Encoding with Radiofrequency Spoiling, Equilibrium States and Inverse Problem for Parametric Mapping

Ludovic de Rochefort[1]

[1]IR4M (Imagerie par Résonance Magnétique Médicale et Multi-modalités), Univ. Paris-Sud, CNRS, UMR8081, Orsay, France

TARGET AUDIENCE: MR physicists.

PURPOSE

Fast steady-state sequences often use RF spoiling to modulate contrast in MRI[1]. The dynamic equilibrium depends on many parameters such as flip angle, longitudinal and transverse relaxations, and diffusion[2,3,4]. Here it is shown that, extending the configuration state formalism[5], RF spoiling can be described as an encoding direction and equilibrium can be efficiently calculated with relaxation and diffusion. The inverse problem can then be solved to reconstruct associated parametric maps. Theory, practical implementation as well as proof-of-concept experiments on a clinical MRI system are given introducing new methods for efficient parametric mapping.

METHODS

Theory: In RF spoiled sequences, gradients are leaving a net dephasing along an arbitrary direction (z here) represented by the complex exponential $Z=\exp(-2i\pi.\Delta k_z.z)$, $\Delta k_z=1/a$ a spatial frequency. In the present work, RF spoiling is described similarly using an apparent spatial frequency Δk_y such that phase is accounted for using $Y=\exp(-2i\pi.\Delta k_y.a)$. The case of quadratic phase cycling is considered assuming short RF pulses (flip angle α). The dynamic equilibrium is studied by extending the configuration state formalism[5], i.e. expressed as polynomials in Y and Z (Eq.1 for the transverse polynomial Q). To account for relaxation, $E_1=\exp(-R_1.TR)$, $E_2=\exp(-R_2.TR)$, with longitudinal R_1 and transverse R_2 relaxation rates, the repetition time TR. Free diffusion can be handled with Gaussian filtering[2,3,5] (Eq. 2 and 3) with $E_d=\exp(-D.TR.4\pi^2/a^2)$ and D the diffusion coefficient. A second order recurrence relation on $Q_k(Y)$ can be obtained (Eq.4) in which the coefficients (a_k, b_k, c_k, r_0, r_{-1}) can be expressed as a function of Y, E_1, E_2, E_d and α (δ is a Dirac). This tridiagonal linear system can be solved efficiently to calculate the equilibrium state with relaxation and diffusion.

$$(1)\ Q = \sum_{k=-\infty}^{+\infty} \sum_{j=-\infty}^{+\infty} q_{j,k} Y^{-j} Z^{-k} = \sum_{k=-\infty}^{+\infty} Q_k(Y) Z^{-k}$$

$$(2)\ D_1 = \sum_{k=-\infty}^{+\infty} E_d^{k^2} Z^{-k}$$

$$(3)\ D_2 = \sum_{k=-\infty}^{+\infty} E_d^{k^2+k+1/3} Z^{-k}$$

$$(4)\ -a_k Q_{k-1} + b_k Q_k - c_k Q_{k+1} = r_{-1}\delta_{k+1,0} + r_0\delta_{k,0}$$

Inverse problem: Based on the acquisition of the k=0 state for multiple Y, implementation of a non-linear least-squares algorithm was developed to fit a measured signal $Q_{0,mes}$ to $M_0.Q_0(E_1, E_2, E_d, \alpha)$. To provide a first estimate of the parameters, D was assumed as $2\ 10^{-9}$ m²/s, α as the prescribed flip angle, and E_1 and E_2 were discretized into a 32x32 grid with values ranging from 0 to 1 providing a 'dictionary' for Q_0. For a calculated Q_0, M_0 was fitted using linear least squares ($M_0=Q_0{}^H Q_{0,mes}/Q_0{}^H Q_0$), where the superscript ^{H} denotes the Hermitian transpose. The set of parameters corresponding to the minimum norm provided initialization. A Gauss-Newton algorithm was then implemented with a numerical evaluation of the Jacobian and a parameter update evaluated using $Q_{0,mes}/M_0$. The procedure was repeated updating M_0 and until relative variations of the parameters were small enough (10^{-4} relative variations).

Experiments: Imaging was performed at 1.5 T (Philips Achieva) using a quadrature head coil for reception. Gd-chelate (10, 5, 2.5, 1.25, 0 mM, Dotarem, Guerbet) and iron oxide nanoparticle (0.32, 0.16, 0.08, 0.04, 0 mM, CL-30Q02-2, Molday ION, Biopal) solutions were prepared. A 3D gradient echo sequence was modified to allow multiple Y acquisitions sequentially. Spoiling gradient was restricted to the readout direction such that $a=1/\Delta k_z$ corresponded to the readout pixel size. Scan parameters were TR/TE=9.2/4ms, acquisition matrix 168x84x9 and voxel size 0.5x1x8mm, reconstructed voxel size 0.47x0.47x8mm, bandwidth 217Hz/pix, T_{acq}=21min, α=45° (0.15ms hard pulse), 180 Y steps with 2° phase increments, acquisition of the k=0 state. A static B$_0$ drift noted during the acquisition was calibrated and corrected for. A region-of-interest analysis on each tube and a pixel-based reconstruction were performed. For the latter, flip angle was set to 45° to accelerate reconstruction.

