## 3D Shear strain analysis of Medial Gastrocnemius muscle based on Velocity Encoded and Diffusion Tensor Imaging data.

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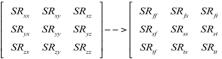
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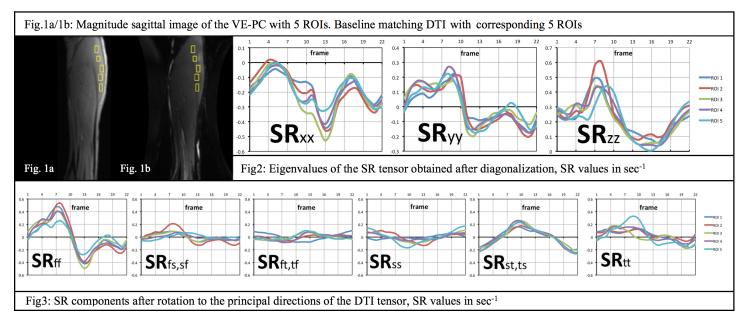
**Target audience:** Physicists, Graduate Students (focus on image analysis/ Muscle mechanics)

<u>Purpose:</u> The objective quantification of regional muscle deformation is a valuable clinical tool to evaluate normal and diseased muscle. 3D strain rate in cardiac muscle [1] and 3D strain in skeletal muscle [2] have been reported. Several studies have shown that the SR tensor is not aligned along with the DTI tensor indicating the presence of shear strain. Our aim is to map the 3D strain rate (SR) tensor and identify the shear strain components from a series of velocity encoded (VE-PC) images acquired during isometric contraction.

Methods: Three subjects, recruited after IRB approval, were scanned on a 1.5-T GE whole-body scanner with a cardiac surface coil. The lower leg was placed a cast with a pressure transducer attached to the cast; the subjects foot pressed against the pressure transducer and the signal from the transducer was projected on a screen to provide feedback to the subject to exert force at 40% MVC. A gated VE-PC (water) imaging sequence (16.5ms TR, 7.7ms TE, 20° FA, 122Hz/pixel bandwidth, 10 cm/s velocity encoding in 3 directions, 4 views/segment, 22 phases, 2 excitations, 256x128 image matrix, 300×120-mm FOV, 3 contiguous slices 3mm (separate acquisition)/skip 0, and 2:14 min scan time) in a sagittal orientation was used to acquire tissue VE-PC dynamic images of the lower leg during isometric contraction. SR tensor was calculated in 3D after the phase images were corrected for phase shading artifacts and denoised using a 2D anisotropic diffusion filter. The spatial gradient tensor, L, and strain rate tensor, SR, were calculated in the lab reference frame. DTI images with diffusion gradients in 32 directions and geometry parameters matching the

VE-PC sequence were also acquired. The 3x3 strain rate tensor was diagonalized and eigenvectors corresponding to the 3 eigenvalues were determined. The shear strain terms were acquired by rotating the SR tensor in the lab frame of reference to the DTI principal axes using the direction cosines of the DTI eigenvectors (directions: f(fiber), s(secondary), t(tertiary) (see on the right).





Results: Fig. 1a and 1b shows the magnitude image of the VE-PC with five ROIs placed in the medial gastrocnemius; corresponding DTI slice and ROIs are shown in Fig. 1b. The three eigenvalues of the strain rate tensor are shown in Fig.2. The first eigenvalue is negative (represents compression), and the third eigenvalue is positive (represents expansion) as anticipated for expansion in one dimension to be accompanied by compression in the other dimension. The second eigenvalue potentially represents the deformation in-plane (fiber cross-section) and shows the least deformation (though not negligible). The SR components rotated to match the DTI show some interesting features (Fig. 3): The strain rate along the fiber (SRff) has the maximum values while strain rate along the secondary DTI eigenvector is the least. Of the shear strain components, the most pronounced shear is in the 'st' (fiber cross section) plane.

Discussion and Conclusions: 3D strain rate and shear strain rate mapping is feasible despite the challenges of 3D spatial/velocity encoded and matched DTI acquisition. The asymmetry of in-plane deformation (high along one direction and low in perpendicular direction) may potentially lead to the high values of the shear strain rate in the fiber cross-section plane (SRst). Further, for the first time, it is shown that strain rate (or deformation) is very low along the direction of the DTI secondary eigenvector. In one model of diffusion, the secondary eigenvector is the direction of sheets. It is possible that very close packing of sheets may restrict muscle deformations along that direction.

References: [1] Selskog P. IEEE Trans Med Imaging. 2002 Sep; 21(9): 1105-9. [2] Englund et al. Am J Physiol Regul Integr Comp Physiol. 2011; 300(5): R1079-9.