Interactive Modelling of Volumetric Musculoskeletal Anatomy

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We present a new approach for modelling musculoskeletal anatomy. Unlike previous methods, we do not model individual muscle shapes as geometric primitives (polygonal meshes, NURBS etc.). Instead, we adopt a volumetric segmentation approach where every point in our volume is assigned to a muscle, fat, or bone tissue. We provide an interactive modelling tool where the user controls the segmentation via muscle curves and we visualize the muscle shapes using volumetric rendering. Muscle curves enable intuitive yet powerful control over the muscle shapes. This representation allows us to automatically handle intersections between different tissues (muscle-muscle, muscle-bone, and muscle-skin) during the modelling and automates computation of muscle fiber fields. We further introduce a novel algorithm for converting the volumetric muscle representation into tetrahedral or surface geometry for use in downstream tasks. Additionally, we introduce an interactive skeleton authoring tool that allows the users to create skeletal anatomy starting from only a skin mesh using a library of bone parts.

CCS Concepts: • Computing methodologies → Mesh geometry models; Volumetric models; Graphics systems and interfaces.

Additional Key Words and Phrases: anatomy modelling, 3D interface, diffusion curves

1 INTRODUCTION

Digital characters are a driving force in the entertainment industry allowing artists to tell stories limited only by their imagination. A lot of effort goes into reaching a point where digital characters are indistinguishable from the real ones. Characters are often modeled by only considering their skin [Jacobson et al. 2014], disregarding...
underlying volumetric muscle, fat, and bone structure.Animating physically realistic effects like muscle bulging, skin sliding, wrinkles, and volume preservation, without an explicit musculoskeletal structure is challenging and, requires skilled and tedious manual effort, to achieve high quality results. Therefore, a truly accurate portrayal of digital characters requires the creation of biologically representative musculoskeletal anatomy.

Different solutions that allow artists to automate tedious manual tasks like the creation of the skin [Yoshiyasu et al. 2014], hair [Saito et al. 2018], rigs [Xu et al. 2020] and others have been explored over the years. However, user-friendly solutions to the problem of creating a musculoskeletal structure that is suitable for character modelling and animation are relatively unexplored. The current solutions either require artists to model every muscle using sculpting software, go through tedious parameter tweaking of geometric primitives, or create a detailed template for retargeting to new geometries. These methods make it hard to produce complex intersection-free muscle shapes that conform to the skin surface. Additionally, defining muscle fiber directions requires users to manually specify attachment points for every muscle. Making incremental changes using these approaches is tedious and hinders the fast exploration of character design.

We propose an interactive modelling tool, that adopts the outside-in [Pratscher et al. 2005] approach and enables the creation of a musculoskeletal system starting from a skin mesh. The user starts by arranging the skeleton from pre-existing templates of bones. Then the user simply sketches curves inside a volume constrained by the skin and our system automatically infers the muscle shapes. Inspired by Orzan et al. [2008], we utilize a diffusion process to segment the volume into muscle and fat tissues based on the user-created curve network. The resulting muscles are intersection free and conform to the skin geometry. We show how to utilize volume rendering to visualize the muscle shapes and hence avoid the need for explicit meshing every time the user edits a curve. We further propose an algorithm for extracting the manifold muscle meshes from our volumetric segmentation for the use in downstream tasks. To the best of our knowledge, our system is the first user-friendly interactive modelling tool, capable of creating intersection free geometry for the musculoskeletal system.

2 BACKGROUND AND RELATED WORK

We provide a brief background on muscle anatomy followed by review of related work categorized by muscle representations in physically-based animation; skinning methods that geometrically attempt to "emulate" the physics of muscle deformation; anatomic templates to aid character modelling, setup and transfer; and interactive interfaces for volumetric and character modelling.

2.1 Musculoskeletal Anatomy:

Muscle is a soft tissue (of type skeletal, cardiac or smooth), whose function is to produce force and motion. A large body of research in Computer Graphics, biomechanics and robotics is focused on studying the physiological properties and of and function of skeletal muscles [Ng-Thow-Hing and Fiume 1997; Scheepers et al. 1997]. For the rest of the paper, we will refer to "skeletal muscles" simply as "muscles". Internally, the muscle is composed of numerous muscle fiber bundles, called fascicles. Large muscles, such as the biceps brachii or the sartorius have fascicles arranged parallel to one another along the length of the muscle. Other muscles exhibit fascicles with a pennation angle, between their tendinous attachments and the longitudinal axis of the muscle (Fig 2 bottom). Skeletal muscle is anchored by tendons to bone. Tendons transmit forces produced by the attached muscle to the bone, enabling locomotion and maintaining posture (Fig. 2 top). We refer the reader to the survey by Lee et al. [2010] which provides a thorough overview of modelling and simulation of skeletal muscles.

2.2 Surface-based muscle primitives:

Musculoskeletal primitives for geometric character skinning is at least three decades old [Chadwick et al. 1989]. Early research has explored the formulation of muscles as collections of ellipsoids [Pratscher et al. 2005; Scheepers et al. 1997; Singh et al. 1995], generalized cylinders [Simmons et al. 2002; Wilhelms and Van Gelder 1997], polygon meshes [Albrecht et al. 2003], extruded parametric curves [Tsang et al. 2005], NURBS [Autodesk 2021], and implicit models [Roussellet et al. 2018]. These surface-based muscle primitives typically serve as proxy geometry to bind and geometrically deform a geometric skin. While these primitives can be imbued with simplified muscle dynamics, they are ill-suited to general purpose anatomic simulation [Ziva Dynamics 2021]. Our representation, based on muscle curves and anisotropically induced muscle volumes, provides the high-level geometric control of muscle shape and skin deformation of these surface-based primitives, but can also produce various muscle shapes (parallel, convergent, pennate) and automate the computation of fiber fields. Being an inherently volume-based representation, it is also well-suited to handle general muscle-muscle, muscle-bone, muscle-skin intersections and muscle fiber bundle computations.

