Magnetic resonance fingerprinting

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Magnetic resonance is an exceptionally powerful and versatile measurement technique. The basic structure of a magnetic resonance experiment has remained largely unchanged for almost 50 years, being mainly restricted to the qualitative probing of only a limited set of the properties that can in principle be accessed by this technique. Here we introduce an approach to data acquisition, post-processing and visualization—which we term ‘magnetic resonance fingerprinting’ (MRF)—that permits the simultaneous non-invasive quantification of multiple important properties of a material or tissue. MRF thus provides an alternative way to quantitatively detect and analyse complex changes that can represent physical alterations of a substance or early indicators of disease. MRF can also be used to identify the presence of a specific target material or tissue, which will increase the sensitivity, specificity and speed of a magnetic resonance study, and potentially lead to new diagnostic testing methodologies. When paired with an appropriate pattern-recognition algorithm, MRF inherently suppresses measurement errors and can thus improve measurement accuracy.

Magnetic resonance techniques such as NMR spectroscopy and magnetic resonance imaging (MRI) are widely used throughout physics, biology and medicine because of their ability to generate detailed information about numerous important material or tissue properties, including those reflective of many common disease states1–4. However, in practice magnetic resonance acquisitions are often restricted to a qualitative or ‘weighted’ measurement of a limited set of these properties; the magnetic resonance signal intensity is almost never quantitative by itself. The same material can have different intensities in different data sets depending on many factors, including the type and set-up of the scanner, the detectors used, and so on. Because of this, the quantitative analysis of magnetic resonance results typically focuses on differences between spectral peaks, spatial locations or different points in time. Even in clinical MRI today, a tissue or material is typically referred to as being ‘hyperintense’ or ‘hypo-intense’ compared to another area, which may not provide a quantitative indication of the severity of the differences, and may have reduced sensitivity to global changes. Thus robust, fully quantitative multiparametric acquisition has long been the goal of research in magnetic resonance5–8. However, the quantitative methods developed to date typically provide information on a single parameter at a time, require significant scan time, and are often highly sensitive to system imperfections. Simultaneous, multiparametric measurements are almost always impractical owing to scan time limits and a high sensitivity to the measurement set-up and experimental conditions. Thus purely qualitative magnetic resonance measurements remain the standard today, particularly in clinical MRI.

Here we introduce a novel approach, namely MRF, that may overcome these constraints by taking a completely different approach to data acquisition, post-processing and visualization. Instead of using a repeated, serial acquisition of data for the characterization of individual parameters of interest, MRF uses a pseudorandomized acquisition that causes the signals from different materials or tissues to have a unique signal evolution or ‘fingerprint’ that is simultaneously a function of the multiple material properties under investigation. The processing after acquisition involves a pattern recognition algorithm to match the fingerprints to a predefined dictionary of predicted signal evolutions. These can then be translated into quantitative maps of the magnetic parameters of interest.

MRF is related to the concept of compressed sensing9–12, and shares many of its predicted benefits. For example, preliminary results show that MRF could acquire fully quantitative results in a time comparable to a traditional qualitative magnetic resonance scan, without the high sensitivity to measurement errors found in many other fast methods. Most importantly, MRF has the potential to quantitatively examine many magnetic resonance parameters simultaneously given enough scan time, whereas current magnetic resonance techniques can only examine a limited set of parameters at once. Thus MRF opens the door to computer-aided multiparametric magnetic resonance analyses, similar to genomic or proteomic analyses, that could detect important but complex changes across a large number of magnetic resonance parameters simultaneously. When an appropriate pattern recognition algorithm is used, MRF also provides a new and more robust behaviour in the presence of noise or other acquisition errors that may lead to the near complete suppression of deleterious effects stemming from these factors. Although we focus on demonstrating the feasibility for MRI in this study, it is rather straightforward to translate these results to other magnetic resonance fields, such as multiparametric NMR spectroscopy, dynamic contrast enhanced MRI and dynamic susceptibility contrast MRI13.

