

# Developing a Protocol for High-Resolution MRI Data Analysis

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## INTRODUCTION

Analysis of brain iron by using Magnetic Resonance Imaging (MRI) is a maturing field of research, and the need for protocols to be developed to assist in the analysis is obvious. The protocol should be such that it provides consistent, accurate and reliable measurements in a quick and efficient manner. **My objective was to develop a protocol for the analysis of high resolution MRI data which has been collected as part of a PhD thesis.**

## BACKGROUND THEORY

Alzheimer's Disease (AD) is a neurodegenerative disease characterised by the formation of amyloid plaques and neurofibrillary tangles (NFTs) in the brain. Iron is linked with the formation of the amyloid plaques and may contribute to cell toxicity [1].

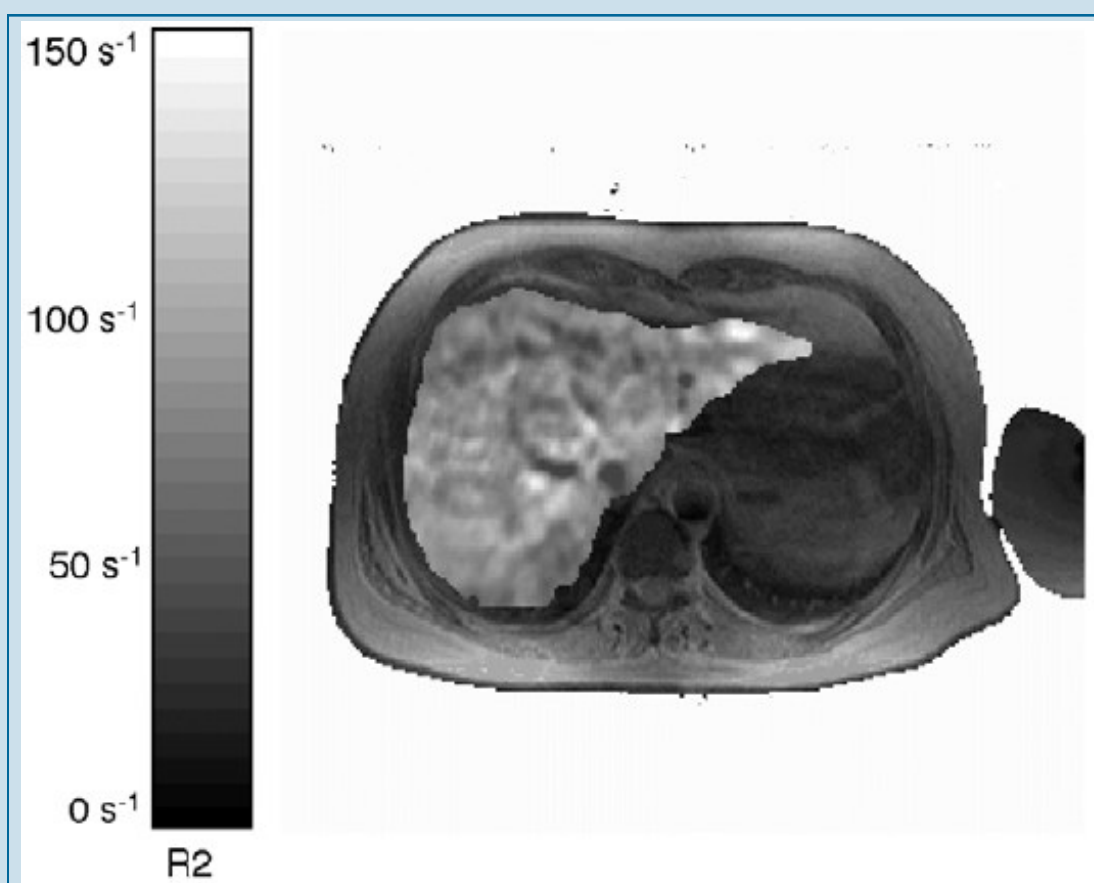


Fig 1:  $R_2$  ( $T_2 = 1/R_2$ ) image of iron-loaded human liver superimposed over a normal  $T_2$ -weighted MRI scan.

Iron influences MRI scans causing hypointense signal (dark areas) in transverse relaxation ( $T_2$ ) weighted and susceptibility-weighted ( $T_2^*$ ) MRI scans. The presence of iron affects the local magnetic field experienced by the hydrogen nuclei and increases their relaxation rate ( $R_2$ ). MRI has been used to quantify iron in the liver (Fig 1) [2].

Work is being done to assess whether iron changes in the AD brain can be observed using high-resolution MRI, with the aim of using iron as a biomarker for AD diagnosis [3]. The ultimate aim is to use clinical MRI to be able to assist in the diagnosis of AD, as currently it is a diagnosis that cannot be confirmed until post-mortem.

