Andrew Melbourne a.melbourne@ucl.ac.uk

CMBI Project: Analysis of MRI T2 Relaxometry

The Problem

Contrast in Magnetic Resonance Images (MRI) is generated by the intrinsic magnetic properties of the tissue; amongst these are the proton density and the T1 and T2 relaxation rates. T1 and T2 relaxation rates relate to the spin-lattice relaxation and spin-spin relaxation respectively. Different tissue types tend to have different values of these key properties, and this is one reason why MRI is such a successful imaging modality as different tissue types can be demarcated [4,5,7].

The different T2 values associated with different tissue types provide contrast in MR images. This contrast is key to many clinical applications of MRI from structural imaging to tumour detection to mapping of tissue inflammation.

The aim in this work is to estimate T2 values for all areas of the brain using a set of MRI images acquired using a technique called MRI T2 Relaxometry.

The model

T2 relaxation describes how quickly a large number of spins de-phase after excitation. The physics of such a homogenous ensemble of spins is described by a decay that is exponential:

Where the signal at echo time t is a function of the initial signal S_0 and the $T2$ time constant (with decay half-life of $T2\ ln(2)$).

Continuous tissues may not be well represented by a single tissue decay time. In this case, the simplest approach is to assume a discrete range of T2 values from non-interacting components within an imaging voxel and thus the signal decay is described by:

Subject to $\Sigma_i v_i=1$.

The T2 relaxation rates estimated from models such as these can be used to investigate both normal tissue and tissue pathology for instance in neurodegeneration and neurodevelopment [2,3].

The Data

The associated project zip file contains six example datasets from different subjects at multiple spin-echo times (TE times) and the corresponding lecture notes

Each dataset has the following items:

case01-qt2_reg.nii.gz = registered multi-echo T2 data in nifti format.

case01-TEs.txt = a text file of corresponding echo times.
case01-mask.nii.gz = a brain mask for the T2 image data.
case01-seg.nii.gz = a multi-class brain segmentation for the T2 image data.
case01-par.nii.gz = a multi-class brain parcellation for the T2 image data.
case01-par_lobe.nii.gz = a simplified multi-class brain parcellation for the T2 image data.

A second dataset consisting of a cohort of extremely preterm born adolescents will be made available at the end of the first week with an additional set of white matter region labels.

Project Tasks

Core tasks

This part of the project is to ensure you understand the imaging data and what factors might affect the signal and the model-fitting.

1) Explore what imaging factors may distort the T2 relaxometry results

Identifying image acquisition problems early in the model-fitting procedure is crucial before making claims about the parameters found after fitting. Have a look at the imaging data and how the images change with varying echo-time. Plot some of the time-intensity curves of individual voxels or regions of interest. Investigate whether the data is both monotonic and mono-exponential. Does the data actually follow an exponential decay curve - if not why not? What imaging factors might affect the results of the model-fitting? Does the data from any subject violate these assumptions more often? How might these artefacts affect the estimation of the model parameters?

2) Fitting a model with one T2 compartment

Using Matlab (or any relevant programming language), write a function that will take in any two images from an imaging volume and generate, analytically, a T2 estimate at every voxel. Does the choice of images affect the T2 estimates? Can you extend this function so that it can take any number of images (more than one!) and generate both a T2 estimate and an S0 estimate? What model-fitting algorithms are suitable for this purpose (e.g. least-squares, weighted least-squares, non-negative least-squares, non-linear least squares)? Compare and contrast the effects of different fitting algorithms in terms of both the results and the computational performance.

3) Fitting a model with two T2 compartments

Extend these models to fit two different T2 components. What constraints on the parameters could you add to improve the ability or plausibility of the model-fitting [3,6]? How does the result depend on the parameter initialisation? Use the provided tissue segmentations to provide average grey matter (GM), white matter (WM) and cerebrospinal fluid (CSF) parameter estimates and confidence intervals for these six datasets.

4) Model comparison and parameter precision

How does the one-compartment model compare to the two-compartment model? Which model fits the data best? Can you investigate the parameter precisions using techniques you have covered in the lectures such as Markov Chain Monte-Carlo methods, Bootstrapping or other methods for estimating the parameter precisions? If you have concerns about the ability to fit multiple parameters can you use methods such as the AIC to guide a decision?

Advanced tasks

5) Multi-compartment models

Using the same data as above, can you extend previous models to multiple (more than two) compartments and compare their performance. Is it advantageous to use a larger number of compartments? What could different compartments mean biologically [4]? How can the number of compartments be chosen? What limitations are there on the number of possible compartments/T2 values that can be fitted?

6) Using priors on parameter estimates

Parameter priors (initial guesses) can be used to speed up the fitting or improve the accuracy in the presence of noise. Can you generate tissue compartment volume fraction or T2 parameter priors from the segmentation data and thus use parameter priors to initialise a non-linear least squares fit? Does the use of a parameter prior allow you to more robustly estimate a myelin water fraction (i.e. a very short T2 component of ~20ms) for these datasets [3,4,6]? Can the spatial prior information be used in other ways to improve the model-fitting, especially in the case of myelin estimation?

7) Inter-subject variation

Using the second dataset, can you investigate how the parameters vary between subjects using the region label maps provided.

Write up what you find in the report. You will need to give evidence of the work that you carried out – did your investigations yield improvements in registration or model-fitting performance and accuracy - if not why not? (marks will be given for adequate discussion of the results obtained, it does not matter whether your work leads to an improvement, only that your work is justifiable). This part is deliberately open ended and the solutions are still an open research question, thus there is no right or wrong answer. If you are able to justify the changes that you make and the results that you find this will be sufficient for the report.

Contact

If you have any questions email: a.melbourne@ucl.ac.uk

References

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