Spin TomogrAphy in Time domain: the MR-STAT project

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Target Audience MRI physicists and engineers. **Purpose** MR image reconstruction is traditionally based on (inverse) Fourier transform operation. Filling the *k*-space requires time and during an acquisition, T_1 , T_2 (T_2*), and B_0 effects cause a weighting of the *k*-space data which deteriorates the quality of the reconstruction. Quantitative information is retrieved *after* multiple images are reconstructed, usually employing steady-state and/or long T_R, causing long scan times. MR fingerprinting[1] has recently offered a possibility to achieve fast, quantitative mapping of T_1, T_2 etc. In this work, we present a different approach to quickly measure MR parameter maps by treating the quantitative MR problem as a dynamic system identification[2] process. The system equations are inverted to match the response of the MR scanner to the data in *time* domain, thus the intermediate FFT step is not necessary. Due to advances in numerical optimization and computing power, this approach has become possible and is routinely applied, for instance, to seismology. In this work, we apply it to MR and we recover all the desired parameters, for example: T_1, T_2, B_1, B_0, M_0. This framework is called MR-STAT: Magnetic Resonance Spin TomogrAphy in Time domain. The advantages of MR-STAT are various: 1) ultra-short scan time, 2) relaxation and other physical system characteristics/imperfections are taken into account for, 3) relationship between sequence parameters and accuracy of reconstruction is explicit and exploited for optimal sequence design, 4) no need for lookup tables, 5) flexibility to include other physical processes than given by Bloch equation, 6) easy scanner implementation with existing standard sequences is possible.

$$\text{Find:}\quad \vec{\theta}_* = \arg\min_{\vec{\theta}} \|s(\vec{\theta},t) - s_m(t)\|^2$$

$$\text{such that:}\quad \begin{cases} s(\vec{\theta},t) = \int_{\mathbb{V}} \theta_\ell(\vec{r}) M_{xy}(\vec{r},\vec{\theta}_n,t)\,d\vec{r} & \text{(Faraday's law)} \\ \dot{M} = \psi(M,\vec{\theta}_n) & \text{(Bloch equation)} \end{cases}$$

(System equations)

$$\text{with:}\quad \vec{\theta}_n(\vec{r}) \equiv [T_1, T_2, \Delta B_0, B_1^+](\vec{r})$$
$$\theta_\ell(\vec{r}) \equiv B_1^-(\vec{r}) M_0(\vec{r}),\ \vec{\theta} \equiv [\vec{\theta}_n(:);\ \theta_\ell(:)]$$

Fig 1: *The framework equations*

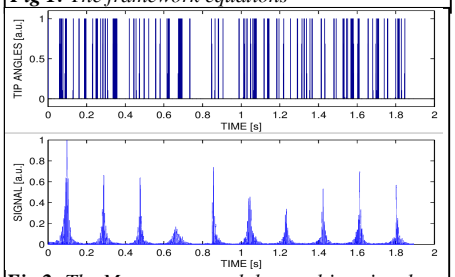

Fig 2: *The M-sequence and the resulting signal*

Theory The Faraday´s law of induction and the Bloch equation represent the model (Fig. 1). The parameters are denoted by θ_n and θ_ℓ and where *n* and ℓ denote, respectively, nonlinear and linear dependence on the signal $s(t)$. The large nonlinear inversion problem has N_{voxels} x N_{param} unknowns where, in case of desired T_1, T_2, B_1 amplitude, B_1 phase, B_0 and M_0: N_{param} = 6. The numerical solution is made feasible by applying efficient derivative approximation schemes and the variable projection method[3], which exploits the distinction between linear and nonlinear dependence of the parameters. A Matlab implementation of the Gauss-Newton method with physical box constraints is used and executed in parallel on a grid of 32 Linux computers, each employing one CPU. To probe the system, we use so-called M-sequences[4] (Fig. 2): series of identical pulses where on/off is determined in a way that the correlation is minimized. The expected accuracy of the M-sequence is given by the optimal experiment design theory[5]. In particular, the number of excitations and the tip angle are determined to minimize the standard deviation (std) of the estimate.

Methods We focus on an easy to implement, 2D GE sequence. The excitation is given by a 60°, slice selective Gaussian pulse. Excitation and readout follow one another without waiting time; T_E and T_R can be the shortest possible since the relaxation and other physical processes are observed over the whole duration of the sequence. Sequence design, noisy scanner response and data reconstruction are first simulated for a numerical head phantom, 64x64 resolution (Fig. 3). The total sequence duration is 3.6 s, SNR = 40. Subsequently, a scanner experiment is performed on a 4.7T VARIAN animal system employing a Helmholtz coil, one single Tx/Rx channel. A homogeneous gel phantom is scanned. Resolution: 32x32, SNR = 35. Sequence duration: 1.9 s. See Fig. 2. For validation purposes, T_1 and T_2 values are measured also with inversion-recovery (IR) and multi-spin-echo (MSE) sequences, respectively.

