Title: Relaxation Time & MT Measures (Sunrise Course: Practical Quantitative Imaging)

Speaker Name: Richard D. Dortch

Target Audience: Clinicians and imaging scientists interested in the basics of quantitative imaging

Outcomes: Following the talk, attendees should be able to: i) identify the basic image acquisition and analysis requirements to perform clinical relaxation time and MT measurements and ii) be familiar with the types of data these sequences produce.

Talk Overview: This talk will discuss the basics of relaxation time (T_1, T_2, and T_2*) and magnetization transfer (MT) measurements with an emphasis on techniques that can be translated into the clinic. For each measurement, we will discuss i) pulse sequence options, ii) "good" sequence parameter choices, and iii) the effect of the effect of experimental imperfections (e.g., B_1 and/or B_0 inhomogeneities). A review of data analysis and model fitting will also be discussed with hands-on relaxation time and MT examples. Note that the data analysis for any of these methods is relatively simply and can be done using a spreadsheet program such as Excel (or with more sophisticated packages such as MATLAB).

Background: Relationships between relaxation parameters and the microanatomical features (e.g., myelination, iron content) of normal and diseased tissues have long been investigated with the goal of developing quantitative imaging biomarkers of these features. Relaxation measurements are also essential for sequence optimization (e.g., optimization of white/gray matter contrast in T_1-weighted scans). Thus, there is a great deal of interest in techniques that allow one to measure tissue relaxation times *in vivo*.

 Any number of pulse sequences can be used to measure relaxation times: one simply needs a model that relates the observed signal to some independent pulse sequence parameter (e.g., TE). For example, in most tissues the spin-echo signal magnitude can be shown to exponentially decay as a function of TE. Thus, if one acquires at least two images at two different TE values (and the same TR values), it is possible to estimate the exponential time constant of this decay, or T_2, by regressing the observed signal intensities against the appropriate model. The effectiveness of this fitting depends on a number of factors including the chosen pulse sequence, its sensitivity to B_1 and B_0 field variations, the chosen independent sequence parameter values, and the signal-to-noise ratio. We will discuss each of these factors in this talk.

 In addition to protons associated with water, there are protons associated with immobile macromolecules in tissue. Conventional sequences cannot capture signal from these macromolecular protons since their T_2s are very short (<<1 ms). They can, however, be indirectly detected by exploiting their interactions with the water pool via chemical exchange and/or dipole-dipole interactions (referred to as MT). Note that while MT is a major factor in determining a tissue's relaxation times (generally speaking more MT = shorter relaxation times), relaxation times are also sensitive to other factors (e.g., B_0 field strength). Thus, MT may offer a more direct means of probing tissue, though relaxation and MT measurements often provide complementary information. Studies have shown that the MT effect in white matter arises primarily from myelin-associated lipids, which suggests that MT contrast may be a specific marker for myelin pathology. As a result, there is interest in exploiting MT contrast to assay changes in myelination associated with a number of diseases.

 The most common way to generate MT contrast is by applying an off-resonance RF prepulse that selectively saturates the spectrally broad macromolecular proton pool (T_2 and linewidth are inversely related). This saturation exchanges with free water via MT, resulting in a decrease in the observed water signal. The magnitude of the MT effect can be characterized by the magnetization transfer ratio: $MTR = 1 - S_{sat} / S_0$, where S_{sat} and S_0 are the observed signal intensities with and without the application of an MT saturation prepulse, respectively. Although the MTR has been shown to correlate with myelin content, it is also sensitive to the choice of experimental parameters (e.g., MT prepulse flip angle). As a result, quantitative MT (qMT) approaches, which allow one to quantify distinct tissue characteristics (e.g., macromolecular pool size) rather than the combined effect of tissue and acquisition parameters, have been developed. In this talk, we will detail protocols used to measure MTR and briefly outline qMT methods.

Suggested Readings:

1. Dortch, RD *et al*. Quantitative Measurement of T_1, T_2, T_2*, and Proton Density. In: *Quantitative MRI in Cancer*. London: Taylor and Francis Press: 53-66 (2011).
2. Ropele, S *et al*. Magnetization transfer MR imaging in multiple sclerosis. *Neuro Clin N Am* **19**:27-36 (2009).
3. Henkelman, RM *et al*. Magnetization transfer in MRI: a review. *NMR Biomed* **14**: 57-64 (2001).