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Magnetic resonance fingerprinting – An overview

Ananya Panda[a], Bhairav B. Mehta[a], Simone Coppo[a], Yun Jiang[a], Dan Ma[a], Nicole Seiberlich[a,b], Mark A. Griswold[a,b] and Vikas Gulani[a,b]

Abstract

Magnetic Resonance Fingerprinting (MRF) is a new approach to quantitative magnetic resonance imaging that allows simultaneous measurement of multiple tissue properties in a single, time-efficient acquisition. The ability to reproducibly and quantitatively measure tissue properties could enable more objective tissue diagnosis, comparisons of scans acquired at different locations and time points, longitudinal follow-up of individual patients and development of imaging biomarkers. This review provides a general overview of MRF technology, current preclinical and clinical applications and potential future directions. MRF has been initially evaluated in brain, prostate, liver, cardiac, musculoskeletal imaging, and measurement of perfusion and microvascular properties through MR vascular fingerprinting.

Addresses

[a] Departments of Radiology, Case Western Reserve University, University Hospitals Cleveland Medical Center, Cleveland, OH, USA
[b] Biomedical Engineering, Case Western Reserve University, University Hospitals Cleveland Medical Center, Cleveland, OH, USA

Corresponding author: Vikas Gulani, Department of Radiology, University Hospitals Cleveland Medical Center, 11100 Euclid Avenue, Cleveland, OH 44106, USA. (vxg46@case.edu)

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Introduction

Magnetic Resonance Imaging (MRI) is a versatile imaging technique for producing exquisite anatomical images. As compared to other cross-sectional imaging modalities, MRI provides superior soft-tissue contrast [1] and has no ionizing radiation exposure. Present-day MR scanning focuses on changing various MR system parameters such as echo time (TE), repetition time (TR) and flip angle (FA) in a systematic manner to produce images generated that are said to be qualitatively "weighted," most often by the T1 and T2 of the tissues. Current MR descriptions such as "hyperintense" and "hypointense" are relative descriptions and do not reflect absolute property values [2]. MRI also allows measurement of various tissue properties such as longitudinal relaxation time (T1), transverse relaxation time (T2), proton density (M_0), diffusion and perfusion, but these properties, particularly T1 and T2, are not typically quantitatively measured in practice.

The last few years have seen an increasing emphasis on rapid and quantitative imaging. Quantitative MR imaging can provide data that can be used as imaging biomarkers for better characterization of tissue pathology, prognostication, follow-up, patient-specific management, and therapy design [3]. While diffusion and sometimes perfusion mapping have been accepted into clinical MRI protocols to provide a modicum of quantitative information, conventional T1 and T2 mapping techniques are limited by their time inefficiency. Conventional T1 and T2 mapping methods measure tissue properties by measuring signal changes obtained by varying a single acquisition parameter, keeping all the others constant. These approaches are relatively time-consuming and typically measure only one tissue property at a time [4,5].

A novel approach to quantitative MRI was recently introduced, called MR Fingerprinting (MRF) [2]. This technique allows simultaneous efficient measurements of multiple tissue properties with one acquisition [2]. This review provides a general overview of MRF technology, current preclinical and clinical applications and potential future directions.

MRF description

MRF can be described as a three-step process comprising of data acquisition, pattern matching and tissue property visualization. The data acquisition involves deliberately varying MR system settings and parameters, i.e. the MRF pulse-sequence, in a pseudo-random manner in order to generate unique signal evolutions, or "fingerprints", for each combination of the tissue properties of interest. The fingerprints from individual voxels are compared with a collection of simulated fingerprints contained in a dictionary generated for that MRF sequence. The best match for the voxel fingerprint is selected from the dictionary through a pattern matching process. Once there is a pattern

