Extracting MRI Sequence Response Kernels from Generalized Extended Phase Graph Simulations

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Introduction and Motivation:

The Extended Phase Graph algorithm is a tool commonly used to predict echo times and echo amplitudes for pulse sequences with repeating pulse succession patterns, yet the full potential of this approach is rarely utilized for arbitrary simulation problems due to their elaborate structure in comparison to direct Bloch Equation simulation. A variation of the Extended Phase Graph algorithm can be used to compute signal that is arbitrarily exact for any sequence if the effects of the RF pulses are simulated instead of assumed to be a rotation¹. The algorithm also yields a separation of the signal into object-related influence and tissue-related influence in addition to the intrinsic separation of all echoes. If then the reconstruction pipeline is applied to the individual signal components, then this separation can be further investigated in image space, making it more intuitive and computationally manageable and allowing for a MRI simulation approach that is conceptually different to direct Bloch Equation simulation.

MR images can be calculated in image space without the need for model assumptions and with a controllable accuracy/speed trade-off that reaches from full direct Bloch Equation simulation accuracy to speed close to a multidimensional lookup of single gray values.

The components hold all information about the response of a tissue or geometry to a MRI sequence in image space, which can be extracted easily and be used to quantify certain properties of a sequence, such as contrast, blurring, chemical shift, B1 sensitivity and artifacts originating from stimulated echoes or insufficiently reached steady states.

Method:

The algorithm previously reported generates signal of the form [Eq1] for one object with homogenous properties. Since the signals of different objects do only negligibly influence each other, they can be treated separately and accumulated later. If a voxel-basis is used to describe the objects, then the Fourier shift theorem can be utilized to assemble each voxel geometry from a small set of basis voxels and shift factors, keeping the set of signal components that need to undergo the reconstruction process small. For simplification, the reconstruction pipeline in this work is assumed to consist of only a Fourier transform, even though all linear operators that have manageable influence on the multiplication-convolution duality of the Fourier transform may also be used. Applying the Fourier transform to the signal equation then yields [Eq2]. If the Echo Pathways can be grouped reasonably, which is the case for sequences with clearly arranged echo properties and approximately constant echo amplitudes, then the resulting Sequence Response Kernels are very sparse and can thus be analyzed easily, or truncated with low, very controllable error. The proposed algorithm is written in C++ and embedded in MeVisLab². The reconstruction pipeline is evaluated by Gadgetron³. ISMRMRD is used as a mediator format to compare simulation results to measured data.

Applications:

For these examples, a TrueFISP sequence (TR=9.6ms, 44° flip angle, 128 base resolution, 20 averages) was investigated.

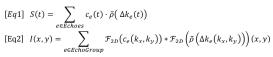
- [a] The generalized Extended Phase Graph [A1] and echo amplitudes [A2] for the first two seconds of the sequence, T1=800ms, T2=100ms.
- [b] The contrast information for a range of T1 (5ms-500ms) and T2 (2ms-200ms) values extracted from the Sequence Response Kernels [B1] and one Sequence Response Kernel for T1=390ms T2=115ms (at the red rectangle of [B1]) the contrast was enhanced and the image was magnified to emphasize the artifact effects [B2].
- [c] To compare the simulation to acquired data, gel phantoms with different T1 and T2 values were imaged on a Skyra 3T and parameter mapped. Then they were exposed to the TrueFISP sequence, producing the image [C2]/[C4] (windowed differently to emphasize contrast or artifacts). After Sequence Response Kernel calculation, a rough contrast [C1] was calculated in 6ms while a more accurate calculation using the 128 most prominent entries of the kernel took 44s [C3] on an i7-2600 CPU.

Conclusion and Discussion:

The combination of the k-space formalism and the reconstruction process reveals complex but at the same time illustrative traits of a sequence that can be used to investigate MRI phenomena and artifacts directly in image space in an intuitive fashion and may also be used to simulate the imaging process with high speed or high accuracy. The approach may be extended to further investigate and quantify the robustness of a sequence or a combination of sequences to extract certain information from the object, or to develop parameter mapping algorithms that do not require a signal model, respect artifacts, quantify parameter-sensitivity and are intrinsically robust due to the multi-scale potential of the Sequence Response Kernels.

References:

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- 2. Ritter, F., Boskamp, T., Homeyer, A., Laue, H., Schwier, M., Link, F., und Peitgen, H. O. (2011). Medical image analysis. IEEE Pulse, vol. 2, 60-70
- 3. Hansen MS, Sørensen TS. Gadgetron: An Open Source Framework for Medical Image Reconstruction. Magn Reson Med. 2013 Jun;69(6):1768-76.



 $\tilde{\rho}$ - Fourier transformed object geometry

c_e - Echo intensity factor [A1]