## EXAMPLE DATASET

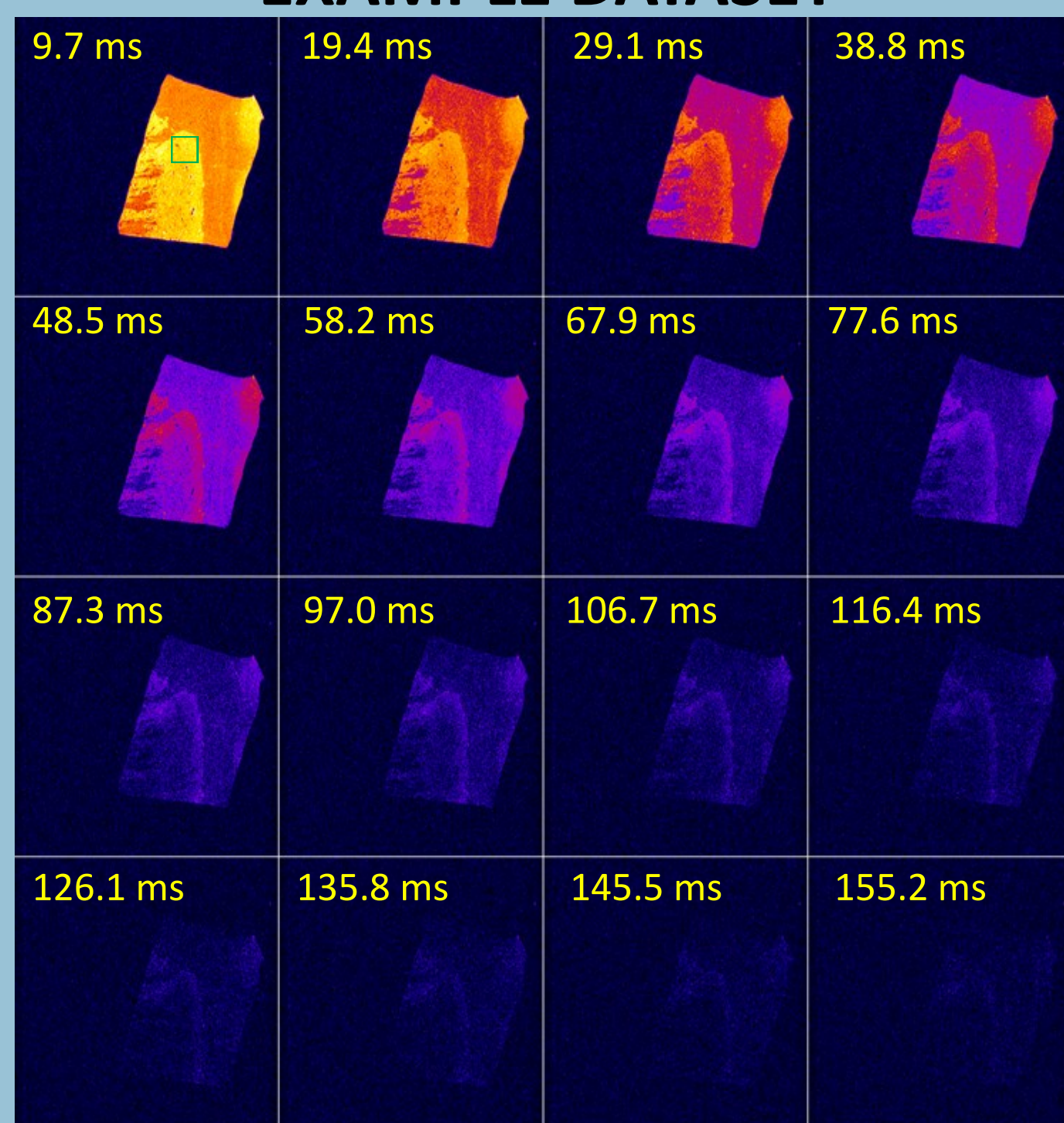


Fig 2: 16 echo times for a slice of control (healthy, age-matched) putamen. The green box in the first echo is a Region of Interest. Regions of Interest were drawn on the images and signal intensity measured as a function of time. This resulted in exponential decay curves (Fig 3).

## METHODOLOGY

A number of different software packages were used to analyse the same dataset and the quality of each analysis evaluated. Each protocol produced results for: i) computed  $T_2$  and  $T_2^*$  times, ii) the mechanism of fitting (pixel or region), iii) the limiting factors of the fitting algorithms and iv) whether a mono- or bi-exponential model should be used.

