Singular Value Decomposition for Magnetic Resonance Fingerprinting in the Time Domain

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Target Audience: This work is relevant for scientists and engineers with an interest in quantitative imaging from magnetic resonance fingerprinting.
Purpose: Magnetic resonance fingerprinting[1] (MRF) is a relatively new technique, and one of its major contributions is to simultaneously provide quantitative maps of different tissue parameters via a novel data acquisition technique. At the heart of this quantitative mapping is a dictionary that models the predicted signal evolutions from different combinations of T_1, T_2, and off-resonance values. After the data are acquired, noisy signal evolutions are matched to the dictionary by computing the inner product between a noisy signal and each dictionary entry to find the maximum. Ma, et al, simulate a dictionary using the Bloch equations with approximately 500,000 combinations of the parameters T_1, T_2, and off-resonance, sampled at each of 1,000 time points, so to classify one signal evolution will require calculating 500,000 inner products between complex-valued vectors of length 1,000. Though this template matching algorithm is shown to be accurate[1], one desires increased speed without sacrificing the high signal-to-noise ratio. We propose to compress the size of the dictionary and observed signal evolutions in the time domain by applying the singular value decomposition (SVD), thereby reducing the number of computations required for the template matching.

Methods: We begin with a dictionary that contains n entries at each of t time points, $n > t$, represented as the $n \times t$ matrix D, whose rows represent the individual entries and columns the time points. The SVD of the dictionary is $D = U\Sigma V^*$, where U and V are unitary matrices of sizes $n \times n$ and $t \times t$, respectively, and Σ is a diagonal matrix of size $n \times t$, with non-increasing diagonal entries satisfying $\sigma_1 \geq \sigma_2 \geq \ldots \geq \sigma_t$. Let the rank of D be r, $r \leq t$, then the first r columns of the matrix V form an orthonormal basis for the dictionary entries. Denoting by $V_k = [v_1, \ldots v_k]$, the first k columns of V, $k \leq r$, we can project the dictionary onto the k-dimensional subspace spanned by the vectors $\{v_1, \ldots v_k\}$, by multiplying $D_k = DV_k$, obtaining a dictionary that has been compressed in the time domain. Observed signal evolutions are compressed in one of two ways. First, let x be a t-dimensional observed signal evolution. Then x is projected onto the same subspace by $x_k = xV_k$, and the template matching is performed between x_k and D_k in the reduced k-dimensional space. Alternatively, the raw data can be projected onto the SVD space before being transformed from the spatial frequency domain to the image domain. In this case, instead of reconstructing t images from one spiral trajectory each, we instead reconstruct k images from t spiral trajectories each, reducing the number of NUFFT[2] computations and resulting in signal evolutions in the reduced space, where template matching is then performed.

Figure 1. SNR of T_1 parameter values calculated via template matching in the reduced k-dimensional subspace.

Results: By projecting the signal evolutions onto the subspace spanned by $\{v_1, \ldots v_k\}$, we are able to reduce the number of computations required in the template matching algorithm significantly without sacrificing the high SNR of the full algorithm. Performing the template match in the reduced space requires $\sim 2k(n + t)$ complex operations, whereas the full algorithm requires $\sim 2nt$ complex operations. The SNR is maintained with as few as $k = 100$ singular vectors; in Figure 1 we plot the SNR of computed T_1 values. When the SVD is applied prior to image reconstruction, more computational savings are possible through fewer NUFFT computations. In Figure 2, we show the parameter map for T_2 obtained using 25 singular vectors and the difference map comparing

Figure 2. Left: T_2 parameter map (units in ms) computed by projecting the raw data onto the SVD space with 25 singular vectors prior to image reconstruction. Right: Difference between the T_2 maps computed with the full template match as compared with the reduced match (units in ms).

the T_2 values to those obtained using the full t-dimensional template match. All computations were performed in Matlab on a standard desktop computer; the reconstruction of each of the k singular images took approximately 27 s, and template matching of the masked image was completed in 5 seconds using 25 singular vectors and 7 seconds using 100 singular vectors. Computation of the SVD took approximately 196 seconds, though this step can be precomputed as it depends only on the dictionary.

Discussion: Compression of the dictionary and the observed signals in the time domain is easily applied due to the many properties of the SVD[3], namely that it provides the best low-rank approximation of a given matrix.

Conclusion: Compression in the time domain is a first step for faster pattern recognition in MRF that maintains the high SNR of the template matching algorithm. Despite adding an additional step of projecting the data onto the reduced subspace, the overall computational load can be significantly decreased.

References: [1]Ma D, et al. Magnetic resonance fingerprinting. Nature. 2013;495 (7440):187-192. [2]Fessler J A and Sutton B P. Nonuniform fast Fourier transforms using min-max interpolation. IEEE Trans.Signal Processing. 2003;51 (2):560-574. [3]Golub G and Van Loan C F. *Matrix Computations*. The Johns 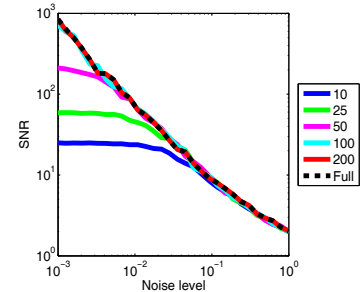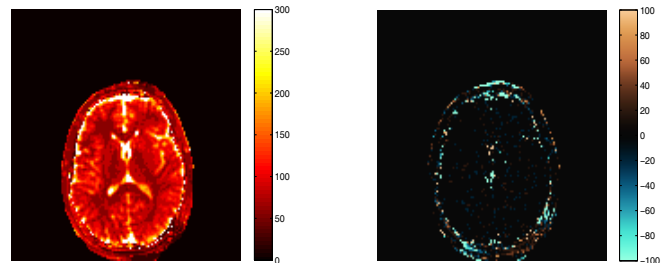Hopkins University Press, Baltimore, 1996.