# GRADIENT ECHO ASSISTED 3D LOOK-LOCKER - A METHOD FOR IMPROVED VOLUME T1-QUANTIFICATION ACCURACY APPLIED TO DGEMRIC

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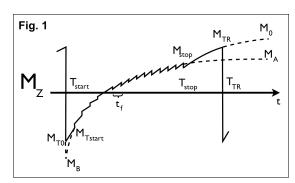
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#### Introduction

3D Look-Locker (LL) can be used for T1 quantification applications such as delayed Gadolinium enhanced MRI of cartilage (dGEMRIC), which is a technique for molecular imaging of the proteoglycan level in cartilage by quantitative T1 measurements [1]. However, such 3D T1 quantifications are often sensitive to flip angle (FA) variations, caused both by B1 inhomogeneities and slice dependent FA variations due to the pulse shape. In this work a method is introduced to correct for all such effects by adding a very quick additional spoiled gradient echo sequence (GRE).

## Methods

In the Look-locker technique, the MR signal is sampled using a train of small FA RF pulses following an inversion pulse. A pseudo-T1 (T1\*) relaxation time is then calculated, together with variables  $M_A$  and  $M_B$ , using a three-parameter fit to the LL data. Traditionally, the true T1 is then calculated from equation 1 [1], using only the nominal FA from the user interface (constant FA correction), with possibly erroneous T1 values as a result. It has previously been shown [2], that equations 2 and 3 will solve the true T1 for any LL data, given that the quality of the inversion, K, is known. However, for in vivo measurements, the inversion cannot be assumed to be ideal (i.e. K<1), not even with adiabatic pulses. Thus, the previous method will fail in calculating the correct T1 value in vivo. By introducing an additional GRE sequence it is however possible to also calculate the K-value (GRE assisted correction). M0 for GRE is calculated using equation 5. If the pulse types for both LL and GRE are the same, the FA for GRE is related to the FA for LL (eq. 4), which in turn can be calculated using equation 1. By combining equations 1-5 and solve iteratively for each voxel, it is possible to find the K-values that result in equal M0 for both LL (eq. 2 and 3) and GRE (eq. 5) for each voxel, together with the corresponding correct T1 values. This approach requires the echo times to be equal for LL and GRE.

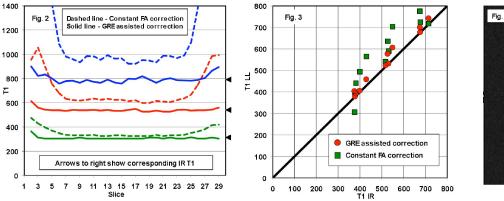


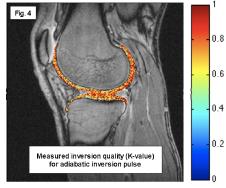
$$\begin{array}{c} \text{Eq 1.} \quad \frac{1}{T_{1}} = \frac{1}{T_{1}} + \frac{\ln(\cos(\alpha))}{t_{f}} \\ \text{Eq 2.} \quad \frac{t_{f}}{\ln\left[1 - \frac{M_{A} - M_{A} \cdot e^{-\frac{t_{f}}{T_{1}}}}{M_{0}}\right]} \\ \text{Eq 3.} \quad M_{0} = \frac{M_{Tstart} + M_{Tstop} \cdot K \cdot e^{-\frac{T_{start}}{T_{1}}} \cdot e^{-\frac{T_{R} - T_{stop}}{T_{1}}}}{1 - e^{-\frac{T_{start}}{T_{1}}} \cdot e^{-\frac{T_{start}}{T_{1}}} \cdot e^{-\frac{T_{R} - T_{stop}}{T_{1}}} } \end{array}$$

All imaging was performed on a Siemens Magnetom Sonata 1.5 T scanner and a CP Extremity coil. Three gel-filled tubes with different T1s were imaged with in-house developed 3D LL (FOV =  $16^2$  cm<sup>2</sup>, Matrix =  $256^2$ , 30 slices, TR 2500 ms, TE 2.68 ms, FA =  $6^\circ$ , 11 contrasts) and 3D GRE (FOV =  $16^2$  cm<sup>2</sup>, Matrix =  $256^2$ , 30 slices, TR 5.85 ms, TE 2.68 ms, FA =  $16^\circ$ ) sequences. The tubes were aligned to the slice-encoding direction, such that the tube ends matched the outer slices. T1 was calculated for all slices using both constant FA correction and GRE assisted correction. The same sequences were also used for in vivo imaging of 6 subjects (sagittal orientation, 3D volume centered at the knee midline between the condyles). LL duration was 10 min 42 s and GRE duration was 45 s. Standard 2D IR dGEMRIC was also acquired as a reference. T1 was evaluated with ROIs in mid-lateral and mid-medial condyle slices.

#### Results

Due to B1 inhomogeneities and RF pulse slice profile, T1 calculated using traditional constant FA correction is generally overestimated in all phantoms, with a rapidly increased overestimation at the outer slices (fig 2, Phantom measurements). This effect is even more prominent in vivo (fig 3), since ROIs are drawn off center and also due to increased B1 inhomogeneity. The GRE assisted correction however, can correct for both deviations in FA and imperfect inversion (fig 4). With this method T1 is essentially correct throughout all slices in the phantoms (fig 2) and also throughout all in vivo measurements (fig 3).





## **Discussion and conclusions**

The constant FA correction does not perform well enough for in vivo applications such as dGEMRIC, particularly not if one wants to make use of the full 3D volume. The method presented here reliably corrects for both B1 inhomogeneities and imperfect inversion, with only a very short amount of extra time (45 seconds) added.

### References

1. Kimelman et al, Inv. Radiol. 41:198-203 (2006), 2. Siversson et al, ISMRM No.5289 (2008)