VERMAGRIS: A Versatile and Realistic Magnetic Resonance Imaging Simulator

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Abstract

Magnetic Resonance Imaging (MRI) has become an invaluable tool for the non-invasive exploration of the human body. However, taking full advantage of its power requires the appropriate setting of numerous parameters. In light of the substantial cost of an MR scan and of the limitations of MR phantoms, MR simulators offer a convenient approach to parameter optimization.

Here we present an MR simulator which produces realistic human brain images for the popular and versatile 3D Magnetic-Prepared Rapid Gradient Echo sequence (3D MP-RAGE). Our simulator physically models the evolution of the magnetization throughout the MR acquisition, as dictated by the Bloch equations, and takes into account all elements (RF pulses, imaging gradients, field inhomogeneities) and timings of the sequence. The output image is then produced in a similar way to that by which it is reconstructed in an MR scanner.

By estimating the Point Spread Function (PSF) of the simulated sequence we can investigate the associated image contrast, partial volume effects and the limit of spatial resolution. The parameters of the sequence can then be tuned to yield an optimal PSF for a given application.

1 Introduction

The remarkable versatility of MRI comes at the expense of operational simplicity: indeed the quality and fit to purpose of a particular acquisition depends on the choice of an appropriate pulse sequence in an ever increasing palette of possibilities and the adequate tuning of a growing number of parameters.

Because of the substantial cost of an MR scan and of the limited possibilities offered by MR phantoms, a number of MR simulators have been developed over the years. They serve a variety of purposes: learning tool for students and clinicians [9], sequence optimisation to reduce acquisition time or increase robustness to noise [2, 3, 7] or validation of image analysis methods in the absence of in-vivo ground truth [6].

In order to cope with the complexity of the MR acquisition process, simulators tend to make a number of approximations. The simplest simulators take T1 and T2 maps as inputs and then synthesize new images for a given pulse sequence by considering the evolution

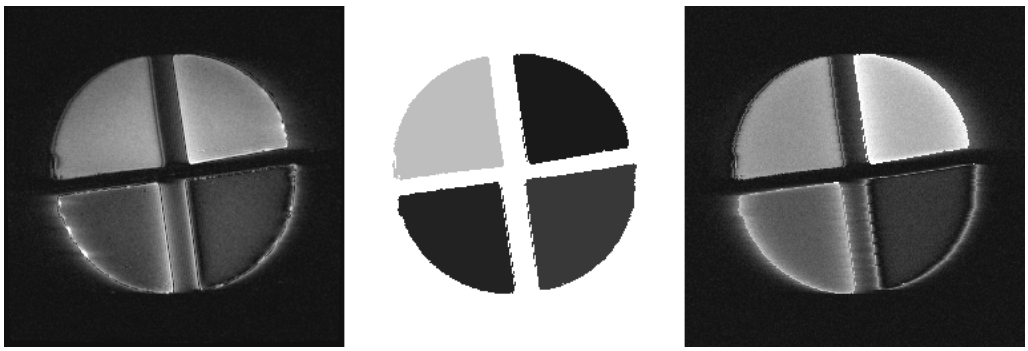

Figure 1: MP-RAGE acquisition of a phantom acquired with linear phase encoding (left); T1 map extracted for use in the simulator (middle); simulated image (right).

of the magnetization during the pulse sequence independently for each voxel [8]. A more sophisticated approach, Kwan et al. uses fuzzy, interpolated templates to allow for partial volume effects and noise to be simulated [6]. However their method does not model the image artefacts produced by the evolution of the magnetization through k-space. The simulator of Petersson et al. overcome this issue by operating in k-space indeed [10]. However it does not take into account the interaction between the position of voxels and the timing of the sequence, and becomes unwieldy if more tissues have to be simulated (i.e. partial volume effect cannot be realistically observed). Finally the most realistic simulators simulate the MR signal directly by solving the Bloch equations for the particular pulse sequence and a highly discretized object [1, 2]. This makes it possible to simulate the effect on the PSF of spin dephasing (T2* decay) and of the evolution of the magnetization during the acquisition. Indeed, the particularly complex relationship between acquisition parameters and PSF naturally makes it a desirable target for optimization. Regrettably, those two approaches suffered from a high computational cost, which restricted them to 2-D sequences.

In this article, we present an MR simulator that can be used both as a validation tool for image processing algorithms, and as a sequence optimizer for high resolution, quantitative MRI. It is based on the solution of the discrete-event Bloch equation, and is capable of handling 3-D sequences and PSF. Realistic field inhomogeneities can also be readily incorporated into the simulations. We chose to simulate the standard MP-RAGE sequence [4] owing to its flexibility and popularity in both qualitative and quantitative studies. The particularly complex relationship between the acquisition parameters of an MP-RAGE sequence and the Point Spread Function (PSF) also makes it a desirable target for optimization. The PSF is defined as the response of an imaging system to a single point source, and quantifies the blurring introduced by an imaging system. In the case of MR imaging, the PSF depends on the object, image acquisition technique and post-processing methods, so the image simulated from a small object can be used to determine the sequence parameters that optimize the sharpness of the PSF. Note that although our simulator was developed for the MPRAGE sequence, it could be easily adapted to a different sequence by defining a new pulse sequence and the associated k-space trajectory (see [2]).

