

Quantitative evaluation of the effect of reduction of signal acquisition number in MR fingerprinting

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Purpose: MR fingerprinting (MRF)¹ is capable of quantitatively mapping multiple parameters simultaneously. A train of pseudorandom radiofrequency (RF) excitations are used to generate unique signal evolution patterns for different tissues, followed by matching of the measured signals to a pre-established dictionary storing signal evolutions simulated by Bloch equation to achieve parameter mapping¹. The signal acquisition number is related to the signal length. Longer signals lead to longer scan time as well as larger dictionaries which increase the computational complexity during signal analysis. In this study, we propose a contour area index to evaluate the effect of reducing signal acquisition number in an MRF sequence.

Methods: In MRF, the signal evolution from one pixel is compared with every signal in the pre-established dictionary by orthogonal matching pursuit², where the dictionary signal pattern showing the largest inner product is treated as the best match. Ideally, the inner product for the best match should be distinctly greater than those for others to ease judgment of the best match. Conversely, an increased number of dictionary signals exhibiting large inner products simultaneously would imply an ill-designed RF excitation scheme. Thus, the number of dictionary signals exhibiting large inner products could be used as an index to evaluate the effectiveness of MRF RF excitation scheme.

To derive the index, all of the inner products are placed in a space with axes constructed by MRF mapping parameters, which are T1, T2 and off-resonance frequency in this study. The points whose inner product values are larger than a pre-specified threshold (0.95 in our study) are encircled to form a 2D contour in the 3D space. The areas within the contours are summed up and multiplied by the square root of the signal acquisition number to reflect the effects of scanning efficiency. This product represents the contour area index corresponding to one pixel. After averaging the contour area index of every pixel in the MRF image, the mean value of contour area index is obtained, which provides a method to evaluate the effectiveness of the MRF acquisition scheme under investigation.

In our study, a fully balanced MRF pulse sequence is implanted on a 3.0T MR system to get a series of 128 MRF images. This sequence is composed of one inversion pulse in the first excitation and following pulses with flip angle varying from 0 to 10 degrees, pseudorandomized phases, TR varying from 7.2 to 16 ms. The dictionary is constructed by simulated signals with T1 parameters ranging from 100 to 4000 ms, T2 ranging from 20 to 1000 ms, off-resonance frequency ranging from -500 to 500 Hz. We test this method by inspecting the effect of reduced signal acquisition number by successively cutting the MRF signal from the end to simulate reduced scan time. New signals and dictionaries constructed by reduced-length sequences are normalized and mapped again, with the contour area indexes under different signal acquisition numbers examined.

Results: The signal-dictionary comparison result from one pixel of the MRF image series and the contour boundary are shown in the form of 2D parameter space in **Figure 1**. Contour area indexes averaged for all pixels of the MRF image are plotted as a function of signal acquisition number in **Figure 2**. As the signal acquisition number reduces, the contour area index increases, which reflects the reduction of mapping precision. The T1 mapping results at 4 signal acquisition numbers are shown in **Figures 3a-d**. While the signal acquisition number reducing from 128 to 88 shows no substantial change, prominent mapping errors over the tissue boundaries can be seen when the signal acquisition number reduces from 64 to 28. The phenomena are reflected by the increase in contour area index in **Figure 2** (arrows).

Discussion: We demonstrate a quantitative method to evaluate the mapping precision under different signal acquisition numbers. This method not only can be used to shorten MRF sequence length under pre-specified error tolerance, but also has potential in evaluating different RF excitation schemes for MRF. Although a three-dimension parameter space is used in this study, the concept can be easily extended to higher dimensions if more parameters were included in the MRF dictionary. Setting of the contour area index threshold for satisfactory mapping is related to signal-to-noise ratio and the desired mapping precision, and is an open topic for further investigations currently underway.

References: 1. Ma D et al. Nature. 2013; 495(7440):187-192. 2. Tropp JA et al. IEEE Trans Inform Theory. 2007; 53(12):4655-4666

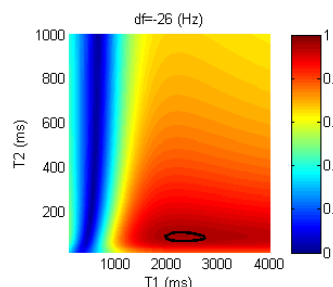


Figure1. A Signal-dictionary comparison map from one pixel in the MRF image series. The bounded contour region contains data points with inner product value greater than 0.95.

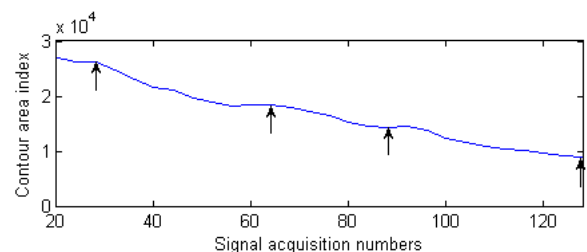


Figure2. The change of the mean value of contour area index under different signal acquisition numbers. Arrows indicate signal acquisition numbers in Figure 3.

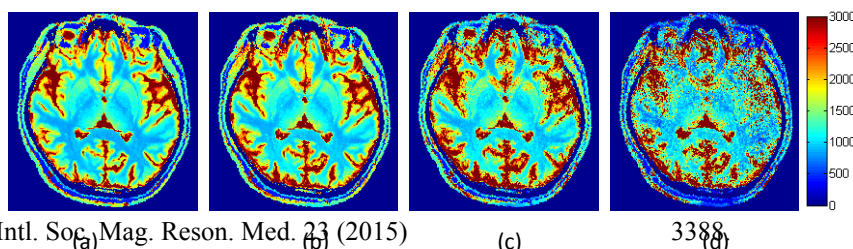


Figure3. T1 mapping results under different signal acquisition numbers. (a)128 (b)88 (c)64 (d)28