

BACKGROUND

BOLD (Blood Oxygenation Level Dependent) imaging is used in fMRI to show differences in activation of the brain based on the relative changes of the T_2^* ($= 1/R_2^*$) signal of the blood. However, quantification of blood oxygenation level based on the T_2^* signal has been hindered by the lack of a predictive model which accurately correlates the T_2^* signal to the oxygenation level of blood.

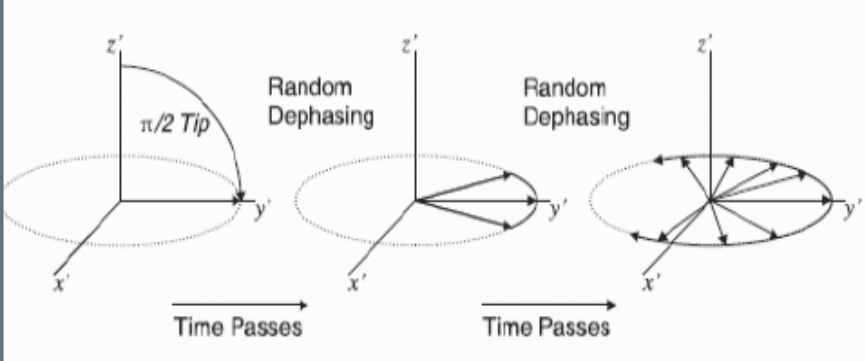


Figure 1: T_2^* relaxation, also termed transverse relaxation, refers to a loss of MR signal due to the dephasing of the magnetic moments of spinning protons in tissue in the transverse plane.²

The T_2^* signal decay in BOLD imaging is generated due to blood containing paramagnetic deoxyhemoglobin (in comparison to diamagnetic oxyhemoglobin). This generates local field inhomogeneities, which cause protons to experience different phase shifts, leading to dephasing and the MR signal decay.

The blood T_2^* signal has been shown to decay with a complex behavior¹, termed Non-Lorentzian, and thus is not adequately described by the traditional model of simple mono-exponential decay.

