Efficient Pulse-Sequence Simulation using Variable Subsampling and Decomposition

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Introduction: Accurate MR pulse-sequence simulators can be used to model pulse-sequence phenomena, to diagnose the source of image artifacts, or to teach and learn MR physics. The most general method of full-sequence simulation [1] involves finely sampling data in all spatial dimensions, then iterating a time-sampled Bloch solution at each readout time point for each sample location. The resulting millions of Bloch iterations require many hours or days to compute even low-resolution synthetic images. Algorithms exist that can improve computation time under certain conditions, such as when only a few tissue types are present [2] or when the signal can be decomposed into a reduced set of Fourier coefficients [3]. While these methods can significantly reduce computation time when their conditions are met, their complexity converges toward the full-sequence simulation for arbitrarily complex conditions.

This work introduces a new method for full-sequence simulation that exploits temporal redundancies inherent in all MR sequences to substantially reduce computation time without additional a priori assumptions. In addition, we propose three alternative experiments that, when combined, can model the vast majority of sequence phenomena.

Methods: All MRI sequences consist of spatial-encoding gradients combined with some form of magnetization preparation (e.g., slice-selective RF, inversions, or steady-state pulse trains). Full-sequence simulations are time-inefficient because simultaneously modeling encoding and preparation results in an effective squaring of iterations. However, encoding alone can be rapidly modeled through the sequence point-spread function, and magnetization-preparation alone can be modeled through a simple steady-state iteration. While these two processes account for most sequence effects, some remaining effects may arise from the interplay between available magnetization and its encoding. For example, if a spin system is not in steady state when it is spatially encoded, then different magnetization is encoded in adjacent phase-encoding lines. To simulate such effects rapidly, simple 1D simulations of signal vs. time can be devised provided that the encoding trajectory is separable. We have developed an integrated, graphical sequence-design and spin-simulation environment that can easily switch between various forms of these sequence analyses.

To accelerate simulation of fully encoded sequences, we exploit the temporal sparsity inherent in all MR pulse sequences to recast the Bloch equations into a non-uniformly sampled basis (Fig. 1). RF pulses are finely sampled to satisfy the hard-pulse approximation, while all other time intervals are sampled at a coarser, variable rate to match the time-varying frequency content of gradient activity. Composite rotations are re-used from TR to TR when possible. This transformation reduces computational complexity by orders of magnitude. All simulations were performed in the SpinBench environment [4], which provides a graphical interface for MRI pulse-sequence specification and Bloch simulation. A 2.0-GHz, dual-core MacBook Pro laptop was used, and tasks were parallelized across both cores in all cases.

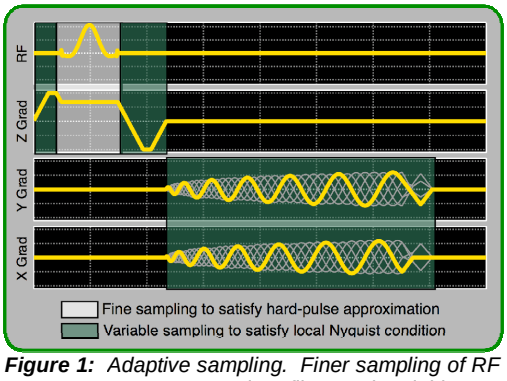

Figure 1: *Adaptive sampling. Finer sampling of RF ensures accurate spectral profiles, and variable-rate gradient sampling reduces computations. Rotation matrices are reused across TRs where possible. Here, only the spiral is re-computed for each TR.*

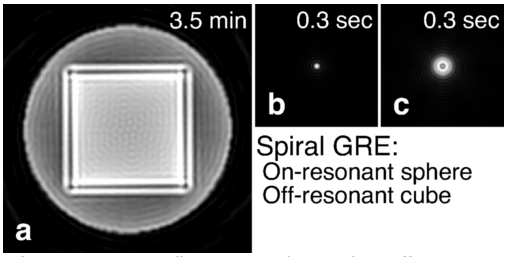

Figure 2: *Encoding example. The off-resonant blurring visible in a full spiral simulation (a) is seen more quickly by instead simulating on-resonant (b) and off-resonant (c) point-spread functions.*

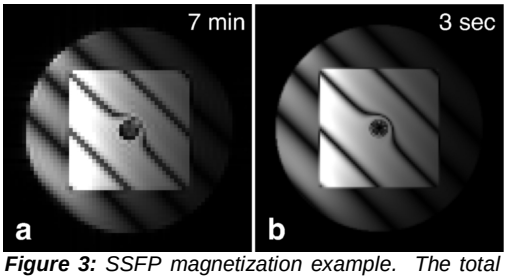

Figure 3: *SSFP magnetization example. The total effects of a linear field variation, paramagnetic particle, and surface-coil shading are visible either with (a) or without (b) simulating spatial encoding.*

Results: In Fig. 2a, the spiral GRE pulse sequence of Fig. 1 was simulated using the adaptive approach. The full simulation completed in 3.5 minutes; for comparison, the same simulation would have taken over 6 hours with optimizations disabled. Point-spread functions of on- and off-resonant spins (Fig. 2b,c) also could be used to anticipate this effect; because they compute in real time, the effects of parameter changes can be interactively visualized. A balanced-SSFP simulation with a host of spatially varying effects included (Fig. 3a) completed in 7 min and used less than 50 MB of system memory. Since these magnetization effects occur irrespective of spatial encoding, a higher-resolution simulation can be completed in less than 1% of the time (Fig. 3b) by visualizing the distribution of magnetization without encoding. Finally, Fig. 4a shows a simulated balanced-SSFP sequence with large in-plane eddy currents. This effect results from the interplay between encoding and the distribution of available magnetization, but similar information can still be obtained by performing a 1D experiment along only the phase-encoding direction (Fig. 4b).

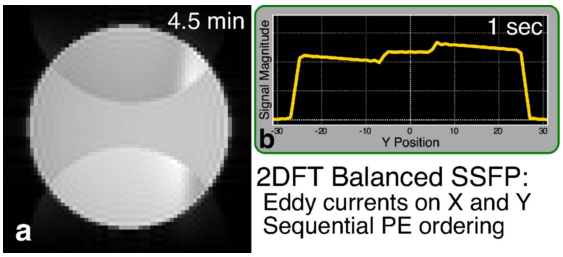

Figure 4: *Reduced dimensionality. While this full simulation (a) depicts ghosting due to non-equilibrated magnetization, much of the information can be gleaned from a faster 1D simulation along the PE direction (b).*

Discussion: Simulation of complete pulse sequences can be accelerated by orders of magnitude through exploiting temporal redundancy in the MR pulse sequence, with no other assumptions on the experiment. By further decomposing a full sequence simulation into three sub-simulations focusing on these less-ambitious goals, computational complexity is again reduced to permit computation in near real time. While no one of these simplified simulations alone gives a complete indication of sequence performance, the ensemble can provide intuition into most commonly encountered sequence phenomena. A simulation tool employing these techniques is available online [4].

References: [1]. Summers, RM, *et al.* MRM 3(3): 363-376, 1986. [2]. Kwan, RKS, *et al.* IEEE Trans Med Imag 18(11): 1085-1097, 1999. [3]. Magland, J, *et al.* Proc. 14th ISMRM: 2365, 2006. [4]. http://www.SpinBench.com/