Generation and recognition of MRF signals

The key assumption underlying the MRF concept is that unique signal evolutions, or fingerprints, can be generated for different materials or tissues using an appropriate acquisition scheme. Here we demonstrate that this is possible through the continuous variation of the acquisition parameters throughout the data collection. Variations in the pulse sequence parameters during acquisition have been used previously in MRI and magnetic resonance spectroscopy to reduce the signal oscillations14 and to improve the spectral response15–17. However, these variations were primarily used in a preparation phase or to make the signal more constant. Randomized sampling patterns have also been used previously to aid in the separation of spatiotemporal signals in moving objects or substances with different resonance frequencies18–20. Here we demonstrate that temporal and spatial incoherence required in MRF can be achieved by varying acquisition parameters—such as the flip angle and phase of radio frequency pulses, the repetition time, echo time and sampling patterns—in a pseudorandom manner.

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After the data are acquired, the separation of the signal into different material or tissue types can be achieved through pattern recognition. In its simplest form, this process is analogous to matching a person’s real fingerprint to a database: once a match is made, a host of additional information about the person, such as name, address and phone number, can be obtained simultaneously once the fingerprint sample is identified. In MRF, this pattern recognition can take place through many means. In the current implementation, we construct a dictionary that contains signal evolutions from all foreseeable combinations of materials and system-related parameters—for example, the longitudinal relaxation time, \( T_1 \), the transverse relaxation time, \( T_2 \) and off-resonance frequency are included in this study. Other properties could also be measured, such as diffusion and magnetization transfer using the well-established Bloch equation formalism of magnetic resonance \( ^{21,22} \). Once this dictionary of possible signal evolutions is generated, a matching or pattern recognition algorithm \( ^{23,24} \) is then used to select a signal vector or a weighted set of signal vectors from the dictionary that best correspond to the observed signal evolution. All the parameters that were used to build this signal vector in the dictionary can then be retrieved simultaneously. At present, the calculation of a complete dictionary containing the realistic range of \( T_1 \), \( T_2 \) and off-resonance frequency requires only a few minutes on a modern desktop computer.

It should be noted that there are near-infinite possibilities for MRF-compatible pulse sequences. Other magnetic resonance parameters of interest can be investigated by identifying pulse sequence components that impart differential sensitivity to the parameters of interest. Moreover, different components can be varied simultaneously, adding the potential for a highly efficient experimental design that allows almost any material characteristic visible using magnetic resonance to be analysed in a quantitative way using MRF.

### Validation of the concept

For a proof-of-principle implementation, an MRF acquisition based on an inversion-recovery balanced steady state free-precession (IR-bSSFP) sequence was used (Fig. 1a). This choice of this basic pulse sequence was based on the extensive existing knowledge about IR-bSSFP signal evolution, and its sensitivity to \( T_1 \), \( T_2 \) and off-resonance frequency \( ^{25} \). After each radio-frequency pulse, one interleaf of a variable density spiral (VDS) read out \( ^{26} \) was acquired, as shown in Fig. 1b. Such a VDS trajectory has been used in fast imaging \( ^{27} \) and for the reduction of undersampling errors \( ^{28} \). Two MRF acquisition patterns with randomized flip angle and repetition time were used as shown in Fig. 1c and d in separate scans to demonstrate the flexibility of the choice of the acquisition parameters.

Figure 2a and b show the simulated signal evolution curves that would be expected from four commonly encountered tissues of the brain (fat, white matter, grey matter and cerebrospinal fluid) using the schematic implementation shown in Fig. 1c and d, respectively. Each tissue type has characteristic \( T_1 \) and \( T_2 \) values and thus each signal evolution has a different shape, which confirms that it is possible to satisfy this fundamental assumption in MRF. Note also that the signal levels in these evolutions represent a large fraction of the equilibrium magnetization (which is normalized to one in these figures.) Conventional spoiled steady-state sequences typically generate signal levels corresponding to 1–10% of the equilibrium magnetization. Figure 2c and d show an acquired signal evolution curve from fully sampled experiments on manufactured agar ‘phantoms’ and its match to the dictionary by using the acquisition pattern shown in Fig. 1c and d, along with the recovered \( T_1 \), \( T_2 \), proton density (\( M_0 \)) and off-resonance frequency values. MRF was able to match the signal to the corresponding dictionary entry and obtain the same \( T_1 \) and \( T_2 \) values from both sequence patterns. A video of the signal evolution from a fully sampled in vivo scan is available (Supplementary Video 1), demonstrating the oscillating nature of the MRF signal observed in vivo.

