Correlation time mapping of the human brain: a new application of the mixed-TSE pulse sequence

H. Jara[1] and O. Sakai[2]

[1]Radiology, Boston University School of Medicine, Boston, MA, United States, [2]Radiology, Bsoton University School of Medicine, Boston, MA, United States

Purpose: To develop a quantitative MRI technique for mapping the volumetric distribution of the MR correlation time (τ_c). Specifically, to derive a T1 equation as a function of the correlation time that is based on the relaxation theories of Bloembergen-Purcell-Pound (**Ref.** 1) (BPP) and of Torrey (**Ref.** 2). Furthermore to develop algorithms and associated computer programs for generating τ_c maps using as input self-coregistered maps of the relaxation times (T1, T2) and of the proton density (PD). To report correlation times observed in primary brain tissues.

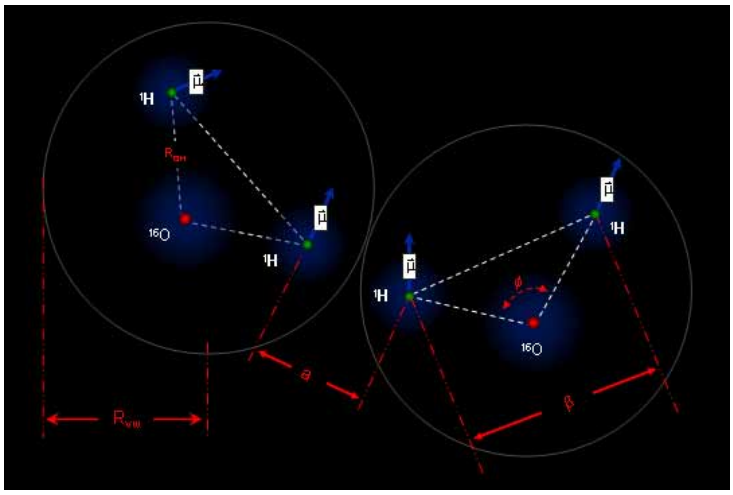

Figure 1: Molecular configuration and relaxation mechanisms in water.

Theory: T1 relaxation of ^{1}H-proton magnetization in aqueous soft-tissues as well as adipose is caused primarily by magnetic dipole-to-magnetic dipole interactions (**Ref.** 1). Such inter-proton dipole-dipole magnetic interactions fluctuate randomly in time due to rotational as well as to translational molecular motions of thermal origin. Such dipole-dipole interactions can occur between two protons of the same molecule – *i.e.* **intra-molecular dipolar interactions**-- or between protons of different molecules –*i.e.* **inter-molecular dipolar interactions**--. Hence, in the absence of paramagnetic solute species, the total diamagnetic spin lattice relaxation rate is the sum of the intra- and inter-molecular relaxation rates. Furthermore, the T1-relaxation effects caused by the intra-molecular proton-proton interactions are modulated by the rotational molecular motions, also known as tumbling molecular motions. On the other hand, the T1-relaxation effects caused by inter-molecular interactions are modulated by the translational motions; accordingly, the following notation will be used for expressing the total diamagnetic spin-lattice relaxation rate: $1/T_1 = 1/T_1^{(rot)} + 1/T_1^{(trans)}$. Using the BPP formula (**Ref.** 1) for $1/T_1^{(rot)}$ and Torrey's formula (**Ref.** 2) for $1/T_1^{(trans)}$, we find:

$$\left[\frac{1}{\left(1+\omega_0^2\tau_{(rot)}^2\right)}+\frac{4}{\left(1+4\,\omega_0^2\tau_{(rot)}^2\right)}\right]\lambda_0\tau_{(rot)}T_1+\left[\frac{1}{\left(1+\omega_0^2\,\xi^2\,\tau_{(rot)}^2\right)}+\frac{2}{\left(4+\omega_0^2\,\xi^2\,\tau_{(rot)}^2\right)}\right]\lambda_1\,\xi\,\tau_{(rot)}T_1\,PD_{(rel)}-1=0 \qquad \text{[Eq.1]}$$