We detail our approach in Section 2 before presenting some results and a qualitative validation based on the comparison of both synthetic phantoms and real brain MR data. We also describe the effect of different simulator parameters, sequences and objects on the simulated PSF.

2 Method

We model the object to be imaged as a collection of discrete voxels, where each voxel contains a number of isochromats with distinct resonance frequencies. Isochromats consist of

small imaginary volumes containing a group of spins which resonate at the same frequency. Those frequencies are drawn from a Lorentzian distribution centered around the Larmor frequency (the average frequency at which the magnetic moment of the protons of the sample precess about the B_0 magnetic field). Note that the relaxation times (T_1 and T_2) also depend on isochromat position and can be given by a priori T_1, T_2 and PD maps. Each isochromat is then defined by a proton density, a set of relaxation times and a frequency offset.

At the initialisation stage, the user also specifies the different parameters of the sequence, such as the size of the output image and the sequence timings. For each time point over the course of the simulation, we compute the magnetization of each isochromat independently by applying the appropriate operators as dictated by the pulse sequence and solving numerically the Bloch equations. The MR signal in each voxel is then computed by summing the signal of its isochromats.

Let $M(r,t) = [Mx(r,t), My(r,t), Mz(r,t)]^T$ be the magnetization of isochromat r at time point t. We approximate the evolution of its magnetization by applying a series of operators, where each operator models the influence on the magnetization of the various components of a particular time step of the pulse sequence. We get:

$$M(r,t+\delta t) = R_{grad}(t)R_{inh}(t)R_{relax}(t)R_{RF}(t)M(r,t) \tag{1}$$

$R_{grad}(t)$ is the rotation operator corresponding to the application of gradient $G(t)$ where $\beta = \gamma \mathbf{r} G(t)\delta t$ relates $G(t)$ to the angle β around the z axis, for each position.

$R_{inh}(t)$ is the rotation operator corresponding to B_0 field inhomogeneities where $\phi = \gamma\,\Delta B(r)\;\delta t$ relates the inhomogeneities $\Delta B(r)$ during the time δt to the angle ϕ around the z axis.

$R_{relax}(t)$ describes the relaxation of the magnetization and is most conveniently described by a 4D matrix acting on the magnetization vector with an additional term corresponding to the equilibrium magnetization (Mx, My, Mz, Mo):

$$R_{relax} = \begin{pmatrix} e^{\frac{-\Delta t}{T_2(\mathbf{r})}} & 0 & 0 & 0 \\ 0 & e^{\frac{-\Delta t}{T_2(\mathbf{r})}} & 0 & 0 \\ 0 & 0 & e^{\frac{-\Delta t}{T_1(\mathbf{r})}} & (1-e^{\frac{-\Delta t}{T_1(\mathbf{r})}}) \\ 0 & 0 & 0 & 1 \end{pmatrix} \tag{2}$$

$R_{RF}(t)$ is the operator describing the effect of an RF pulse tipping the magnetization by an angle α about the x axis, applied instantaneously at time t. Because of RF field inhomogeneities, the tip angle α generally depends on the position of the isochromat, and could therefore be controlled by an a priori RF map, if available.

Field maps of inhomogeneities in the RF and static (B_0) field can be introduced to modulate the effect of R_{RF} and R_{inh}. Any relevant scanner preparation steps, such as driving the magnetization to an steady state, are taken into account by applying the appropriate combination of R_{RF} and R_{relax} to the magnetization.

Finally, each time point corresponds to a different point in k-space (the Fourier reciprocal space of the image), which we populate by summing the transverse magnetization of all isochromats. In practice, the MR signal is contaminated by thermal noise so complex white noise with a specified variance is added to the complex data, before performing any post-processing. The signal can be filtered in k-space, as is generally performed on an MRI scanner to minimize effects such as Gibbs ringing. The simulated 3-D image is then obtained by Fourier transforming the k-space data.

