Magnetic resonance fingerprinting (MRF)

Gaby Pell

We continue our series of articles on “hot topics” in MRI with a post on an exciting approach for rapid quantification of tissue parameters.

What is MRF? In a nutshell, it is a novel approach for rapid quantification of important MRI structural and physics properties based on pattern recognition and machine learning.

Understanding the need - Quantitative vs Qualitative MRI data: The vast majority of common clinical MRI protocols rely on qualitative images reflecting the weighted effect of different tissue parameters. These contrast parameters include relaxation times, principally T1, T2 and T2*, as well as structural or functional quantities such as diffusion and blood flow. The absolute level of the signal values in these images is largely meaningless and the radiologist has to rely on prior knowledge and experience to discern abnormalities. This was however not how it was meant to be. Initial work during the formative years of MRS and MRI sparked great interest in the ability of the new technology to “quantify” tissue status with the goal of assessing pathological states. However, this promise has largely been left unfulfilled. This is due to a number of reasons, among which are the practical limitations in the common methods for quantification in which one sequence parameter is manipulated over multiple image acquisitions. Moreover, even if acquired, this information has not been found to be accurate and robust enough to identify states such as tumor staging. While efforts to speed up mapping sequences such as those for relaxometry has continued unabated, the application of these techniques has remained controversial.

Procedure of MRF: More lately, quantification of MR parameters has received a massive boost with the development of the technique of MRF by Mark Griswold’s team in Case Western in Cleveland, Ohio (Ma 2013). See Figure 1 for an overview of the process. This approach is based on a new approach of acquiring MR images that shares many characteristics as compressed sense. This is a signal processing technique for the reconstruction of signals and images from significantly fewer measurements than were traditionally thought necessary. It relies on the relative empty or sparse nature of the signal domain. Applied to MRI, it can be used to significantly reduce imaging times (Lustig 2007). In place of the steady progression through the image-encoding space (known as k-space) by accumulating ordered steps of phase gradient, MRF takes a different tack. Image acquisition parameters that directly manipulate image contrast are deliberately varied in a pseudo-random fashion (commonly combinations of sine distribution curves or algorithmic noise patterns such as Perlin noise), each followed by a rapid, under-sampled acquisition of a portion of k-space, following again a randomized trajectory. These acquisition parameters that are varied...
commonly constitute the repetition time (TR) and the flip angle (FA) but could also include other parameters, such as TE and diffusion times. Common imaging sequences are inversion-prepared TrueFISP (with the inversion pulse fortifying the T1 contrast) or basic FISP sequence, while the most common acquisition strategy is the variable gradient spiral (Lee 2003; Ma 2013). This same process is repeated a large number of times (commonly 1000 or more), creating a series of “time-points”. The combined pattern describes a signal evolution dictated by tissue parameters in each pixel. This pattern is then compared to a “dictionary” made up of a large number (commonly >500,000) of simulated signal evolution patterns calculated for a wide range of physiologically relevant tissue parameters over the same time-points. These tissue parameter sets commonly include a range of relaxation times as well as off-resonance effects since the rapid imaging sequences that are candidates for MRF are highly sensitive to susceptibility.

Pattern recognition algorithms can then be used to select the closest match from the dictionary to the measured signal evolutions, thereby determining the calculated tissue parameters at each pixel. This most simply corresponds to the maximal dot product between each measured and stored evolutions in the dictionary. In this matching process, the tissue equilibrium magnetization, $M_0$, is commonly left as a scaling parameter. Importantly, as a result of its reliance on pattern recognition rather than Fourier transform-based reconstruction, MRF is relatively insensitive to motion and other sources of noise.

This process is akin to standard fingerprinting in which the unique impression of the finger is matched against a vast database of such impressions and the resulting match thereby determines the likely identity of the individual, and along with that various associated pieces of personal information, such as age, height, date of birth etc.
MRF today

These derived parameter maps of quantities such as relaxation times that are now being used to reignite the early promise of objective tissue discrimination. These parameterized maps can also be used to reconstitute synthetically weighted images at common clinical combinations of acquisition parameters that the radiologists are used to reading. However, it may only be a matter of time when these parameter maps become the norm.

