Materials and Methods
From 03/2009 to 09/2009, 50 patients underwent digital Full Field Mammography (detector: resolution 70μm) (Fa. Siemens) and, after diagnosis and preoperative wire localization, digital Full Field Mammography (detector: resolution 50μm) (Fa. FujiFilm) with the same exposure parameters. Five investigators retrospectively determined the diagnosis after the operation from randomly distributed mediolateral views (monitor reading). These results were correlated with the final histology.
Results
The accuracy of the digital Full Field Mammography (detector 70μm) and the digital Full Field Mammography (detector 50μm) for microcalcifications (n = 50) was 73.2% resp. 77.8%. The difference in the results was not significant (p<.001).
Conclusion
Our findings indicate an equivalence of the both digital Full Field Mammography systems with the trend towards a superiority of the new constructed detector (Fa. FujiFilm).

Fast time-resolved cardiac functional imaging in mouse on a clinical 3T MR scanner using l1-minimization for reconstruction

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Keywords MRI · Cardiac · Mouse · Function

Introduction
Small animal cardiac magnetic resonance imaging is an important research topic for biology and medicine. 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 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 to 10 ms). 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,

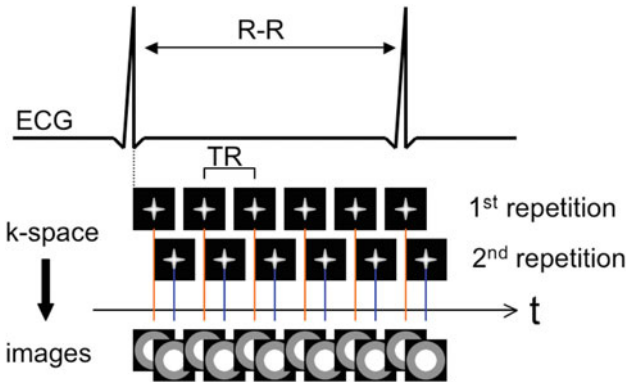

Fig. 1 Schematic representation of the proposed sequence

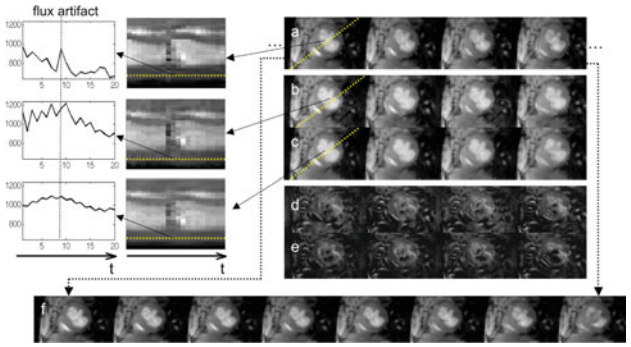

Fig. 2 4 out of the 20 cardiac phases for the reference sequence (TR 13ms, 2av, images are taken on 2RR cycles) (a), the proposed sequence (TR 26 ms, 1 av, 2 repetitions) (b), and the filtered proposed sequence (c). Left: time course of the yellow profile for (a), (b) and (c) as well as time course for 1 line of this profile. (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

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' time courses; 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.
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 432 × 432 × 20 stack of images in Matlab®. The data term for the validation experiment (i.e. $\|I - I_{ref}\|^2$ where I is the considered image and I_{ref} the reference) was computed for each cardiac phase in

order to evaluate the performance of the regularization. Soft thresholding allows us to decrease the standard deviation of the data term 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.

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.

An efficient composing method for Dixon sequence whole-body-MRI

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Keywords Whole-body MRI · Dixon sequence · Image enhancement · Composing · Adipose tissue

Purpose

Whole-body magnetic resonance imaging (MRI) in combination with an automatic moving table is a novel technique of recent years and improves the clinical workflow by being capable of acquiring images of a large field of view in short time. [1]

The Dixon sequence is a custom-built MRI protocol for the analysis of adipose tissue and separates fat from water tissue, utilizing the different resonance frequencies protons bound in fat and water [2]. Due to the high computational effort, the integrated method of the MRI panel aborts during the composing step and only individual sections are saved, which makes further data processing necessary. To date, just a few scientific papers have been published that deal with the automatic generation of whole-body data [3]. The main problem of creating a whole-body data from the individual sections comes from field inhomogeneities of the MRI, which becomes more pronounced closer to the boundaries of the image. Furthermore, the inhomogeneous magnetic field brings forth a phase error and generates mismatches between the fat and water sequence making precise segmentation impossible. In general, the unwrapping algorithm based on Region Growing compensates the artifact automatically [2]. However, this correction is frequently unsuccessful in the region of the legs and the output image is defective (see Fig. 1(a) and (d)). Until now there is no scientific work which corrects this distinctive failure in a post-process.