2.3 Volume-based muscle primitives:

Physically-simulated skinning of the skin layered over volumetric muscle primitives [Li et al. 2013] is a desirable solution to producing the subtle details of skin motion [Weta Digital 2021; Ziva Dynamics 2021]. The initial musculoskeletal setup of a character as comprised of skin, fat, muscle and bone, in a simulation pipeline

![Fig. 2. Muscle structure. Image courtesy of [Lee et al. 2010]](image-url)
is tedious and requires multiple iterations of laboriously rebuilding hand-crafted bone and muscle geometry [Deepak Rajan 2021], to elicit the desired simulation behavior from the musculoskeletal anatomy. These sculpted geometries then need to be processed to resolve intersections, and define fiber fields to support anisotropic muscle contraction. While MRI/CT scan data can aid the reconstruction of accurate live anatomy [Jacobs et al. 2016; Teran et al. 2005], such data must be artist-inspired for fictional characters. Muscles have also been built by physically simulating inflatable 3D patches defined by a user on a character’s skin [Turchet et al. 2017], or as parametric solid volumes [Ng-Thow-Hing and Fiume 1997], but these muscles tend to leave undesirable gaps between muscles, bones and other internal structures. Angles et al. [2019] models a muscle as a bundle of position-based rods augmented with isotropic scale to enable simulation of volumetric effects. However, their rod-based representation requires users to either manually create bundles or acquire pre-existing tetrahedral geometry of muscles which is then automatically converted to their representation. Yu et al. [2020] introduces an efficient algorithm for (self)-repulsion of space curves that can be used to design biologically-inspired curve networks such as muscle fibers. However, their optimization-based approach is not suitable for interactive modelling of a large number of muscles.

2.4 Anatomic Templates:
The first semi-automatic method for creating anatomical structures, such as bones, muscles, viscera, and fat tissues was proposed by Ali-Hamadi et al. [2013]. Their method can be seen as a partial registration process, where skin surfaces are first registered based on the data, and the interior tissues are estimated using interpolation and anatomical rules. Saito et al. [2015] create a wide range of human body shapes from a single input 3D anatomy template by simulating biological processes responsible for human body growth. Kadleček et al. [2016] use a set of 3D scans of an actor in various poses to compute subject-specific and pose-dependent parameters of an anatomical template model, to explain the captured 3D scans as closely as possible. Our method is complementary to these approaches and can be used to produce the initial template.

2.5 Interactive volumetric and character modelling:
Takayama et al. [2010] proposed a novel diffusion surface (DS) representation to model the smooth color variation seen in fruit and vegetables. User input to their approach, and others [Owada et al. 2008; Pietroni et al. 2007] is based on cross-sections, which are ill-suited to modelling complex muscle geometry and connectivity. Solid texture synthesis [Pietroni et al. 2010] is focused on modelling homogeneous material like wood or marble and Cutler et al. [2002] uses scripting to define internal volumetric structure of mesh(es). Yuan et al. [2012] do facilitate solid modelling of heterogeneous objects with multiple internal regions using multiphase implicit functions. However, these approaches are not artist-centric or require segmented and labeled 3D biomedical images as input. Wang et al. [2011] represent complex internal 3D structure using multiscale vector volumes. The object is decomposed into components modelled as SDF trees. However, the user needs to actually create the “building-blocks” of an object, such as SDF instances and region definitions, and then assemble them together into linked SDF trees.

Several sketch-based interfaces for character modelling [De Paoli and Singh 2015; Nealen et al. 2007; Schmid et al. 2011; Takayama et al. 2013] use a 3D geometric skin as a canvas on and around which to project 2D sketch strokes. Our work is similar in spirit to [De Paoli and Singh 2015; Schmid et al. 2011] in that we are focused on drawing curves, around the skin, and specifically within a volumetric domain constrained by the surface of the skin.

The actual shape of the muscles is inferred from the scalar values defined on the curves via a volumetric rendering approach. We do not explicitly generate the geometry (triangle or tetrahedral meshes) of the muscles until the user completes the modelling session. Unlike previous methods, our approach allows the user to rapidly explore and experiment with both the topological connectivity and shape of musculoskeletal structures, with a guarantee of precisely constrained and intersection-free structures that conform outside-in to the given skin surface.

3 OUR SYSTEM
The user starts by providing the skin mesh of a model. The bone meshes can also either be provided by the user or built using our interface (Fig.3 left). We generate the tetrahedral mesh $T \in \mathbb{R}^{T \times 4}$, $V \in \mathbb{R}^{V \times 3}$ from combined skin and bone geometries to make sure our tetrahedralization conforms to the bone geometry. We remove all tetrahedra belonging to the bone geometry. This simultaneously induces desirable natural boundary conditions (see, e.g., [Stein et al. 2018]) and increases computational performance. A tablet or a mouse can be used to draw an open 2D stroke that starts and ends over the bone surface. The muscle surface corresponding to the drawn curve is presented to the user. The user can continue to draw more strokes or edit the existing ones to create a full muscular system (Fig.3 right). The results can then be exported as surface or tetrahedral meshes and further edited in other software packages. In the following sections, we describe each part of our muscle modelling system and discrete implementation in detail.