### Accelerated MRF acquisitions

In addition to simultaneously quantifying multiple parameters, the error tolerance of MRF can be significantly better than that of conventional MRI. Because MRF is based on pattern recognition in a setting where the form of all predicted signal evolutions is known, MRF should be less sensitive to errors during the measurement. This is similar to conventional fingerprint recognition techniques, which often contend with smudges and partial fingerprint information. In particular, the interaction of the temporal and spatial incoherence possible in MRF provides new opportunities to accelerate image acquisition through rejection of spatial undersampling errors. In order to test the limits of this acceleration, the same MRF sequence as shown in Fig. 1a–c was modified to use only one spiral readout in each acquisition block. Therefore, the data collected are only 1/48th of the normally required data at each time point, resulting in a total acquisition time of 12.3 s, corresponding to 1,000 sampled time points. (See Fig. 3a and Supplementary Video 2.) The signal evolutions from all 1,000 undersampled time points were used directly to match one entry from the dictionary to quantify \( T_1 \), \( T_2 \), \( M_0 \) and

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**Figure 1** MRF sequence pattern. a. Acquisition sequence diagram. In each subsequent acquisition block, identified by a repetition time index (TR index; TR(1)...TR(N)), various sequence components are varied in a pseudorandom pattern. FA, flip angle. b. Here, one variable density spiral trajectory was used per repetition time. The Fourier coefficients sampled by the variable density spiral trajectory (given by the coordinates \( k_x \) and \( k_y \)) are rotated from one repetition time to the next. c, d. Examples of the first 500 points of flip angle and repetition time patterns that were used in this study.
White matter (−30 Hz off-resonance) RESEARCH

clearly visualized in the off-resonance map. We also note that the roughly
observation of
methods DESPOT1 and DESPOT2 (driven equilibrium single pulse
ively. The concordance coefficient correlations for
between MRF and spin-echo sequence were 0.988 and 0.974, respect-
sequences34 as well as modern rapid combined
with alternative mapping strategies, namely, standard spin-echo
The accuracy and efficiency of the MRF acquisitions were compared
Accuracy and efficiency of MRF

The high concordance correlation coefficients indicate that both
methods are in good agreement with standard spin-echo measurements,
and that MRF shows a better accuracy than DESPOT1 and DESPOT2.
The theoretical comparison of the efficiency from various mapping
methods has been presented35,36 and is based on a measure of precision
per square root of scan time. In those publications, DESPOT1 and
DESPOT2 were shown to have greater efficiency than all previously
known conventional and accelerated mapping strategies36. As can be
seen in Fig. 5b, MRF outperforms both DESPOT1 and DESPOT2 by an
average factor of 1.87 and 1.85, respectively. For example, at a
of
1,280 ms, MRF shows an average efficiency for estimation of
2 of 24.2, whereas DESPOT1 has an average efficiency of 10.89. This means
that for this
value, MRF achieves a precision of ±15.2 ms (or 1.2%) in
12 s of scan time, whereas the precision in DESPOT1 would be
±33.9 ms (or 2.6%) for the same scan time. The DESPOT methods
apparently display higher efficiency from the single phantom, with
1 of 360 ms and
1,280 ms, MRF shows an average efficiency for estimation of
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14 MARCH 2013 | VOL 495 | NATURE | 189

Motion error tolerance in MRF

Because motion is one of the most common sources of error in an MRI
scan, a motion-corrupted scan was performed using the accelerated
MRF acquisition described in the previous section. The subject was
instructed to randomly move his head for the last 3 s of a total 15-s
scan. Supplementary Video 3 shows the random motion as well as
severe undersampling artefacts in the reconstructed images. Figure 4
describes the quantitative maps from the data with and without the
motion-corrupted data. The maps acquired during motion show
almost no sensitivity to the motion, and show nearly the same quality
and anatomy as the maps from the motion-free data, thus indicating
that the signal changes resulting from motion were uncorrelated with
the evolutions included in the dictionary, and were largely ignored by
the pattern recognition algorithm.