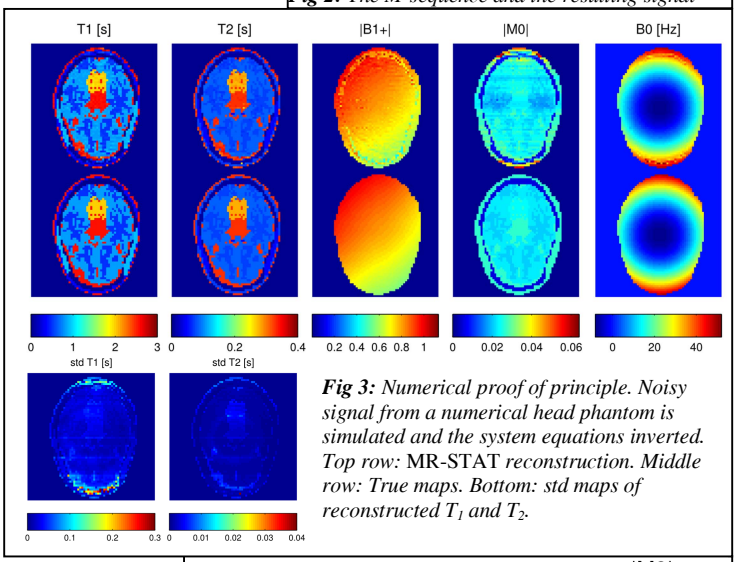

Fig 3: *Numerical proof of principle. Noisy signal from a numerical head phantom is simulated and the system equations inverted. Top row:* MR-STAT *reconstruction. Middle row: True maps. Bottom: std maps of reconstructed T_1 and T_2.*

Results The numerical proof of principle is successfully performed and shown in Fig. 3. MR-STAT is capable of recovering all physical parameters. The experimental reconstruction is shown in Fig. 4, together with the std maps for the T_1 and T_2 estimates. The (T_1,T_2) average values are (0.52s, 0.043s) with average std of (0.05s, 0.002s). For comparison, the (T_1, T_2) values from the IR and MSE sequences are (0.42s, 0.049s) with std (0.03s, 0.006s).

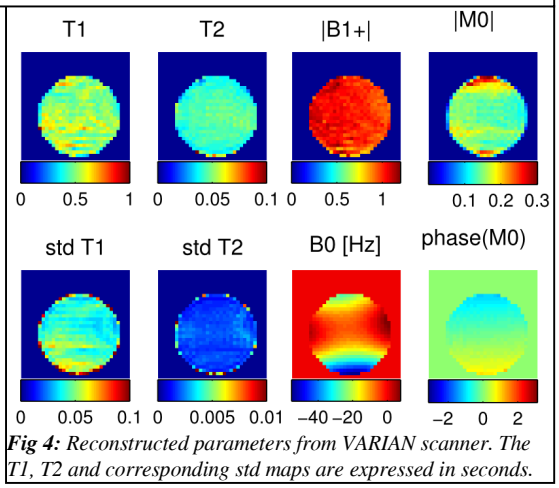

Fig 4: *Reconstructed parameters from VARIAN scanner. The T1, T2 and corresponding std maps are expressed in seconds.*

Discussion The MR dynamical system can be probed by a very short, simple to implement sequence and there is no need for restrictive sequence characteristics like steady states, full relaxation, inversion, long T_R, etc. To show the flexibility of MR-STAT, we have employed standard 2D GE sequences. This is not restrictive and other readout schemes, e.g. single-shot, spiral or radial, could be employed. Note that MR-STAT does not require necessarily linear gradients, any encoding scheme could be applied. Accuracy of the reconstruction is assessed by the standard deviation maps, which are output of the reconstruction. Sequences that achieve lower std could be designed, this will be addressed in the future. Extension to parallel imaging/transmit is straightforward. The reconstructed quantitative values can be directly used to generate synthetic images of standard clinical sequences and/or for computer aided diagnostic purposes. High-dimensional look-up-tables are not needed thus the system equations can be expanded to include other physical phenomena (e.g. flow, motion, diffusion).

Conclusion Exploiting techniques from nonlinear dynamic system identification theory, we set up an ultra-fast quantitative MR framework which is validated through numerical and experimental proofs of principle. MR-STAT represents a systematic and comprehensive approach to quantitative MR where the explicit relationship between sequence design and reconstruction is exploited to probe the system in a very efficient way. **References** [1] Ma Dan et al, Nature 2013. [2] Franceschini G et al. Chem Eng Sc. 2008. [3] Golub GH and Pereyra V, Inv Prob 2003. [4] Buracas GT et al, Neuroimage 2002. [5] Bauer I. et al. J of Comp App Math, 2000.