3.1 Skeleton Authoring
If pre-existing skeletal geometry is not available, we provide a tool for creation of the skeletal system from the pre-existing library of bones. We define a three categories for the types for bones: cylinder bone, curve bone, shape bone. The user can select a pre-defined
templates for each of the categories. Then each of template bones are properly placed inside the body mesh with the algorithm described below.

3.1.1 Cylinder bone. A cylinder bone is a type of bone that can be represented as a line segment (e.g. arm or leg bone). When a user clicks on a point on the surface of the skin mesh, we cast a ray through the mesh and record the first two hits, which correspond to the ray entering and exiting the mesh, respectively. We take the midpoint of these two intersections as one endpoint of the cylinder bone, and the other endpoint is determined interactively using the same ray-casting procedure while the mouse button is held down. A cylinder bone template is pre-rigged with two point handles and it is deformed accordingly as its two point handles are attached with the endpoints of the line the user draw.

3.1.2 Curve bone. Curve bone is a type of bone that can be represented as a curve. For example, a spine can be described as a sequence of vertebrae bones placed along a curve. When the user draws a curve, it is projected onto a user-defined plane of symmetry. Then for easy editing of the curve, we fit a Catmull–Rom spline to a sequence of vertebrae bones placed along a curve. When the user draws a curve, it is projected onto a user-defined plane of symmetry. Then for easy editing of the curve, we fit a Catmull–Rom spline to a sequence of vertebrae bones placed along a curve. When the user draws a curve, it is projected onto a user-defined plane. Finally, a user selected template is distributed along the spine.

3.1.3 Shape bone. A shape bone is a type that cannot be represented as a line segment nor a curve. Essentially, it describes all the bones with complex shapes. We place the shape bone as local fitting on the user-specified region. We determine the center of the template with a mouse click, using the same ray-casting procedure used to compute the endpoints of a cylinder bone. Then from that initial shape, the template is iteratively fitted to its local region of the skin mesh.

3.1.4 Local fitting. We pre-rigged the template with a cage deformer. Using data that already has skin and corresponding bone mesh, we define a cage by cutting a local region of the skin mesh with high decimation and with manual editing. We fit the cage using both step of rigid ICP (Iterative Closest Point) and nonrigid ICP, and the templates are deformed using this registered cage. We first perform rigid ICP to find an optimal transformation of its closest corresponding target points. After it has converged within the threshold, we then perform nonrigid ICP by deforming the cage with an additional squared Laplacian smoothness term to prevent abrupt deformation. Corresponding target points are determined by finding the closest points to cage vertices on the skin mesh. We discard the correspondence point whose normal directions are almost opposite to their closest projected points.

3.2 Muscle Curve Authoring

The user draws a curve for each muscle. Skeletal muscles require an origin and insertion points where the muscle tendons are being attached to the bone. In our interface we expect the user to always begin and end the stroke over the bone surface and provide the necessary visual feedback to achieve that. The first and last points of the curve are automatically projected via ray-casting onto the surface of the bone to find their corresponding 3d coordinates.

The depth value for all the points drawn in between is ambiguous, so we simply linearly interpolate the depths of the first and last points. Because we want the curves to be easily editable we fit a Catmull–Rom spline $S_i$ in a least squares manner with 4 control points $p_1^i, ..., p_4^i$ by default: one for each end point and two along the curve (see inset). We denote the resulting muscle curve network as a set of splines $\{S_1, S_2, ..., S_m\}$. Each control point $p_0^i$ is augmented with an additional attribute representing a tissue value $D^p_i$. Users can adjust the tissue value to shape the muscle: a larger value results in a “thicker” shape around the control point.

3.3 Muscle and Fat Functions

Let $Ω \subseteq \mathbb{R}^3$ denote the volumetric domain defined by the tetrahedral mesh $V, T$. Our goal is to find a scalar muscle function $f_i : Ω \rightarrow \mathbb{R}$ for each muscle $i$ that describes the likelihood of any point $p \in Ω$ to belong to a muscle $i$. Similarly we define a fat function $s_i$ that describes the likelihood of any point to belong to a fat layer. We propose to define $f_i$ and $s_i$ as minimizers of the Dirichlet energy subject to constraints:

$$\begin{align*}
&\arg\min_{f_i, s_i, i = 1, ..., m} \sum_{i=1}^m \int_Ω \nabla f_i^T A_i \nabla f_i + \int_Ω ||\nabla f_i||^2 dV \\
&\text{subject to} \\
&f_i|_{δΩ_i} = D_i \\
&s_i|_{δΩ_i} = 0 \\
&f_i|_{δΩ_i} = 0 \\
&s_i|_{δΩ_i} = d_{fat} \\
&s_i|_{δΩ_i} = 0
\end{align*}$$

where $A_i$ is an optional user-defined diffusion tensor field which biases the directions in which material flows at a point in space. Intuitively, we “diffuse” each muscle curve such that the tissue values at the curve points ($δΩ_i$) are set by the user (via interpolation of tissue values $D^p_i$ at the control points) and the tissue values at all other muscle curves ($δΩ_j$) and skin ($δΩ$) are set to zero. We additionally diffuse from the skin to represent the fat layer (fat function $s_i$, where “s” stands for skin) by setting its tissue value to a user-defined $d_{fat}$ and constraining the values at all muscle curves.
The muscle splines usually do not coincide with the vertices of the tetrahedral mesh and to discretize the splines we need to identify a set of tetrahedrons that contain each muscle curve \(S_i\). For each tetrahedron \(t\) and each muscle curve \(i\) passing through it, we identify a point \(c^t_i \in \mathbb{R}^3\) on the curve that is contained inside the tetrahedron (see inset).

