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A Bayesian approach to distinguishing interdigitated tongue muscles from limited diffusion magnetic resonance imaging

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ABSTRACT

The tongue is a critical organ for a variety of functions, including swallowing, respiration, and speech. It contains intrinsic and extrinsic muscles that play an important role in changing its shape and position. Diffusion tensor imaging (DTI) has been used to reconstruct tongue muscle fiber tracts. However, previous studies have been unable to reconstruct the crossing fibers that occur where the tongue muscles interdigitate, which is a large percentage of the tongue volume. To resolve crossing fibers, multi-tensor models on DTI and more advanced imaging modalities, such as high angular resolution diffusion imaging (HARDI) and diffusion spectrum imaging (DSI), have been proposed. However, because of the involuntary nature of swallowing, there is insufficient time to acquire a sufficient number of diffusion gradient directions to resolve crossing fibers while the *in vivo* tongue is in a fixed position. In this work, we address the challenge of distinguishing interdigitated tongue muscles from limited diffusion magnetic resonance imaging by using a multi-tensor model with a fixed tensor basis and incorporating prior directional knowledge. The prior directional knowledge provides information on likely fiber directions at each voxel, and is computed with anatomical knowledge of tongue muscles. The fiber directions are estimated within a maximum a posteriori (MAP) framework, and the resulting objective function is solved using a noise-aware weighted ℓ_1-norm minimization algorithm. Experiments were performed on a digital crossing phantom and *in vivo* tongue diffusion data including three control subjects and four patients with glossectomies. On the digital phantom, effects of parameters, noise, and prior direction accuracy were studied, and parameter settings for real data were determined. The results on the *in vivo* data demonstrate that the proposed method is able to resolve interdigitated tongue muscles with limited gradient directions. The distributions of the computed fiber directions in both the controls and the patients were also compared, suggesting a potential clinical use for this imaging and image analysis methodology.

1. Introduction

The tongue is a critical organ for a variety of functions, including swallowing, respiration, and speech [1,2]. It contains intrinsic and extrinsic muscles that play an important role in changing its shape and position [3]. Tongue muscles have been studied using diffusion tensor imaging (DTI) [4–9], which provides a noninvasive tool for investigating fiber tracts by imaging the anisotropy of water diffusion [10]. For example, in Gaige et al. [5], based on diffusion tensors, the technique of fiber tracking [10–13] was used to reconstruct 3D curves representing key muscle fibers and visualize the tongue anatomy. In Felton et al. [6], muscle fibers were studied together with strain rate to demonstrate the relationship between fiber organization and tissue deformation during swallowing. Using DTI, studies on the influence of interventions on the tongue muscles have also been performed. In Shinagawa et al. [8] and Shinagawa et al. [9], preliminary studies were carried out to track the deformed muscle fibers in patients with oral appliances. In Murano et al. [7], tongue muscle fibers were tracked for a patient after the glossectomy and compared with a control subject.

These studies [5–9] all used DTI-based fiber tracking [11,13]. However, many of the tongue muscles interdigitate, and it is well known that DTI cannot represent crossing fiber directions [14]. Thus, using the tensor model is insufficient for reconstructing

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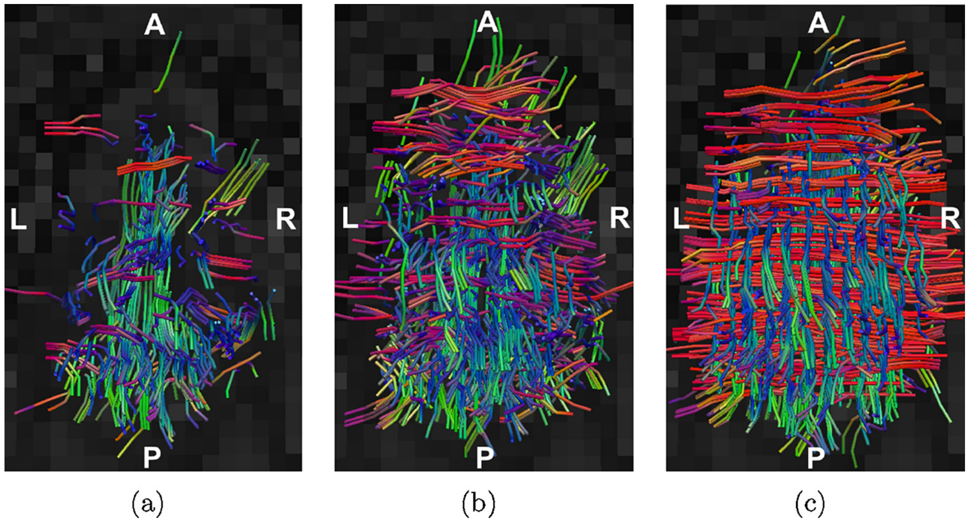