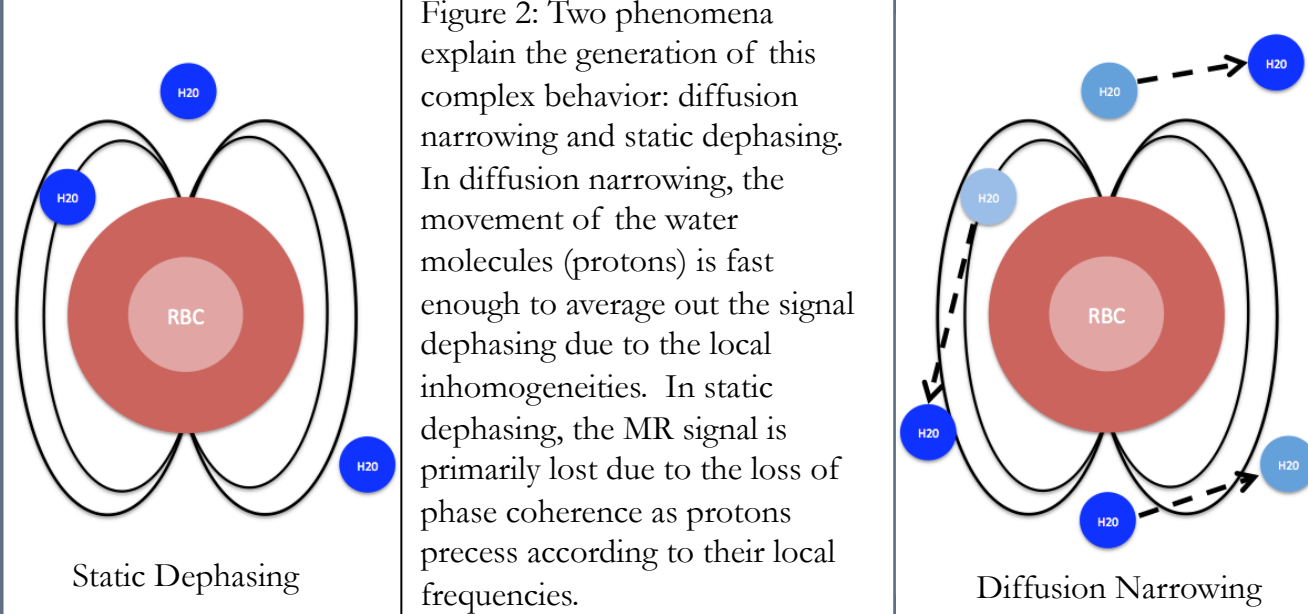


Figure 2: Two phenomena explain the generation of this complex behavior: diffusion narrowing and static dephasing. In diffusion narrowing, the movement of the water molecules (protons) is fast enough to average out the signal dephasing due to the local inhomogeneities. In static dephasing, the MR signal is primarily lost due to the loss of phase coherence as protons precess according to their local frequencies.

Theoretical calculations show that diffusion narrowing substantially affects signal loss in our data. Over the past decade, several theoretical models have been proposed to describe this Non-Lorentzian behavior in the blood T_2^* signal in BOLD fMRI imaging. The goal of this project was to investigate different models which have been proposed over the years and determine a semi-phenomenological model for the T_2^* behavior using actual MR blood data.

POTENTIAL MODELS

Spees ¹	$S(t) = S_0 \cdot \exp[-R_2^* \cdot (t - TE) - AR^* \cdot (t - TE)^2]$
Stables and Gore ⁴	$S = S_0 e^{-\lambda(e^{-\omega t} + \omega t - 1) - R_2 t}$
Stables and Gore ⁴ - TSE	$S = S_0 e^{-\lambda \left(2e^{-\frac{TSE \cdot \omega D}{2}} + 2e^{-\omega D \frac{TSE + 2t}{2}} - e^{-\omega D(TSE + t)} + \omega D(TSE + t) - 3 \right) - R_2 t - (R_2 \times TSE)}$
Novikov ⁵ - GRE	$S(t) = S_0 \left[\frac{\alpha^2}{1 - 2\alpha^2} e^{-(1-\epsilon)\omega t} + \frac{1 - \alpha^2}{1 - 2\alpha^2} e^{-\epsilon\omega t} \right] e^{-R_2 t}$
SQRT	$S = S_0 e^{-\lambda(\sqrt{1+(\omega t)^2} - 1) - R_2 t}$

METHODS and MATERIALS

The MR blood data used originated from the work of Spees et al¹.

Preparation of Blood

Fresh human whole blood were prepared at varying oxygenation levels and sealed in entirely blood-filled NMR tubes without gas bubbles prior to every experiment Spees et al¹ performed.

MR Acquisition

Spees et al¹ performed all MR measurements on a Siemens Magnetom Vision system operating at 1.5T (Siemens, Erlangen, Germany). Blood samples were contained in NMR tubes placed horizontally inside the magnet in a temperature-controlled (37.0°C) box. To avoid settling of the erythrocytes, the blood sample was rotated about its axis at a rate of approximately 100 rpm.

Pulse Sequence

Data were obtained by Spees et al¹ using a single spin-echo-based 1D volume localized spectroscopy technique in which 90° and 180° RF pulses were applied in the presence of slice-selective gradients. A single 4-mm thick slice perpendicular to the NMR tube axis at the center of the tube was examined. Individual FIDs were acquired starting at spin-echo time $TE = 2\tau$, varying the TE's from 18ms to 178ms throughout the experiments.

Bayesian Analysis

Potential models describing the blood MR signal were analyzed using the Bayesian Analysis Package (<http://bayesiananalysis.wustl.edu/index.html>) to determine parameter values and fit. Over 200 blood datasets were run with most parameters being determined for each data set except for ω , which was determined to a single value for all datasets.