In practice, we choose the point to be the midpoint of the curve segment bounded by the tetrahedron. We call this point a collocation point. All collocation points can be found efficiently by finding the tetrahedron containing the first curve point and then finding all the other tetrahedrons by tracing the curve, given that the adjacency is computed beforehand. This amounts to at most three ray triangles intersections per tetrahedron and therefore very fast.

For each curve \(i\), we stack all collocation points in a matrix \(C_i \in \mathbb{R}^{[C_i] \times 3}\) and compute a tissue \(d_i^t\) value for each collocation point by interpolating values at control points \(p^P_t\). One of the primary constraints to be satisfied (Eq. 2, 3) are the curve constraints, i.e., the tissue value at the vertices \(V\) must be determined to agree with the values at the collocation points. We use barycentric coordinates to interpolate the tissue values for each tetrahedron, such that the value \(d_i^t\) of the collocation point \(c^t_i\) is expressed as:

\[
d_i^t = \sum_{j=1}^{4} b_j \cdot d_j
\]

where \(d_j\) denotes the tissue value of a vertex \(j\) of a tetrahedron \(t\) (for \(j = 1, 2, 3, 4\)) to which the collocation point \(c^t_i\) belongs to, and \(b_j\) are the barycentric coordinates of \(c^t_i\) with respect to the vertex \(j\). Stacking the barycentric equation (7) for a set of desired values of the collocation points into a matrix constitutes a linear equality constraint equation:

\[
B_t f_i = \begin{bmatrix} B_1 \\ \vdots \\ B_m \end{bmatrix} \begin{bmatrix} d_1 \\ \vdots \\ d_m \end{bmatrix} = d_i \in \mathbb{R}^{[C_i]} \tag{8}
\]

where for every curve \(i = \{1, \ldots, m\}\) we have \(B_i \in \mathbb{R}^{[C_i] \times [V]}\) which is a sparse matrix of stacked barycentric coordinates of collocation points for all curves with non-zero entry \(B_i(k, j)\) being a barycentric coordinate of the collocation point \(k\) with respect to vertex \(j\), \(d_i \in \mathbb{R}^{[C_i]}\) is a vector of stacked tissue values of collocation points s.t. \(d_i(j)\) is nonzero only if collocation point \(j\) belongs to curve \(i\) and \(f_i \in \mathbb{R}^{[V]}\) are values of muscle function \(f_i\) at each vertex of the tetrahedral mesh. The fat tissue constraint (Eq. 6) can be similarly discretized as

\[
B_t f_s = \begin{bmatrix} B_1 \\ \vdots \\ B_m \end{bmatrix} f_s = 0 \in \mathbb{R}^{[C_i]} \tag{9}
\]

The Dirchlet Energy in Eq.1 is discretized as

\[
\min \sum_{i=1}^{m} (f_i^T \hat{L} f_i + ||B_i f_i - d_i||^2) + f_i^T \hat{L} f_s + \alpha||B_i f_s||^2 \tag{10}
\]

subject to

\[
f_i|_{\text{skin}} = 0 \tag{11}
\]

\[
f_i|_{\text{skin}} = d_{\text{fat}} \tag{12}
\]

\[
\hat{L} = G^T \hat{M} A G \tag{13}
\]

where \(G\) is the gradient matrix (see [Botsch et al. 2010] for derivation) and \(M\) is a mass matrix representing an inner-product accounting for the volume associated with each tetrahedron, \(G^T \hat{M} A G\) is the anisotropic cotangent Laplacian ([Andréux et al. 2014]), \(L_c\) is the standard (isotropic) cotangent Laplacian, \(\alpha\) parameter that defines the tradeoff between smoothness of the resulting scalar field and respecting the tissue values at the collocation points (set to 5 in our experiments). Because the collocation points are not necessarily located at mesh vertices and many may appear in the same element, using soft constraints avoids overshooting. Vertex values \(f_i\) of each muscle function can be computed separately and hence computation of Eq.10 is easily parallelizable. Compared to regular-grid-based methods, the boundary-conforming tetrahedral mesh makes it easy to set precise boundary conditions.

### 3.5 Segmentation

Each point \(p \in \Omega\) in our volume will either belong to a muscle, bone, or fat. The fat is visually represented as an "empty" space between muscles, skin, and bones. The points that belong to the bone tissue are simply all the points that are contained inside tetrahedrons comprising the bone geometry. So we only need to differentiate between muscles and fat. We treat the muscle and fat functions as probabilities and assign the point \(p\) to the tissue with the highest probability (Fig. 6):

\[
tissue(p) = \arg\max_i \{f_1(p), \ldots, f_m(p), f_s(p)\} \tag{14}
\]

In the discrete case we find the tetrahedron \(t\) that contains the point \(p\) and use barycentric interpolation to determine tissue values for
Fig. 6. Each point in our domain has a vector of tissue values that represent the likelihood of this point to belong to one of the tissues (left). We assign the point to the tissue with the highest probability (right).

muscles and fat at $p$ given tissue values $(f_1, f_2, f_3)$ at the vertices of the tetrahedron $t$. We skip the normalization step of our probabilities because the muscle visualization (Sec 3.6) and muscle extraction (Sec 4) are invariant to normalization.

