T₂ based analysis of fat infiltration in muscular dystrophy using quantitative, sub-voxel estimation of fat and water fractions

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1. INTRODUCTION

- T₂ relaxation time is a highly efficient biomarker of muscle health, being sensitive to both macro- and microstructural changes in muscle tissues, which can be caused by various muscle dystrophies, inflammatory processes, or neuromuscular disorders.¹
- These diseases result in an infiltration of subcutaneous fat and a corresponding loss of muscle volume, leading to a mixture of two tissue types, fat and muscle, and results in the appearance of two T₂ components in each imaged voxel.²
- Quantification of these fat and water components holds great diagnostic and prognostic value by allowing an accurate assessment of the muscle status and the stage of the disease.³
- Achieving a reliable quantification of single-T₂ values in clinical setting is a challenging task due to the bias of fast Multi Spin-Echo (MSE) protocols by stimulated and indirect echoes.⁴ The Echo-Modulation-Curve (EMC) algorithm⁵ can overcome these limitations and deliver accurate and reliable maps of the true tissue T₂ values, independent of the scanner and protocol implementation.⁶
- In this work, an extension of the EMC algorithm for two-component fitting is presented, simultaneously estimating sub-voxel fat and water fractions, along with the T₂ and Proton Density (PD) corresponding to each component.

2. METHODS: EMC Algorithm

- **Data acquisition**: The calf muscle of a healthy volunteer and a patient with Dysferlinopathy was scanned on a whole-body 3T Siemens Prisma scanner using a standard MSE protocol.
- **Data postprocessing**: Bloch simulations of the MSE protocol were performed using identical scan parameters. Simulations were repeated for a range of T₂ [ms] and Bₐ [mT/m] inhomogeneity values [%], producing a database (DB) of EMCs, each associated with a unique [T₂, Bₐ] pair (DBwater). A similar DB was created for the fat signal by repeating this process at 3.5 ppm off-resonance (DBfat).
- **Generation of quantitative maps**: Water T₂,fat T₂, and water fraction (fwater) maps were generated on a pixel-by-pixel basis by matching the experimental MSE time-series to the simulated EMCs, calculated as the weighted sum of two decay curves:
  \[ EMC_{\text{experimental}} = f_{\text{water}} \cdot EMC_{\text{water}} + (1 - f_{\text{water}}) \cdot EMC_{\text{fat}} \]
- Matching was done via L2-norm minimization of the difference between experimental and theoretical EMCs over the range of simulated [T₂, Bₐ] values.

3. RESULTS

- Figure 2: (a) Example of 20 simulated EMCs for a range of T₂ values and a single Bₐ scale. (b) Actual EMC database, consisting of ~5000 simulated EMCs, each corresponding to a unique [T₂, Bₐ] value pair.

4. CONCLUSIONS

- The ability to quantify sub-voxel tissue components is highly valuable for clinical applications.
- The framework allows to separately track changes in the water and in the fat components.
- An appealing feature of this approach is that it employs a standard MSE protocol scheme, making it readily available on any clinical or animal scanner.
- EMC based quantitative maps are invariant across vendors, scanners and scan settings.

5. REFERENCES


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• The fat-infiltrated muscle regions are indicated with arrows: The Medial Gastrocnemius muscle (GM) and the Tibialis Anterior muscle (TA).