Measurement of R1 Dynamics using a 3D FLASH Variable Flip Angle Sliding Window Technique

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Introduction

Physiological parameters such as vessel permeability, perfusion and relative blood volume can be quantified in dynamic contrast agent studies. To calculate these parameters, dynamic MR signal intensities are first converted into relaxation rates R1 that are often assumed to be linearly correlated with contrast agent concentration. Unfortunately, R1 can often not be measured directly in dynamic studies, as R1 measurement times are much longer than the typical time scale of the contrast agent bolus passage. To increase the reconstructed temporal resolution in 3D R1 measurements, in this work we combine a variable flip angle acquisition scheme with a sliding window R1 calculation.

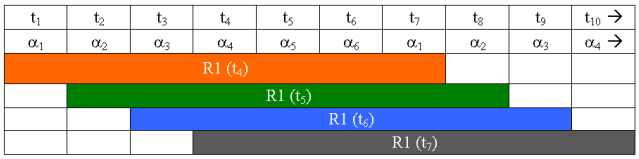

Fig.1: Schematic of the sliding window reconstruction: One R1 value is calculated by a fit of seven different signal intensities into a model assuming a linear variation of R1 with time.

Materials and Methods

To measure R1 as a function of time, a series of 6 spoiled gradient echo (FLASH) images with different excitation flip angles α_i is acquired repeatedly before, during and after contrast agent infusion. For R1 calculation, the FLASH signal equation is rearranged into a linear form

$$\frac{S_i}{\sin\alpha_i} = e^{-R1\cdot TR}\cdot\frac{S_i}{\tan\alpha_i} + e^{-R2^*\cdot TE}\rho(1-e^{-R1\cdot TR}) \qquad (1)$$

$$y = m \cdot x + b$$

and R1 is extracted from the slope m as R1 = - ln(m)/TR [1]. The individual measurement times of the 3D FLASH data sets typically last for several seconds. Therefore, R1 might change over the acquisition time of the 6 FLASH data sets, and the R1 calculation in Eq. (1) can only be considered as a zero-order approximation. To improve the precision, a first-order approximation was used in combination with a non-linear least-squares fit which fits the signal intensities to a model assuming a linear variation of R1 with time. To increase the stability of the fit, 7 consecutive data sets were used. For the fitting procedure a sliding window technique was applied that replaced only one data set for each new fit. The sliding window reconstruction allows reconstructing R1 maps with a temporal resolution that equals the acquisition time of a single 3D data set (Fig. 1).

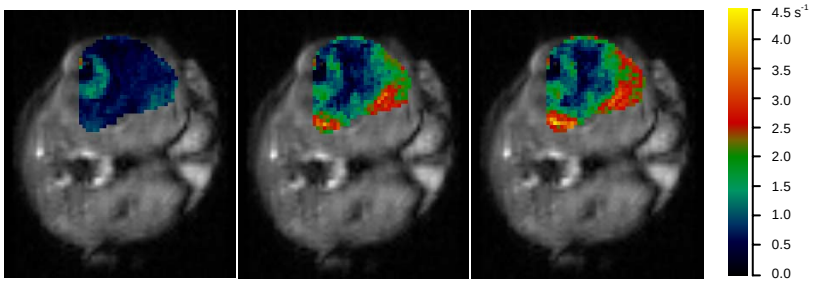

Fig. 2: Single slice of a 3D FLASH data set of a tumor-bearing mouse with overlaid R1 maps before (left), 1 min (center) and 7 min (right) after contrast agent injection.

Simulations and Optimization

To determine the optimal set of flip angles a numerical simulation was carried out for all possible combinations of flip angles between 5° and 85° in steps of 5°. Noise was added to the simulated data assuming an SNR of 100. The optimal flip angle combination was determined by minimizing the relative error in R1 for all R1 values of interest between 25.0 – 12.5 s^{-1} and 1.0 – 0.8 s^{-1}. Furthermore, in simulations the influence of noise, B1 inhomogeneity, and tissue heterogeneity were investigated.

Animal Imaging Protocol

R1 measurements were carried out in tumor-bearing mice on a clinical 1.5 T MR system (Siemens Symphony Quantum, Erlangen, Germany) using a home-built small animal Tx/Rx coil. To assess the R1 changes a 3D FLASH pulse sequence was used with the following parameters: TR / TE / FOV / matrix / partition thickness = 7.21 ms / 2.58 ms / 50×25 mm² / 128×64×30 / 3 mm. With these parameters, the imaging time per volume amounted to 10 s. Before, during and up to 10 min after contrast agent injection a series of 6 3D data sets were sampled with different flip angles.

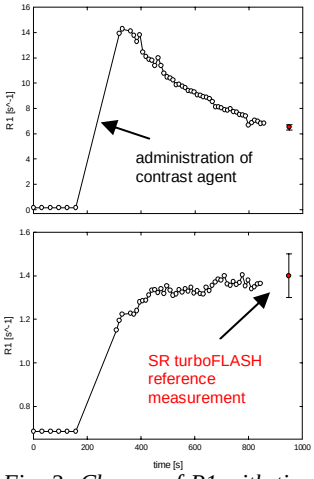

Fig. 3: Change of R1 with time in tumor tissue (bottom) and the vena cava (top) of a mouse after injection of contrast agent.

Results and Discussion

The flip angle optimization yielded a set of flip angles of α_i = 5°, 15°, 20°, 25°, 30°, and 85°. The simulations showed that a B1 inhomogeneity (i.e. a systematic error in the flip angle calibration) leads to characteristic artifacts in the R1 time-courses. In the animal experiments R1 maps show a heterogeneous increase in R1 in the tumor (Fig. 2). The R1 time courses in the tumor and the vena cava show the decrease of contrast agent concentration in blood and the slow uptake in tumor tissue (Fig. 3). R1 data measured at 950 s with a saturation recovery method [2] are in excellent agreement with the proposed R1 measurement technique. The reconstructed temporal resolution is 10 s, however, data from 70 sec-long acquisitions are used to compute one R1 value. Furthermore, image data acquired directly before and after the administration of contrast agent should not be combined as the linear approximation does not account for very rapid signal changes. To conclude, our method permits the direct monitoring of a time-varying relaxation rate R1 in a whole 3D volume with a temporal resolution of 10 s.

Acknowledgment

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References

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