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Quantitative Magnetic Resonance Fingerprinting in Ovarian Tumors for T_1 and T_2 Mapping

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Abstract

Multi-parametric magnetic resonance imaging (MRI) can be used to characterize many cancer subtypes including ovarian cancer. Quantitative mapping of MRI relaxation values, such as T_1 and T2 mapping, is capable of improving tumor assessment beyond usual qualitative T1- and T2-weighted images. Though, quantitative MRI relaxation mapping methods frequently engage long scan times because of sequentially measuring many parameters. Magnetic resonance fingerprinting (MRF) is a new technique that creates fast quantitative MRI by exploiting the transient signals caused by the variation of the pseudorandom sequence parameters. These transient signals are now matched with simulated dictionary of T1 and T2 values to create quantitative maps. The ability of MRF to simultaneously measure multiple parameters could represent a new approach to characterizing cancer and assessing treatment response. This paper investigates the MRF for simultaneous T1, T2, and relative proton density mapping treating ovarian cancer as a model system.

Keywords- *Matlab; Ovarian Tumors; MRF; Finger printing; T1 and T2;*

I. INTRODUCTION

Clinical MR imaging acquires multiple images with different approaches to generate contrast and are usually assessed qualitatively. Contrast on MR imaging is based on differences in magnetic resonance parameters in tissue, such as longitudinal T1 relaxation, transverse T2 relaxation, and relative proton density (rPD). Multiple images with different weightings are obtained by varying the acquisition, including parameters such as repetition time (TR) and flip angle (FA).

Although the contrast that is generated is qualitative, contrast is highly dependent on operator specifications, which can complicate the interpretation at multiple centers. In order for the results to be more repeatable and representative of the underlying biological factors that control signal, quantitative mapping of MRI relaxation values is promising for improving tumor diagnosis, for monitoring of disease progression, and for assessment of treatment response beyond simple qualitative assessments.

However, traditional quantitative imaging can be inefficient, requiring multiple serial acquisitions from which a single quantitative map can be derived. The measurement of multiple MR parameters is almost always time-consuming and is particularly challenging in moving regions such as the abdomen MR Fingerprinting (MRF) has recently been introduced, as a novel acquisition and reconstruction strategy to overcome these challenges and time-constraints with the potential to be used for the clinical imaging, MRF could improve the speed and accuracy of the PET/MRI parameter quantitation for the cancer imaging . MRF in prostate, abdomen and brain cancer has shown nearly double the T1 values when compared to normal-appearing tissue, and T2 differences as large as 70% have been demonstrated between low and high grade tumors MRF enables fast, simultaneous and efficient multi-parametric mapping by exploiting the transient signals produced from the variation of pseudo-random sequence parameters.

These generated transient signal evolutions or "fingerprints" are unique for different tissues and are dependent on the various magnetic resonance properties of the tissue After data acquisition,

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the signals are matched to a simulated dictionary including (but not limited to) a range of T1 and T2 values to create quantitative maps. The relative proton density (rPD) is the scaling factor used to match the simulated signal evolution with the measured signal.