Accuracy and efficiency of MRF

The accuracy and efficiency of the MRF acquisitions were compared
with alternative mapping strategies, namely, standard spin-echo
time evolution curves corresponding to four normal brain tissues using the
sequence patterns in Fig. 1c and d, respectively, as a fraction of the
equilibrium magnetization. The curve from white matter with off-resonance
is also plotted. c, d, Measured signal evolution from one of eight
phantoms using different sequence patterns and their dictionary match. The estimated
T1, T2 and off-
resonance frequencies are 340 ms,
50 ms and −41 Hz (c) and 340 ms,
50 ms, −13 Hz (d). The plots are
normalized to their maximum value.
about the material, tissue or pathology of interest. Because there is no a priori requirement on the shape of the signal evolution curves, there are more degrees of freedom in designing an MRF acquisition, where parameters such as repetition time, echo time, radio frequency pulses and sampling trajectories (among others) can be varied together to produce the simultaneous sensitivity to numerous tissue properties. The ability to analyze oscillating signals in MRF also provides the opportunity to use larger fractions of the available magnetization than methods that rely on a steady-state signal, which is a significant factor contributing to the higher efficiency in MRF. In addition, the oscillatory signal in MRF allows one to sample more informative points along a longer signal evolution as compared to conventional methods which always reach a steady state level after some finite amount of time. Specifically, our initial results here demonstrate that the efficiency of MRF is approximately 1.8 times higher than the DESPOT methods, which were previously the most efficient methods for the measurement of relaxation parameters. Thus the direct prediction of the oscillating, incoherent signal evolutions through the Bloch simulation provides us the potential to obtain new quantitative information that is impractical today because of the prohibitively long scan times required, especially in biological samples and patients.

As demonstrated by the results shown here, MRF has the potential to significantly reduce the effects of errors during acquisition through its basis in pattern recognition. Acquisition errors may globally reduce the probability of a match of an observed signal to any given fingerprint, but as long as the errors do not cause another fingerprint to become the most likely match, the correct quantitative identification will still be made. Ideally, the sequence pattern will be designed so that the various fingerprints from different tissues and materials are as independent as possible, thus ensuring this robustness against motion and other practical errors.

Commercial magnetic resonance scanners include methods to minimize the effects of unavoidable system imperfections. However, these inaccuracies are becoming increasingly important as magnetic resonance technology is pushed to its limits, such as the use of very high magnetic fields or physically larger systems. MRF provides a route to model and account for system imperfections, such as inhomogeneities in both the static magnetic field (B₀) and the

### Table 1 | In vivo data

| Tissue Type                                      | T₁  (ms) | T₂  (ms) |
|-------------------------------------------------|----------|----------|
| White matter (this work)                        | 685 ± 33 | 65 ± 4   |
| White matter (previously reported)              | 608-756  | 54-81    |
| Grey matter (this work)                         | 1,180 ± 104 | 97 ± 5.9 |
| Grey matter (previously reported)               | 998-1,304 | 79-98    |
| Cerebrospinal fluid (this work)                 | 4,880 ± 379 | 550 ± 251 |
| Cerebrospinal fluid (previously reported)       | 4,103-5,400 | 1,800-2,460 |

Shown are comparisons of MRF results and reference values in different brain regions.
and compare the measured signal evolutions against the set of known states of interest. This measurement could either indicate the presence of the material or disease of interest, or indicate its absence within a margin of error. This feature could result in very rapid and accurate screening procedures. In particular, this feature may help to relax the required spatial resolution of an MRI examination, thus increasing the speed, and potentially reducing the cost, of such an examination.

A preliminary example of this kind of visualization is shown in Supplementary Information Section 3. Using the MRF concept, the operation of the magnetic resonance unit will also be greatly simplified, because the ‘all in one’ scan concept of MRF has the potential to reduce the dozens of parameters currently presented to the magnetic resonance operator to a simple ‘scan’ button.

