Accelerated post-processing of MR fingerprinting data using partial signal library construction

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Purpose

MR fingerprinting (MRF) has recently been introduced to rapidly estimate tissue parameters including T1, T2, and chemical shift by applying a partially randomized pulse sequence to a tissue of interest and comparing measured data to a library of simulated signal evolutions spanning the range of reasonable tissue parameters [1]. Although it can be performed offline, the process of constructing a signal library is computationally expensive and unique to the pulse sequence. Here, we describe speed improvements that can be attained with a simultaneous simulation-matching approach that requires only partial library construction. This approach will be useful for experiments in which the MRF sequence parameters are randomized independently for each acquisition.

Methods

MRI signal evolution was simulated using a Bloch simulator written in Matlab (Mathworks, Inc., Natick, MA). As in the original MRF description [1], the pulse sequence consisted of an initial inversion pulse followed by RF pulses of alternating phase applied at each of 500 TR intervals. TR was specified according to a Perlin noise pattern [2] ranging from 10.5 to 14 ms, and flip angles were defined by a sinusoidal component combined with uniformly distributed noise (**Figure 1**). The lattice points of the signal library corresponded to T1 and T2 in increments of 100 ms between 100 ms and 2000 ms, and resonance offset in increments of 5 Hz between -40 Hz and 40 Hz. A test signal was then generated with T1=500 ms, T2=200 ms, and resonance offset of 10 Hz (**Figure 2**). A normally distributed noise signal with standard deviation σ_{noise} was added to the test signal. Signal evolution at each lattice point was simulated for the first N_{TR} TR intervals. These partially constructed signals were then compared against the sample signal using a root mean square difference metric. Library signals with difference metrics above the *p*th percentile were not considered viable candidates, and further simulation of these signals was halted. This process was repeated after each N_{TR} TR intervals until only one candidate signal remained. The speed and accuracy of this simultaneous simulation-matching algorithm were assessed for a variety of σ_{noise}, N_{TR}, and *p*.

Results

The execution speed of the simultaneous simulation-matching algorithm relative to full library construction is shown in **Table 1**. With appropriate choice of *p* and N_{TR}, the speed could be increased by nearly two orders of magnitude. As expected, signal matching accuracy decreased as σ_{noise} increased (**Table 2**), with relatively greater propensity for signal misidentification at small *p* and small N_{TR}. However, at SNR>5, the test signal was correctly matched within the library of 6800 signals with 95% or greater accuracy. In all cases of signal misidentification, the algorithm identified a neighboring lattice point.

Conclusion

The simultaneous simulation-matching algorithm described herein allows for partial construction of a signal library and thereby permits substantial acceleration of the simulation process that underpins the MRF method. Partially constructed libraries still resulted in accurate estimation of tissue T1, T2, and resonance offset at a variety of noise levels. As such, this technique may represent a practical improvement of the originally described method of library construction. Extension of this technique to multiple voxels is straightforward and expected to still yield substantial speed improvements since the number of distinct tissue types is expected to be far lower than the number of lattice points in the signal library. Additionally, different signal similarity criteria than the root mean square error may result in decreased susceptibility to noise.

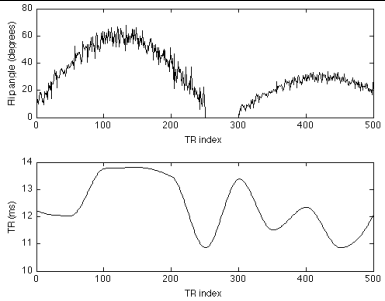

Figure 1. Flip angle (top) and TR spacing (bottom) for each of 500 RF pulses. Parameters are prescribed as in Ref. [1].

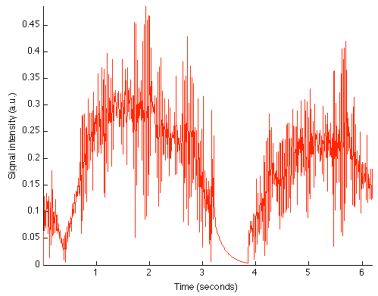

Figure 2. Simulated MRI signal with T1=500 ms, T2=200 ms, and resonance offset=10 Hz.

p	N_{TR} = 5	10	25	50
5	87.2	44.1	17.6	8.8
10	82.7	41.7	16.7	8.4
25	69.2	34.8	14.0	7.1
50	46.3	23.2	9.5	4.9
75	23.0	11.8	4.9	2.6

Table 1. Speed compared to full library construction for different p and N.

σ_{noise}	SNR	Accuracy
0	∞	100%
0.01	19.83	100%
0.02	9.92	100%
0.03	6.61	95%
0.04	4.96	85%
0.05	3.97	85%
0.10	1.98	75%

Table 2. Signal matching accuracy from a library of 6800 reference signals as a function of noise level.

References

[1] Ma D, et al. Nature 2013;495:187-192. [2] Perlin K. SIGGRAPH Comput Graph 1985;19(3):287-296.