Rapid and Accurate Single and Multicomponent Relaxometry Using Steady-State Acquisitions

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Magnetic resonance imaging (MRI) is a medical imaging modality capable of generating images of the soft tissues of the human body in exquisite detail. Unlike most imaging devices, which are based on the attenuation or reflection of visible or x-ray radiation, the image formation process in MR is based on the radiofrequency excitation of water molecules in the body. The level of signal observed and the contrast between various tissues depends on the interaction of these molecules with their local tissue and microstructural environment, and may be described by the fundamental NMR parameters *T1* and *T2*. Additionally, MRI scanners may be programmed with different radiofrequency and magnetic field gradient timings to modify image contrast. Conventional imaging relies on adjusting these timings to weight the signal towards a particular parameter, while quantitative imaging seeks accurate and precise measurements of the fundamental NMR parameters *T1* and *T2*. MRI is an extremely powerful tool for diagnostic imaging as well as basic science studies of the brain, and this work will be focused on neuroimaging applications.

In particular, steady state sequences are an attractive choice for performing relaxometry experiments due to their short scan times and moderate to high-resolution volumetric coverage. In spite of these advantages, these methods suffer from a number of effects that reduce their accuracy, in particular strong dependence on the strength and variations of the radiofrequency excitation field (flip angle). A significant portion of this work investigates two methods, Actual Flip-angle Imaging (AFI) and Bloch-Siegert *B1* mapping (BS), for correction of these effects. A novel fitting method for AFI is proposed, implemented, and validated. This method improves the accuracy of AFI over a wider range of *T1* values and reduces its sensitivity to sequence settings (spoiling). A novel combination of AFI and BS is also proposed, implemented, and validated, enabling correction of imaging sequences employing multiple types of radiofrequency excitation pulses.

Most relaxometry techniques measure a single value of *T1* and *T2* in each voxel. This is valid under the assumption of a single well-mixed pool of water, a condition that does not typically hold for the complex microstructural features of neural tissues. Multicomponent relaxometry is a technique to model multiple pools of water, each with its own *T1* and *T2* value. The mcDESPOT method is investigated for performing multicomponent relaxometry, using a model of two exchanging pools of water. As this method involves a complicated signal model with as many as seven free parameters, an analysis of the theoretical and practical precision is performed. mcDESPOT is then demonstrated *in-vivo* on an animal model of dysmyelination that exhibits an extreme paucity of myelin at birth.