3.6 Visualization

In the end, we only want to visualize all points belonging to the muscles, while points belonging to fat should be invisible. A common solution to this problem in scientific visualization and computer graphics is volume rendering. We take inspiration from the literature on volume rendering on unstructured grids ([Silva et al. 2005; Weiler et al. 2003]) which deals with rendering iso-surfaces of a scalar function defined on vertices of the tetrahedral mesh. To achieve interactive rates we perform ray casting on the graphics hardware via a ray propagation approach and perform all computation inside a fragment shader.

To render the model we split each tetrahedron into 4 triangles and submit them for rendering on the GPU. For each vertex of the triangle, we assign a vertex attribute with the value of the tetrahedron index it belongs to and set it to not be interpolated when moving from vertex to fragment shader. That way each fragment can be traced back to the tetrahedron it belongs to. We store all the information (vertex positions, normals, muscle and fat functions) about each tetrahedron on the GPU and access it inside the shader.

Inside the fragment shader, we start with computing the entry point into the tetrahedron that the current fragment belongs to by simply converting the fragment from screen space into camera space. We determine the corresponding exit point by computing three intersection points of the ray with the planes containing faces of the entered tetrahedron and choosing the intersection point that is closest to the eye point but not on a face that is visible from the eye point. With the eye point $e$, and the normalized direction $r$ of the viewing ray, the intersection points with the faces of the tetrahedron are $e + \lambda_i r$ with $0 \leq i < 4$:

$$\lambda_i = \frac{(v_3 - e) \cdot n_i}{r \cdot n_i} \quad (15)$$

where $i \in \{0, 1, 2, 3\}$ denote the face index, $v_3$ is the vertex opposite to the $i$-th face, $n_i$ is the normal vector of the face $i$ pointing outside of the tetrahedron (see inset). A face is visible if the denominator in the previous equation is negative; thus, this test comes almost for free. If $\lambda_i$ is set to an appropriately large number for all visible faces, $\min\{\lambda_i\,|\,0 \leq i < 4\}$ identifies the exit point. Once the minimum $\lambda_i$ and its face $i$ are identified, the intersection point $x$ may be computed as $x = e + \lambda_i r$.

The muscle surface is only potentially visible if the entry point belongs to fat in which case we ray march through the single tetrahedron from the entry point to the exit point until we detect that the tissue changed from fat to muscle. At which point we stop and compute the normal to shade the surface of the muscle. If the whole tetrahedron belongs to fat we call the GLSL discard command and the GPU will call the shader again until we find a tetrahedron that contains the surface of a muscle (if one exists). Figures 1, 7 show an example of a volume-rendered muscles.

3.7 Anisotropy

To provide an additional control over the muscle shape we allow users to change the rate of diffusion along the certain directions. This is achieved by introducing a tensor field that biases the directions in which tissues diffuse at a point in space. Tensor field is represented by a tensor matrix $A_i \in \mathbb{R}^{G \times G}$ in Eq. 13.
We provide an easy way for the user to construct the tensor fields for the individual muscles. The first point of each muscle curve is assigned a 3D frame \( Q = [e_1, e_2, e_3] \) in \( \mathbb{R}^{3 \times 3} \) representing eigenvectors of a tensor. The first vector in the frame \( e_1 \) is always aligned with the curve tangent while the other two eigenvectors lie in its null space. The user has control over the rotation of \( e_2, e_3 \) along the axis defined by \( e_1 \) (Fig. 7ab). Additionally, the user can control the magnitude of eigenvalues \( \lambda_2, \lambda_3 \) to bias diffusion rate along \( e_2, e_3 \) directions (Fig. 7cdef). We use the method of [Hanson and Ma 1995] to compute the frame \( Q_i \) at each collocation point \( c_i^j \), and assign frames to each vertex of the tetrahedrons containing collocation points (using the frame of the closest collocation point).

Each frame \( Q \) can be considered as a set of nine scalars and the problem of propagating values from the fixed vertices of the tetrahedrons containing collocation points to the remaining vertices is thus same as computing nine scalar fields over the mesh. To find the unknown values at the remaining vertices, we use the Laplacian smoothing framework, i.e. for each scalar field, we create a harmonic vertex-based scalar field on \( T \) given the boundary conditions (from the values at the fixed vertices) [Palacios et al. 2016]. Once all 9 scalar fields have been obtained, we compute the per-vertex tensor \( Q^T AQ \) where \( \Lambda \) contains eigenvalues \( \lambda_1, \lambda_2, \lambda_3 \) along the diagonal and assemble the tensor field matrix \( A_i \) for the muscle \( i \).