Wachinger and Glocker proposed a deformable mosaicing approach to generate high-resolution whole body images [3]. Still, the computation time for three composing steps is approximately 25 minutes, which is due to simultaneous registration. In this paper we introduce a fast and automatic composing method for generating artifact-free whole-body MRI of multiple image sections in a post-processing step. The new method improves image quality by normalization and interpolation of the intensity between each section. Furthermore, artifacts of the Dixon sequence are automatically compensated by correcting the phase error using differential images. According to the results, the proposed method is suitable to create artifact-free whole-body MRI images with smoothed transition between different sections.

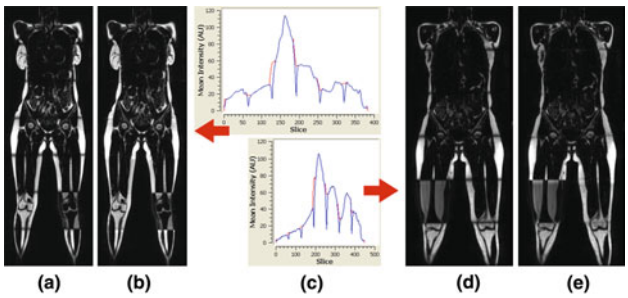

Fig. 1 Generation of whole body images with smoothed transition between different section. (**a**) Original, (**b**) result, (**c**) intensity distribution, (**d**) original, (**e**) result

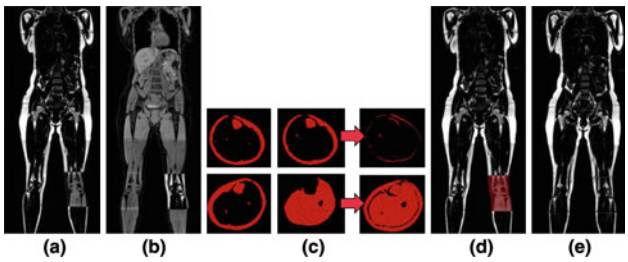

Fig. 2 Correction of the Dixon artifact in the lower extrimities. (**a**) Fat image, (**b**) water image, (**c**) differential image, top: right leg, (**d**) result, bottom: left leg with an artifact

Methods

The presented methods are evaluated on data of 11 subjects. The Dixon sequence automatically generates four datasets per subject in a single scan (in-phase, opposed phase, fat and water data), so the evaluation of generating whole-body data can be made on 44 data sets. The resolution of the image segments is 384 × 288 × 64 voxels, with a spacing of 1.3 × 1.3 × 3mm. A full data set consists of six to seven segments. The images were taken with an Avanto MRI of Siemens. The implementation is based on the Medical Imaging and Interaction Toolkit (MITK) [4].

Generation of whole-body images

In our approach we use non-overlapping MRI image sections. The number of sections is arbitrary. We assume no body movement between each section as the patient's position is stabilized during scanning by multiple phased array coils. In the first step, we compose all sections by loading them in the correct order and adding them up to a whole-body image (Fig. 1 (a) and (d)). For correction of low intensity distortion at the upper and lower border we implement a normalization algorithm. It increases the intensity by a factor, calculated from the mean and maximum intensities of the distorted slices and the slices above and below (reference region). Acquisition artifacts are reduced by interpolation of distorted slices (first and last slice of a section) with slices above and below them. In summary, the methods generate a whole-body image with smoothed transition between different sections (Fig. 1 (b) and (e)).

Correction of the Dixon artifact

In the first step, the right and left leg are segmented and masked separately. This separate consideration is necessary because the artifact generally occurs only in one leg (see Fig. 1(a) and (d)). To determine which section contains an artifact, a differential image between the adjacent slices of the segments is generated and the volume of the resulting image calculated. This procedure is carried out in any distinct combination between the water (Fig. 2 (b)) and fat image (Fig. 2 (a)). If the volume of the differential image is small, the adjacent image slices are similar and belong to a common sequence