# LOCAL FLIP ANGLE CORRECTION FOR IMPROVED VOLUME T1-QUANTIFICATION IN 3D DGEMRIC USING THE LOOK-LOCKER TECHNIQUE

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## Introduction

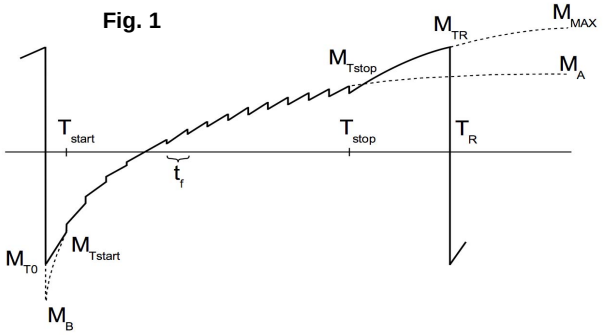
3D Look-Locker (LL) delayed Gadolinium enhanced MRI of cartilage (dGEMRIC) is a technique for molecular imaging of the proteoglycan level in cartilage using quantitative T1 measurements [1]. However, in 3-D imaging the flip angle (FA) will vary in the slice encoding direction. This is usually not taken into account but may cause erroneous T1 values. The aim of this work was to evaluate the extent of this effect and try to correct for it in in vivo data.

## 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 biased by the applied pulses is then calculated from the acquired signal. The true T1 is normally retrieved by compensating for the effect of the RF pulses using Eq. 1 (constant FA correction). The nominal FA from the user interface is often used, with possibly erroneous T1 values as a result.

However, from Eq. 1 and the steady signal equation for the spoiled gradient echo sequence, a new set of equations can be derived which can be used to calculate a T1 value inherently compensated for the actual local FA (Eq. 2-3, Fig. 1) (local FA correction). K is the quality of the inversion pulse, which is assumed to be 1 for the adiabatic inversion used here.

Fig. 1




Eq. 1

$$\frac{1}{T} = \frac{1}{T_1^*} + \frac{\ln(\cos(\alpha))}{\tau}$$

Eq. 2

$$M_{MAX} = \frac{M_{Tstart} + M_{Tstop} \cdot K \cdot e^{-\frac{T_{start}}{T_1}} \cdot e^{\frac{T_R - T_{stop}}{T_1}}}{1 - e^{-\frac{T_{start}}{T_1}} - K \cdot e^{-\frac{T_{start}}{T_1}} + K \cdot e^{-\frac{T_{start}}{T_1}} \cdot e^{\frac{T_R - T_{stop}}{T_1}}}$$

Eq. 3

$$T_1 = -\frac{t_f}{\ln\left(1 - \frac{M_A - M_A \cdot e^{-\frac{t_f}{T_1}}}{M_{MAX}}\right)}$$

All imaging was performed on a Siemens Magnetom Sonata 1.5 T scanner and a CP Extremity coil. Three gel-filled tubes with different T1's were imaged with an in-house developed 3D LL sequence (FOV = $20^2$ cm$^2$, Matrix = $256^2$, 30 slices, TR 2500 ms, FA = 6°, 12 contrasts). 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 the constant FA correction as well as the local FA correction. The same 3D LL sequence was also used for in vivo imaging of 9 subjects (FOV = $12^2$ cm$^2$, sagittal orientation, 3D volume centered at the knee midline between the condyles). Standard 2D IR dGEMRIC was also acquired as a reference. T1 was evaluated with ROI's in mid-lateral and -medial condyle slices.

## Results

The calculated FA for the three different T1 phantoms decreases rapidly at the outer slices as compared to the central slice, where the FA closely resembles the nominal flip angle value (Fig. 2). If this variation is not taken into account (i.e. using a constant FA correction) the T1 calculation fails at the outer slices with large deviation from the expected T1 value (fig. 3). If local FA correction is used instead, a stable T1 is obtained in all slices (Fig. 3). For in vivo data in off center 3D slices (ROI drawn in slices 6-10, and 22-24 for the respective subjects), the constant FA correction obviously fails in restoring the T1 obtained by reference IR measurements (Fig. 4). If instead the calculated FA slice profile from the phantom measurements is used for correction, the 3D data better resembles the reference values (fig. 4).

Fig. 2

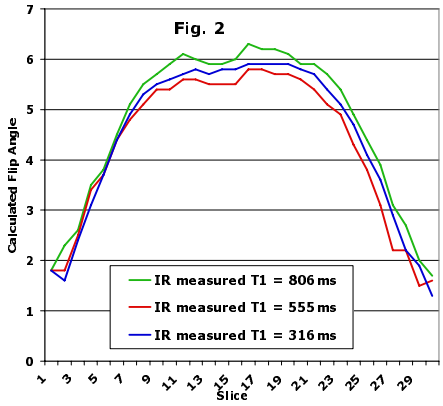



Fig. 3

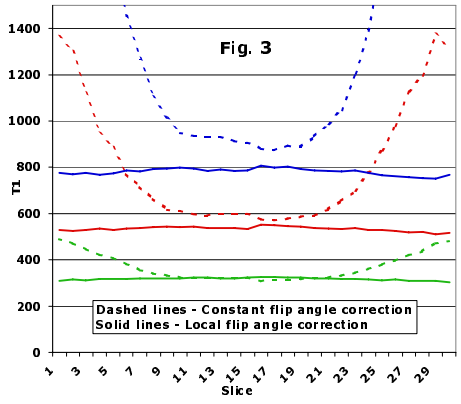
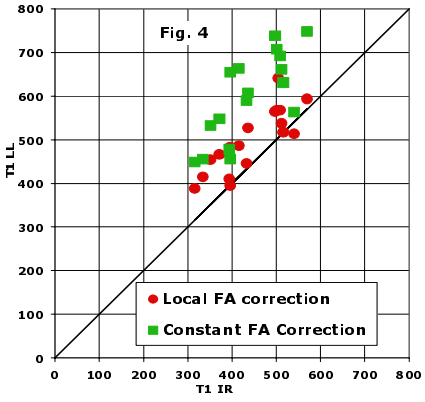



Fig. 4




## Discussion and conclusions

A constant FA correction is not enough for calculation of correct T1 values from 3D LL data if one wants to make use of the full 3D volume. The method presented here for local correction of T1 data better restores the expected T1 value in outer slices of a 3D volume. From Eq. 2-3 a T1 is obtained directly, which gives a true pixel-wise local correction. This T1 calculation is however more noise sensitive, and in the in vivo case here, with high-resolution, low-SNR data, the calculated FA's from the phantom measurements was instead more suitable to use for T1 correction. For 3D-dGEMRIC data with higher SNR (e.g. obtained at 3T and/or with multi channel coils) the directly obtained T1 might become suitable also for in vivo pixel-wise T1 calculations.

## References

1. Kimelman et al, Inv. Radiol. 41:198-203 (2006)