PERFUSION IN MURINE MYOCARDIUM: A RETROSPECTIVELY TRIGGERED LOOK-LOCKER ARTERIAL SPIN LABELING SEQUENCE USING MODEL BASED RECONSTRUCTION

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Introduction:

A retrospectively triggered Look-Locker Arterial Spin Labeling (ASL) sequence for robust quantification of perfusion in murine myocardium is proposed. The method is based on T_1 mapping after slice selective and global inversion using an Inversion Recovery Snapshot Flash (IRSF) sequence [1,2]. Retrospective triggering yields several advantages. The continuous acquisition of data strictly maintains the Look-Locker condition without the need for additional dummy pulses used in the original prospectively triggered Look-Locker sequence [2,3]. This allows implementation of the sequence on almost any MRI system without requiring the hardware ability to switch dynamically between acquisition and dummy pulses on trigger input. Furthermore, keeping the strict Look Locker condition ensures improved robustness and quality of T_1 fits. In addition, analyzing the trigger data retrospectively enables the use of advanced algorithms to increase the robustness of the triggering and respiratory gating.

Look-Locker ASL sequences for perfusion measurement rely on averaging to achieve sufficient SNR for quantification. However, this introduces additional errors as the data to be averaged may belong to different inversion times due to variations in heart and respiratory rate. The averaging problem is addressed by using a random Cartesian sampling scheme in combination with Principal Component Analysis (PCA) interpolation techniques [4,5].

Methods

All experimental work was carried out on a 7 T small animal system (Bruker BioSpin, Germany) using a 72 mm quadrature birdcage for excitation and a 29 mm 4-channel hole slotted receiver array to attain high SNR [6]. The animals used in this work are NMRI mice (Charles River Laboratories) anesthetized by isoflourane.

An IRSF sequence using Cartesian random sampling in phase direction was implemented. The acquisition was weighted by a Hann function. A first order motion compensation was applied for each gradient direction. The sequence parameters were: Matrix size of 68 x 58 for a 30 x 20 mm² field of view. The imaging slice thickness was 2 mm, the inversion slice thickness was 6 mm in width. An asymmetric readout with 25 % echo position was used. With a repetition time of 3.3 ms 3000 readouts can be acquired during a time frame of 9.9 s which is followed by a 15 s waiting period. The study protocol for one perfusion map consists of 32 global and 32 slice selective inversions. The cardiac and respiratory information is monitored and recorded by a home built electrocardiogram (ECG) trigger unit using ECG-leads attached to the fore-paws and a pressure transducer connected to a balloon which was placed underneath the mouse. Additionally, a trigger signal from the MRI system is recorded, marking the position of each readout pulse. The inversion pulses are triggered to the diastole.

Each readout is assigned a relative position in the heart phase. With this information the data used for reconstruction is selected using a fixed window in the heart phase or KWIC-like filters centered on the end diastole. The undersampling in the k-t-space is eliminated using interpolation along the time direction for each k-space point. The interpolation scheme is based on the framework of partially separable functions using principal components [4,5]. The principal components are attained from a training dataset constructed for the specific measurement parameters [5]. The use of this protocol results in 3000 fully sampled frames for each the global and selective inversion. These frames can then be fitted using standard methods to obtain T_1-Maps after global and selective inversions. In addition to animal experiments the reconstruction algorithms were validated in numerical simulations.
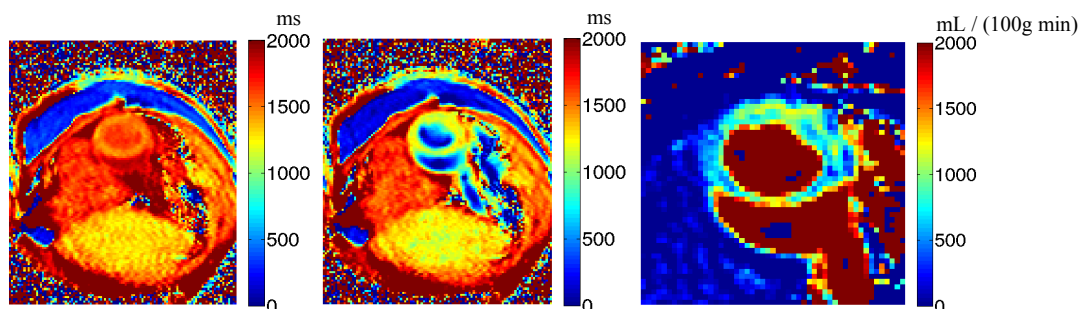
1) T_1 Global [ms] **2)** T_1 selective [ms] **3)** Corresponding perfusion maps [mL / (100g min)]

Result and Discussion

Exemplary T_1 maps are shown in figure 1 (global) and figure 2 (selective), each from 32 inversions with retrospective triggering using PCA reconstruction with five principal components and a fixed window selecting 50 % of the heart rate. The corresponding perfusion map is shown in figure 3.

In this work quantitative T_1 and perfusion maps of murine myocardium were acquired. These maps were in good agreement with literature values [3]. The problem of averaging k-space points with different inversion times was bypassed using PCA. The perfusion maps may be further improved by application of filters [7,8]. A more in detail analysis of the parametric reconstruction is required.

Conclusion

Retrospective IRSF appears to be a robust alternative to its prospectively triggered counterpart for quantification of myocardial perfusion. Its reduced hardware requirements should allow it to be implemented on a broad range of preclinical scanners.

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