It is important to note that the proof-of-principle implementation of MRF shown here is but one of the many possibilities that could be used for this technique, and both the sequence design/implementation and post-processing methods will continue to be a significant open area of research, just as sequence design has advanced over the decades since the conventional methods have been introduced. Other, more advanced pattern recognition algorithms would probably improve the performance of MRF. For spatially encoded MRI applications, the parameters retrieved from MRF are far fewer than the number of pixels in the images, and because the signals generated are largely incoherent, MRF has the additional potential to be highly accelerated through combination with other compressed sensing methods for accelerated spatial encoding, in addition to the now standard parallel imaging methods, neither of which were included here. Any of these methods would reduce the undersampling errors seeing in Fig. 3a even before the pattern recognition step, which should result in higher quality results. We have recently published data indicating that we can achieve a reduction in imaging time of about ten times for a two-dimensional slice using parallel imaging alone. Also, it should be noted that the proof-of-principle results shown here only take advantage of two spatial dimensions for undersampling, whereas it is well known that taking full advantage of undersampling in all three spatial dimensions gives higher performance than a two-dimensional acquisition owing to the reduced power of the resulting errors at any given undersampling factor. Thus a combination of an optimized three-dimensional MRF pulse sequence with parallel imaging and more advanced pattern matching algorithms will allow realization MRF in very short scan times.

METHODS SUMMARY

Sequence design. After an initial inversion pulse, the sequence pattern shown in Fig. 1c used a pseudorandomized series (Perlin noise) of flip angle and a random repetition time from 10.5 to 14 ms. The flip angle pattern in Fig. 1d contained repeating sinusoidal curves with a period of 250 acquisitions and alternating maximum flip angles. The repetition time was a Perlin noise pattern. The radio frequency phase for both of the patterns alternated between 0 and 180° on successive radio frequency pulses. The variable density spiral-out trajectory was designed using minimum-time gradient design.

Dictionary design. A total of 563,784 signal time courses, each with 1,000 time points, with different sets of characteristic parameters (T₁, T₂, and off-resonance) were simulated for the dictionary. One dictionary entry was selected for each measured pixel location using template matching. In this case, the vector dot-product was calculated between the acquired data and all dictionary entries using complex data for both. The dictionary entry with the highest dot-product was then selected as most likely to represent the true signal evolution. The M₀ value is then the multiplicative constant derived by fitting the acquired data to this dictionary entry.

Data acquisition. All data were acquired on a 1.5-T whole body scanner (Espree, Siemens Healthcare) with a standard 32-channel head receiver coil. Images from each acquisition block were reconstructed separately using non-uniform Fourier transform. The resultant time series of images was used to determine the value for the parameters (T₁, T₂, M₀ and off-resonance) as described above.

Statistical analysis. Quantitative estimates of the errors and efficiencies of MRF, DESPOT1 and DESPOT2 were calculated pixel-wise using a bootstrapped Monte Carlo method. The means and standard deviations of T₁ and T₂ along the 50...
repetitions were calculated, and averaged within a square (5 pixel × 5 pixel) region of interest for each phantom. The concordance correlation coefficients and efficiency were calculated as in refs 30 and 52.

**Full Methods** and any associated references are available in the online version of the paper.

**Received 11 September 2012; accepted 30 January 2013.**

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**Supplementary Information** is available in the online version of the paper.

**Acknowledgements** Support for this study was provided by NIH R01HL094557 and Siemens Healthcare. We also thank H. Saybasili and G. Lee for technical assistance during the implementation of these concepts; M. Lustig and W. Grissom for discussions regarding this work; and A. Exner, S. Brady-Kalnay, E. Larivé and H. Salz for their assistance in preparing the manuscript.

**Author Contributions** D.M., concept development, technical implementation, data collection and analysis, manuscript development and editing; V.G., concept development, manuscript development and editing; N.S., concept development, manuscript development and editing; K.L., concept development, technical implementation, manuscript development and editing; J.L.S., concept development, manuscript development and editing; J.D.L., concept development, manuscript development and editing; M.A.G., concept development, data collection and analysis, manuscript development and editing.

