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RULE-BASED APPROACH FOR ASSIGNMENT OF MYOFIBER DISTRIBUTION TO HUMAN TONGUE MODELS

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INTRODUCTION

The overall quality of human life is directly dependent on (and affected by) processes involving motion of the tongue, including production of sounds for speech, mastication of food, and breathing. For this reason, oral cancer has deep negative consequences on individuals despite not having a high mortality rate [1-2]. Because the incidence of this type of cancer is growing, there is an increasing need for effective therapeutic techniques, not only in terms of tumor removal, but also in preserving tongue function afterwards [2]. Mechanical modeling offers insights that can aid in the design of surgical techniques. For example: simulations enable relatively rapid assessment of functional changes due to changes in geometry or stiffness that can result from postsurgical tissue remodeling. As a rule, the input to computer simulations must faithfully represent the system under investigation in order to produce accurate and reliable results. This is especially true for the tongue's myofiber orientation, because it is intimately related to muscle contraction. Structural assessment is often achieved via diffusion-tensor MRI (DT-MRI) [3], but this is often insufficient to extract fiber directions (due to noise), or is unavailable altogether. While manual approximation is possible, it can introduce user variability and can be increasingly difficult in intricate geometries.

This study explores the creation of synthetic fiber directionality information using the rule-based algorithm, which has previously been used to construct cardiac models [4]. The main tenet of the approach is to apply a priori anatomical knowledge to the boundary of a subject-specific domain and resolve the interior via Laplace's equation. In the heart, the strategy consists of applying conditions to the endo- and epicardium, where some aspects of fiber directionality are generally known. While the myofiber distribution in the tongue is complex (including crossing fiber families), it follows a distinctive pattern [5]. Thus, it is possible to describe the overall pattern from subject-specific anatomy to generate an approximation of fiber distribution. In particular, we hypothesized that mechanical simulations with approximate fiber orientations (via the aforementioned approach) would be functionally similar to those obtained using experimental measurements from high-resolution DT-MRI.

METHODS

The experiments herein focus on the genioglossus (GG), which is the largest tongue muscle by volume [6]. Therefore, it has a large influence in the organ's motion, as well as a well-defined diffusion signal, which enables its structural characterization in vivo [6-3]. To test the hypothesis, finite-element (FE) biomechanical simulations (Fig. 1) of GG contraction with either approximated, or experimentally measured, fiber distributions were compared against each other.

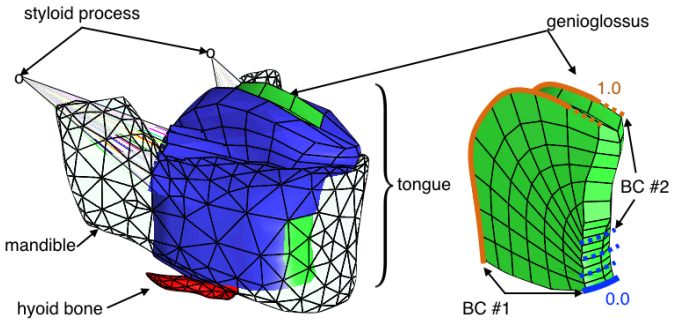

Figure 1: Tongue model. The FE mesh (left) was used to simulate GG contraction. Fiber distribution was obtained via DT-MRI, or via Laplace's Equation using the boundary conditions (BC, right).

The model consisted of the hyoid and mandibular bones, which were considered rigid and constrained to be stationary, and the tongue geometry, which was based on a published shape [7]. The material constitutive model was assumed to be an isotropic neo-Hookean solid with coefficients based on literature values [8].

The model was matched (via manual affine registration) to the imaging domain. DT-MRI of a healthy adult male was performed to extract fiber directions using 64 diffusion directions (2 averages), 80x80x80 matrix size, 3 mm isotropic voxel size, and a b-value 500 s/mm^2. Diffusion tensor reconstruction was obtained using DSI Studio [9]. Fiber information was extracted from the first eigenvalue of the diffusion tensor via nearest-neighbor interpolation.

While simulations with imaging-derived fibers used as the benchmark, two approximated fiber distributions were constructed by solving Laplace's equation. These differed in their boundary conditions (BC), which consisted of setting nodal values to 1.0 or 0.0. The first consisted of simply placing known values at the inferior-anterior corner of the GG (Fig. 1, right) and along the longitudinal surface. In the second, anterior values were extended to the entre insertion to the mandibular bone, and discarded towards the anterior tip of the tongue. These changes appear in Fig. 1 with dotted lines. Comparisons were quantified via displacement percent error.

