

Water Fat Separation with Undersampled TSE BLADE Based on Three Point Dixon

Q. He^{1,2}, D. Weng^{1,3}, X. Zhou^{1,2}, M. Beckmann¹, and C. Ni^{1,2}

¹Siemens Mindit Magnetic Resonance Co. Ltd., Shenzhen, Guangdong, China, People's Republic of, ²Life Science and Technology School, Tongji University, Shanghai, China, People's Republic of, ³Beijing MRI Center for Brain Research, Institute of Biophysics, Chinese Academy of Sciences, Beijing, China, People's Republic of

Introduction

In the three-point Dixon water fat separation method, one in-phase echo and two out-of-phase echoes are sampled in Cartesian k-space trajectory conventionally [1][2]. The Cartesian sampling is sensitive to motions, such as from pulsation and flow, which cause artifacts degrading the image quality. To address this problem, a non Cartesian sampling method, TSE BLADE three-point Dixon, is proposed in another abstract. This technique acquires one in-phase image and two out-of-phase images with two consecutive TSE BLADE sequences. Before the computation of the water-fat separation, the images are reconstructed by regridding methods traditionally [3], which require a high enough sampling rate and thus long scanning time to overcome streaking artifacts. The present work demonstrates that the integration of a total variation (TV) regularized iterative reconstruction of each image and water-fat separation calculation with undersampled BLADE k-space trajectory will reduce the scanning time, suppress streaking artifacts while maintaining a high quality of water-fat separation. Meanwhile, the proposed reconstruction method will keep the benefits of BLADE sampling, which is much less sensitive to motions.

Methods

Sequence: A normal TSE BLADE sequence (Fig. 1A) is used to acquire the in-phase image, a double echo TSE BLADE sequence (Fig. 1B) with equal time shift from spin echo time is designed to generate the two out-of-phase images. This design ensures that gradient delays and eddy current effects will have the same impact on all acquired images. The reconstruction consists of a 2D TV regularized iterative reconstruction to work out in-phase and out-of-phase images, which is shown in the optimization problem by means of equation (1) [4][5], and followed by a water-fat separation calculation based on phase unwrapping [1]. Fig. 2 indicates the BLADE k-space trajectories with different coverage of 100% (23 blades), 82.6% (19 blades, undersampling rate=1/0.826=1.2) and 52.2% (12 blades, undersampling rate=1.9) with 18 phase encoding lines on each blade, respectively.

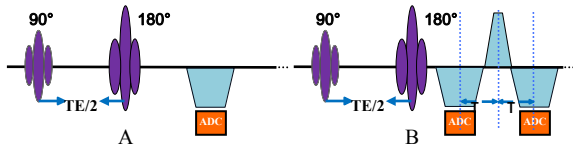


Fig. 1: In-phase and out-of phase sequence diagram.

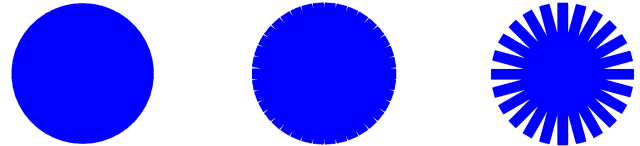


Fig. 2: BLADE trajectories with different undersampling rates.

$$f^* = \arg \min_f \left[\|NUFFT(f) - y\|_{L_2}^2 + \lambda TV(f) \right] \quad (1)$$

In equation (1), f is the reconstructed image; y represents the raw measurement data in k-space; $TV(\bullet)$ is the operator of total variation; $NUFFT(\bullet)$ is a non-uniform fast Fourier transformation operator, which is generated together with the system matrix according to the actual BLADE k-space trajectory [6]; and λ is the weighting for the TV term, which is set to 0.01 in this work.

Human Study at 1.5T: Volunteer knee images in the transverse plane were scanned on a Siemens MAGNETOM ESSENZA 1.5T scanner. The TSE BLADE Dixon acquisition parameters were: FOV=165mm×165mm, matrix size=256×256, TE=145ms, TR=4450ms, slice thickness=3.0mm, slice number=11, turbo factor=18, blade=12, coverage=52.2% (undersampling rate 1.9), total scanning time=113s (211s when coverage=100%). The parameters for the TSE Dixon sequence were: FOV=165mm×165mm, matrix size=256×256, TE=145ms, TR=4450ms, slice thickness=3.0mm, slice number=11, turbo factor=19. The parameters for the TSE sequence with spectral fat saturation measured (FatSat) for comparison were: FOV=165mm×165mm, matrix size=256×256, TE=142ms, TR=4450ms, slice thickness=3.0mm, turbo factor=19.

Evaluation: The water and fat images from the TSE BLADE Dixon sequence using a TV regularized iterative reconstruction are compared with regridding method reconstruction, respectively, with undersampling rate 1.9. For comparison, images acquired with a Cartesian sampling TSE Dixon sequence and a TSE sequence with FatSat are also shown in Fig. 3.

Results



Fig. 3: Water and Fat images acquired with different TSE based sequences. See text for details.

A comparison between the images reconstructed with the TV regularized iterative reconstruction and regridding reconstruction methods with undersampled TSE BLADE Dixon, TSE Dixon and TSE with FatSat is shown in Fig 3. The results show that water and fat images have been separated correctly with the undersampled TSE BLADE Dixon raw measurement data with TV regularized iterative method by comparing with the TSE Dixon method. The fat image reconstructed with regridding (Fig. 3B) shows obvious streaking artifact. In the Cartesian TSE Dixon fat image (Fig. 3C) pulsation artifacts are visible. Also the TSE image with FatSat (Fig. 3G) shows pulsation artifacts. In the water images, the structures are shown more clearly in the TV regularized iterative reconstruction than using the regridding method, and with comparable results as from the two other methods.

Discussion & Conclusion

A Dixon method based on the TSE BLADE sequence is shown to separate water and fat images correctly. It inherits the known benefits of the BLADE sequence, such as less sensitivity to artifacts caused by motions from pulsation, flow etc., and it has higher SNR due to the multiple sampling of the k-space center. By integration of the TV regularized iterative reconstruction with the Dixon water-fat separation algorithm, the scanning time can be reduced by undersampling while maintaining a robust water-fat separation, a good suppression of motion artifacts and suppression of streaking artifacts.

References

[1] Glover GH, *et al.* MRM, 18:371-83 (1991). [2] Scott B, *et al.* MRM, 54:636-44 (2005). [3] Pipe JP, *et al.* MRM, 42:963-969 (1999). [4] Block KT, *et al.* MRM 57: 1086-98 (2007). [5] Chang T-C, *et al.* Proc. ISMRM 14: 696 (2006). [6] Fessler JA, JMR 188: 191-5 (2007).