4 MUSCLE EXTRACTION

Given the complete muscle curve network and the corresponding muscle functions defined over the volumetric domain, we need to extract the geometry of the muscles suitable for downstream applications.

isosurface extraction methods [Chentenez et al. 2009; Labelle and Shewchuk 2007; Lorensen and Cline 1987] do not trivially solve our problem, because we are not simply extracting an isosurface of a scalar function. Instead, we want compute a pointwise maximum of multiple scalar functions inside each tetrahedron and extract a boundary separating each function while ensuring the final output is a manifold tetrahedral mesh. In other words, inside each tetrahedron, each tissue function can be thought of as a point-wise vote for ownership. We want to split the tetrahedron along boundaries that delineate changes in the maximum vote and assign each sub-tet to the tissue with maximum value. We cast the problem of extracting the muscle surface geometry as a solution to the computation of the upper envelope of scalar functions representing each tissue over each tetrahedron. First, lets look at a simple example of the upper envelope problem in Fig. 9. Four line segments are defined over the 1D domain \([a, b]\) (Fig. 9, left). The upper envelope is the pointwise maximum of all segments over the domain. The maximization diagram is a subdivision of the domain \([a, b]\) into cells, where each cell’s identity is induced by the upper envelope. Alternatively, we can think of the maximization diagram as a projection of the upper envelope onto the domain (Fig. 9, right).

Let us now define the general upper envelope problem. Let \( S = \{s_1, s_2, \ldots, s_n\} \) be \( n \) \( d \)-simplices in \((d + 1)\)-dimensional space. A \( d \)-simplex has \((d + 1)\) vertices, i.e. \( d = 1 \) is a line segment, \( d = 2 \) is a triangle and \( d = 3 \) is a tetrahedron. We can thus view each \( s_i \), as the graph of a partially defined linear function \( x_{d+1} = f_i(x_1, x_2, \ldots, x_d) \), whose domain of definition is a \( d \)-simplex, namely the orthogonal projection of \( s_i \) onto the hyperplane \( x_{d+1} = 0 \). The upper envelope, \( M \), of the given simplices is the pointwise maximum of these functions [Edelsbrunner et al. 1989], that is,

\[
M(x_1, x_2, \ldots, x_d) = \max_{1 \leq i \leq n} f_i(x_1, x_2, \ldots, x_d) \tag{16}
\]

The maximization diagram \( M \) of \( S \) is the subdivision of \( \mathbb{R}^d \) into connected cells obtained by the projection of the upper envelope of \( S \) in the \( x^d \) direction. The example in Fig. 9 corresponds to \( d = 1 \) where each line segment is a 1D simplex in 2D space. Fig. 8a shows an example of two 2-dimensional simplices in 3-dimensional space whose maximization diagram is shown in (Fig. 8b). Solutions for solving the general upper envelope problem for \( d = 1 \) and \( d = 2 \) ([Agarwal et al. 1996; Meyerovitch 2006]) and computing their corresponding maximization diagrams have been proposed. Abdrashtov et al. [2019] computes \( d = 2 \) upper envelope of "part" functions to extract the smoothed part boundaries.

We consider tissue functions \( T = \{f_1, \ldots, f_m, f_t\} \) (combination of muscle and fat functions) defined as scalar fields over the vertices of our tetrahedral mesh and we notice that Equation 14 is the pointwise maximum (Eq.16) of tissue functions. In our problem (\( d = 3 \)) we are interested in finding maximization diagrams of all tissue functions over the volume constrained by the surface of the skin. This problem can be solved by considering finding the maximization diagrams of the tissue functions over each tetrahedron. In which case in contrast to the general upper envelope problem where our domain is a continuous hyperplane, we restrict our domain by a 3-simplex on that hyperplane. Fig. 8c shows an example of the maximization diagram of the functions defined by the scalar values at the vertices of the tetrahedron and (Fig.8d) shows the tetrahedralization of each cell. As a result, the tetrahedron is split into more sub-tets where each sub-tet has only one function that is the maximum. In other words, we can "assign" the sub-tet to one of the tissues. Performing this operation for every single tetrahedron results in a new tetrahedral mesh where each tetrahedron is assigned to one tissue. We can extract individual tissue shapes by simply combining all tetrahedrons that are assigned to that tissue. Fig. 8e shows an example of taking a uniform 3x3 tetrahedral mesh with two scalar functions defined over it and splitting it into two tetrahedral meshes (Fig.8f). The split is the result of computing tetrahedralized maximization diagrams of every tetrahedron. However, the resulting tetrahedral meshes representing each muscle are not guaranteed to be manifold unless we are consistent with how we tessellate adjacent tetrahedrons (Fig. 10). In reality, we would just be getting a tetrahedral "soup" that is difficult to work with. Instead we want our resulting mesh to be manifold and hence we can easily use it for downstream applications. We propose an algorithm for computing manifold tetrahedralized maximization diagrams of functions defined as scalar fields over the vertices of a tetrahedral mesh. We first define auxiliary operations in Sections 4.1, 4.2 and then discuss the main algorithm in Sections 4.3.

4.1 Prune tissues

We notice that if the tissue function \( f_j \in T \) is strictly below any other tissue function \( f_i \), then it will not be part of the maximization
Fig. 8. Two triangles (a) and the corresponding maximization diagram (b). Example of the maximization diagram cells of 5 different functions over the tetrahedron (c) and tetrahedralization of each cell (d). Tetrahedral mesh (e) with 2 different functions defined over its vertices and the resulting tetrahedralized maximization diagram (one of the parts is slightly moved in the figure to show the internal tessellation)

Fig. 9. Four line segments (red, green, purple, gray) are defined over a single 1D element \([a, b]\) (left). The upper envelope (light blue) and the maximization diagram (right).