Continued development of MRF is a major area of focus in the research MR community. Over forty articles on the topic were found in a search on PubMed for 2017. The incorporation of other...
tissue parameters into the protocol are being explored such as T2*, diffusion, cerebral blood flow, 31P metabolites and chemical exchange (Wang 2017). Ways of even further accelerating acquisition are also being intensively explored, including the use of different imaging sequences, readout trajectories, techniques of dictionary compression and pattern recognition algorithms. The technique is fertile territory for machine and deep learning techniques to be incorporated (Hoppe 2017). Dictionary compression has been attempted in both the temporal and parameter combination dimensions using approaches such as single value decomposition (SVD) (McGivney 2014). Recently, “dictionary-less” methods of MRF have been presented which rely on linear fitting of parameters and therefore can dispense with the dictionary (Sbrizzi 2017).

The technique is not without its detractors, principal amongst these being Peter Rinck, a highly respected MR scientist and president of European Magnetic Resonance Forum (EMRF). He wrote one of the best introductory MR physics text books which is now available on-line¹ (which I highly recommend!). He was one of the early advocates of using tissue relaxometry for tumor grading and classification. However, he later became disillusioned following what he saw were the unfounded claims and uncertain methodology that was being used in its implementation although acknowledging certain successes (such as use of T2* maps to assess cardiac iron). He made statements in the same vein about MRF criticizing its lack of novelty and claiming that the problems that dogged those early studies have not at all been confronted in the excitement surrounding the new technique².

The killer application of MRF has yet to be found but a number of studies have shown its utility in assessing tumor status with greater classifying accuracy than regular weighted images (Badve 2014; Badve 2016; Springer 2016). See Figure 2 for an example. Here is a list of some of the issues that still need to be fully resolved before MRF hits the mainstream

1) Accuracy, repeatability and robustness of parameter quantification  
2) Sensitivity to all forms of motion and other artefacts  
3) Sensitivity to noise  
4) Base image sequence  
5) Readout strategy including trajectory, interleaves, degree of undersampling  
6) Acquisition parameter space to be manipulated  
7) Number of time-points to be acquired  
8) Dictionary complication and compression  
9) Pattern recognition algorithm

For a more extensive information on MRF, the reader is referred to the original text (Ma 2013) and a growing series of reviews on the topic (for example, Coppe 2016, ESR 2015).

¹ http://www.magnetic-resonance.org/ch/00-03.html  
Figure 2  (1A) Contrast-enhanced T1-weighted MPRAGE images show one central necrotic lesion in the left temporal lobe, with contrast media uptake at its margin. A solid part of the lesion is visible at its dorsal margin. Another equally appearing lesion is located in the left cerebral peduncle. Dorso-laterally adjacent, this part of the tumor migrates into another solid part of the tumor that ranges along the hippocampus towards dorsal. This part shows little contrast media uptake, only in the lateral portion, and no central necrosis. Spectroscopic assessment of the central necrotic lesion (not shown here) revealed Choline NAA disproportion and a lipid peak, while the more dorso-laterally located lesion also showed Choline/NAA disproportion, but to a lesser extent and no lipid peak. Consequently, in comparison to the central necrotic and strongly enhancing high grade part (Glioblastoma WHO IV) of the tumor, a lower grade part of the tumor has to be considered here. (1B-D) Corresponding calculated T2 image, T1 map and T2 map, derived from MRF data. ROIs were placed in the solid part of the tumor (red), the central necrosis (green), the lower grade part of tumor (blue), and in the surrounding edema respectively area of suspected tumor infiltration (yellow), as well as in normal appearing, contralateral white matter (pink). (1E) The scatterplot of T1 over T2 shows visible differences between the solid part of the centrally necrotic lesion (red), the central necrosis (green), the lower grade part of the tumor (blue), the surrounding edema potential infiltration (yellow) and a clear distinction from normal appearing white matter (pink).

Image and legend from (Springer 2016).
References