THE MODEL

Our Model is based on one presented by Stables and Gore⁴.

$$S = S_0 e^{-\lambda(e^{-\omega t} + \omega t - 1) - R_2 t - at^2} + S_2 \cos(\omega_2 t + \varphi) e^{-R_{22} t}$$

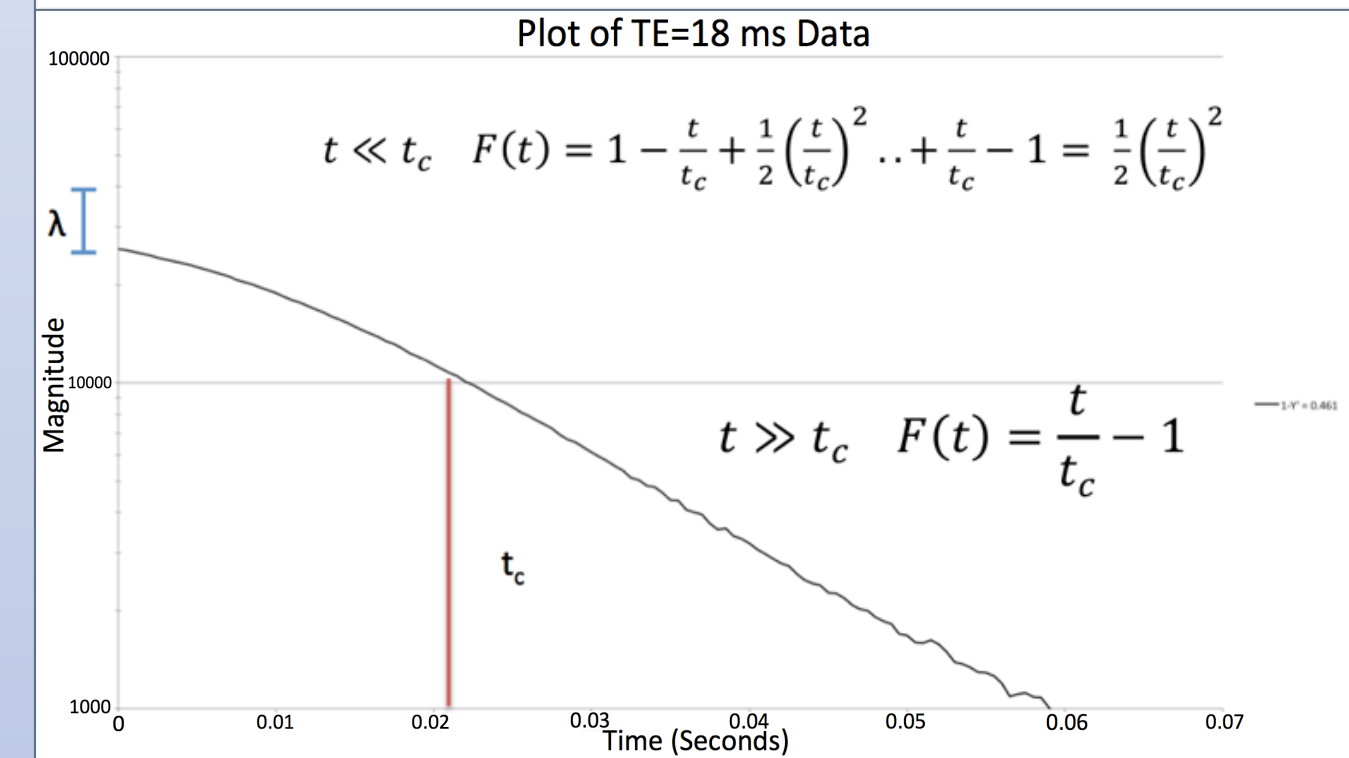


Figure 3: Graph of a data set with $TE = 18$ ms on a logarithmic scale. In the model, $\omega = 1/t_c$, and arises from shift in frequencies experienced by the protons. At time t_c , the behavior of the exponent switches from mono-exponential to linear. The Taylor expansions of the exponent for the two different time regions are shown. λ is calculated from the volume fraction of RBCs and determines the weighting of the mono-exponential part of the model.