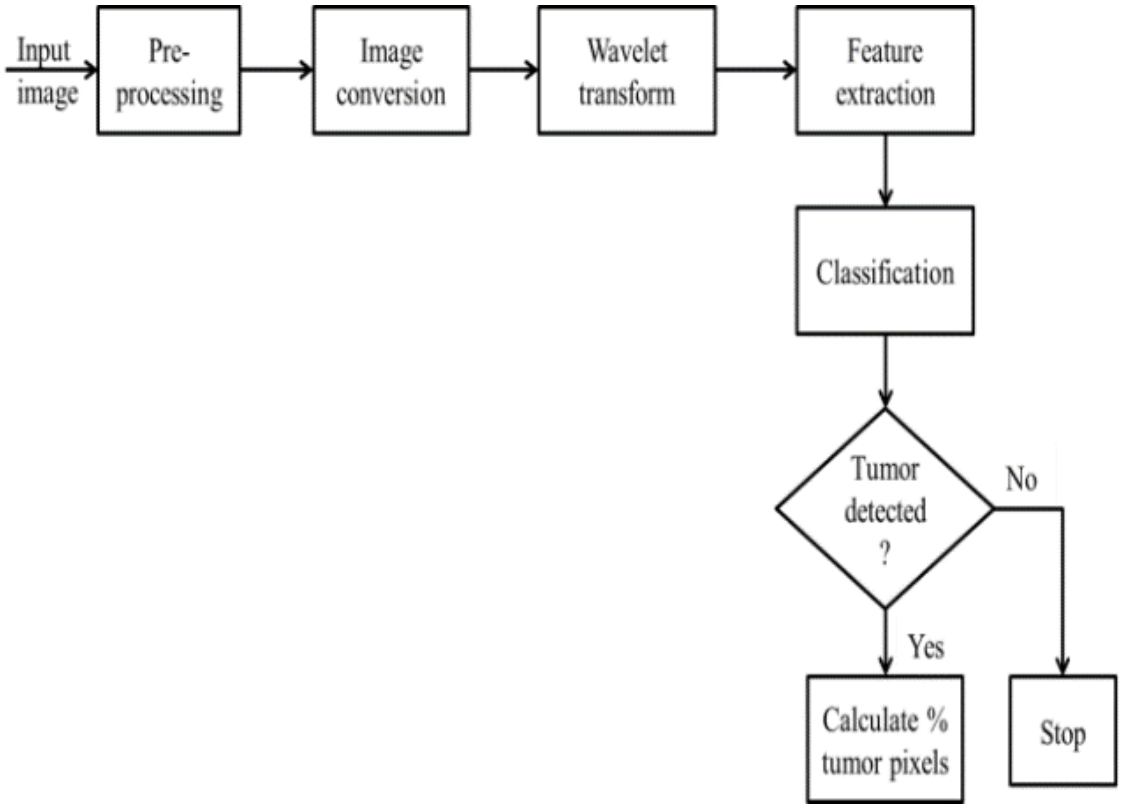

Fig 1: Proposed System Block Diagram

II. GENERATION OF MRF SIGNALS

The key assumption of the MRF concept is that one can generate unique signal, or fingerprints, for different materials or tissues using an appropriate acquisition method. 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 MR spectroscopy to reduce the signal oscillations and to improve the spectral response. However, these variations were primarily used in the preparation phase or to make the signal more constant type. Randomized sampling patterns have also been used previously to aid in the separation of spatiotemporal signals in moving objects or substances with different resonance frequencies. Here we demonstrate that temporal and spatial incoherence required in MRF can be achieved by varying acquisition parameters such as the flip angle (FA) and phase of RF pulses, the repetition time (TR), echo time (TE), and sampling patterns in a pseudorandom manner.

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 system, pattern recognition can take place by 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, T_1, T_2, off-resonance frequency are included in this study, or other properties such as diffusion and magnetization transfer (MT) using the well-established Bloch equation formalism of MR. Once this dictionary of possible signal evolutions is generated, a matching or pattern recognition algorithm is

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then used to select a signal vector or a weighted set of signal vectors from dictionary that best represent 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 requires only a few minutes on a modern desktop computer. It should be noted that there are about infinite possibilities for MRF compatible pulse sequences. Other MR parameters of interest can be investigated by identifying pulse sequence components that impart differential sensitivity to the parameters of interest. Moreover different components also can be varied simultaneously adding the potential for a highly effective experimental design that allows almost any material characteristic visible using MR to be analysed in a quantitative way using MRF.

III. VALIDATION OF CONCEPT

For a proof of implementation, an MRF acquisition based inversion-recovery balanced steady state free-precession (IR-bSSFP) sequence was employed. This choice of this basic pulse sequence was based on the extensive existing knowledge about the evolution of the IR-bSSFP signal evolution, and its sensitivity to T_1, T_2 and off-resonance. After each RF pulse, one interleaf of a variable density spiral (VDS) read out was acquired, as shown in. Such a VDS trajectory has been used in fast imaging and for the reduction of under sampling errors. Two MRF acquisition patterns were used as shown in Figure in separate scans to demonstrate the flexibility of the acquisition parameters.