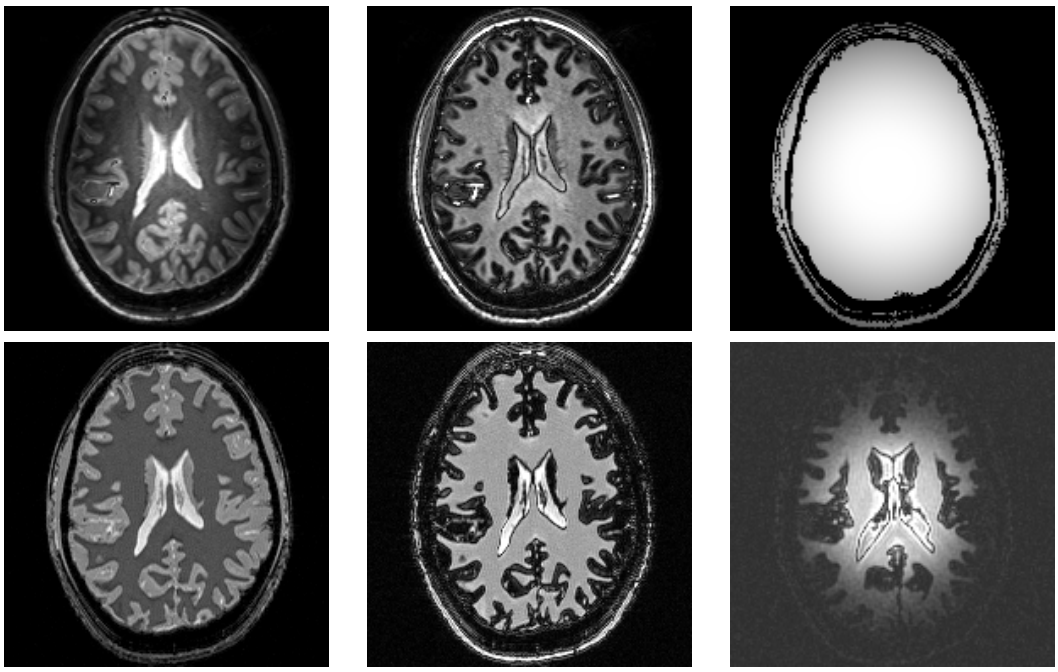

Figure 2: MP-RAGE acquisitions (top) and simulations (bottom): 1mm isotropic with 300ms inversion time (left); 1mm isotropic with 850ms inversion time (middle); simulated B_1 map and corresponding image simulation with added noise (right column).

Note that this simulation of the k-space MRI data lends itself very well to parallelisation, as each isochromat is simulated separately. Consequently, the overal volume can be easily broken down into several sub-volume simulation processes, to be run in parallel. Still, a compromise must be found between simulation accuracy and computation time.

3 Results

3.1 Point Spread Function and isochromats

Simulating the PSF of the scanner (the image of a small volume of isochromats, typically of the order of the reconstructed voxel) gives valuable information about the spatial resolution of the imaging sequence. In turns, this facilitate the sequence optimization process. In order to determine the minimum number of isochromats required, per voxel, for an adequate simulation, different PSF with a varying number of isochromats were computed. We then measured the intensity profile across the simulated image in the readout (x) direction. We observed that 7 isochromats per direction (giving 7x7x7 discrete values of off resonance) provided an adequate trade off between simulating an exponential T_2^* decay and computational time, for a width of the offset frequency distribution of 1MHz. As the width of the distribution increase, more isochromats per volume were required. We also observed that as the width of the Lorentzian increased, and T_2^* decreases, the width of the PSF increased for a given number of isochromats, as expected. Finally, the PSF in the the phase encoding direction (y) was unaffected by the number of isochromats or the frequency offset, also as expected.

3.2 Qualitative phantom validation

We used a spherical phantom made of four quadrants filled with saline solution containing various concentration of agar (Sigma-Aldrich) and gadolinium (Magnevist, Schering) to cover a range of relaxation times. The phantom was scanned using an MP-RAGE sequence (256x256x20 acquisition matrix with a linear phase encoding scheme and 160ms

inversion time, 5s shot length). We then segmented the acquired image using FAST FSL (http://www.fmrib.ox.ac.uk/fsl) before measuring the T_1 in each quadrant [5] to produce a T_1 map. T_2^* values and proton density were assumed constant. We simulated the exact protocol run on the scanner with noise added at 0.5% of the maximum signal. The ability of our approach to adequately simulate the artefacts in the phase encoding direction makes for a simulation result particularly close to the acquisition one (Figure 1).

3.3 Simulating an in vivo image

We acquired a series of MP-RAGE images with different T1-weighting of a volunteer's brain and picked the one closest to a standard T1-weighted scan for tissue segmentation. This served to create a T1 map where the appropriate relaxation times were assigned to each tissue. Standard T_1-weighted MP-RAGE images were simulated for different inversion time and with an inhomogeneous B1 field. Visual inspection of Figure 2 shows a promising similarity between the simulated and original images.

4 Conclusion

We have presented a physically realistic MR simulator suitable for 3-D imaging sequences. We have used it to investigate the PSF in MP-RAGE. The effect of variations in RF and $B0$ fields could similarly be studied with the end goal of determining the imaging protocols that will be most robust to those inhomogeneities. We are also planning to make the simulator available online in the near future.

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