RESULTS

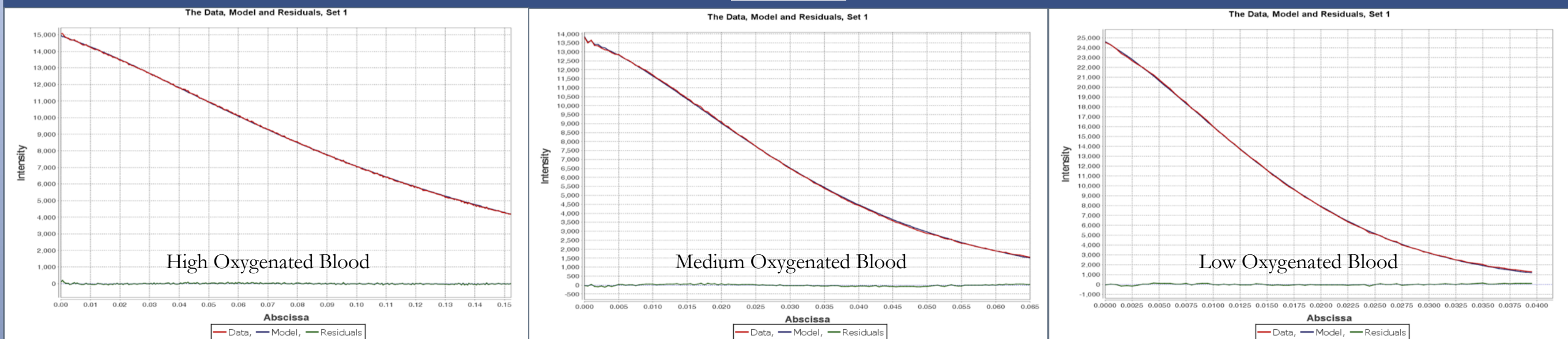


Figure 4: Plots of blood data (blue line) and our model based on Stables and Gore (red line) for blood data at three different oxygenation levels. Our model can accurately describe the blood data for different oxygenation levels with little residual (green line). The plots were generated within the Bayesian Analysis Package.

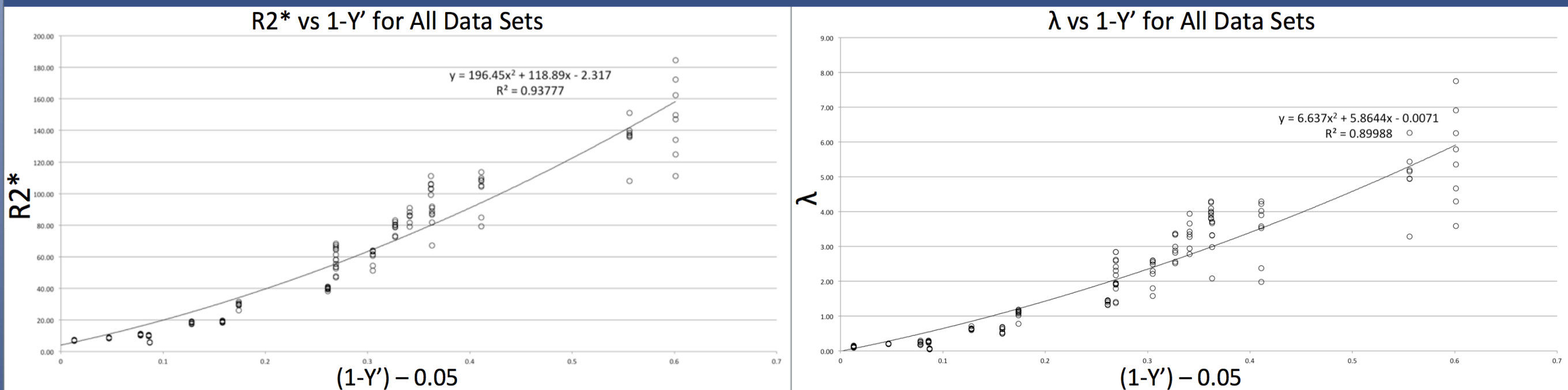


Figure 5: Plots of all model calculated R_2^* and λ values according to blood oxygenation level. R_2^* and λ grew according to the oxygenation level of the blood in a predictable manner. Polynomial fits are shown on the graph. $(1-Y)$ is the fraction of hemoglobin present in paramagnetic form, consisting of deoxyHb and metHb.