Fig. 10. Maximization diagram is defined over two adjacent tetrahedrons 1234 and 1345 (a). During the tessellation there is no guarantee that the shared face 134 is split the same way (b). By making sure the order of edge splits is consistent we can guarantee that the face is split the same way (c).

4.2 Split tetrahedron

Given only two different tissue functions \(f_1\) and \(f_2\) over a tetrahedron we need to find the tetrahedralized maximization diagram that results from computing the upper envelope of those two functions. This problem is similar to the *Marching tetrahedra* [Doi and Koide 1991] algorithm that finds an isosurface of a scalar field \(f_1 - f_2\) passing through isovalue of 0. However, in our case we are not interested in extracting the isosurface but rather splitting the tetrahedron along the isosurface and tetrahedralizing the resulting polyhedrons.

**Input:** tetrahedron defined by 4 vertices \(V \in R^{4x3}\), per-vertex values \(f \in R^4\) of a scalar function \(f\).

**Output:** tet mesh \(T_{split}, V_{split}\) resulted from splitting the input tet along the isosurface of \(f\) at isovalue of 0.

**Algorithm:** We find a set of sorted unique edges \(E\) of the tetrahedron that are intersected by the isosurface of \(f\). The number of edges \(|E|\) is either 3 or 4. We then define a *split_edge* operator that given a tetrahedron \(t\) and an edge \(e\) first splits the edge at a vertex \(v\) and then splits \(t\) into two tetrahedrons by connecting \(v\) with two vertices of the edge opposite \(e\) (Fig. 11). Similarly to *Marching tetrahedra* the location of \(v\) is determined by interpolating vertices of \(e\) using weights defined by \(f\). We simply run *split_edge* recursively on each \(e \in E\) to produce the resulting tetrahedral mesh \(T_{split}\). The order of edges in \(E\) determines the order in which we split the edges and hence determines the final topology of the tessellation. By simply sorting the interested unique edges we solve the problem of inconsistent tessellation (Fig.10b) between adjacent tetrahedrons (Fig.10c). We additionally maintain a history of unique edge splits before splitting an edge \(e\) at vertex \(v\) by a call to *split_edge* on one of the adjacent tetrahedrons we do not create a new vertex \(v\) but simply make it point to \(\hat{v}\). To improve the robustness of the algorithm, when \(v\) almost coincides with one of the vertices in \(V\) (when one of the values in \(f\) is close to zero within some threshold) we simply remove that edge from \(E\) so it will not be split.

4.3 Tetrahedralized Maximization Diagram

We iterate through every tissue function \(f_i \in T\) and use \(W\) to find a set of tissue functions \(\tilde{T}\) such that for any \(f_j \in \tilde{T}, W(i, j) > 0\). In other words \(\tilde{T}\) contains all tissue functions that appear in the maximization diagrams with \(f_i\) in at least one tetrahedron. We compute
4.4 Fiber direction

Fiber directions play an important role in simulation by defining the directions the muscle contracts. Fibers tend to point in the same directions as gradients of a hypothetical flow from one end of the muscle to the other [Choi and Blemker 2013; Saito et al. 2015]. Given muscles tetrahedral mesh $V_m, T_m$, we leverage our muscle curve to guide the global flow of the fiber field. The flow should align with the tangent space of the muscle curve. This can be formulated via constraint that for each tetrahedron along the curve we would like to create and use half of the mesh for creating the muscles. Therefore, we cut both skin and bone meshes along the half-plane. The mesh vertices belonging to the cut boundary can be excluded from the constraints in Eq. 11, 12 to help create muscles that are supposed to cross the cut boundary. The half-skin and half-bone meshes are loaded by the muscle-curve authoring tool and we use TetGen [Si 2015] to generate a tetrahedral mesh. The quadratic solver is implemented using the modified version of libIGL’s min_quad_with_fixed function with Eigen’s PardisoSupport module which provides significant speed ups. The tool was tested on a computer with Intel Xeon CPU @ 2.40GHz, Nvidia GTX1080 and 64GB of RAM and can perform at interactive rates for tetrahedral meshes with > 500k tetrahedrons. The geometry stays intact between curve editing operations, and we only update GPU buffers containing per-vertex diffusion values which is fast.

Figure 16 showcases the results created by the authors using our tool. We informally evaluated our tool with a professional animator who has experience with using Maya Muscles [Autodesk 2021] for creating musculoskeletal systems. They mentioned that using existing tools requires a significant amount of tedious work for ensuring that muscle geometry respects the geometry of its surroundings (bones, skin, other muscles), and the overall workflow is “unintuitive” and “awkward”. They liked the fact that our tool allows one to simply draw the location of the muscle while handling these issues automatically and provides enough intuitive controls (changing tissue values, moving control points, enabling anisotropy) to create complex muscle shape (Fig.12). One feature they wanted
Fig. 13. We consider the Lion model in Fig. 16 with 39 muscles and 642224 tetrahedrons. The plot shows the number of tetrahedrons and the maximum number of tissue functions that can appear in their corresponding maximization diagram. This shows that for the vast majority of tetrahedrons (78%) computing their tetrahedralized maximization diagrams requires no splitting or only trivial non-recursive splitting of 2 tissues (19%). No tetrahedrons require resolving intersection of 6 or more tissues.

to see added is volume preservation of the muscle: when a muscle is being flattened in one direction, there is a corresponding stretching in another direction so that the volume stays the same. They also wanted an ability to specify multiple attachment points instead of just two to enable finer control, especially for triangular types of muscle shapes. We further informally evaluated our tool with an orthopedic surgeon with extensive knowledge of human anatomy but who does not have experience with 3D modelling applications. They see the potential of using this tool to explain the surgery process to their patients. By using a pre-existing anatomical muscle model made with our tool, they would be able to edit the muscles to explain their medical procedure. However, similar to the animator, they mentioned that to create truly anatomically correct muscles, they need to be able to specify multiple attachment points.

