

Quantitative MR imaging method: All of the main MR parameters can be obtained in little more than a single scan

Bruno Madore¹, W. Scott Hoge¹, Tai-Hsin Kuo², and Cheng-Chieh Cheng¹
¹Brigham and Women's Hospital, Harvard Medical School, Boston, MA, United States, ²Philips Healthcare, Taipei, Taiwan

Target Audience: Researchers and clinicians interested in quantitative MR imaging.

Purpose: MR exams typically last 45 min or so, during which time the anatomy of interest may get repeatedly imaged to generate a variety of tissue contrasts. While image contrast can be manipulated to great effect to produce clinically-useful images, one rarely obtains maps of the actual physical parameters that give rise to this contrast. The present method generates maps of all of the main MR physical parameters: T_1 , T_2 , T_2^* , the equilibrium magnetization M_0 , the flip angle and the offset frequency Δf . While established methods exist to map each one of these parameters, obtaining them individually would typically require scan times beyond reasonable constraints. Here we present a method that can estimate them in little more than a single scan.

Several inspired methods such as GESFIDE¹, DESPOT², MP-DESS³, TESS⁴ and MR fingerprinting⁵ have aimed at mapping several parameters at once. The main strengths of the present work are that it requires little more than a single scan, it treats the flip angle as a parameter to be evaluated rather than a known quantity, and all parameters are evaluated one at a time and/or through linear equations as opposed to numerically solving larger and non-linear systems of equations involving many or all parameters at once. The method is an improvement upon a two-scan strategy introduced last year⁶, where data requirements have been reduced from two to little more than one scan. Compared to MR fingerprinting⁵, because parameters are calculated analytically rather than simulated and matched, a leaner method that acquires only the minimum amount of needed data can be more naturally aimed for and obtained.

Method: One full-resolution 3D scan is acquired using the pulse sequence from Fig. 1, with repetition time TR_1 and nominal flip angle $\hat{\alpha}_1$. The present implementation uses hard (non-selective) RF pulses for simplicity and to help keep SAR under control. Because hard pulses are used the frequency-encoding direction should be in the superior-inferior direction to avoid aliasing, and the FOV encompasses the whole object along y and z . A small region near k -space center, about 40×40 in the k_y - k_z plane, gets re-acquired with repetition time TR_2 and a much-larger nominal flip angle $\hat{\alpha}_2$. Total scan time is about equal to $N_y \times N_z \times TR_1 / f_1 + 1600 \times TR_2 / f_2$, where f_1 and f_2 are acceleration factors achieved for these scans (through parallel imaging). Scan time tends to be dominated by the first term, the high-resolution scan, hence the statement that the method requires little more than one scan. Simulated results in Fig. 2 show how very different flip angle settings are beneficial to reconstructed SNR, a setting $\hat{\alpha}_1 / \hat{\alpha}_2 \approx 20 / 300^\circ$ was chosen here. Because so few k -space lines are acquired in the second scan a longer TR can readily be used for extra SNR at little cost in scan time, for example, $TR_1 / TR_2 = 40 / 60$ ms (green X in Fig. 2) rather than $TR_1 / TR_2 = 40 / 40$ ms (red X). A setting of about 300° was considered the highest we might go while staying well below degeneracies that inevitably occur for angles that exceed 360° . It should be noted that a flip angle of 300° in the present context is very different from -60° , as wherever the B_1 field drops to half its nominal value the former would become 150° while the latter would be -30° , two very different angles.

Step 1: Using the high-resolution data and the method from⁷, R_2 and R_2' (or $T_2=1/R_2$ and $T_2^*=1/(R_2+R_2')$) are found.

Step 2: Using a spatially-filtered version of the signal from the first scan and the low-resolution signal from the second scan, the flip angle map can be calculated. A (presumably quite robust) assumption that B_1 and the flip angle distribution should be smooth spatially is made here. Using $\hat{\alpha}_2 / \hat{\alpha}_1 = \alpha_2 / \alpha_1$ the following equation with the single unknown $c_1 = \cos(\alpha_1)$ is solved as described in⁶, with X a function of acquired MR signals:

$$(X_{1,k}c_1 - 1) \frac{TR_2}{TR_1} \times (X_{2,k} - c_2) - (X_{2,k}c_2 - 1) \times (X_{1,k} - c_1) \frac{TR_2}{TR_1} = 0$$

$$T_{1,i,k} = TR_i \left/ \ln \left(\frac{X_{i,k} \times c_i - 1}{X_{i,k} - c_i} \right) \right.$$

Step 3: Using the flip angle map from Step 2 and the high-resolution dataset obtained with $\hat{\alpha}_1$

T_1 and $C \times M_0$ are found where C is the sensitivity of receive coil(s), the equation for T_1 is⁶:

Step 4: Finally, the offset frequency Δf is evaluated from the multi-echo acquired data.

