

Simultaneous T_1 , T_2 , Diffusion and Proton Density Quantification with MR Fingerprinting

Yun Jiang¹, Dan Ma¹, Katie Wright¹, Nicole Seiberlich¹, Vikas Gulani², and Mark A. Griswold^{1,2}

¹Department of Biomedical Engineering, Case Western Reserve University, Cleveland, OH, United States, ²Department of Radiology, Case Western Reserve University, Cleveland, OH, United States

Target audience: Those interested in developing novel methods in quantitative imaging.

Purpose: We present a method for simultaneous quantitative mapping of T_1 , T_2 , proton density, and diffusion within the MR Fingerprinting (MRF)¹ framework. The method is based on diffusion-weighted steady-state free precession (DW-SSFP) which has previously been suggested as a way to estimate the apparent diffusion coefficient (ADC)². However, the measurement of diffusion with SSFP is highly dependent on the relaxation parameters, thus requiring additional experiments to quantify T_1 and T_2 . MRF has been shown to be efficient in generating multiple quantitative maps by matching acquired transient-state signal to a pre-calculated dictionary. Here we demonstrate ADC quantitation along with the relaxation parameters with a single sequence, by acquiring the transient-state signals of a double-echo sequence.

Methods: Fig.1 shows a diagram of the diffusion-weighted double-echo pulse sequence with a spiral readout. Two signals (FID and echo) are formed within one repetition time. The FID is acquired with a variable density spiral-out trajectory, and the echo is acquired with a variable density spiral-in trajectory. The FID signal is more T_1 -weighted, and the echo signal is more T_2 -weighted, and has the potential to be made additionally sensitive to diffusion when diffusion gradients are applied. In order to increase the diffusion sensitivity of the sequence, a monopolar diffusion gradient can be inserted between the FID and the echo. In this work, we acquired both signals in each repetition with varying flip angles (Fig. 2a), repetition times (Fig. 2b), and diffusion gradient moments (Fig. 2c). The spiral trajectories for both FID and echo require 6 interleaves to fully sample the inner 10x10 region, and 48 interleaves to fully sample the outer 128x128 region of k-space. Undersampled double-echo MRF data were acquired with 6 spiral interleaves. A dictionary of the signal evolutions with a range of T_1 (50-3000 ms), T_2 (10-300 ms) and ADC ($0-3 \times 10^{-3} \text{ mm}^2/\text{s}$) was simulated using the extended phase graph algorithm³. We employed a template-matching algorithm to match the obtained signal evolution to the closest dictionary entry and thus extract the corresponding T_1 , T_2 , proton density and ADC values. This method was evaluated on a phantom of 5 cylindrical tubes constructed with varying concentrations of agarose, Gd-DPTA, and sucrose to yield compartments with different T_1 , T_2 and ADC values⁴. All studies were performed on a Siemens Magnetom Skyra 3T (Siemens AG Medical Solutions, Erlangen, Germany) with a 12 channel head receiver array. T_1 and T_2 values were measured by the balanced-SSFP MRF method¹ that is not sensitive to diffusion. Spin-echo, diffusion-weighted EPI sequences ($b=0, 500, 1000$ and 1500 s/mm^2 with TE of 86ms) were used to quantify ADC values.

Results and Discussion: Fig. 2d and Fig. 2e show the signal time courses of both the FID and the echo from one pixel of acquired signal and its matched dictionary entry. Fig. 3 shows the reconstructed T_1 , T_2 , ADC and M_0 maps from a double-echo MRF experiment. Fig. 4 shows the comparison of T_1 , T_2 , and ADC to their standards. These results indicate that this novel method quantify the relaxation parameters together with diffusion within the MRF framework. The double echo MRF sequence generates different signal evolutions that can be employed to quantify these important parameters simultaneously. Like DW-SSFP, the proposed method is also sensitive to macroscopic motion, and options to mitigate the motion effects are currently under investigation.

Acknowledgements: Siemens Medical Solutions, NIH grant 1R01EB017219, and Brian Hargreaves for his code and assistance with the EPG formalism.

