A Model-based Reconstruction Technique for Look-Locker FAIR Gradient Echo ASL Perfusion Data

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Purpose: Arterial Spin Labeling (ASL) provides quantitative measurements of tissue blood flow and has been used for quantification of myocardial perfusion in small animals. The most common methodological approach is a FAIR preparation combined with an ECG-gated Look-Locker gradient echo (LLFAIRGE) acquisition scheme [1-4]. The fast heart rates of rodents enable a high sampling rate of the T_1 relaxation curve but limit the acquisition to only one phase-encoding (PE) per inversion (IR) pulse if blurring by cardiac motion is to be avoided. The IR pulse needs to be repeated for each PE step leading to long scan times of about 20-25 min. In the initial implementation [2], inversion times (TI) are obtained as an average over the measured TI of all PE steps. A long scan time associated with variable heart rates can cause inconsistencies in the TI used for the T_1 fitting process which has been addressed in [4]. In this work, an adjustment of the model-based MAP reconstruction technique presented in [5] to a LLFAIRGE acquisition (IR-MAP) was developed featuring two major improvements: (i) the ability to take into account any variations of TI in the reconstruction and (ii) the ability to apply k-space undersampling for eventually reducing the total acquisition time. This technique paves the way for quantitative myocardial blood flow mapping on small animals from prospectively undersampled datasets, promising shorter scan times in future studies.

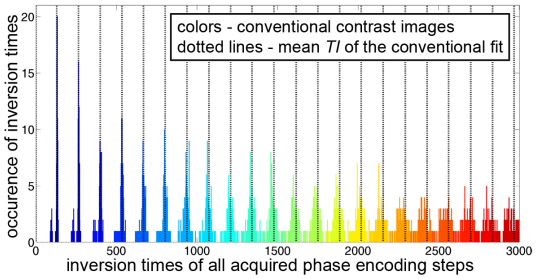

Fig. 1*: Partial histogram of all inversion times < 3 s.*

Methods: In the course of an LLFAIRGE experiment, varying heart rates as well as missed ECG-triggers usually lead to a variation in the TI of every PE step growing with the temporal distance to the inversion pulse (see histogram in Fig. 1). Thus, the use of averaged TI (dotted lines in Fig. 1) is a source of error in the T_1 fit and therefore in the measured perfusion values. To improve the precision of the fit, the exact time points of every acquired PE step after the IR pulse were recorded during the experiment. Based on this time log, all PE steps were assigned to bins of a temporal resolution of 20 ms. The result was a set of highly undersampled k-spaces. For reconstruction, the IR-MAP algorithm (based on the MAP algorithm presented in [5]) was applied to these undersampled k-spaces in order to reconstruct one fully sampled k-space for each of the temporal bins. The mono-exponential function

$$M(TI) = M_0^* - (M_0 + M_0^*) \cdot \exp(-TI/T_1^*) \qquad (1)$$

was used to model the signal after the IR pulse (M_0: equilibrium magnetization, T_1^*: apparent relaxation time, M_0^*: steady-state magnetization in presence of continuous RF excitation [6]). The reconstruction scheme of the IR-MAP algorithm is shown in Fig. 2. For initialization, all *undersampled k-spaces* were Fourier transformed into image space. Subsequently, a pixel-wise least-squares fit of Eq. 1 was applied, resulting in a set of parameters $M_0(x,y)$, $M_0^*(x,y)$ and $T_1^*(x,y)$ for every pixel (x,y). Using these parameters, model images were calculated for all TI (*model*). In order to ensure data consistency, the initial k-spaces were finally substituted into the corresponding model k-spaces (*consistent model*). The consistent model was then passed on to the subsequent iteration. A fixed number of 100 iterations was used as termination criterion throughout this work.

