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MRF-ZOOM for the Unbalanced Steady-State Free Precession (ubSSFP) Magnetic Resonance Fingerprinting

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Abstract

In magnetic resonance fingerprinting (MRF), tissue parameters are determined by finding the best-match to the acquired MR signal from a predefined signal dictionary. This dictionary searching (DS) process is generally performed in an exhaustive manner, which requires a large predefined dictionary and long searching time. A fast MRF DS algorithm, MRF-ZOOM, was recently proposed based on DS objective function optimization. As a proof-of-concept study, MRF-ZOOM was only tested with one of the earliest MRF sequences but not with the recently more popular unbalanced steady state free precession MRF sequence (MRF-ubSSFP, or MRF-FISP). Meanwhile noise effects on MRF and MRF-ZOOM have not been examined. The purpose of this study was to address these open questions and to verify whether MRF-ZOOM can be combined with a dictionary-compression based method to gain further speed. Numerical simulations were performed to evaluate the DS objective function properties, noise effects on MRF, and to compare MRF-ZOOM with other methods in terms of speed and accuracy. In-vivo experiments were performed as well. Evaluation results showed that premises of MRF-ZOOM held for MRF- FISP; noise did not affect MRF-ZOOM more than the conventional MRF method; when SNR ≥ 1 , MRF quantification yielded accurate results. Dictionary compression introduced quantification errors more to T2 quantification. MRF-ZOOM was thousands of times faster than the conventional MRF method. Combining MRF-ZOOM with dictionary compression showed no benefit in terms of fitting speed. In conclusion, MRF-ZOOM is valid for MRF- FISP, and can remarkably save MRF dictionary generation and searching time without sacrificing matching accuracy.

Keywords

magnetic resonance fingerprinting; fast searching; ubSSFP; FISP; T1; T2

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1. INTRODUCTION

Magnetic resonance fingerprinting (MRF) is an emerging technique for the estimation of multiple magnetic resonance (MR) parameters with a single time-resolved fast scan [1, 2]. It is based on the premise that the MRI signal of different tissue types can be resolved by virtue of pseudorandomized fast dynamic acquisition. As shown in Fig. 1, measured MR signal is matched to a dictionary, containing the theoretical MR signal evolution of different combinations of MR parameters, such as T1 and T2, generated by the Bloch equations [3] or extended phase graph (EPG) [4]. The MR parameters of the dictionary entry that best matches the measured MR signal are taken as the parameter estimates. The major advantages of MRF include the relative short acquisition time, a potential for multi-modal tissue segmentation, and the flexibility to incorporate parameters other than T1 and T2, etc. However, MRF has two major limitations, namely, dictionary size and dictionary searching (DS) time. The size of a dictionary increases exponentially with the number of parameters to estimate, the precision of each parameter, and the number of time points of the MRF acquisition. On the other hand, the DS time is proportional to the size of the dictionary and acquisition matrix. Both problems make the process of DS computationally demanding. Solving the two related problems therefore represents an urgent research need in MRF.

Several methods have been proposed to address the said issues but are mainly by virtue of a combination of dictionary compression [5-7] and the standard brute-force (BF) searching process as was originally proposed [1]. We have recently proposed a new fast MRF DS algorithm, dubbed MRF-ZOOM, based on optic zoom-like DS [8, 9]. MRF-ZOOM exploits two unique properties of the objective function of DS (the Pearson correlation coefficient (CC)) [1, 2], namely, separability and convexity. It has a number of advantages. Because of the parsimonious number of DS steps required to find the global maximum, MRF-ZOOM can be operated with a small pre-computed dictionary or even without a dictionary, making it highly flexible for practical use. The precision of DS can be dynamically adjusted. The fidelity of the algorithm does not depend on the range of the MR parameters associated with a pre-defined dictionary.

Because the fidelity of MRF-ZOOM was previously demonstrated only for the balanced steady-state free precession (bSSFP) sequence as used in the original MRF paper [1], it is imperative to investigate that for the unbalanced steady-state free precession sequence (ubSSFP, also called Fast Imaging with Steady-state Precession (FISP)) [10]. Furthermore, considering that MRF-ZOOM can be accelerated if full dictionary exists, an important question is whether dictionary compression can be utilized. The purposes of this work are therefore to address these two issues with the following contributions: 1) evaluations of MRF optimization objective function and MRF-ZOOM in MRF-FISP, which have not been done thus far; 2) evaluations of noise effects; 3) verifying the validity of MRF-ZOOM for the compressed dictionary; 4) comparing MRF-ZOOM to the dictionary compression-based MRF DS algorithm; 5) validating the combination of MRF-ZOOM and the dictionary compression based methods.