References: 1. Ma D et al. *Nature*. 2013;495(7440):187–92. 2. McNab JA, Miller KL. *NMR Biomed*. 2010;23(7):781–93. 3. Weigel M et al. *J. Magn. Reson.* 2010;205(2):276–85. 4. Lavdas I et al. *J. Magn. Reson. Imaging*. 2013;38(1):173–9.

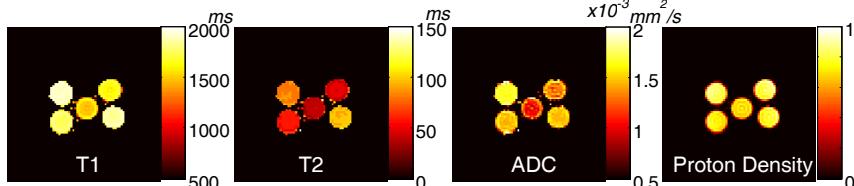


Fig. 3. T_1 , T_2 , ADC and proton density maps generated from double-echo MRF acquisition from the phantom

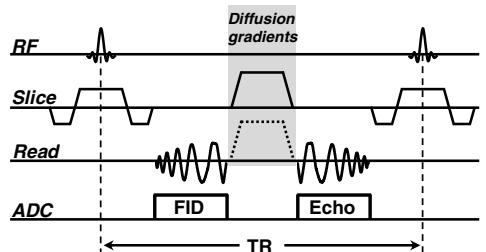
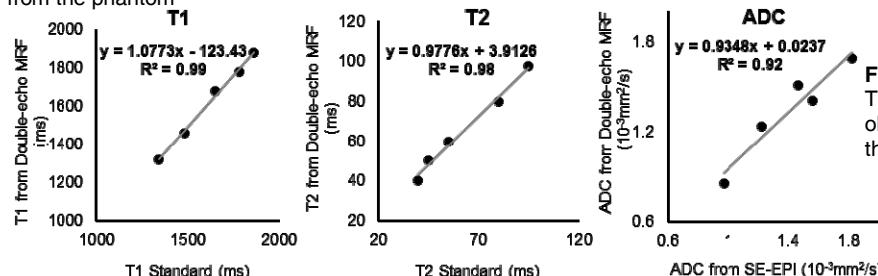


Fig. 1. The diagram of the diffusion-weighted double-echo sequence with the spiral readout.

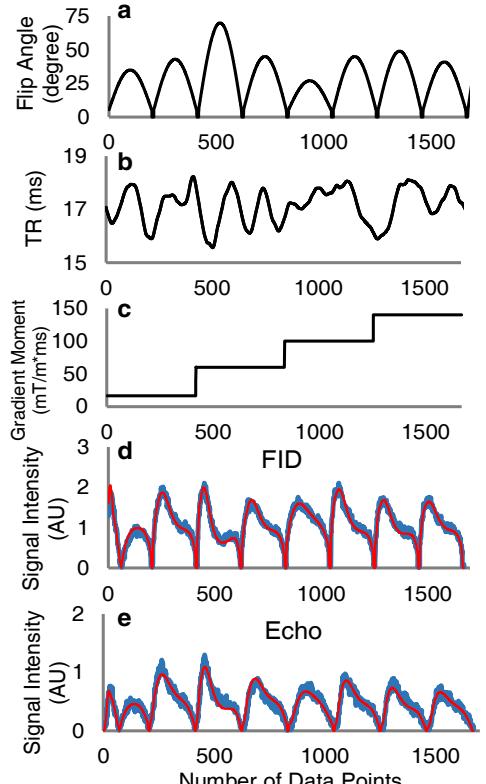


Fig. 2. An example of a) varied flip angles ($0\text{--}75^\circ$), b) repetition times (15.5–18.5ms), and c) gradient moment (16–140 mT/m*ms) used in the double-echo MRF sequence. The corresponding signal evolutions of d) the FID and e) the echo from the acquired signal (blue) and the matched dictionary entry (red) are shown to demonstrate the fitting.

Fig. 5. The comparison of T_1 (left), T_2 (middle) and ADC (right) values obtained from double-echo MRF to their standards.