ADDITIONAL ANALYSIS

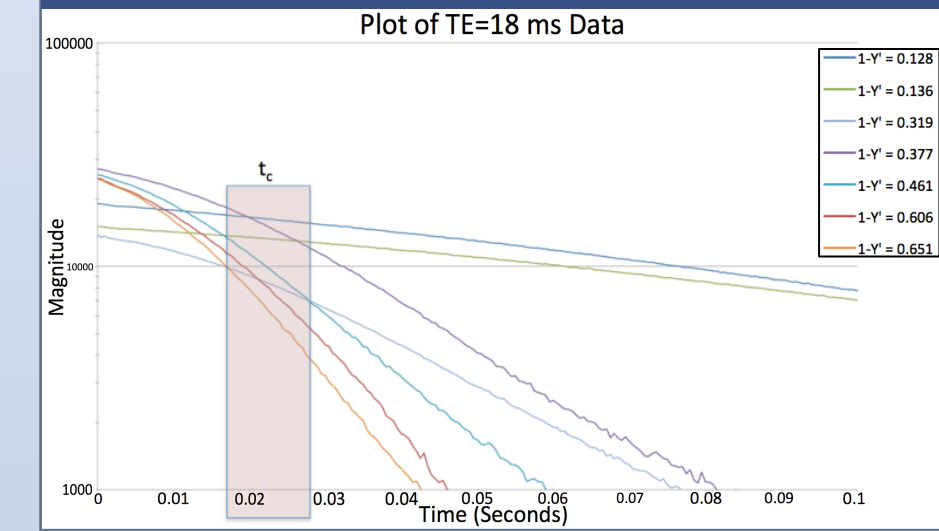


Figure 6: Plot of the blood MR data for different oxygenation levels on a logarithmic scale. Parameter t_c is approximately the same for every data set, showing that t_c does not vary with oxygenation level.

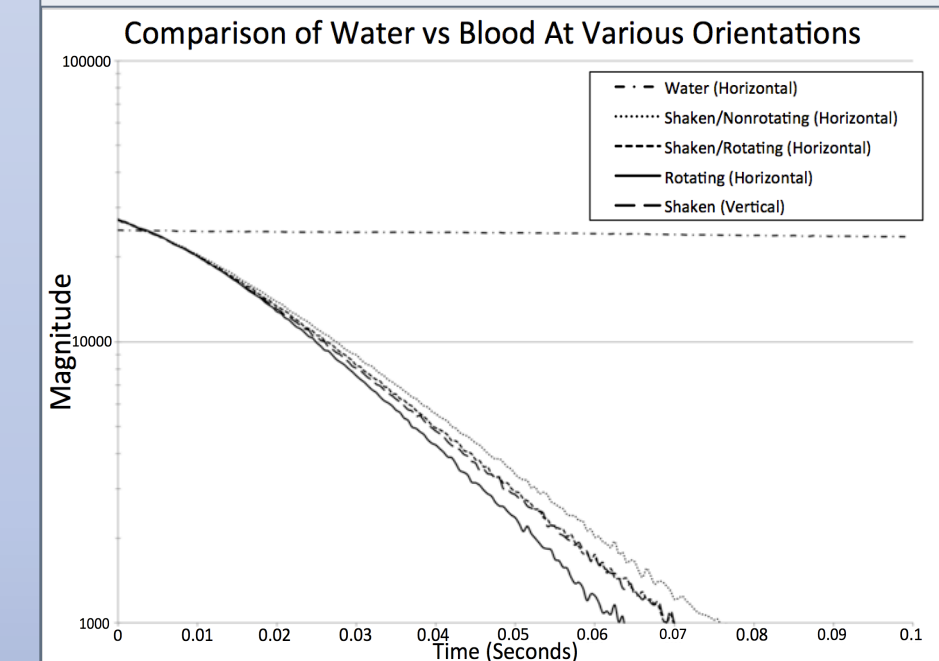


Figure 7: Plot of MR blood data (on logarithmic scale) obtained under different experimental conditions: vertical vs. horizontal position of NMR tube, rotating vs. not rotating vs. shaken. The complex T_2^* relaxation behavior is seen under all conditions, thus confirming the fundamental non-Lorentzian nature of the blood MR signal.

CONCLUSIONS

Our results reaffirm that the traditional model of mono-exponential decay does not accurately describe the behavior of the blood T_2^* signal. Based on our analysis we have proposed a new semi-phenomenological model, describing the blood T_2^* signal decay as initially quadratic and changing to linear after a characteristic time, t_c . This model connects blood T_2^* signal to blood oxygenation level, thus allowing MRI-based measurements of blood oxygenation level.

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