Fig. 1. An example of fiber tracking seeded in the transverse muscle, which in this axial view should be seen as left to right (red) streamlines. Each segment of the fibers is color-coded by the standard DTI color scheme (red: left–right; green: front–back; and blue: up–down). (a) DTI model, (b) multi-tensor model and (c) proposed method with prior information. (For interpretation of the references to color in this figure legend, the reader is referred to the web version of the article.)

interdigitated tongue muscles. For example, the transverse muscle interdigitates with the genioglossus, and DTI fails to reconstruct the transverse muscle. Fig. 1(a) gives a typical example of fibers tracked with DTI when seeded in the transverse muscle; it can be seen that the majority of the transverse muscle fibers, which should be reconstructed as left to right (red) streamlines, are missing. Therefore, a fiber tracking method that is able to resolve crossing fibers is crucial for correct representation of the tongue muscles.

To address the problem of tracking crossing fibers, different imaging modalities that seek to obtain more comprehensive directional information, including high angular resolution diffusion imaging (HARDI) [15] and diffusion spectrum imaging (DSI) [16], have been proposed. Since these modalities typically acquire around 100 gradient directions and demand long scan times (which limits their application in clinical research), a number of attempts to accelerate the imaging process have been made [17–19]. However, because of the involuntary swallowing, which limits the available time to around 2–3 min for *in vivo* acquisition in the tongue, especially in cases where pathology is present, only a dozen (or so) gradient directions are achievable in practice. Thus, there is insufficient time for the acquisition of HARDI and DSI, despite the efforts to accelerate image acquisition. In addition, a great number of existing DTI data sets have been acquired and need better analysis. Therefore, although both HARDI and DSI data could be used for the methods described in this paper, we limit the presentation of results to the conventional DTI acquisitions that are presently achievable.

There are also methods designed to better exploit the information in DTI to resolve crossing fibers. For example, Behrens et al. [20] and Peled et al. [21] use two-tensor models to recover crossing directions. In Behrens et al. [20], a Bayesian estimation is used to fit the parameters of the model, which is achieved by Markov chain Monte Carlo sampling. The method in Peled et al. [21] places a number of constraints on the tensors in the two-tensor model to reduce the number of free parameters, and resolves two crossing fiber directions using a nonlinear least squares method. Ramirez-Manzanares et al. [22], Landman et al. [23], and Zhou et al. [24] use multi-tensor models with a fixed tensor basis to resolve crossing fibers. In Ramirez-Manzanares et al. [22], diffusion signals are modeled as a discrete mixture of Gaussian random variables and are deconvolved using a set of diffusion basis functions which represent fiber directions. In Landman et al. [23], a sparse reconstruction technique is used, where a dictionary is constructed with a fixed tensor basis. The fiber directions are estimated by solving the ℓ_1-norm regularized least squares problem. Zhou et al. [24] adds an isotropic component in the multi-tensor model and solves the problem with ℓ_1-norm and TV-norm regularization.

Using the number of gradient directions that is common in clinical research (around 30), these two-tensor or multi-tensor models are able to resolve crossing fibers. However, due to the limited number of gradient directions in *in vivo* tongue diffusion data acquisition, there is insufficient information for successful resolution of crossing fibers using these methods. Fig. 1(b) gives an example of fibers tracked using the multi-tensor model in Landman et al. [23], when the fibers were seeded in the transverse muscle. Although part of the transverse muscle is reconstructed, it is clear that the major body is missing. Thus, distinguishing interdigitated tongue muscles, which constitute a large percentage of the tongue volume, is very challenging.

In this paper, we present a multi-tensor method for distinguishing interdigitated tongue muscles by incorporating prior directional knowledge within a Bayesian framework. The proposed method is named Fiber Interdigitation Estimation by Bayesian Reconstruction (FIEBR). In FIEBR, the prior directional knowledge provides information on likely fiber directions at each voxel, and can be computed with anatomical knowledge of tongue muscles. Note that this work is an extension of our conference paper [25]. Compared to Ye et al. [25], here we have included more comprehensive muscle information and we also propose a way to determine the parameters of the algorithm. In addition, while only one control subject was included in Ye et al. [25], here we have included both control subjects and patients after glossectomies to show the influence of surgeries on the muscles and demonstrate the potential of applying FIEBR for clinical use.

An example of the FIEBR result is shown in Fig. 1(c). In contrast to the DTI model and the multi-tensor results in Fig. 1(a) and (b), FIEBR successfully reconstructs the transverse muscle. In FIEBR, we use a fixed tensor basis to model the diffusion weighted signals in each voxel, and then we determine the contribution of each basis tensor using maximum a posteriori (MAP) estimation. The prior distribution contains both the prior directional information and sparsity constraints, and data fidelity is modeled in the likelihood term. The resulting objective function can be solved as a noise-aware version of a weighted ℓ_1-norm minimization [26]. Using the estimated fiber directions from FIEBR, we also propose a streamlining fiber tracking strategy to reconstruct tongue muscles.