2. Materials and Method

2.1. The MRF DS optimization problem

Denoting the measured and Bloch-simulated MR signals respectively by $\vec{M}_a = \{A_j e^{i\theta_j}\}_{j=1}^N$ and $\vec{M}_d = \{B_j e^{i\varphi_j}\}_{j=1}^N$, where A_j and θ_j represent the magnitude and phase of $\vec{M}_a$, B_j and φ_j the magnitude and phase of $\vec{M}_d$, and N is the data length. The goal of MRF DS (Fig. 1) is to minimize the Pearson correlation coefficient function [1, 9]:

$$CC(\vec{M}_a, \vec{M}_d) = |\langle \vec{M}_a, \vec{M}_d \rangle| = \left| \sum_{j=1}^N A_j B_j e^{i(\theta_j - \varphi_j)} \right|. \quad (1)$$

Note that $\vec{M}_a$ and $\vec{M}_d$ are normalized. We have previously shown that CC was found to be pseudo periodic with respect to (w.r.t.) off-resonance, and quasi-separable and convex w.r.t. T1 and T2 [9]. The quasi-separability of off-resonance and T1/T2 allows a separate searching process for off-resonance and T1/T2. The convexity of CC permits fast searching algorithms such as Golden-section [11], Fibonacci searching [12], and etc. Golden-section was adopted in MRF-ZOOM with optimization.

2.2. Numeric simulations

The aforementioned properties of CC were derived from Bloch-simulated MR signals for bSSFP sequence. To verify whether these properties still hold for an ubSSFP sequence, we performed simulations of MR signal evolution using the extended phase graph (EPG) method [4]. 1000 timepoints were simulated. T1 value was in the range of 200 - 3500 ms (a step size of 5 ms for 200 - 2020 ms, and 20 ms for 2040 - 3500 ms) and T2 10 - 2000 ms (a step size of 2 ms for 10 - 130 ms, 4 ms for 134 and 200 ms, and 10 ms for 200 - 2000 ms). The effect of noise on the fidelity of MRF-ZOOM was also evaluated.

Two datasets were obtained: 1) 100 noise-free MR signal evolutions with different combinations of T1/T2, and 2) 20 MR signal evolutions with different combinations of T1/T2, each contaminated by 5 different levels of noise repeated over 40 times. As ubSSFP-based MRF is insensitive to off-resonance and the proton density can be quickly determined from the norms of the acquired signal and dictionary entry, only the effects of T1 and T2 on CC remains to be investigated.

In this work, a 2D MRF-ZOOM [8] was used for human brain tissue T1 and T2 quantification to avoid the potential need of a recursive T1 and T2 update process especially when the searching process is approaching the maximum where CC may become less separable with w.r.t. T1 and T2. Fig. 2 illustrates the overview of 2D MRF-ZOOM. Detailed MRF-ZOOM algorithm entails the following steps:

1. Initialization – set the center of 2D ZOOM at T1/T2=1200/40 msec, and set the ZOOM length for T1/T2 as 200/200 msec. Move the ZOOM until it centers at the maximum at a given ZOOM length.

2. Reduce ZOOM length by 4 times and repeat 1).
3. Repeat 2) until reaching the maximal precision or the stop criteria of the CC function.

The stopping criteria is that the change of absolute CC is less than $1e-5$.

Because MRF-ZOOM can be accelerated if full dictionary exists, the effect of dictionary compression using singular value decomposition (SVD) [5] on the MR parameter estimation was evaluated. Comparisons on the fidelity of MR parameter estimation from various algorithms were performed. These algorithms include, the BF searching method, MRF-ZOOM, BF with dictionary projected on the 300 singular vectors (BFSVD300), MRF-SVD [5] with 600 singular vectors (SVD600), MRF-ZOOM with dictionary projected on the 300 singular vectors (MRF-ZOOMSVD300), MRF-ZOOM with 600 singular vectors (MRF-ZOOMSVD600). For MRF-SVD, both the measured MR signal evolution and dictionary were projected into the singular vectors. DS was subsequently performed in the lower-dimensional subspace using the representation coefficients. Similarly, MRF-ZOOM was applied to those singular vector representation coefficient vectors using the same process. The same CC map assessment was performed in the lower-dimensional subspace by calculating the CC between the singular vector representation coefficient vectors of the MR signal evolution and dictionary entries. Different Gaussian noise was added to the real and imaginary part of the synthetic fingerprints separately. SNR was defined by the ratio of the mean magnitude of the noise-free fingerprints and the standard deviation of the noise. The mean SNR of our in vivo data was 0.71. To provide a similar noise environment, 5 different SNRs: 0.2, 0.5, 1, 2, 5 were tested. For each SNR level, the experiments mentioned above were repeated. All MRF DS algorithms were implemented in C++ and tested in a laptop with an Intel i-7 2.5GHz CPU with 8GB memory. The computational time was recorded.