The muscle extraction algorithm in Section 4 uses the divide and conquer approach by considering pairs of tissue functions. In Figure 13, using the example of the Lion model (Fig.16), we show that in practice the vast majority of tetrahedrons only contain 1 tissue function in their maximization diagram and therefore are not split. While the vast majority of tetrahedrons that do need to be split only contain 2 tissue functions, which means they are only split once.

Because our volumetric domain is represented as an unstructured mesh, the resulting topology of the muscle meshes ends up containing skinny tetrahedrons as shown in Figure 14. However, because we guarantee that the resulting meshes are manifold, it is straightforward to extract the boundary faces (faces that belong to only one tetrahedron). The resulting muscle surface triangular meshes can be easily remeshed and tetrahedralized again. In practice, we simply run TetWild [Hu et al. 2018] with default parameters on the surface mesh to improve the topology.

During the modelling process the muscles seen by the user are directly volume rendered upper-envelopes: rendering does not require performing any meshing operations during the modeling process. Every time the user creates or edits muscle curves we recompute values of the tissue functions (Eq. 10) for each vertex of the tetrahedral mesh and update those values in the corresponding GPU buffer. These values are later accessed by the fragment shader to perform the volumetric rendering using the ray-marching method (supported by all modern GPUs). The muscle visualization using fragment shaders is fast (>30fps) on our system. The bottleneck of our system during modeling is computing the solution to (Eq. 10) for which we currently use the Eigen library with Pardiso enabled. This solve immediately benefits from any generic Poisson solving optimizations which are orthogonal to our main contributions. We only perform a meshing operation (Sec. 4) after the modelling session is complete, to export muscles as tetrahedral meshes for downstream applications. Using muscle extraction every time we create/edit a muscle would negatively impact performance, which is the motivation for our volumetric rendering approach.
Fig. 16. Results. We refer the reader to the provided supplemental video to see the modelling process of the Ape model. We refer the reader to the provided Additional Modelling and Simulation Demos video to see the modelling process of the Lion model. Lion (top) and Dinosaur Leg (bottom left) are provided by ©SideFx Software. Used under permission. Ape model (middle) is obtained from https://www.3dscanstore.com/ecorche-3d-models/gorilla-ecorche-3d-model. Used under permission. Bone geometry of the arm (bottom right) is provided by ©Ziva Dynamics. Used under permission.
6 LIMITATIONS AND FUTURE WORK

Although we demonstrated that our tool enables users to create complex muscular-skeletal geometries, there are limitations, subject to future work.

The quality of the muscle shapes depends on the quality of the tetrahedralization (VT) of the input skin and bone meshes. On one hand, coarse meshes prevent the creation of smooth and thin muscles; on the other hand, very high quality meshes can affect the performance of computing muscle functions and hinder the interactive experience. This makes it hard to create muscles in the areas where bones are too close to the skin, unless the area is densely tessellated. We also notice that often a large portion of the model ends up being unused (the intestines area), yet it’s still being used for computation of muscle functions which wastes computation. In practice, for all models, we were able to find a balance between the quality of the tetrahedralization and performance. In the future, we want to explore adaptive boundary conforming tessellation of the volume with increased tessellation quality only around boundaries of the muscles.

We use a simple heuristic (Sec. 3.2) for creating initial muscle curves, which leads to multiple editing operations of control points to get the muscle curve shape just right. This makes it challenging to create muscle curves around complex bone geometry, since control points must be edited from multiple viewpoints. In the future, we would like to explore a more robust curve creation techniques that simultaneously utilizes skin and bone geometry to create the best guess for the initial shape of the muscle curve.

Currently, each muscle is represented by a single curve. Based on the feedback we received from users, we plan to explore how we can use multiple curves to represent a single muscle. This would allow us to create more anatomically correct and complex muscle shapes with multiple origin and insertion points. Additionally, there are many muscles in which fiber direction does not match the flow between origin and insertion and therefore we plan to explore ways to specify the pennation angle (the angle between the longitudinal axis of the entire muscle and its fibers) as it is an important parameter in muscle contraction dynamics.

We have investigated the potential use of the resulting muscle geometry for simulation (Fig. 15) but more work needs to be done to test simulations with the complex and densely packed full-body muscle systems. With the help of professional artists, we plan to evaluate how animation-ready our resulting muscle geometry is using industry-standard software like Houdini [SideFx 2021] and Ziva Dynamics [2021].

Our system is designed with the idea of creating muscle geometry from scratch but we have experimented with extracting curve networks from pre-existing artist-made muscle shapes (using methods for computing curve skeletons of 3D shapes) and importing them into our system, which can provide a good starting point.

We currently do not support locking of the muscle shape. However, we could extract the mesh of a muscle, and treat it similarly to bones so that other muscles wrap around it. This requires to redo the initial tessellation to make sure it conforms to imported muscle geometries but TetGen only takes a few seconds. Similarly an artist can import existing muscle meshes and continue to create muscles around them.

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