# Contrast Optimization for Knee MRI at 7 T

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FREEDOM TO RESEARCH

## Introduction

MRI properties of knee joint tissues including cartilage, bones, fat, synovial fluid, menisci, ligaments, and tendons, could act as markers for the pathologies of this anatomically complex joint in the human body. Osteoarthritis (OA) is for example a knee joint disease for which thickness and volume of cartilage, area and shape of bones, size and severity of lesions in bone marrow, menisci or ligaments, and inflammation of synovium (synovitis) are some of the well-recognized and established MRI markers.

Among physical parameters, T2 and T1ρ of cartilage have been considered as other MRI features reflecting different stages of OA. MRI offers a variety of contrast mechanisms based on pulse sequences which are employed.

In this work, we aim at generating different and optimal contrasts to track human knee pathologies at 7T, beneficially at high spatial resolution. An aligned goal is to produce tissue specific contrast at desired level with support of simulation.

## Methods

Initially, two pulse sequences are considered for this purpose. Among the spin-echo based pulse sequences, we employ 2D and 3D TSE [1] and among the gradient-echo based pulse sequences, we use 3D FLASH [2].

The MR signal dependency on sequence parameters and tissue properties is well-known [3]. We simulated it to derive sequence parameter values to achieve any certain level of contrast between two different tissues.

The number of free parameters on which the MR signal depends is sequence specific. For TSE we feed the simulation with desired range of TE and TR and obtain their optimal values to generate any certain level of contrast between two tissues. For FLASH we have the flip angle as another free parameter.

## Results

To get an insight into reliability of the parameters derived from the simulation, they were compared with the values used by Springer et al [4] in their comparison study of knee MR imaging at 3 T and 7 T. As highlighted in Figure 1, TE of approximately 19 ms and TR of 5200 ms used in the reference study [4] were among the values derived with simulation for contrast level of 75% between cartilage and bone marrow (BM) in PD-weighted MR image generated with TSE. With the same TE and slightly lower TR we can reach contrast level of 95%. Figure 2 presents the range of TE and TR for T1-weighted MR image acquired with TSE for four different ranges of contrast level. TE of 10 ms and TR of 1600 ms used in [4] are among the values obtained with simulation for contrast level of 95% between cartilage and BM.

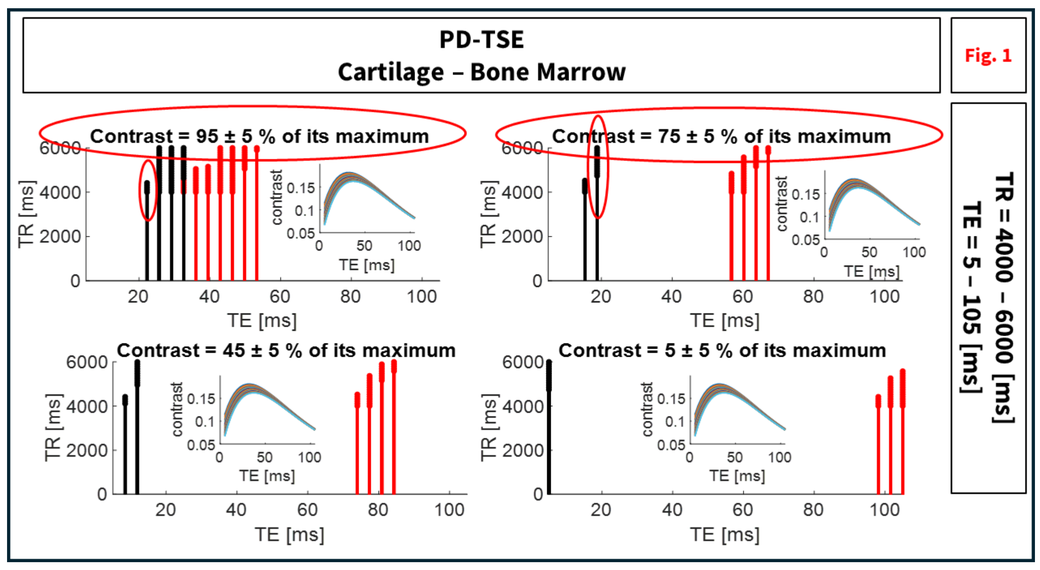
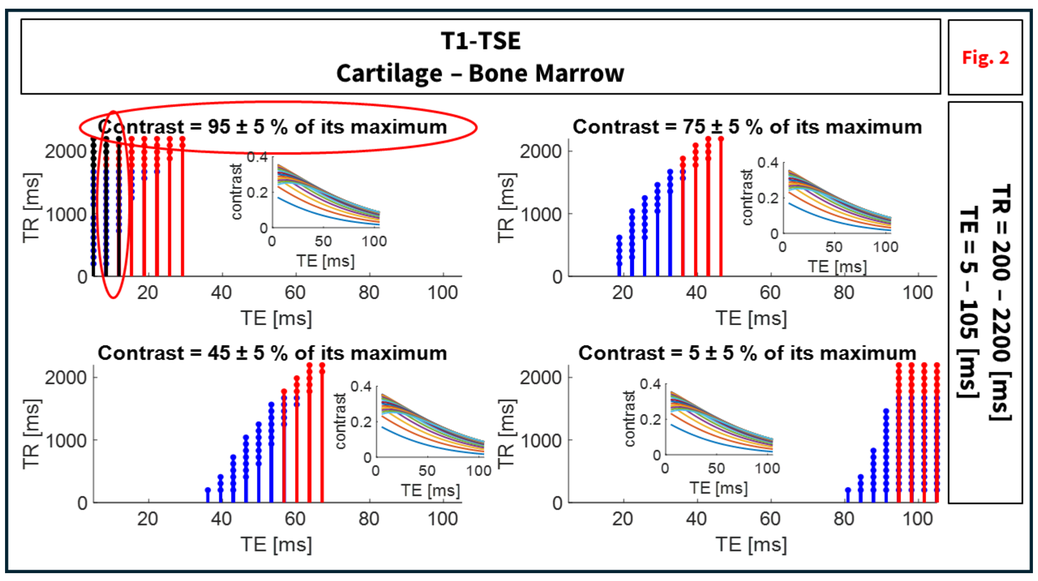



Table 1 compares the values used in [4] for a FLASH sequence to acquire T2-weighted MR images with the values calculated with simulation for four different contrast levels between cartilage and BM ranging from 90% down to 15%.

**Table 1**

| 3D GRE | Springer et al, 2017 [4] | Simulation | | | |
|---|---|---|---|---|---|
| TR [ms] | 8.1 | 8.1 | 8.1 | 8.1 | 8.1 |
| TE [ms] | 3.57 | 3.55 | 3.55 | 3.55 | 3.55 |
| FA [degrees] | 7 | 10-11 | 8 | 6 | 4 |
| Contrast Level | - | 90% | 75% | 45% | 15% |
| Tissues | - | Cartilage-Bone Marrow | | | |




## Discussion

To gain more reliable values of the sequence parameters, the relative proton density level should be included and the contrast better to be reported as its ratio relative to the thermal noise. Simulation provides us with the ability to calculate some of the sequence parameters to generate different contrast levels between two different tissues assuming their relaxation times are known at a certain field strength which is the case for knee joint tissues at 7T [5]. This could also provide the possibility to establish multi-tissue contrast optimization.

## References

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