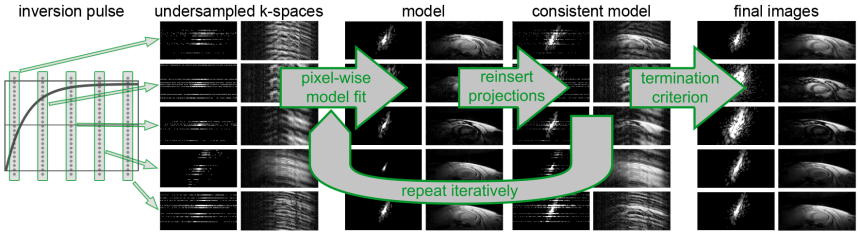

Fig. 2: *Basic IR-MAP reconstruction scheme.*

For proof of concept, an experiment was performed with a healthy C57Bl6J mouse on a Bruker 4.7T animal scanner. As described in [2], every repetition started with an ECG- and respiratory-gated IR pulse, followed by the acquisition of 55 ECG-gated gradient echoes. This was repeated for all 64 PE steps with an additional repetition delay of 3 s. Post-processing was performed in three different ways: (A) the complete dataset including all 55 acquired images of the relaxation process was used for slice-selective (SS) and global (GL) measurement, (B) all images visibly affected by respiratory movement were excluded, (C) the binning process resulted in sets of 357 highly undersampled k-spaces for both the SS and the GL measurement (5 examples for the GL case are given in Fig. 2). Applying the IR-MAP algorithm resulted in 357 complete model images and a set of parameters M_0, M_0^* and T_1^* for every pixel. There parameters were used with the mean values of TI (dotted lines in Fig. 1) to calculate a new model dataset which was used for post-processing. Perfusion maps were calculated as described in [2].

Results: Figure 3 shows three perfusions maps of the in-vivo measurement obtained by the different post-processing techniques (A-C) as described above. Table 1 lists the corresponding perfusion values obtained from different myocardial regions (anterior and lateral) as well as the entire myocardium and the chest muscle. Good concordance was found between myocardial perfusion assessed after excluding images affected by respiratory movements (B) and the model-based reconstruction (C).

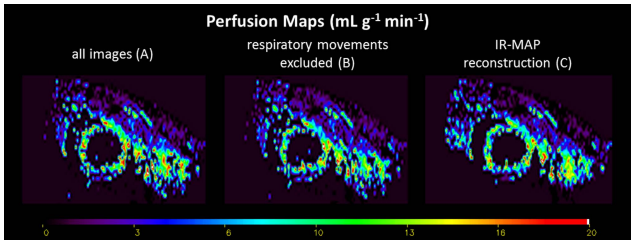

Fig. 2: *Perfusion maps.*

region	conventional reconstruction		IR-MAP reconstruction (C)
	all images (A)	respiration movement excluded (B)	
anterior	10.4 ± 5.2	8.6 ± 5.5	8.0 ± 5.9
lateral	12.0 ± 4.3	7.4 ± 5.5	7.5 ± 6.2
global myocardium	10.3 ± 5.0	8.1 ± 5.8	8.1 ± 5.8
chest muscle	0.3 ± 1.5	0.3 ± 1.5	0.4 ± 1.7

Table 1: *Perfusion values.*

Discussion / Conclusion: An extension of the MAP algorithm for the model-based reconstruction of LLFAIRGE datasets is presented. The IR-MAP algorithm can perform parameter mapping from highly undersampled k-spaces acquired after IR magnetization preparation. In conjunction with a time log of all acquired PE steps, it allows taking into account any variations in TI, which can be caused by variable heart rates or imperfect R-wave detection. Sorting the acquired data more accurately leads to an excellent temporal resolution smaller than 20 ms in TI for the model-based T_1 fit. Although the three perfusion maps seem visually similar, perfusion is overestimated if images affected by respiratory movements are not excluded from the T_1 fit (A vs. B). By using the constraint of a mono-exponential relaxation, the IR-MAP algorithm automatically suppresses respiratory artefacts. Additionally, a time log of the respiratory movement of the animals could be included in the post-processing to further decrease respiratory artefacts. Finally, the new technique holds the potential for a quantification of myocardial perfusion from further undersampled k-spaces, promising shorter scan times in the future.

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References: [1] Belle, J Magn Reson 8:1240-5 (1998), [2] Kober, Magn Reson Med 51:62-7 (2004), [3] Streif, Magn Reson Med 53:584-92 (2005), [4] Vandsburger, Magn Reson Med 63:648-57 (2010), [5] Tran-Gia, Proc ISMRM 20:359 (2012), [6] Deichmann, J Magn Reson 96:608-612 (1992)