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METHODS

Sequence design. After an initial inversion pulse, the first sequence pattern shown in Fig. 1c used a pseudorandomized series (Perlin noise45) of flip angle and a random repetition time between 10.5 ms and 14 ms based on a uniform random number generator. A linear ramp was added to the flip angle train since we have seen that this can increase differential sensitivity to both \( T_1 \) and \( T_2 \).

The second flip angle pattern in Fig. 1d used a series of repeating sinusoidal curves with a period of 250 repetition times and alternating maximum flip angles. In the odd periods, the flip angle (FA) is calculated as \( FA_i = \frac{10 + \sin \left( \frac{2\pi r}{500} \right)}{250} \), where \( r \) is from 1 to 250, and random(5) is a function to generate uniformly distributed values with a standard deviation of 5. In the even periods, we divide the previous period’s flip angle by 2. A 600 ms delay was added between each of the periods to allow for both differential magnetization recovery according to \( T_1 \) and differential signal decay according to \( T_2 \). In this case, the repetition time was a Perlin noise pattern. The radio frequency frequency phase for both of the patterns in Fig. 1 alternated between 0 and 180° on successive pulses.

The variable density spiral-out trajectory was designed to have 5.8 ms readout time in each repetition time and to have zero and first moment gradient compensation using minimum-time gradient design49. (The code used for this design is available at http://www-mrsl.stanford.edu/~brian/minitgrad/). This trajectory required one interleaf to sample the inner 10 × 10 region, while 48 interleaves were required to fully sample the outer portions of k-space. During acquisition, the spiral trajectory rotated 7.5° from one time point to the next, so that each time point had a slightly different spatial encoding.

Dictionary design. The dictionary used in the matching algorithm was simulated using MATLAB (The MathWorks). Signal time courses with different sets of characteristic parameters (\( T_1 \), \( T_2 \) and off-resonance) were simulated. The ranges of \( T_1 \) and \( T_2 \) for the in vivo study were chosen according to the typical physiological limits of tissues in the brain: \( T_1 \) values were taken to be between 100 and 5,000 ms (in increments of 20 ms below a \( T_1 \) of 2,000 ms and in an increment of 300 ms above). The \( T_2 \) values included the range between 20 and 3,000 ms (with an increment of 5 ms below a \( T_2 \) of 100 ms, an increment of 10 ms between 100 ms and 200 ms, and an increment of 200 ms above a \( T_2 \) of 200 ms). Since magnetic resonance is sensitive to parts per million (p.p.m) level deviations in the \( B_0 \) field, different off-resonance frequencies (1 Hz increment between ±40 Hz, 2 Hz between ±40 to ±80 Hz, 10 Hz between ±80 to ±250 Hz, and 20 Hz between ±270 to ±400 Hz) were simulated for each combination of \( T_1 \) and \( T_2 \) parameters to incorporate the effects of signal evolutions in different \( B_0 \) fields. A total of 563,784 dictionary entries, each with 1,000 time points, were generated in 399 s on a standard desktop computer. One dictionary entry was selected for each measured pixel location using template matching. In this case, the vector dot-product was calculated between the measured time course and all dictionary entries (appropriately normalized to each having the same sum squared magnitude) using the complex data for both. The dictionary entry with the highest dot-product was then selected as most likely to represent the true signal evolution. The proton density (\( M_0 \)) of each pixel was calculated as the scaling factor between the measured signal and the simulated time course from the dictionary. For this experiment, four parameters were retrieved simultaneously from each of the 128 × 128 pixels using MRF. This calculation required about 3 min on a standard desktop computer.

Data acquisition. All MRI and MRF data were acquired on a 1.5 T whole body scanner (Siemens Espree, Siemens Healthcare) with a 32 channel head receiver coil (Siemens Healthcare). A square field of view of 300 mm × 300 mm was covered with a matrix of 128 × 128 pixels. The slice thickness was 5 mm. Images from each acquisition block were reconstructed separately using non-uniform Fourier transform (NUFFT)39. The resultant time series of images was used to determine the value for the parameters (\( T_1 \), \( T_2 \), \( M_0 \) and off-resonance) as described above.

In vivo experiments were performed with IRB guidelines, including written informed consent. For the fully sampled spiral acquisition shown in Supplementary Video 1, 48 repetitions were acquired, each with a different interleaf of the total acquisition. A recovery time of 5 s was used in between various acquisitions and this was taken into account in the simulated dictionary.

