Faster acquisition of MR images with Double Quantum Filtering by regularization

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INTRODUCTION

MRI with Double Quantum Filter (DQF) gives a direct access to water linked to ordered macromolecules, but requires a large number of repetitions of the acquisition scheme (16 up to 64 steps), with different phases of the RF pulses in the DQ filter, to select the double-quantum signal and to suppress unwanted single-quantum ones[1]. However reconstruction of MR images from a partial knowledge of the k-space is more and more commonly used especially in dynamic MR applications and in parallel MRI[2-3]. We examined the possibility to reduce the number of phase encoding lines kept in the data for each step of the DQ filter, employing a regularization method to compute the image.

MATERIALS AND METHODS

MRI in a SE mode (single-slice) with DQF-MT was implemented on a home-developed 4.7 T scanner controlled by a Tecmag sequencer, with TE/TR=1 ms/1 s and a slice thickness of 5 mm (FOV 28 mm). The parameters in the DQF-MT sequence were τ (creation time)=26 μs and tLM (magnetization transfer time) = 100 ms. All RF pulses were hard pulses (90° duration of 10 μs) except the last 90° which was the slice-selective pulse (duration of 320 μs). The full k-space data set corresponded to a matrix 128*128, with 16 different steps and 2 repetitions. Samples of bovine Achilles tendon and bovine muscle obtained from the local butcher (a few days after death) were separately wrapped in a plastic foil and put in a glass tube. The sample fibers were aligned with the main magnetic field. Typical signal to noise for images computed from the full k-space at each step was around 70 for muscle and 48 for tendon.

Image reconstruction from a partial knowledge of k-space was done for each step in the phase cycle by minimizing an energy function, sum of the squared differences between data in the k-space and their estimated values, and two regularization terms, each with its own weighting factor λ_C and λ_Z: the first term was designed to preserve contour information, and the second term to draw towards low gray-values the background region, both terms being introduced in the image domain. For both regularization terms, an appropriate convex function (Huber function) was used, reflecting signal variation within neighbor pixels in the image, each with an appropriate threshold (resp. T_C and T_Z). Optimization was achieved by using a pseudo-conjugate gradient descent method. The computation time of one image was about 10 s.

RESULTS AND DISCUSSION

Images reconstructed with different choices of a reduced number of k_Y-lines (in the phase direction) were compared after normalization to 1, keeping only pixels from the sample ROI. The comparison was done with the image computed by 2D FFT from the full k-space. The criterion was the sums of the differences squared, Chi2. First a choice of the 4 hyperparameters (λ_C, λ_Z, T_C, T_Z) for which Chi2 was about 4% was determined, keeping only the 40 central lines in k-space (Fig 1); then the same 4 hyperparameters were used for different choices of the k_Y-lines kept, and the choice giving the lower Chi2 was kept (Fig 2), it corresponded to 22 lines non symmetrically distributed around the center, in addition to 19 central lines. Finally, with the latter choice of k_Y-lines kept, images were computed for a range of possible values for the 4 hyperparameters (76,176 different combinations). For about 20,000 combinations, Chi2 was found lower than 0.02. The values corresponding to the maximum occurrence in their respective histograms were then kept: λ_C=0.4, λ_Z=0.1, T_C=0.8, T_Z=0.1. Then images were separately computed for each step in the phase cycle with these parameters, giving each Chi2 around 0.02. Fig 3 shows the DQF-MT image of the sample from the full k-space data, and after regularization. Regularization caused a significant narrowing of the background noise histogram and loss of some contour details in the images, but signal levels in different ROIs in the image (tendon, muscle, fiber) were in excellent quantitative agreement within better than 0.8%.

CONCLUSION

The acquisition time in MRI with DQ filter could be reduced by 2/3 without any significant loss of contrast and minor loss of contrast on contours. The choice of the hyperparameters should be carefully done depending on available SNR and image contrast. In future work, we intend to use other k-space filling methods (radial, spiral) which should give access to even faster acquisition for DQF applications
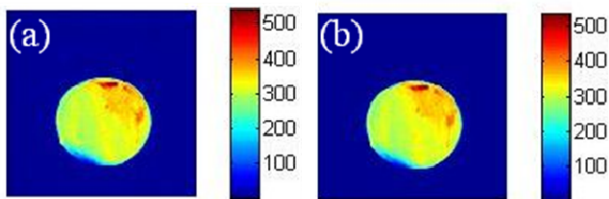

Fig 1: image of a tendon-muscle specimen, one step in the DQF-MT phase cycle: (a) full k-space kept, (b) regularized image computed from the 40 central k_Y-space lines with λ_C=1.6, λ_Z=0.6, T_C=0.4, T_Z=0.4.
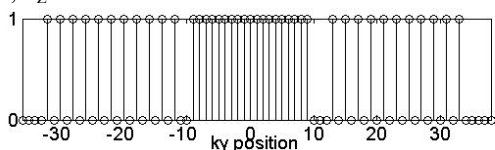

Fig 2 : k_Y-lines kept before regularization giving Chi2=0.019 as compared to full k-space, with λ_C=1.6, λ_Z=0.6, T_C=0.4, T_Z=0.4.
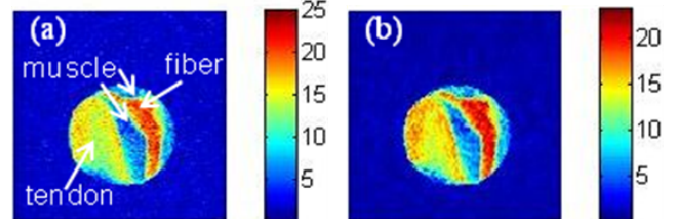

Fig 3: image with DQF-MT of the same sample as in Fig 1: (a) full k-space kept, (b) regularized image computed from 41 k_Y-space lines distributed as shown in Fig 2 with λ_C=0.4, λ_Z=0.1, T_C=0.8, T_Z=0.1. With DQF-MT, signal remains visible mainly in tendon and in muscle fibers.

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