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MRICOM–MRI COntrast Modelling using 2D T_1–T_2 correlation spectra and relaxation signatures

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Abstract

Image contrast is calculated by inputting experimental 2D T_1–T_2 relaxation spectra into the ODIN software interface. The method involves characterising a magnetic resonance imaging pulse sequence with a "relaxation signature" which describes the sensitivity of the sequence to relaxation and is independent of sample parameters. Maximising (or minimising) the overlap between the experimental 2D T_1–T_2 relaxation spectra and the relaxation signature can then be used to maximise image contrast. The concept is illustrated using relaxation signatures for the echo planar imaging and Turbo spin-echo imaging sequences, together with in-vitro 2D T_1–T_2 spectra for liver and cartilage.

Keywords: Image contrast; Relaxation; ODIN; EPI; Turbo spin-echo; Cartilage; Liver

1. Introduction

Apart from its noninvasive nature, one of the advantages of magnetic resonance imaging (MRI) is the almost limitless variety of pulse sequences that can be designed for clinical diagnosis. This enormous diversity can, however, be a problem when it comes to identifying the 'optimum' sequence for diagnosing a specific clinical condition that is not easily detected with standard MRI sequences. All too often, a hospital MRI radiologist working with a commercial scanner has only a limited menu of these standard imaging sequences and this limited choice, together with constraints on research time, means that a trial-and-error approach has to be used and this is unlikely to identify the optimum sequence. There is therefore a need for user-friendly, in silico computer simulations that can be used independently of the hospital or clinical research environment to explore the space of pulse sequences and choose optimum imaging protocols.

A second related problem is the optimum choice of the main magnet field strength, or, equivalently, resonance frequency. A 1.5-T magnet continues to be the standard for many clinical MRI applications, but the desire for higher spatial and chemical shift resolution is driving the move to higher fields. However, as a number of authors have pointed out [1], provided sufficient resolution is available to identify the regions of interest, it is usually image contrast that needs optimising, and for some clinical conditions, this might be greater at lower, rather than higher fields. The in silico simulation therefore needs the capability to explore the space of spectrometer frequencies as well as imaging sequences.

Optimising image contrast is, of course, greatly assisted if there is prior information on spin density and relaxation times, but this can also be a problem because of the limited nature of most in vivo T_1 and T_2 measurements on biological tissue. An MRI T_1 map is usually created from a very limited number of inversion recovery or saturation recovery steps, and the recovery curve is then fitted with only a single exponential function. The resulting T_1 is therefore a rather crude, average value. Similarly, effective, average T_2's are usually derived for each image voxel by acquiring Hahn Echoes at just a few echo times, or, less frequently, from a

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limited number of echoes in a CPMG sequence. A T_1 or T_2 map therefore preserves spatial resolution but it sacrifices valuable relaxation time information. To optimise relaxation contrast we need to use the maximum amount of relaxation data for the biological tissues of interest. For T_1 and T_2 contrast this information is contained in the two-dimensional T_1–T_2 correlation spectrum, such as those shown in Fig. 4, preferably acquired over a range of different field strengths. Of course, the 2D relaxation spectrum is most easily acquired on a dedicated bench-top relaxometer using dissected tissue [2–5]. But a number of authors have also acquired 2D relaxation spectra in vivo [6,7], and novel volume-selective [8] and ultrafast [9] methods are being developed to facilitate this.

In this article, we therefore present an in silico approach to MRI sequence optimisation that fully exploits the information in the 2D T_1–T_2 correlation spectrum. It is based on the ODIN sequence programming interface [10–12] and uses experimental 2D T_1–T_2 spectra together with the novel concept of a "relaxation signature." For convenience, we call the new approach "MRICOM" (MRI COntrast Modelling). For the moment, we focus on the class of imaging sequences, such as echo planar imaging (EPI) and turbo spin echo, whose contrast depends mainly on spin density and relaxation time differences and exclude flow and diffusion-weighted imaging.