For the phantom study shown in Figs 2 and 4, eight cylindrical phantoms were constructed with varying concentrations of GdCl3 (Aldrich) and agarose (Sigma) to yield different \( T_1 \) and \( T_2 \) values ranging from 67 to 1,700 ms and 30 to 200 ms, respectively. Standard spin echo sequences were used to quantify \( T_1 \) and \( T_2 \) separately (\( T_1 \) quantification: 13 repetition times (TRs) ranging from 50 to 5,000 ms, echo time TE = 8.5 ms, total acquisition time = 33.4 min; \( T_2 \) quantification: spin echo sequences with \( T_E = [15, 30, 45, 60, 90, 150, 200, 300, 400] \text{ ms}, \text{TR} = 10,000 \text{ ms, total acquisition time = 3.2 h} \). \( T_1 \) values were calculated pixel-wise using a standard three-parameter nonlinear least squares fitting routine to solve the equation: \( S(\text{TR}) = a + be^{\text{TR}/T_1} \). \( T_2 \) values were determined in a pixel-wise fashion using a two-parameter nonlinear least squares fitting routine to solve the equation \( S(\text{TR}) = a + c e^{\text{TR}/T_2} \).

Efficiency and accuracy of MRF. For DESPOT1 and DESPOT2 sequences using a fully sampled spiral readout were implemented based on the acquisition values from ref. 30. DESPOT1: FA: \( 4^\circ \) and \( 15^\circ \), TR: 13.6 ms, DESPOT2: FA: \( 15^\circ \) and \( 55^\circ \), TR = 10.8 ms. The \( T_1 \) and \( T_2 \) values were calculated from the equations provided in ref. 30. A 20 s waiting period was used in between the different acquisitions. The initial 10 s of data acquisition was not used in order to ensure that the signal was in steady-state for each of the DESPOT acquisitions. In the following analysis of efficiency, only the pure time of data acquisition for the steady-state DESPOT images is used. For DESPOT1 this was 1.27 s and for DESPOT2 it was 2.29 s (which includes the time for the required DESPOT1 acquisition).

Statistical analysis. Quantitative estimates of the errors and efficiencies of MRF, DESPOT1 and DESPOT2 were calculated pixel-wise using a bootstrapped Monte Carlo method51. Two sets of raw data were acquired for each sequence: the encoded signal and a separate acquisition that only contained noise. Fifty reconstructions were then calculated by randomly resampling the acquired noise and adding it to the raw data before reconstruction and quantitation. The means and standard deviations of \( T_1 \) and \( T_2 \) along the 50 repetitions were calculated, and both were averaged within a 5 pixel × 5 pixel square region of interest for each phantom. The concordance correlation coefficients (\( r_c \)) were calculated using the equation47:

\[
p_c = \frac{2S_{12}}{S_1^2 + S_2^2 + (T_2 - T_1)^2}
\]

where \( Y_1 \) and \( Y_2 \) denotes the \( T_1 \) or \( T_2 \) values from two different methods, \( n \) is the number of phantoms, \( Y_{ij} = \frac{1}{n} \sum_{i=1}^{n} Y_{ij} \), \( S_1^2 = \frac{1}{n} \sum_{i=1}^{n} (Y_{ij} - Y_1)^2 \), \( j = 1, 2 \) and \( S_{12} = \frac{1}{n} \sum_{i=1}^{n} (Y_{ij} - T_1)(Y_{ij} - T_2) \).

The efficiency of the methods was calculated using:

\[
\text{Efficiency} = \frac{T_{NR}}{\sqrt{T_{q}}}, n = 1, 2
\]

where \( T_{NR} \) is the \( T_1 \) or \( T_2 \) to noise ratio (defined as the \( T_1 \) or \( T_2 \) value divided by the estimated error). \( T_{q} \) is the total acquisition time for MRF, and the relevant acquisition times for DESPOT1 and DESPOT2 (where the waiting times required for the approach to steady state and the time between each of the DESPOT1 and DESPOT2 scans to allow for complete recovery of magnetization were ignored).