Radiology

Reproducing Fingerprints: A Step toward Clinical Adoption

Frederik Barkhof, MD • *Geoff J. M. Parker, PhD*

From the Center for Medical Image Computing and Institute of Neurology, University College London, London, England (F.B., G.J.M.P.); and Department of Radiology and Nuclear Medicine, Amsterdam UMC, Vrije Universiteit, De Boelelaan 1117, Amsterdam, the Netherlands (F.B.). Received May 20, 2019; revision requested May 23; final revision received May 28; accepted May 29. **Address correspondence to** F.B. (e-mail: *f.barkhof@vumc.nl*).

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See also the article by Körzdörfer et al in this issue.

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Classic MRI sequences optimize image contrast based on physical properties such as proton density and T1 and T2 relaxation times by applying fixed combinations of radiofrequency pulses and repetition times across various pulse sequences to obtain consecutive series of images with different types of image contrast. MR fingerprinting was introduced in 2013 as a revolutionary data acquisition scheme, in which radiofrequency pulses and repetition times are applied in a pseudorandom fashion to create signal evolutions that simultaneously characterize the various relaxation processes unique for each type of tissue—the MR "fingerprint" (1). The signals acquired are referenced against a (simulated) data dictionary, allowing extraction of multiple tissue properties such as T1 and T2 relaxation times, proton density, and diffusion with a single acquisition in the order of 5 minutes.

The promise of MR fingerprinting is the provision of robust quantitative MRI measurements within a short imaging time, which has the potential to enable widespread standardized MRI tissue characterization. However, to date, to our knowledge, clinical applications of MR fingerprinting are only emerging slowly (eg, to determine brain maturation or to characterize brain tumors [2,3]). The slow clinical translation in part reflects technical barriers in implementing the MR fingerprinting technique, such as the availability of suitable pulse sequences and image reconstruction methods. In addition, little is known about the reproducibility and repeatability of MR fingerprinting in a clinical setting, which reduces the confidence of practitioners who may otherwise be motivated to deploy MR fingerprinting.

In this issue of *Radiology*, Körzdörfer and colleagues (4) explore the use of MR fingerprinting to determine the within-scanner and between-scanner variability of relaxation times in various regions of the healthy brain. Ten healthy volunteers were imaged multiple times with 10 different machines—all Siemens Healthcare (Erlangen, Germany) operating at 3.0 T—to determine repeatability (within-scanner variation) and reproducibility (between-scanner variation). The MR fingerprinting implementation tested was a fast imaging with steady-state free precession sequence; seven sections with a thickness of 5 mm were acquired in 5 minutes. T1 and T2 relaxation times were determined by comparing the acquired signals to a dictionary of simulated T1 and T2 relaxation times. Results showed that the between-scanner reproducibility, defined by using the 95% confidence intervals on relative deviation, is around 3.4% for T1 and around 8% for T2 in solid tissues. Within-scanner repeatability was slightly better, with best values of around 2% for T1 and 3.1% for T2 in solid tissues. Values in cerebrospinal fluid were much less favorable, probably because the acquisition scheme did not have appropriate flip angle and repetition time combinations to sample longer relaxation times in cerebrospinal fluid, or due to cerebrospinal fluid motion during image acquisition. The measured values of T1 and T2 fall within the previously reported range for white and gray matter at 3.0 T, although tend to be on the long side for T1 and on the short end for T2. Measurements using a calibrated relaxation time phantom showed deviations from the expected values of less than 10% for both T1 and T2.

Why has there been relatively little progress in translating MR fingerprinting to clinical applications since its initial description in *Nature* in 2013 (1)? The answer has multiple components, as is so often the case with groundbreaking MR methods. MR fingerprinting requires a complex pulse sequence for data acquisition, a sufficiently large dictionary, and computing power to process the data. Robust implementation for clinical use, therefore, inevitably takes time. The revolutionary approach of quantitative image formation makes it important to fully understand the accuracy, precision, and generalizability of the outputs of the method. The work presented in this issue by Körzdörfer and colleagues (4) makes a substantial contribution by confirming the accuracy and precision of the method, providing further confidence in the technical validity of MR fingerprinting. The requirement for such detailed characterization means that, to date, no vendor has provided a commercial regulatory-approved implementation, although this is likely to change in the near future. Performance of MR fingerprinting with other scanner brands should be investigated, as well as extensive investigation of performance in the setting of patients with disease and in a range of anatomic locations.

It is important to note that MR fingerprinting continues to evolve as a method, with widespread active research taking place. The sequence used by Körzdörfer and colleagues (4) is a two-dimensional steady-state gradient-echo sequence (eg, fast imaging with steady-state free precession), with inherent limitations to measure proton density

and other tissue properties. Alternative sequences are being developed to measure proton density, diffusion, perfusion, chemical exchange, and B1 homogeneity (5). Improvements are also being made in terms of tissue coverage and spatial resolution, with three-dimensional versions being developed (6). Finally, parameter map reconstruction may benefit from deep learning, both in speed and accuracy.

A more fundamental question that may limit adoption of MR fingerprinting is why one would want to measure T1 and T2 relaxation time, or for that matter any quantitative MR parameter, given the astounding success of MRI as a qualitative imaging modality? Tissue property quantification has been shown to be useful in well-controlled research studies to detect small differences between groups of patients, but is hardly used in clinical routine (with the exception, perhaps, of the apparent diffusion coefficient). Indeed, measuring T1 and T2 relaxation times per se may not be the ultimate clinical use of MR fingerprinting, as the obtained parameter maps may be more useful when used to generate synthetic image contrast. This allows a full set of clinical images (including fluid-attenuated inversion recovery) to be generated from a single acquisition. We are at a pivotal point in the clinical use of MRI, as never before has quantitative measurement been so readily available. MR fingerprinting may be the technique that makes common use of quantification a clinical reality.

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