RESULTS

Steady-state signal as a function of Y could be efficiently modelled using the proposed simulation (Fig.1). Data is presented in the complex plane to emphasize the informative nature of the full complex signal as compared to the usual absolute value reported[1,4]. Exploring Y along the unit circle, the equilibrium state rotates around the fully spoiled signal $M_0.\sin(\alpha)(1-E_1)/(1-\cos(\alpha)E_1)$ without reaching it (green circle in Fig.1). For the 1.25 mM Gd tube exemplified in Fig.1, fitted α was 44.07° and diffusion coefficients was 2.32 10^{-9} m²/s, consistent with the prescribed angle and water free diffusion coefficient, demonstrating the ability to recover these parameters. Regarding measured relaxation rates (Fig.2), they were consistent with the expected ones, linear with concentration and providing molar relaxivities r$_1$=3.85/r$_2$=4.52 mM^{-1}s^{-1} for Gd and r$_1$=11.8/r$_2$=88.1 mM^{-1}s^{-1} for ION. Longitudinal and transverse relaxation rates, as well as diffusion coefficient maps could be obtained (Fig.3) demonstrating that RF spoiling Y-encoding can be used for multiparametric mapping using steady-states sequences.
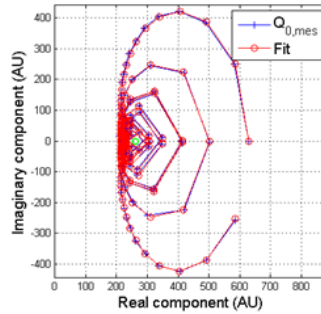

Fig.1: Representative measurement (blue crosses) and fit (red circles) for 1.25 mM Gd displayed in the complex plane. Maximum real value corresponds to Y=1.
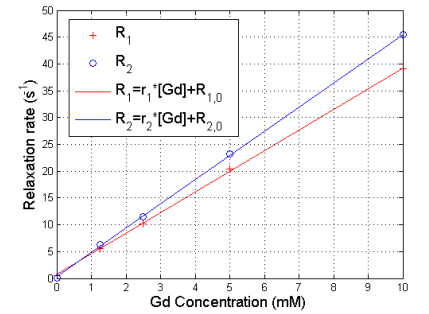

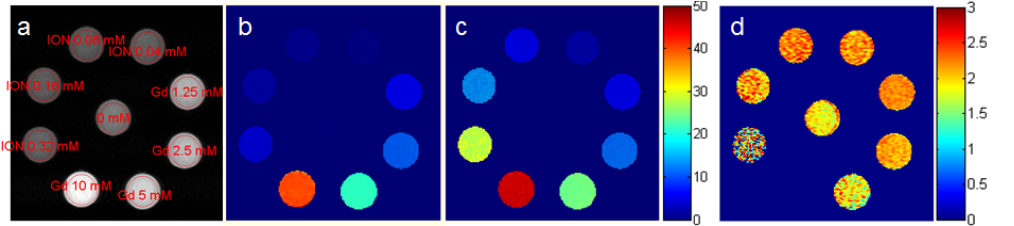Fig.2: Fitted relaxation rates in the tubes for Gd displaying linearity as a function of concentration.

DISCUSSION/CONCLUSION

Multiparametric mapping using Y-encoding was demonstrated over a wide range of R_1, R_2 and R_2/R_1 ratio. M_0 amplitude and phase, flip angle, free diffusion coefficient and relaxation parameters could be measured. E_2 and E_d compete to attenuate the transverse component and diffusion coefficient cannot be probed accurately for fast relaxation (see concentrated samples in Fig.3). An error propagation analysis can be performed to estimate the fitted

Fig.3: Y=1 image with sample locations (a), R$_1$ (b) and R$_2$ (c) maps (same colorbar in s^{-1}), D map (d, 10^{-9} m.s^{-1}).

parameter precision and reduce the sampled Y steps. To reduce scan time *in vivo*, hermitian symmetry in Y can be used together with parallel imaging or sparse acquisitions. *In vivo*, diffusion can be direction-dependent, restricted, magnetization transfer can occur or partial volume interfere. These phenomena could be accounted for by sampling various spoiling gradient orientations, using more complex filtering polynomials, modeling exchange or multi-compartments, and may be probed using fast steady-state sequences with the Y-encoding concepts.

REFERENCES 1. Zur et al. MRM 1991-21:251. **2.** Kaiser et al. J Chem Phys 1974-60:2988. **3.** Zur et al. MRM 1997-37:716. **4.** Ganter, MRM 2006-55:98. **5.** Weigel, JMRI 2014, to appear. **Acknowledgments**: The author thanks Patrick Le Roux and Geneviève Guillot for useful discussions.