2.3. In-vivo experiments

To validate MRF-ZOOM and its variant with dictionary compression, in-vivo MRF data were acquired from a healthy volunteer with informed consent. A 3.0 Tesla human MRI scanner (Achieva TX, Philips Healthcare) and an in-house MRF- FISP sequence [10] were used. The imaging parameters were TE = 2 ms, TI = 20 ms, FOV = $300 \times 300 \text{ mm}^2$, acquisition matrix = 128×128 , voxel size = $2.34 \times 2.34 \times 5 \text{ mm}^3$, and number of time points = 1000. Complex-valued images were first reconstructed from the k-space data using NUFFT [13].

MRF-ZOOM without a pre-defined dictionary was also implemented for MRF- FISP. The searching steps were the same as described above except that each dictionary entry was generated on-the-fly when MRF-ZOOM reached the position in the T1/T2 space. The initial searching step was 200/200 msec and was set to be 2/2 msec for T1/T2.

3. Results

3.1. $CC(T_1, T_2)$ mapping results for MRF- FISP

Fig. 3 shows the CC map of a synthetic MR fingerprint simulated with EPG and T1/T2=1040/60ms. The map clearly demonstrated the convexity and pseudo-separability as

previously identified in the bSSFP-MRF [8, 9]. *CC* properties did not change after compressing the dictionary (Fig. 3B). Slight difference was observed in the *CC* map when 300 singular vectors were used for dictionary compression. The map (Fig. 3C) for dictionary compression with 600 singular vectors was almost identical to Fig. 3A. All 3 maps peaked at the target position in the T1/T2 space. These properties permit the use of MRF-ZOOM in MRF- FISP regardless of whether the dictionary is compressed or not.

3.2. The effect of noise on different MRF DS methods

Fig. 4 shows the performance of the six different MRF DS algorithms. MRF-ZOOM yielded the same quantification results as BF regardless of whether SVD is used or not (Figs. 4A, 4C, 4D). SVD600 produced the same results as BF or MRF-ZOOM, whilst SVD300 showed large errors (Figs. 4A, 4C, 4D). On average, MRF-ZOOM is 1886.7, 733, and 1200-fold faster than BF, SVD300, and SVD600, respectively. SVD300 and SVD600 are 2.6 and 1.5 times faster than BF. MRF-ZOOM with SVD is 36 times faster than SVD (Fig. 4B). As compared to BF, SVD caused larger errors in T1/T2 for all noise levels but MRF-ZOOM did not introduce additional errors. Fitting errors reduced when SNR increased (Figs. 4C and 4D). Dictionary compression using SVD introduced quantification errors (Fig. 4C and 4D) compared to no compression.

3.3. In-vivo MRF

Fig. 5 and 6 show the estimated T1 and T2 maps from different DS algorithms. The parametric maps obtained from MRF-ZOOM and BF (Figs. 5A and 6A) are almost identical for the conditions of no SVD compression (Figs. 5B and 6B vs Figs. 5A and 6A), SVD300 (Figs. 5D and 6D vs Figs. 5C and 6C), and SVD600 (Figs. 5F and 6F vs Fig. 5E and 6E) though minor discrepancies were observed in the ZOOM-BF difference maps (Figs. 5-B1, 5-D1, 5-F1, and Figs 6-B1, 6-D1, 6-F1). As compared to the results from dictionary without compression (Figs. 5A, 5B, 6A, and 6B), SVD300 yielded aliasing artifacts (Figs. 5C, 5D, 6C, 6D) while SVD600 showed much less artifacts (Figs. 5E, 5F, 6E, and 6F). The artifacts were better displayed in the SVD vs non-SVD difference maps (Figs. 5-C1, 5-E1, Figs. 6-C1, 6-E1). Fig. 7 shows the results of MRF-ZOOM without a precomputed dictionary. By dynamically generating the dictionary on-the-fly, MRF-ZOOM took on average 0.05 sec to fit one voxel and yielded nearly the same results in the gray matter and white matter as the dictionary-based algorithms (Fig. 5A, 5B, 6A, 6B) but with discrepancy presented in CSF mainly due to the difference in dictionary resolution.