Where $\lambda_0 \equiv \frac{3}{10}\left(\frac{\mu_0}{4\pi}\right)^2\frac{\hbar^2\gamma^4}{\beta^6}$ and $\lambda_1 \equiv \frac{2\pi}{5}\left(\frac{\mu_0}{4\pi}\right)^2\frac{\hbar^2\gamma^4}{a^3}\rho_0$. In these formulas (SI units), (ω_0) is the Larmor angular frequency, PD is the absolute proton density expressed as the number of ^{1}H-protons per m^3, (β) is the intra-molecular ^{1}H-proton distance, and (a) is the closest inter-molecular proton-to-proton distance of approach. In this model, molecules interact with one another as "solid" spheres (**Fig.** 1).

Methods: Equation [1] was solved numerically with standard root finding algorithms. The proposed correlation-time mapping technique consists in root finding the correlation time as a numerical solution of **Eq.** 1. Images of a phantom and a research subject (brain) were acquired with a 1.5 T superconducting MR imaging system (NT-Intera Philips Medical Systems, N.A.). Mixed turbo spin echo (**Ref.** 3) (mix-TSE) is a multislice 2D pulse sequence that combines the principles of T1-weighting by inversion recovery and T2-weighting by multi-echo sampling into a single mixed MRI acquisition. Directly acquired images were post-processed, first with Q-MRI algorithms to generate the PD, T1, and T2 maps. PD maps were generated by reversing the T1 and T2 weightings of one of the mixed-TSE directly acquired images.

Results: Representative τ_c maps are shown in **Fig.** 2. High image quality correlation time maps of the human brain have been generated. In vivo quantitative results (37°C): CSF (2.4±0.4 ps), GM (10±2 ps), and WM (17±2 ps). In vitro quantitative results (23°C): D-water (3.4±0.1 ps).

Conclusion: A quantitative MRI technique for generating volumetric distributions of the correlation time has been developed and applied to study the human brain. To our knowledge, this is the first report of correlation time MR imaging.

References

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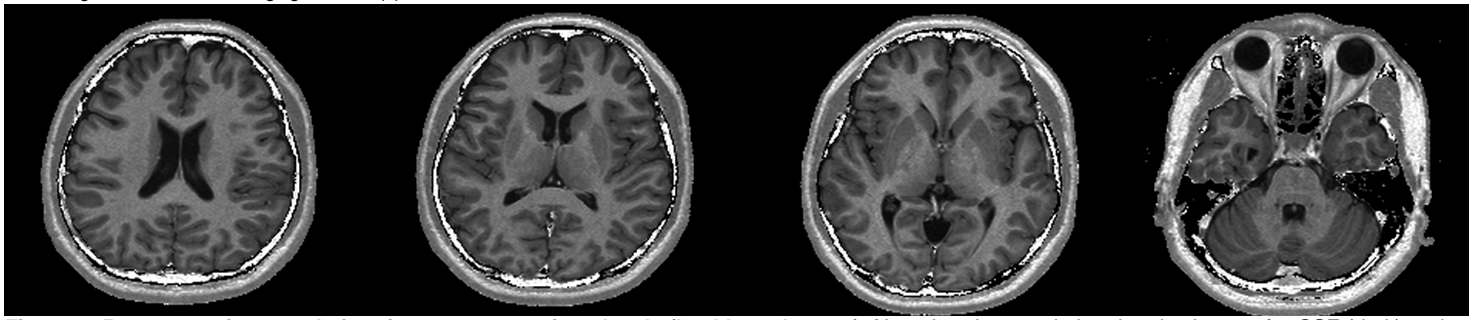

Figure 2: Representative correlation time maps at various levels (healthy volunteer). Note that the correlation time is shortest for CSF (dark) and longest for adipose (brightest).