Results: The approach has been validated through several phantom experiments (e.g., Fig. 2,

$\hat{\alpha}_1 = 20^\circ$, $TR = 40$ ms, higher-resolution dataset $192 \times 192 \times 160$ and $1 \times 1 \times 1.12$ mm³ voxel, lower-resolution dataset only 6% the size of the 1st one, 3 pathways, 4 TEs). No singularities or infinities have been encountered. Solutions can sometimes be degenerate but the correct root was always readily identified using the common-sense rule that $\alpha_1 \approx \hat{\alpha}_1$ near the center of the excited volume and α_1 should vary smoothly from there. At the time of writing the first 3 *in vivo* datasets had been acquired, with IRB-approved informed consent, but the appropriate parameter space (TR_1 , TR_2 , $\hat{\alpha}_1$, $\hat{\alpha}_2$, right choice for the 3 pathways to sample, etc) and offline processing were not optimized yet. In these exploratory *in vivo* scans both datasets were sampled with the same spatial resolution, and a few representative images are displayed in Fig. 4 for both the brain and knee applications we are pursuing. These images represent initial steps toward optimization.

Discussion and Conclusion: The present approach allows the main MR parameters that determine contrast to be rapidly and quantitatively evaluated, so that any desired contrast might in principle at least be computed rather than acquired. What SNR will ultimately be achievable in the parameter maps remains the biggest unknown, but results in Fig. 3 can give an indication for a 1.12 mm³ voxel size, with a standard deviation of 9 ms on T_2 and 90 ms on T_1 . No regularization has yet been included in the algorithm, but doing so may prove advantageous for SNR.

References: [1] Ma J, Wehrli FW. J Mag Res B 1996, 111:61–9. [2] Deoni SCL et al. MRM 2003, 49:515–26. [3] Stöcker T et al. MRM 2014;72:103–11. [4] Heule R et al. MRM 2014;71:230–7. [5] Ma D, Gulani V, Seiberlich N, et al. Nature 2013, 495:187–93. [6] Madore B et al. ISMRM 2014:0336. [7] Cheng C-C et al. ISMRM 2013:4216. Support from grants R01CA149342, P41EB015898 and R01EB010195 is acknowledged.

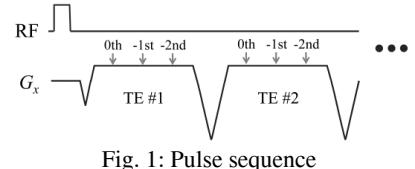


Fig. 1: Pulse sequence

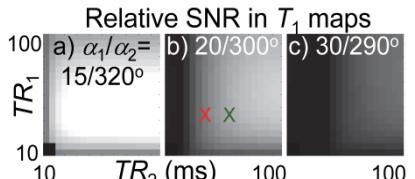


Fig. 2: On selecting TR and flip angle values.

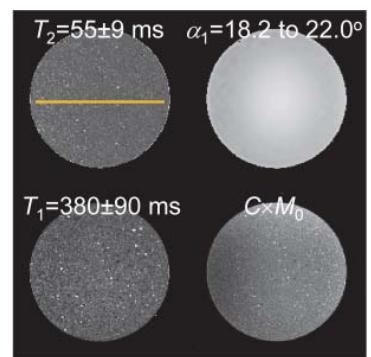


Fig. 3: Gel phantom, erratic pixels are caused by air bubbles

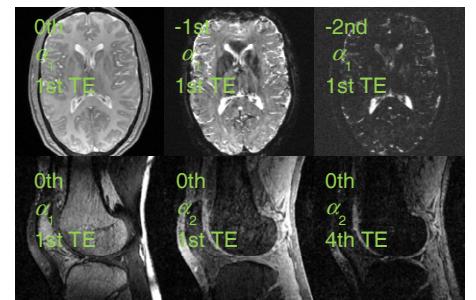


Fig. 4: Examples of images obtained using the sequence from Fig. 1.