

Tri-Exponential T2 Quantification In Vivo

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PURPOSE

T2 relaxation decay curves from in vivo human brain tissue are rarely mono-exponential due to both physiology and partial volume averaging. With increasing hardware performance, and hence data quality, studies have demonstrated that the relaxation of the T2 MR signal cannot be described by a single exponential. Realistic analysis of T2 relaxation curves in biological tissues therefore requires multi-exponential techniques. However, the limited signal-to-noise (≈ 50) from clinically feasible imaging sequences due to limited acquisition time available has severely restricted a multi-exponential analysis of the T2 decay. We propose a tri-exponential model parametric fitting of the T2 relaxation curve, restricting the range for the T2 in each compartment, and estimating the probability of the existence of each of the components on a pixel-by-pixel basis.

METHODS

Imaging data were acquired on a 3T Siemens (Siemens Medical Solutions) magnet, equipped with 8-channel head coil, from six normal healthy adults using a CPMG multi-echo imaging sequence, employing phase cycling. The echo spacing was varied between 22.5, 12 and 8 ms (shortest possible time with the hardware used) for 16 and 32 echoes. Images were acquired for all volunteers with a matrix size of 256x256, field of view 21cm, and TR of 2000 ms. Both single and double acquisitions were acquired. The images acquired with two averages had the expected 1.4 higher signal-to-noise ratio and served as the gold standard. The proposed analysis technique modeled the T2 in three discrete compartments as described by the following equation:

$$\text{SignalIntensity} = Ae^{TE/T_{2a}} + Be^{TE/T_{2b}} + Ce^{TE/T_{2c}}$$

The following parameter bounds were enforced: Myelin ($T_{2a} = [20\ 50]$ ms), White / Gray Matter ($T_{2b} = [50\ 120]$ ms), and CSF ($T_{2c} = [120\ 500]$ ms) compartments. Magnitude components (A, B and C = [0 1000]) represent a combination of signal magnitude due to proton density and the relative contribution of each compartment. Constrained nonlinear fitting was performed using the trust-region methods for nonlinear minimization implemented in Matlab (Mathworks Inc.). The algorithm used a subspace trust region method based on the interior-reflective Newton method. For any given pixel, the three T2 components were forced to lie within each compartment. However, the magnitude for each of these components was allowed to take any non-negative value including zero. As a result, if any component were absent, its magnitude would be zero and hence not contribute to the fit. Points towards the tail of the decay which were below a signal-to-noise ratio of three were rejected during fitting. The results from the analysis yielded three T2 components, three respective magnitudes, chi-square of the fit, and the standard deviation of the parameters. The magnitude maps of the three components were normalized to one thereby indicating the relative fraction for each T2 component.

RESULTS

Typical results from the processing of a representative subject have been presented in the adjacent figure for an acquisition with TE = 8 ms and two averages. The short T2 components with mean ≈ 38 ms were concentrated in white matter as can be seen in the corresponding magnitude map. The middle T2 component shows an even distribution of values, mean ≈ 80 ms, primarily in regions of white and gray matter with gray regions having higher values. The long T2 and associated magnitude maps show the pixels concentrated within the CSF with mean ≈ 370 ms. These values are in excellent agreement with values reported in the literature.

The following table compares the different imaging sets with varying parameters for the same subject shown in Figure 1. The range of T2 values seen across the six image acquisition protocols for this subject is representative of the variance seen across all six subjects.

TE (ms)	Avg	Echoes	SNR	Short (ms)	CV	Middle (ms)	CV	Long (ms)	CV
8	1	32	44	39.5	3.60%	80.4	1.20%	330	4.40%
	2	32	66	38.5	4.10%	80.9	1.20%	334	6.30%
12	1	32	48	39.7	2.10%	78.3	1.20%	380	3.20%
	2	32	64	39.8	1.90%	78.9	1.20%	372	3.20%
22.5	1	16	43	38.8	6.80%	78.9	1.30%	385	2.30%
	2	16	58	37.9	5.40%	79.2	1.10%	372	6.20%

CONCLUSIONS

Multi-exponential decomposition is a type of linear inverse problem with discrete data. Small errors in the data, typically noise, can produce large errors in the solutions, which may therefore force solutions that lose physical meaning. Multi-exponential analysis, thus far, commonly utilizing the levenberg-marquardt optimization technique, routinely place no constraints on the parameters or utilize the non-negative least squares method in order to restrict the parameters to a positive range.

Our technique places discrete rigid bounds on the T2 components, forcing them to lie within acceptable values with the magnitude parameters allowed to take a zero value to account for a missing component. By bounding the T2 values within a physiological range, we can determine the multiple components of the T2 relaxation with high accuracy. This technique is useful in clinical situations where the SNR is limited, performs robustly for a variety of imaging sequences, and may potentially aid in clinical diagnosis and follow-up of patients with white matter abnormalities.

REFERENCES

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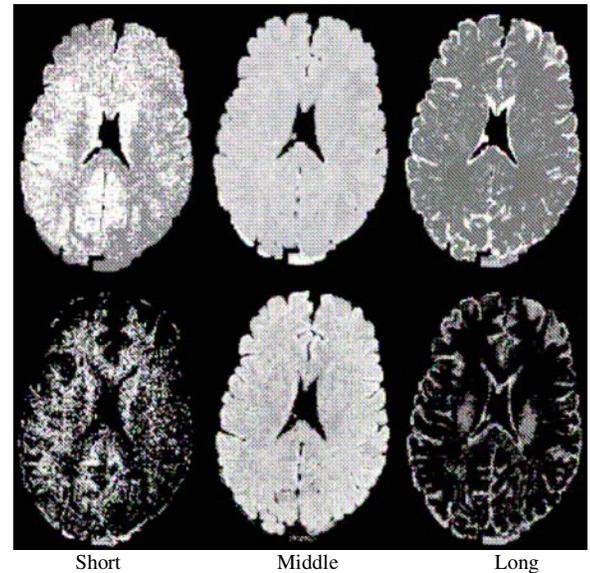


Figure 1. The short, middle and long T2 component maps are shown in the top row with corresponding magnitude maps on the bottom row. For the short component map, the magnitude map has high intensities in the white matter, indicating that the significant short components are only in white matter. The middle component has a uniform distribution in white and gray regions. The long component distribution is concentrated primarily in the CSF.