2. MRICOM methodology

2.1. Calculation of the "Relaxation Signature" and "MRI-weighted T_1–T_2 spectra"

ODIN is intended to run MRI experiments on a variety of real hardware, but it also includes a simulation facility whereby the effect of a given pulse program and all the associated parameters (called the imaging "protocol") on a given digital phantom can be simulated. The phantom is specified by four matrices defining the spin density, T_1 and T_2 and chemical shift for each voxel in the sample (see Fig. 1). The four matrices, saved in text files, are combined with information about the physical dimensions of the sample into a single binary file that can be read and simulated by ODIN. This step is done by an ODIN DOS program called Gensample. The present work goes beyond this standard "image creation" procedure by leveraging the ODIN simulation facility in a manner not originally intended by its authors. A digital phantom is first specified by

(i) Setting all voxels to unit spin density.
(ii) For each voxel (j,k), the T_1 value is initialized according to $\log_{10}[T_1(j,k)]=a*j+b$ where a and b are convenient constants, chosen to give a suitable gradient of T_1s across the sample in the x-direction. A linear distribution of $\log_{10}(T_1)$ is used, rather than

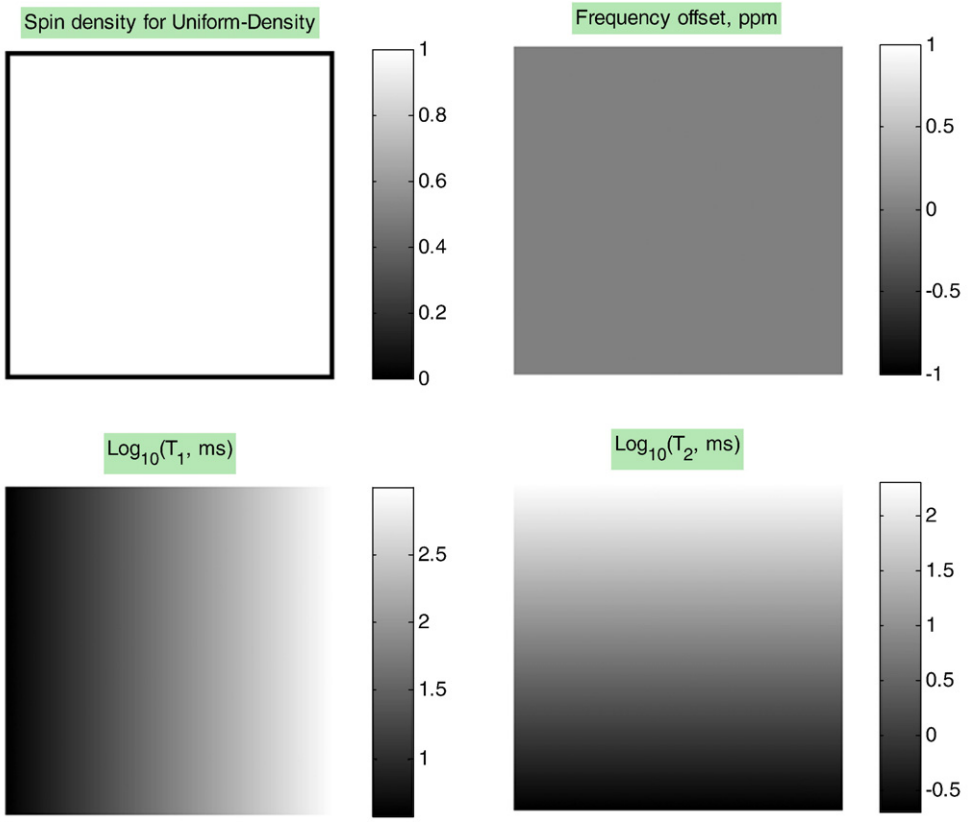

Fig. 1. The "uniform phantom" used to calculate relaxation signatures using the ODIN interface. It comprises a uniform spin density (top left); a gradient of T_1 (bottom left) and of T_2 (bottom right). A uniform chemical shift has been assumed in this example (top right).