Contractile stress in the GG was set to 25% of its maximum capacity of 0.35 Mpa [8]. An additional simulation of 25% activation in the styloglossus (SG) muscle was performed to evaluate error when GG motion was passively generated. Biomechanical simulations were carried out using FEBIO Software Suite [10].

RESULTS

The solutions to Laplace's equation (potential distributions) for the two BC sets appear in Figure 2. As described, approximate fiber distributions relate to these solutions via gradients.

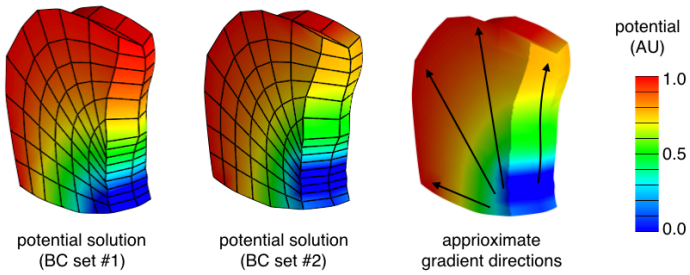

Figure 2: Differences between boundary conditions sets. The potential distributions (in arbitrary units, AU) are equivalent to the solution of Laplace's equation with the different BC sets.

Despite the similarities in their potential distributions, the resulting fiber orientations are noticeably different (Figure 3). Fibers from BC set #2 are visually similar to DT-MRI results across a greater area than BC set #1, but some discrepancies are noticeable on the superior (top) portion. Some noise is present on DT-MRI results.

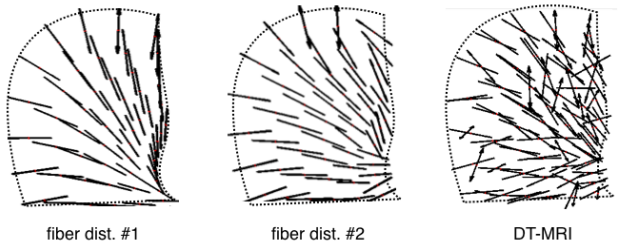

Figure 3: Fiber distributions. Approximate fiber distributions (left, center) are distinct and less noisy compared to DT-MRI.

Error maps between simulated GG activation with either of the approximations, against imaging-based results are shown in Figure 4. Using fiber distribution #1 (Fig. 3) results in relatively large displacement error particularly above the mandible insertion of the GG. The mean error across the tongue was 49%, with an SEM of 2%. In contrast, application of fiber distribution #2 results in a visibly reduced error, although error was still concentrated in the same area. The mean error across the tongue in this case was 28%, with an SEM of 3%. Displacement percent error during SG contraction was 8.8x10^{-3} using fiber distribution #1 and 1.3x10^{-3} using distribution #2.

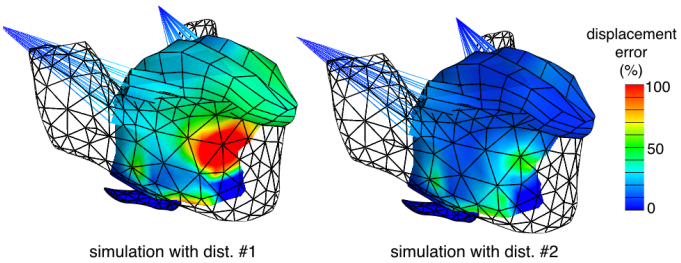

Figure 4: Differences between simulated GG contractions. The color maps shows the displacement error from each of the simulations with approximate fiber distributions (Fig. 3) with respect to the benchmark (DT-MRI solution). Using fiber distribution #1 (left), results in larger error than #2 (right).

DISCUSSION

The magnitude and dispersion of error in Fig. 4 suggests that simulated active contraction is very sensitive to fiber distribution. This result highlights the necessity for adequate modeling of fibers. Figure 4 also shows that if the approximated distribution is too simplistic (as with BC set #1), simulated results can greatly disagree with what would be expected when using experimental data. By incorporating more anatomical details in the boundary conditions of the Laplace's equation solution (as done in BC set #2), it is possible to improve the quality of the estimated fiber distribution. This improves the overall agreement with the experimental data (Fig. 3), and reduces simulation discrepancy (Fig. 4).

Note that DT-MRI data includes some noise. Thus, complete agreement with experimental data may not be necessarily better, and an approximate fiber distribution may be used in conjunction with (rather than in lieu of) experimental measurements. As expected, there was little error associated with passive displacement of the GG via SG contraction, because the material was isotropic.

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