

An Integrated MR Console / MR Physics Simulation System

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Introduction

In MR research today there is a high level of pulse sequence complexity and an increasing need for verifiable, quantitative measurements. The arising need for quantitative understanding of actual complex MRI experiments requires consideration of many experimental issues and multiple physical, magnetic and magnetic resonance phenomena. The tool we describe here - an integrated MR console / MR physics simulation system - is designed for this purpose.

System: The system consists of a research MR console with a full-function hardware-independent pulse programming environment, and a parallel computer cluster running full Bloch equation simulations on a 3D digitally-defined spin phantom. This allows side-by-side comparisons of experimental vs. simulated data for any real (not simplified) pulse sequence. The simulator employs multiple spins per voxel which allows the development of stochastic tissue models and the simultaneous simulation of multiple physical phenomena.

Applications: The integration of acquisition with simulation has applications on **many levels:** verification of sequence implementations; verification of data processing and analysis procedures; diagnosis of the origin of image artifacts; diagnosis of the presence and effects of hardware limitations and defects; development and testing of tissue models; evaluation of quantitative image acquisition and analysis protocols; and finally the precise comparison of theory with experiment – an essential part of the scientific process.

Implementation of the Integrated MR Console / MR Physics Parallel Simulation System

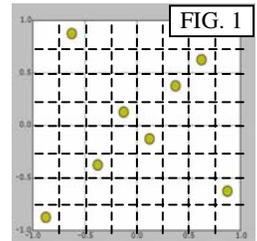
Console Hardware: The console sequencer software executes on a Pentium III running a real-time operating system (RTOS) and generates waveform data and digital control data on the PCI bus. A PCI DAC card produces up to 8 channels of analog waveform output. A multi-channel digital receiver data acquisition system runs on a separate computer with synchronization tasks performed by FPGAs.

Simulation: For our application it is necessary that the Bloch equation simulator function with any sequence whatsoever. To achieve this full generality spins are treated individually – coherence or k-space concepts are not used. Since this is computationally demanding, the simulator is configured to run in parallel on one or more PCs (Linux PVM). The largest cluster used to date contains 22 nodes (44 x 2.8GHz Xeon) processors..

Integration: The core console code (sequencer, data system, GUI, database) is configurable to operate with either real hardware or with the simulator by use of dynamic loading of hardware/simulator drivers (DLLs). The MR console and the MR physics simulator are thus highly integrated and share most code. This is achieved by the use of a software-based (hardware independent) sequencer and waveform-based simulation.

Pulse Sequence Library: A full pulse sequence library, including over 40 imaging, spectroscopy and utility sequences, has been implemented including: SSFP; FSE; CPMG; SE/GE/DW-EPI; 3D TOF/2DFT/Spiral/Turbo/IR-GE; Radial/IR/Double-SE; PROPELLER; DW/STEAM imaging; 3-Pt-Dixon-GE/SE; T1/T2rho; VSI; OSIRIS; PRESS; SSFP/2D-CSI; STEAM and others.

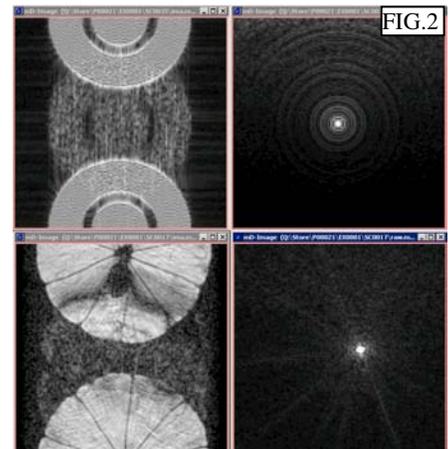
Multiple Spins per Voxel & Stochastic Model: Spin randomization strategies were selected to model physical effects while minimizing artifacts. The use of multiple randomly positioned spins per voxel allows the development of stochastic tissue models and the simultaneous simulation of multiple physics phenomena (e.g. T2*, diffusion). A constant number of spins per voxel was maintained, while randomizing (with constraints) the positions within the voxel. Multiple levels of randomization were employed as follows: (a) initial randomization to sparsely populate NxNxN lattice locations with N spins within each voxel (**FIG.1**); (b) initial local randomization away from these lattice positions to eliminate spurious coherences due to non-physical periodicity (1); (c) static spatial randomization of B0 fields (T2* effects); (d) Brownian motion during spin evolutions.



Results

The console has been successfully installed on a 9.4T/21cm animal MR imaging system. The system can simulate 100,000 spins over 240,000 time-points in 107 seconds and is being used initially to test new pulse sequence implementations. **Figure 2** shows simulated data (upper) and real data (lower) from a balanced SSFP sequence. Image ghost and image wrap are apparent in both simulated and real data – and thus are attributed to implementation errors (software); however the off-center echo and banding (both visible only in the real data) must have an experimental cause (hardware). The immediate and definitive diagnosis of artifacts in this manner is one example of the power of the integrated approach.

Simulation Physics and “Spin Noise”: As expected, the spin positional randomization eliminates all orders of spurious echoes, but introduces some simulation “spin noise” (visible in Fig.2, upper), which appears as magnetization fluctuations when spins are in a dephased state (1). We find that spin noise is very often preferable over the alternative of spurious coherences - since firstly the origin of the spin noise is always known and understood (often not the case for coherent effects), and secondly the overall impact on image formation is less damaging. Avoidance of spurious coherences is important for sequences producing strong dephasing conditions such as steady-state, multi-echo, and diffusion and any sequence using gradient crushers. Successful diffusion simulations have been performed with between 4 and 16 spins/voxel with results in agreement with analytical formulae, (within limits due to simulation spin noise). The numerical approach allows signal attenuations for different spin diffusion models to be calculated for any pulse sequence.



Conclusions

This is the first demonstration, to our knowledge, of the integration of MRI Bloch equation simulation with a full function research MR console. Future work will include incorporation of more sophisticated spin and tissue models.

References: (1) Yin-D, Deng-Q & Sharp-JC Proc. ISMRM 11 p.2402 (2003); (2) Sharp-JC et al. Proc ISMRM p.1146 (2001).

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