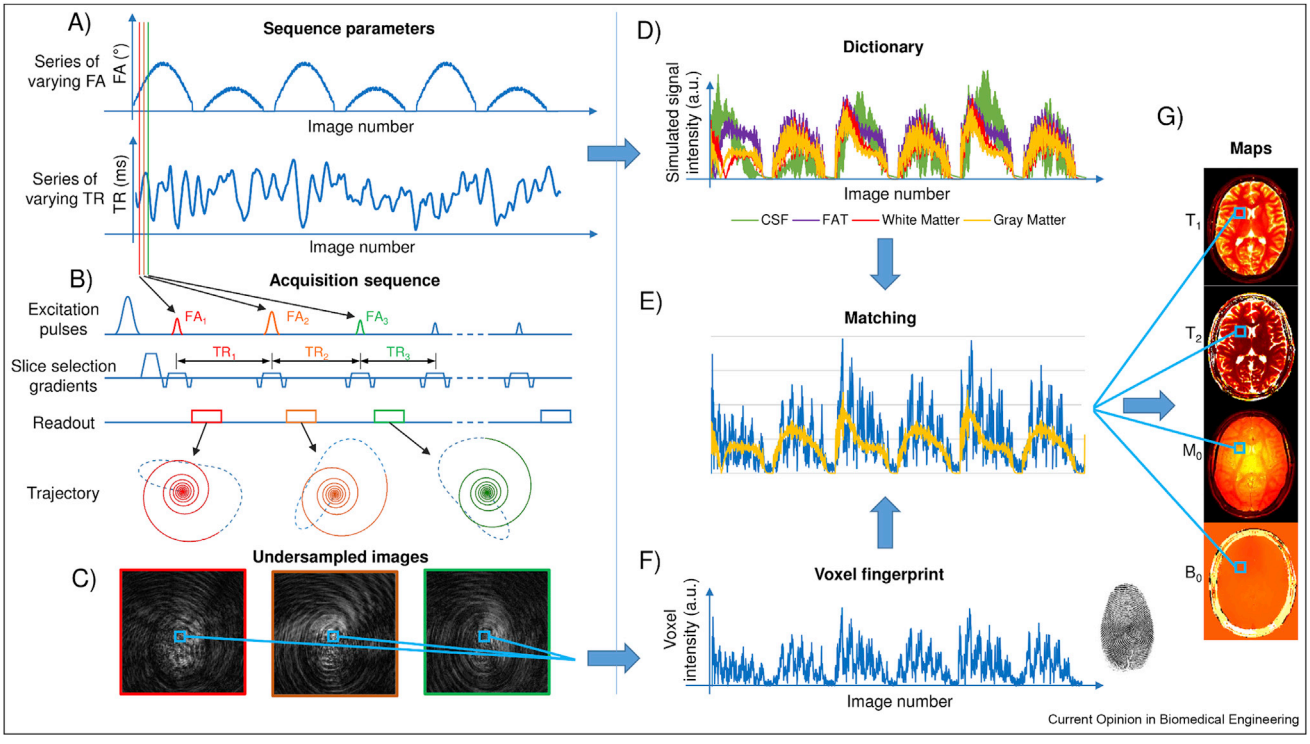
match, the combination of tissue properties that were used to generate the simulated fingerprint are identified as the underlying tissue properties in that voxel and these tissue properties are depicted as pixel-wise maps that are perfectly registered to one another, thereby providing quantitative and anatomic information [4] (Figure 1). Each of these steps is discussed in more detail below. While the original MRF description focused on measuring T1, T2, static magnetic field (B_0) inhomogeneity or off-resonance frequency and proton density M_0 [2], recent work has shown the feasibility to measure other properties such as radio frequency (RF) transmit field inhomogeneity (B_1) [6,7], T2* [8], perfusion [9] and microvascular properties [10–12].

Data acquisition

In MRF, there is a fundamental difference in the way data are acquired, as compared to conventional MRI. Instead of repeating the same acquisition parameters over time in a particular sequence until all the data in k-space have been obtained and used to reconstruct images with weighting by a particular property; in MRF the acquisition parameters such as the radiofrequency excitation angle (FA) and phase, repetition time and k-space sampling trajectory, are varied throughout the acquisition, which when implemented properly can generate a unique signal timecourse for each tissue. Proper implementation of the sequence design is crucial for obtaining useful information and determines the relevant combination of tissue properties that can be measured, how time-efficient, accurate, precise and clinically useful that MRF sequence is.

Reduction of acquisition time is important for volumetric coverage and coverage of large body regions. As originally described, MRF acquisitions were already extremely undersampled (only 1/48th of full image data set was acquired for each time point) [2]. This undersampling results in severe artifacts in the image from each individual time point. However, a philosophical decision is made in MRF: Unlike traditional mapping techniques, the focus is solely on generating quantitative maps of interest, and the artifacts in each individual image are not of concern as long as they do not compromise the matching process. Thus high quality individual time point images are explicitly not sought. Despite the significant undersampling, the signal evolution obtained from all the undersampled data can still

Figure 1



MRF overview. The flowchart shows an overview of the MRF framework as used for MR-True Fast Imaging with Steady State Precession (TruFISP) acquisition. (A) Shows an example of variable flip angles (FA) and time of repetition (TR) used for this acquisition. (B) Sequence diagram showing the excitation pulses, slice selection gradients, readout and k-space trajectory for each TR (C) shows three undersampled images acquired in different TR. (D) Shows examples of four "dictionary" entries representing four main tissues; cerebrospinal fluid (CSF) (T1 = 5000 ms, T2 = 500 ms) fat (T1 = 400 ms, T2 = 53 ms), white matter (T1 = 850 ms, T2 = 50 ms) and gray matter (T1 = 1300 ms, T2 = 85 ms). (E) Shows pattern matching of the voxel fingerprint with the closest entry in the dictionary, which allows to retrieve the tissue features represented by that voxel. (F) Shows intensity variation of a voxel across the undersampled images. (G) Shows parameter maps obtained by repeating the matching process for each voxel.