4. Discussion

The analysis of the *CC* map demonstrated that the *CC* function is convex, smooth and pseudo-separable w.r.t. T1 and T2, suggesting that the MRF-ZOOM algorithm is applicable to either non-balanced or balanced SSFP sequences. As compared to BF DS, MRF-ZOOM with pre-dictionary is thousands of times faster. When SNR is greater or equal to 1, MRF quantification yielded accurate results. Dictionary compression introduced quantification errors more to T2 than T1 quantification, likely due to the fact of that T2 is shorter than T1 and can be comparable to TR used in MRF and then be more sensitive to noise. SVD dictionary compression with up to 600 singular vectors still lead to large quantification

errors, not to mention when dictionary was compressed with 300 singular vectors, which contradicts to [5], where 200 eigen vectors were claimed to be sufficient. The difference might reflect the MRF imaging implementation difference. Different implementation will produce different datasets which will have different data variance structures and then different eigen value distributions as we know from our previous SVD-related research experience [14-16]. Nevertheless, we showed that when more variance (energy) was preserved, the fitting accuracy increased. However, as computation time increases with the number of singular vectors, larger number of singular vectors does not speed up the DS process as compared to BF. Combining MRF-ZOOM with dictionary compression does not yield significant DS speed gain because the additional computation time incurred for projecting the fingerprints onto the subspace of the singular vectors offsets the computation time saving during the CC calculation between the projected fingerprints and the projected dictionary entries. SVD compression does not alter the CC map properties because SVD-based compression is a linear transform and linear transform will not change domain properties, which also explains why MRF-ZOOM produced the same fitting results no matter whether the dictionary was compressed or not.

We didn't directly compare the pre-dictionary free MRF-ZOOM to BF because of the additional time used in MRF-ZOOM for generating the dictionary entries on-the-fly. The pre-dictionary free MRF-ZOOM took much longer time than MRF-ZOOM with a pre-dictionary mainly because of the heavy computation involved in the EPG-based simulation of MR signal evolutions. While this might discourage the use of pre-dictionary free version of MRF-ZOOM for MRF-FISP, parallel computing via video cards with graphic processing units can potentially alleviate this problem as many voxels can be processed simultaneously. Another approach to reduce the computation time of MRF-ZOOM is to use fewer time points for both the acquired MR fingerprints and the generated dictionary entries. For example, in Fig. 8, we showed that even with 200 timepoints, the CC remains to be convex and smooth, and most importantly peaks at the correct target T1 and T2. $CC(T2)$ becomes flatter as T2 further increases because the signal difference caused by different T2 becomes smaller or even negligible when T2 increases. Longer time evolution of MR signal (more time points) will be necessary to enlarge the small signal difference caused by different T2 and subsequently resolve the right T2 value by locating the right peak of $CC(T2)$. Nevertheless, Fig. 8 suggests that current MRF-ZOOM can be further accelerated by reducing the length of timeseries to be 600 or 400.

We still observed minor difference between the MRF-ZOOM results and those from BF, which might be caused by noise interference to the CC map near the peak locations. Our in-vivo data showed a mean temporal SNR of 0.71, and the difference between MRF-ZOOM and BF was then in the same range of that shown in our simulation results. Both T1 and T2 difference between MRF-ZOOM and BF became bigger in CSF when no pre-defined dictionary was used in MRF-ZOOM. This may be mainly caused by the different searching step used in the dictionary-based BF and dictionary-free MRF-ZOOM. Constrained to dictionary grid points, solutions of the dictionary-based BF can have errors in one or two multiples of the local grid resolution as we showed previously [8, 9], which the dictionary-free ZOOM doesn't have that issue.

