Fast time-resolved cine sequence using temporal regularization for small animal cardiac imaging on a clinical 3T scanner

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Introduction:

Small animal cardiac imaging is an important research topic for biology and medicine [1]. Functional imaging on clinical scanners allows effective contribution to translational medicine. However, hardware limitations such as gradient slew rate or amplitude prevent obtention of the necessary space and time resolution [2] that can be easily reached with dedicated instrumentation. Here, we propose a novel method to improve time resolution for cardiac mouse imaging, reaching parameters comparable to the ones obtained with dedicated scanners in the context of cardiac stress study (TR = 8.6 ms [3]). In particular, we combine two fast repetitions with temporal regularization based on l1-minimization in the Fourier domain. Temporal regularization is a necessary step since the combination of two repetitions taken at different instants of the cardiac cycle introduces artifacts between each acquisition that need to be compensated.

Methods:

Experiments were performed on a clinical Siemens 3T scanner (magnetom TIM Trio) with a dedicated mouse coil. Maximal gradient amplitude and slew rate are 26 mT/m and 170 T/(m·s), respectively. The reference sequence is a segmented turbo flash cine adapted to small animal requirements; parameters were as follows: FOV 111 mm, TR/TE=13/6.2 ms, in-plane resolution 257 µm^2, slice thickness 1 mm, 2 averages, typical acquisition time is 2 min. Sequences are ECG and respiratory gated and cine acquisition is done on 2 R-R cycles. The TR (13 ms) is the minimal time resolution achieved considering the spatial resolution since one segment is acquired at a time for each cardiac cycle. The proposed sequence has exactly the same parameters but without averages. However, the sequence is repeated twice, where the second time a trigger delay equal to the half of TR value is added. By combining both repetitions, the effective TR is reduced to half of the hardware TR, in our case 6.5 ms, as shown by figure 1, while keeping the same acquisition time. The main difficulty encountered by combining the two series is a flickering effect that is not in phase with repetitions and mainly due to the different flow artifacts of both series. Since no averaging is performed, resulting images are also more prone to noise. To reduce these contributions we take advantage of the periodicity of the cardiac cycle by performing l1-minimization in the temporal Fourier domain for the pixels' timecourses; this can be done efficiently by soft thresholding of Fourier coefficients. To validate our method, TR was artificially lengthened to 26 ms and the proposed sequence was used to reach 13 ms temporal resolution and compared with the reference sequence. The sequence was then applied to acquire fast time-resolved cine in mouse.

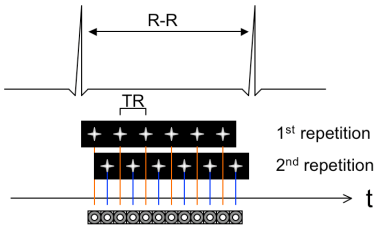

Figure 1 : Schematic representation of the proposed sequence.

Results and discussion:

Experiments were performed on healthy and pathological mice (n=4). Figure 2 shows results for mouse with a permanent ligation of the LAD artery 24h after surgery. For visualization purposes, we show a cropping around the heart of only four phases of the cardiac cycle. The observed differences between the proposed and the reference method are due to different TR, flow artifacts, as well as number of averages. Temporal regularization clearly reduces the artifacts that mainly appear as flickering artifacts. This operation took only 2 sec for a 432x432x20 stack of images in Matlab®. Figure 3 shows the data term for the validation experiment (i.e. $||I - I_{ref}||^2$ where I is the considered image and I_{ref} the reference) for each cardiac phase. Soft thresholding allows us to decrease the standard deviation of the dataterm by an average factor of 5 (range: 2 to 8 for n=4) and thus reduce the flickering. The visual improvement due to regularization is quite striking, as can be appreciated from the spatio-temporal cut in Fig. 2.

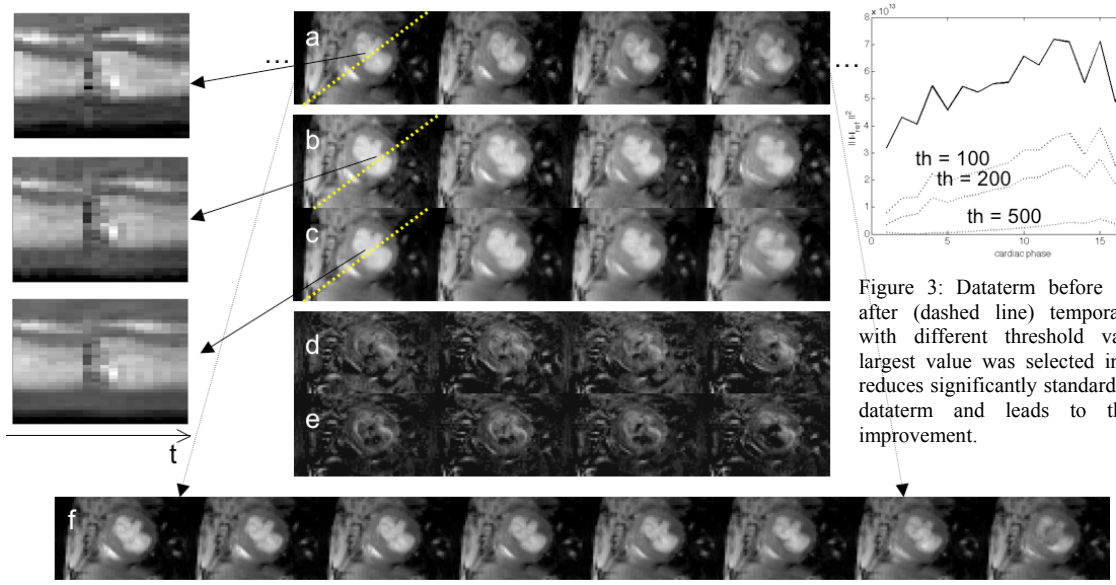

Figure 2: 4 out of the 20 cardiac phases for the reference sequence (TR 13ms, 2av, images are taken on 2RR cycles) (a), the proposed sequence (TR 26 ms, 1 av, 2 repetitions) (b), and the filtered proposed sequence (c). Left: time course of the yellow profile for (a), (b) and (c). (d) and (e) are the differences between (b) and (c) respectively and the reference sequence (a). (f) is the regularized proposed sequence (TR 13 ms, 1av, 2 repetitions) with effective TR 6.5 ms.

Figure 3: Dataterm before (solid line) and after (dashed line) temporal regularization with different threshold values (th). The largest value was selected in this case as it reduces significantly standard deviation of the dataterm and leads to the best visual improvement.

Conclusion:

Our results demonstrate that the proposed method can achieve an effective TR corresponding to half of the hardware TR, in our case 6.5 ms. The main advantage of the method is that it deploys the classical cine sequence as a basis and works directly in the image domain; i.e., it does not prevent the use of parallel imaging acceleration approaches such as SENSE or GRAPPA that are commonly used in clinical environment to further reduce acquisition time. Temporal regularization deals effectively with the flickering artifact generated by combining both repetitions.

References: [1] Epstein NMR Biomed. 20 : 238-255 (2007) ; [2] Steser et al. JMRI 12(3) :430-438 (2000) ;[3] Wiesmann et al. Circ. Res. 88 :563-569 (2001) ;