

# MUSCLE DIFFUSION TENSOR IMAGING: INFLUENCE OF SEGMENTATION ON THE DETERMINATION OF MUSCLE ARCHITECTURE

Sebastian Vetter (1), Hans-Peter Köhler (1), Maren Witt (1), Jeanette Henkelmann (2) & Christian Roth (2)

1. Leipzig University, Germany; 2. Universitätsklinikum Leipzig, Germany

## Abstract

**Introduction.** A skeletal muscle fascicle length is a primary determinant for its functioning. Determining a muscle's arrangement in a reliable way, requires a standardized imaging method. MRI-based diffusion tensor imaging of muscle (mDTI) gives three-dimensional and complex insights in a muscle structure. Within neurosciences DTI is an already accepted method and shows the arrangement of nerves by measuring the diffusion of water molecules along the nerve fibers<sup>[1]</sup>. Since muscles also contain a certain amount of water, mDTI also allows for a valid<sup>[2-4]</sup>, reliable and robust<sup>[5,6]</sup> measurement of a muscle's arrangement. Nevertheless, mDTI data processing seems time-consuming and dependent on consistency between operators and therefore less applicable for different purposes.

To turn mDTI into a tool of practical importance, the adjustment of the slice-by-slice muscle segmentation prior to fiber reconstruction provides most potential<sup>[7,8]</sup>. Therefore, it is of practical relevance to know how different muscle model shapes affect mDTI analysis. This study aims to analyze the influence of segmentation-based analysis (SBA) by two different operators on muscle fiber tractography. Furthermore, we want to compare these results to model-free analysis (MFA).

**Methods.** 15 healthy male subjects underwent a standard 3T MR diagnostics using a 16-channel shoulder coil (XL). A T1w and 2D echo planar DTI sequence were applied for the right shoulder. Total scan time was about twelve minutes. After acquisition, two different operators (SBA 1 and SBA 2) independently segmented each M. supraspinatus by using an individual routine. MFA did not contain a segmentation prior to tractography (Figure 1). Deterministic fiber tracking was performed using DSI Studio with the following stopping criteria: maximum angle between tract segments 10°, 40 mm ≤ tract length ≤ 130 mm; step size = 1.0 mm. Recommended DTI pre-processing steps were applied. For reliability analysis (ICC) we calculated values for the parameters fractional anisotropy, axial diffusivity, radial diffusivity, mean diffusivity, muscle volume and fascicle length.

**Results.** Overall methods ICC ranged between 0.615 (fascicle length) and 0.943 (fractional anisotropy). Interrater-reliability analysis for SBA 1 and SBA 2 showed an ICC between 0.872 and 0.991, with

exception for muscle volume (0.711). In contrast, MFA revealed an ICC between 0.404 and 0.544. Without considering the results for the parameter fascicle length, ICC values for MFA varied between 0.726 and 0.933 (Table 1).

Parameter	Method	ICC	95% CI	
FA	SBA 1 vs. SBA 2	.991	.973	.997
	SBA vs. MFA	.933	.805	.978
MD	SBA 1 vs. SBA 2	.962	.887	.987
	SBA vs. MFA	.810	.512	.935
AD	SBA 1 vs. SBA 2	.959	.882	.987
	SBA vs. MFA	.822	.538	.939
RD	SBA 1 vs. SBA 2	.969	.908	.990
	SBA vs. MFA	.832	.558	.943
FL	SBA 1 vs. SBA 2	.872	.658	.957
	SBA vs. MFA	.404	-.071	.751
MV	SBA 1 vs. SBA 2	.711	.036	.915

Table 1: intraclass coefficient (ICC) and 95% confidence intervals (CI) for segmentation-based (SBA) and model-free analysis (MFA) for the parameter fractional anisotropy (FA), axial diffusivity (AD), radial diffusivity (RD), mean diffusivity (MD), fascicle length (FL) and muscle volume (MV).

**Discussion.** mDTI allows a detailed and excellent reliable<sup>[9]</sup> analysis of shoulder muscle structure independent of the segmentation. Since it is known that the human shoulder joint is challenging for any imaging technology, this study shows very promising results. Further, even the model-free, less time-consuming method (MFA) showed acceptable results. This makes mDTI suitable as a tool in prevention and rehabilitation. Therefore, mDTI claims practical relevance and may be considered as a standard sequence within a musculoskeletal MR application. Nevertheless, complex image processing and segmentation seems mandatory for an accurate measurement of fascicle length. It remains unclear whether MFA could be applied for any muscles with different fiber orientation.

## References

1. Maier-Hein et al, Nat Commun, 8, 2017.
2. Damon et al, Magn Reson Med, 48:97-104, 2002.
3. Schenk et al, J Anat, 223:61-68, 2013.
4. Bolsterlee et al, J Biomech, 48:1133-1140, 2015.
5. Heemskerk et al, NMR Biomed, 23:294-303, 2010.
6. Bolsterlee et al, J Biomech, 86:71-78, 2019.
7. Forsting et al, NMR Biomed, 34, 2021.
8. Muzic et al, Acta Myol, 40:116-123, 2021.
9. Koo et al, J Chiropr Med, 15:155-163, 2016.