It is worth to note that deep learning has recently been applied to MRF DS [17, 18]. We didn't compare MRF-ZOOM to them because deep learning method is often difficult to be repeated without the original implementation code. A fair comparison will also need a parallel computing-based new implementation of MRF-ZOOM using GPU, which is out of the scope of this study. Undersampling patterns and aliasing artifacts are known to affect MRF quantification accuracy [19, 20], which might need to be evaluated for MRF-ZOOM as well. But as we shown in this paper and previous papers [8, 9, 21], MRF-ZOOM is able to provide the same accuracy as that of the gold standard method, the brute-force method, so we won't expect to see additional errors due to the use of MRF-ZOOM for new applications. When more parameters are modeled in MRF such as the MRF-based arterial spin labeling perfusion MRI [22] or CEST imaging[23], the objective function properties should be re-evaluated using simulations.

5. Conclusion

In conclusion, we have successfully demonstrated that MRF-ZOOM is applicable to MRF-FISP, and shown the validity of the convexity of the Pearson correlation coefficient function. Using pre-computed dictionary, our data showed that MRF-ZOOM was thousands of times faster than BF. Dictionary compression didn't alter *the MRF CC* properties, so MRF-ZOOM holds true for with dictionary compression. MRF-ZOOM combined with SVD showed no benefit in terms of fitting speed. More eigenvectors in SVD produced less artifacts, making the results closer to those of BF but more eigenvectors would reduce the benefit of data compression and DS speed. We also showed that MRF-ZOOM can obviate pre-computed dictionary. Although the algorithm and experiments were tested and performed for a field strength of 3T and for brain imaging, we expect to see similar results in other field strengths and other organ imaging.

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List of abbreviations used:

MRF	magnetic resonance fingerprinting
DS	dictionary searching
FISP	Fast Imaging with Steady-state Precession
ubSSFP	unbalanced steady state free precession
SVD	singular value decomposition
EPG	extended phase graph
BF	brute force
SNR	signal-to-noise-ratio

CC correlation coefficient

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Fig. 1.

Illustration of MRF imaging and parameter quantification. Data acquisition is by executing the pulse sequence A) in the MR scanner B). The virtual machine E) is built upon the Bloch equations. The dictionary entries F) are the output of the virtual machine when taking the pulse sequence A) and different combinations of parameter values D) as the input. MR signal acquired with the real scanner C) is then matched G) to the dictionary F). Parameter values generating the best matched entry are assigned to the measure voxel H). The red box overlaid on the right image slice indicates the voxel involved in C, G, and H.

Fig. 2.

Illustration of a 2D MRF ZOOM. After initialization, the center of MRF-ZOOM will recurrently move to the maximum of its 9 grid points (the green circles and purple squares) until reaching a local peak (the thick black big square in the figure) where the center has a CC greater than all other boundary points (marked by green circles). A finer resolution is then used to start a new MRF ZOOM process until the specified resolution is reached. The white arrow indicates moving direction; the green circles indicate the boundary points that are closest to the center; purple squares indicate the corner points. The dashed big square indicates an intermediate location.

Fig. 3. CC(T1, T2) maps of a synthetic MR fingerprint with T1/T2=1040/60 ms. The pre-defined dictionary was compressed with A) no SVD compression, B) SVD compression using 300 eigenvectors, C) SVD compression using 600 eigenvectors. The plus signs indicate the matched location in each subfigure.

Fig. 4. Performance comparisons between 6 different MRF dictionary searching algorithms for noise-free (A and B) and noise contaminated MRF signal (in C and D). The errorbars indicate the standard deviation.

Fig. 5.

T1 maps (A to F) determined by different dictionary searching algorithms. B1, C1, and E1 are the difference of B, C, E to A. D1 and F1 are the difference between BF and MRF-ZOOM when the dictionary was compressed in the same way. The two colorbars indicate the display window of T1 values and the difference maps, respectively.

Fig. 6.

T2 maps determined by different dictionary searching algorithms. B1, C1, and E1 are the difference of B, C, E to A. D1 and F1 are the difference between BF and MRF-ZOOM when the dictionary was compressed in the same way. The two colorbars indicate the display window of T2 values and the difference values, respectively.

Fig. 7.

T1/T2 map determined by MRF-ZOOM without a pre-computed dictionary. All dictionary entries were calculated on-the-fly when MRF-ZOOM was searching the T1/T2 space. Figs. 7A1 and 7B1 shows the T1 difference between Fig. 7A and Fig. 5A (the BF T1 results), between Fig. 7B and Fig. 6A (the BF T2 results), respectively. The color scales for T1 and T2 are the same as in Fig. 5 and Fig. 6, respectively.

Fig. 8.
CC(T1, T2) maps of the same MR fingerprints with different time lengths.