The simulated signal evolution curves that would be expected from four commonly encountered tissues of the brain (fat, White Matter (WM), Grey Matter (GM) and Cerebral Spinal Fluid (CSF)) using the schematic implementation. Each tissue type has characteristic T_1 and T_2 value and thus each signal 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 1 in these figures.) Conventional spoiled steady-state sequences typically generate signal levels corresponding to 1-10% an acquired signal evolution curve from fully sampled phantom experiments and its match to the dictionary by using the acquisition pattern shown in Figure, 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 also included demonstrating the oscillating nature of the MRF signal.

IV. ACCELERATED MRF ACQUISITIONS

In addition to simultaneously quantifying the multiple parameters, the error tolerance of MRF can be better than 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 final measurement. This is similar to conventional fingerprint recognition techniques which contend with partial fingerprint information. In particular, the interaction of the temporal and spatial incoherence possible in MRF provides new opportunities are developed to accelerate image acquisition through rejection of spatial under sampling errors. To test the limits of this acceleration, It was modified to use only one spiral readout in each acquisition. Therefore the data collected are only $1/48^{th}$ of the normally required data, resulting in a total acquisition time of 12.3 seconds corresponding to 1000 sampled time points. The signal evolutions from all 1000 under sampled time points were used directly to match one entry from the dictionary to quantify T_1, T_2, M_0 and off-resonance simultaneously. Because these errors are incoherent with the expected MRF signals they are

largely ignored by the following processing steps. high quality estimates of the MR parameters are generated even with this significant level of under sampling. WM, GM and CSF regions were then selected from the resultant of maps. The shortened T_2 value in CSF is likely due to out-of-plane flow in this 2D experiment. A similar effect is observed in conventional T_2 mapping. Also that the roughly 220 Hz chemical shift of fat protons is clearly visualized in the off-resonance map.

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V. MOTION ERROR TOLERANCE IN MRF

Since motion is one of the most common sources of error in an MRI, a motion corrupted scan was performed using the accelerated MRF acquisition described in the prior section. The subject was instructed to move his head for the last 3s of a total 15s scan. The maps acquired during motion show almost no sensitivity to the motion and shows the same

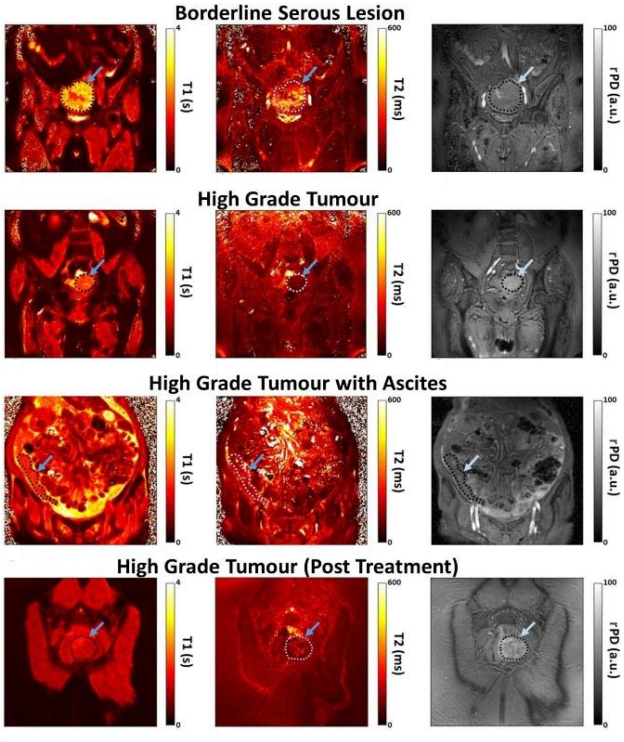

Fig: ovarian tumor images

quality and anatomy as the maps from the motion-free data, thus indicating that the signal changes resulting from motion were unrelated with the evolutions included in the dictionary, and they were largely ignored by the pattern recognition algorithm.

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