Efficient Quantification of Metabolite Concentration and T_1 Relaxation by ^{31}P Spectroscopic Magnetic Resonance Fingerprinting

Charlie Yi Wang[1], Mark Alan Griswold[2], and Xin Yu[2]

[1]*Biomedical Engineering, Case Western Reserve University, Cleveland, Ohio, United States,* [2]*Radiology, Case Western Reserve University, Cleveland, Ohio, United States*

Target Audience: Researchers and clinicians interested in quantitative spectroscopic measurements.

Background/Purpose: Quantitative ^{31}P spectroscopy has a wide range of potential biomedical applications. However its lengthy acquisition time has limited its use, especially in dynamic or *in vivo* studies. Recent development of Magnetic Resonance Fingerprinting (MRF) provides a novel framework for data acquisition that allows simultaneous measurement of multiple tissue properties, including relaxation times, at high speed[1]. In this study, we assessed the accuracy and efficiency of a novel spectroscopic MRF sequence for multi-species T_1 measurement in phantom.

Pulse Sequence Design: The pulse sequence consisted of a nonselective hyperbolic secant inversion pulse followed by 512 acquisitions. The 512 acquisitions consisted of 16 repeated blocks, with each block comprised of 32 acquisitions using linearly ramped up and ramped down flip angles ranging from 1.5° to 22.5° using hard pulses with alternating phases. A constant repetition time (TR) in the range of 11.2 to 13.5 ms was used for all the acquisitions. 544 data points were collected for each acquisition with a dwell time of 11 μs. Total acquisition time of one fingerprint was ~7 s. Each fingerprint acquisition was followed by an 8 s inter-scan delay.

Dictionary Construction and Matching Method: Signal evolutions for each metabolite were simulated across a range of characteristic T_1 relaxation times. The B_0 inhomogeneity was accounted for by applying a set of shim-derived weights to the simulated data and the weighted-sum for each fingerprint was calculated. For each metabolite, a dictionary was constructed with T_1 varying in a range of 1-2 s around its expected values and at a resolution of 10 ms. Fingerprint matching was performed in the corresponding spectral bins, with the signal normalized by the sum of square magnitudes. Specifically, the vector dot product between the fingerprint and each dictionary entry was calculated, and the T_1 for the dictionary entry that gave rise to maximal dot product was returned as the matched T_1. Subsequently, M_0 was determined by minimizing the sum of the error vector between the acquired fingerprint and the M_0-scaled matched dictionary entry.

Phantom Study: A solution phantom comprised of 15 mM PCr, 10 mM ATP, and 3 mM Pi and titrated to 7.1 pH was used for sequence testing. All data acquisitions were performed on a 9.4T vertical bore system. Three MRF sequences differing in TR and carrier frequency were examined. A total of 120 datasets with 1 signal average were acquired for each sequence. Standard Inversion Recovery (IR) was used to compare T_1 measurements by MRF methods.

Results: Shown in Fig. 1a&b is a complete fingerprint obtained from the phantom. The fingerprint comprised of 512 spectra. Individual spectrum showed reduced spectral resolution due to the short acquisition time (Fig. 1c). However a T_1 encoding signal evolution is obtained for each metabolite (Fig. 1d). M_0 and T_1 measurements by the three MRF variations showed strong agreement with IR method for all three metabolites (Fig 2a&b). Efficiency, calculated as precision per square root of acquisition time, for MRF was substantially higher than IR in the quantification of T_1 (2.46, 1.57 and 1.44 fold increase in PCr, γATP and Pi respectively) (Fig. 2c&d). M_0 measurement in PCr and γATP also showed similar improvements (1.65 and 1.46 fold increases in efficiency respectively), while comparable efficiency for Pi measurement was also achieved despite its long T_1 value (on average 0.99 relative efficiency).

Discussion/Conclusion: A novel spectroscopic MRF method has been developed that demonstrates enhanced efficiency in multi-species T_1 and M_0 quantification.

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References:

1. Ma, D. *et al*., Nature 2013;495:187–92.

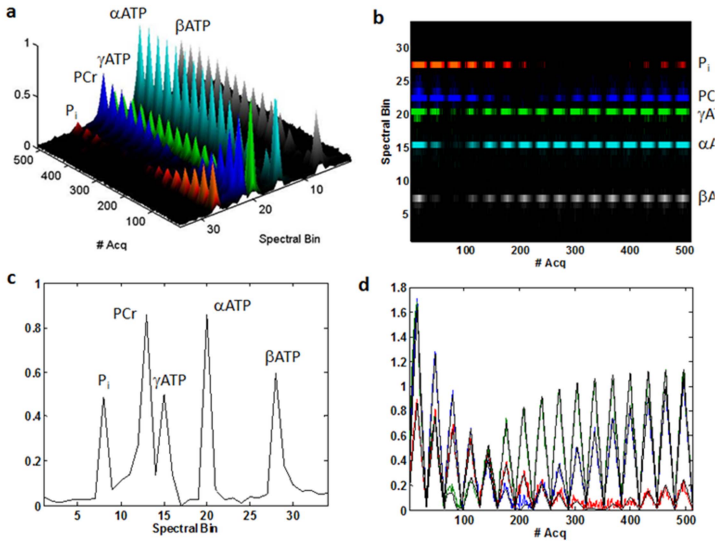

Figure 1, MRF signal from a phantom. a. A representative fingerprint with 512 31P spectra; b. Magnitude map of a fingerprint; c. A representative spectrum out of the 512 acquisitions of a fingerprint; d. Signal evolution from spectral bins corresponding to PCr (blue), γATP (green) and Pi (red) signal superimposed with matched dictionary entries (black).

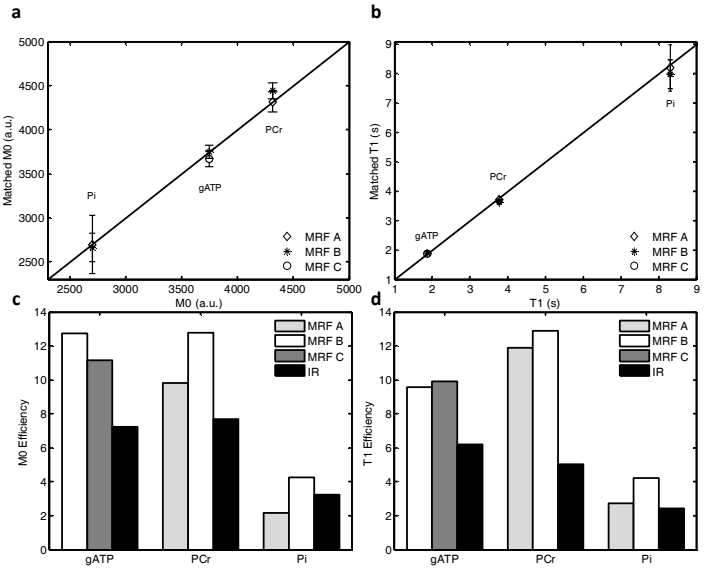

Figure 2. Accuracy and efficiency of MRF and IR. a&b. Comparison of 120 repeated MRF measurements of T_1 (a) and M0 (b) with the classic IR method. c&d. The efficiency of MRF compared to classic IR for T_1 (c) and M0 (d) measurements. Solid lines in a&b represent the line of identity.