

# Segmentation of Lingual Muscles Based on Diffusion Tensor Imaging

S. Kim<sup>1</sup>, C. Pierpaoli<sup>2</sup>, A. S. Barnett<sup>3</sup>, G. Chi-Fishman<sup>1</sup>

<sup>1</sup>Physical Disabilities Branch, Department of Rehabilitation Medicine, WGM Clinical Center, National Institutes of Health, Bethesda, MD, United States, <sup>2</sup>National Institute of Child Health and Human Development, National Institutes of Health, Bethesda, MD, United States, <sup>3</sup>National Institute of Mental Health, National Institutes of Health, Bethesda, MD, United States

## Introduction

The human tongue is diverse in function and plays crucial roles in speech production and deglutition. Its myoarchitecture is unparalleled in complexity by any other organs in the human body. Nonetheless, human lingual myoarchitecture has not been investigated rigorously. A limited number of studies to date have shown that different perspectives may be gained from different gross structural and histological investigation methods, and that an adequate understanding of the complex lingual myoarchitecture requires a complete 3-D analytical approach that is difficult to undertake through histological sections [1]. The purposes of this study are to develop a regularization and segmentation method for 3-D morphological analysis of the tongue in an animal model, and to determine the feasibility of using high-resolution diffusion tensor imaging (DTI) to study the compartmentalized lingual myoarchitecture.

## Method

DTI was performed on six fresh unembalmed calf tongues within 24 hours of harvest. They were scanned with a standard quadrature head coil in a 1.5T GE Signa MR scanner (GE Medical Systems, Milwaukee, WI) equipped with a whole-body gradient coil producing gradient pulses up to 50 mT/m. A custom diffusion-sensitive stimulated-echo pulse sequence was used with 8-shot echo-planar spatial encoding (acquisition matrix: 128 x 64, FOV = 260 x 130 mm<sup>2</sup>, slice thickness = 2 mm, 50 slices, TM=400 ms, TR=16.0 s, diffusion gradient amplitude = 44.5 mT/m, diffusion gradient directions: [1, 1, 0], [1, 0, 1], [0, 1, 1], [1, -1, 0], [1, 0, -1], and [0, 1, -1]). The total scan time for 8 repetitions was approximately 7 hrs 30 min.

Prior to segmentation, the acquired tensor field was regularized using normalized convolution. Normalized convolution is a general framework to filter missing and uncertain data based on certainty measures and has also been applied to the regularization of tensor field through magnitude and angular similarity measures of neighboring voxels without blurring the boundary between tensor fields of different orientations [2]. In our study, a new skewness similarity measure was added to maintain the boundaries between linear and planar tensor regions during regularization. The measure is defined as:  $C_s = \exp[-((SK(D_0) - SK(D))/\sigma_s)^2]$ , where  $SK(D)$  is the third order momentum of the eigenvalues,  $\lambda^D$ , of diffusion tensor  $D$ . The overall certainty measure is defined as the product of the new skewness similarity and all other certainty and similarity measures. The regularized model  $f'$  for tensor elements is found by minimizing the square error between  $f'$  and the measured data  $f$ :  $f' = BR = B(B^T W_a W_c B)^{-1} B^T W_a W_c f$  where  $B$  is a matrix of basis functions,  $W_a$  applicability weight vector, and  $W_c$  certainty measure vector. The regularization was performed on the entire 3-D data, not on individual 2-D image planes.

Segmentation was implemented based on a concept similar to directional correlation, which was first used to segment white matter tracts in the rat brain [3] and recently in the human brain [4]. Directional correlation is a simple algorithm to group anisotropic voxels based on the inner product of their primary eigenvectors, starting from manually selected seed points. Newly grouped voxels then become the new starting points for region growing iteratively until there are no more neighboring voxels to include in the group. Although directional correlation has been demonstrated to work reasonably well for the white matter tracts, its usage is limited to the linear anisotropic regions, because it utilizes the primary eigenvector orientation only. In order to segment muscles and muscle groups regardless of their tensor shape and to measure the coherence in direction as well as in shape, the double inner product of the reference and neighboring tensors was calculated, instead of the inner product of primary eigenvectors, followed by normalization to calculate orientation coherence (OC). The double inner product between a reference voxel tensor,  $D_R$ , and a neighboring voxel tensor,  $D_N$ , is defined as in Eq.(1) where  $\lambda_{A,B}$  and  $e_{A,B}$  are the  $B$ th eigenvalue and eigenvector of voxel  $A$ , respectively. OC is defined as in Eq.(2) where  $\alpha$  is a constant, set to a value of 4, to increase the sensitivity of the measure near 1.