Software Package	Fitting Algorithms	Fitting Mechanism	Exponential Models investigated			
			Mono	Mono-offset	Bi	Bi-offset
Origin Pro 8.5 (used as a validation check)	Levenburg-Marquadt	N/A	✓	✓	✓	✓
Bruker Paravision	Levenburg-Marquadt	Region Fitting	✓	✓	✗	✗
ImageJ 'MRI Processor' plugin	Levenburg-Marquadt Simplex	Pixel Fitting	✓	✓	✓	✗
ImageJ 'MRI Analysis Calculator' plugin	Levenburg-Marquadt	Pixel Fitting	✓	✗	✗	✗

The importance of including the offset in the fitting process was seen by comparing goodness-of-fit statistics ( $R_{adj}^2$ ) from the plotted data in Origin Pro 8.5 (Fig 4). Background subtraction was also used to correct the offset manually (before fitting) and its effect on parameter value investigated.

## RESULTS

After comparing the analysis methods and software packages, ImageJ 'MRI Processor' plugin was found to be the most suitable. It was established both 'MRI Processor' and 'MRI Analysis Calculator' were fitting the data for each pixel and producing a reliable  $T_2$  or  $T_2^*$  map.

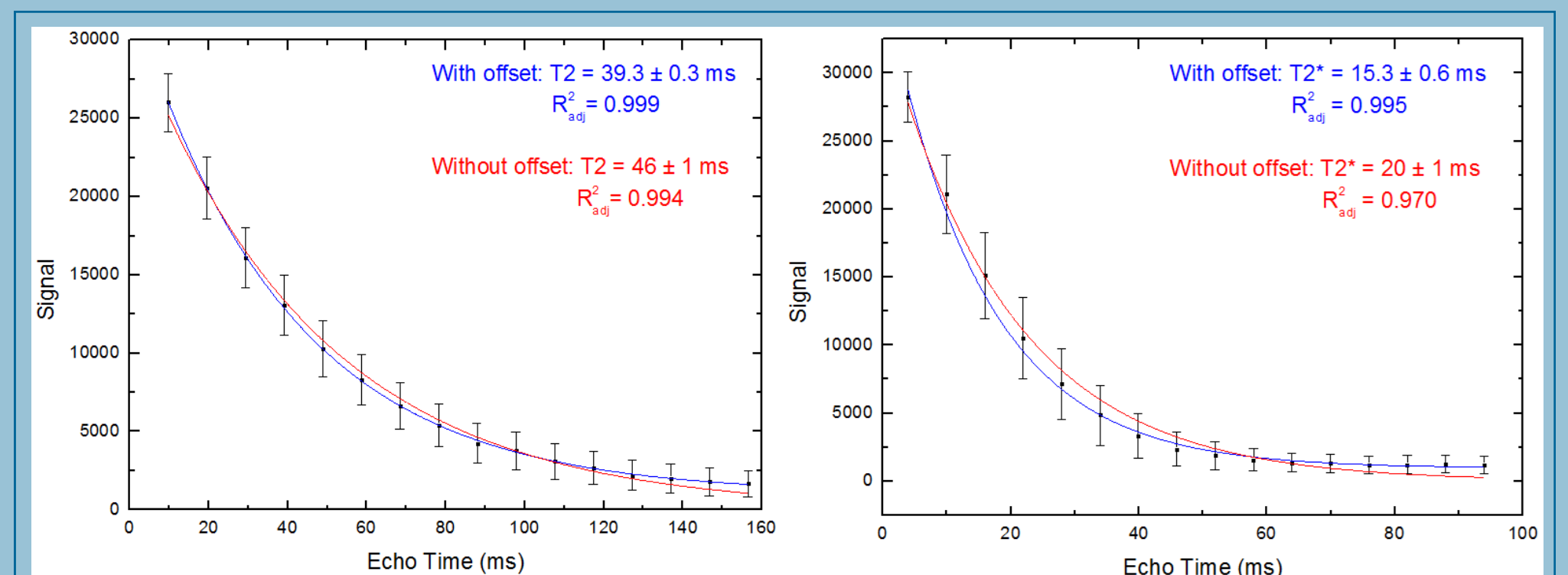


Fig 3: Effect of fitting model on parameter values in  $T_2$ -weighted (left) and  $T_2^*$ -weighted (right) images. The lines of best fit are for  $y = y_0 + Ae^{-x/t}$  and  $y = Ae^{-x/t}$ .

Fitting the data to an offset mono-exponential function gave the best fit. Bi-exponential fitting was an over-parameterisation of the dataset, as indicated by the dependency of the model parameters being equal to 1. Manual correction of the offset gave equivalent results to fitting to an exponential plus an offset, but is more prone to error and so should be avoided.

## CONCLUSION

Due to reliable results and ease of use, the protocol for MRI data analysis using ImageJ with the 'MRI Processor' plugin was chosen. This protocol can be used with confidence for MRI analysis for a current PhD project nearing completion, as well as by the Trace Metals in Medicine group for future MRI analysis. There is potential to publish these results as a conference or journal paper.

## ACKNOWLEDGEMENTS & REFERENCES

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- [3] V. Antharam *et al.*, *Neuroimage.* **59**, 2, p1249–1260 (2012)