$$D_R : D_N = \sum_{k=1}^3 \sum_{l=1}^3 \lambda_{R,k} \lambda_{N,k} (e_{R,k}^T e_{N,k})^2 \quad (1)$$

$$OC = \left( \frac{D_R : D_N}{\sqrt{D_R : D_R} \sqrt{D_N : D_N}} \right)^\alpha \quad (2)$$

Similar concept was introduced earlier to estimate the local order within the vicinity of the reference voxel by taking a weighted sum of normalized tensor products [5]. In our application, OC was calculated for any neighboring voxel with fractional anisotropy higher than 0.15 for voxel recruitment. Multiple seed points were selected within the same muscle or muscle group. Their results were added to reconstruct the given muscle or muscle group.

## Results & Discussions

Morphologic details were obtained from visualization of diffusion tensor eigenvector orientations of tongue muscles as shown in Fig.1. The primary eigenvectors were found to be adequate to delineate the superior and inferior longitudinalis, genioglossus, and hyoglossus. Tertiary eigenvector orientations effectively revealed the homogeneous and systematic change of muscle orientation in the tongue core. Regularization of the tensor field using the proposed algorithm was successful as shown in Fig.2. The result of segmentation of lingual muscles is shown using volume rendering in Fig.3. Our DTI-based morphologic data agreed with qualitative analysis of tissue characteristics from our gross dissection slices. With technical advances in imaging and substantial reduction in scan time, DTI can be applied in vivo toward a better understanding of the relationship between lingual myoarchitecture and function in health, aging, and disease.

## References

- [1] Takemoto H. J Speech Lang Hear Res 2001;44:95-107. [2] Westin et al., EUROCAST 2003; LNCS 2809:565-572. [3] Mori et al., Magn Reson Med 2001;46:18-23. [4] Klose et al., J Magn Reson Img 2004;20:25-30. [5] Basser PJ, Pierpaoli C. J Magn Reson B 1996:209-219.

\*Physical Disabilities Branch is a collaboration between the National Institute of Child Health and Human Development and the Warren G. Magnuson Clinical Center, NIH

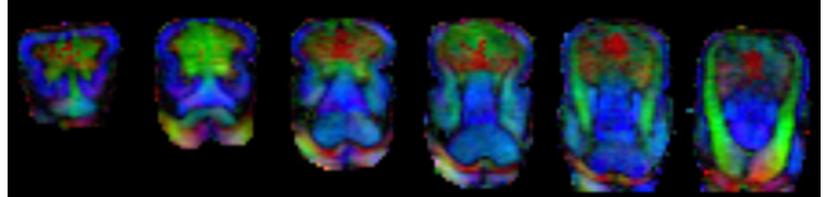


Fig.1 Coronal images of directionally encoded color mapping of the primary eigenvectors weighted by lattice index; red for horizontal, green for vertical, and blue for through-plane directions.

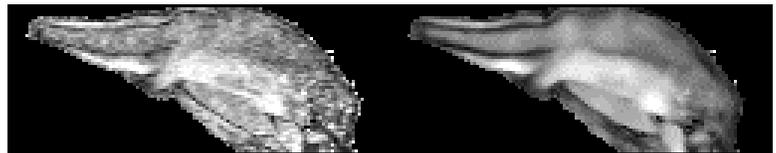


Fig.2 Example of regularization result shown by fractional anisotropy map. Left: original data in mid sagittal view. Right: regularized data of the same slice.

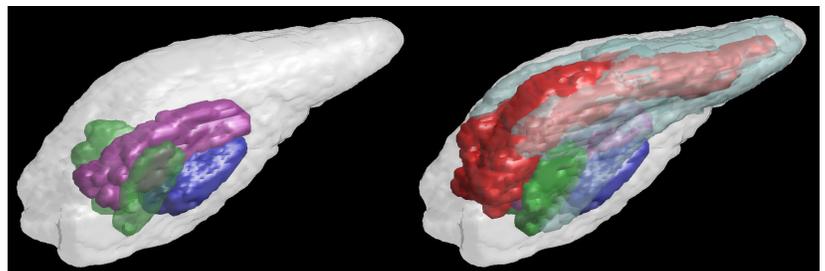


Fig.3 3D rendering of segmented muscle groups. The tongue surface is shown by translucent white color. Left: genioglossus in purple, geniohyoid in blue, and hyoglossus in translucent green. Right: composite of all segmented muscle groups with the tongue core (transverse and vertical muscles) in red and longitudinal muscles in cyan.