Rapid calculation of correction parameters to compensate for imperfect RF spoiling in quantitative R1 mapping

Martina F. Callaghan[1], Shaihan J Malik[2], and Nikolaus Weiskopf[1]

[1]*Wellcome Trust Centre for Neuroimaging, UCL Institute of Neurology, London, London, United Kingdom,* [2]*Division of Imaging Sciences and Biomedical Engineering, King's College London, London, United Kingdom*

<u>Target Audience:</u> Those interested in quantitative mapping of longitudinal relaxation rate, R_1

<u>Purpose:</u> Quantitative MRI is attractive because of its standardised nature and increased specificity to particular underlying tissue microstructure. A high level of precision is required in order to detect subtle differences across time points or between populations. Combining spoiled gradient echo datasets acquired with different flip angles is a time efficient approach to mapping the longitudinal relaxation rate (R_1=1/T_1) allowing for high resolution and whole brain coverage. However, this approach relies on complete spoiling of the transverse magnetisation between successive excitations. When this is not the case the apparent R_1 estimated from the Ernst equation differs from the true value. This effect has been characterised and a correction scheme proposed[1]. This scheme requires the steady state signal to be simulated for the specific set of sequence parameters over a range of R_1 and transmit field values in order to quantify the bias between the apparent and true R_1 and determine global correction parameters. Full Bloch-Torrey simulations[2] are required to incorporate diffusion effects[3,4], which are particularly relevant when strong spoiler gradients are used. To achieve accurate results, many thousands of isochromats, or more, need to be simulated. This is computationally demanding and still only provides an approximate solution. Here we use the extended phase graph (EPG) formalism, incorporating diffusion effects[5], to rapidly produce an exact solution for the steady state signal from which the required correction parameters can be calculated.

<u>Methods:</u> Two FLASH sequences were simulated in Matlab (The Mathworks, USA): flip angles of 6^0 and 21^0, TR = 25ms, 137^0 RF spoiling phase increment (an optimal value for spoiling), 0.8mm resolution, a spoiler gradient with a 6π dephasing moment across a voxel, transmit field bias ranging from 70% to 130% in steps of 5%. To determine the correction parameters accounting for imperfect RF spoiling, the steady state signal was calculated over a range of T_1 and T_2 values using both the full Bloch-Torrey simulations with 100 isochromats per voxel and the EPG formalism incorporating diffusion effects. Data were acquired from a healthy volunteer on a 3T system (TIM Trio, Siemens Healthcare) using the same sequence parameters that were simulated along with calibration data to determine the transmit field bias[6]. Two R_1 maps were calculated. One map was corrected for imperfect RF spoiling using the correction parameters derived from the Bloch-Torrey approach, the other with parameters derived from the EPG approach.

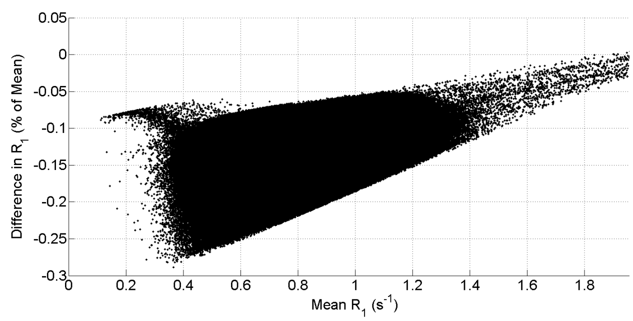

Fig.1: Bland-Altman plot examining the difference in R_1 values derived from the two correction schemes, which is higher at lower R_1 values where the impact of imperfect spoiling will have greater consequence, but still remains below 0.3% across a wide range of R1 values.

<u>Results:</u> The computation time of the EPG simulations was 0.25% that of the Bloch-Torrey simulations. The bias between the apparent and true T_1 predicted by the two approaches were in close agreement, though the EPG approach predicts marginally higher bias. Analysis of the corrected R_1 maps (fig 1) shows the approaches are within 0.3%.

<u>Conclusions:</u> The accuracy of Bloch-Torrey simulations is dictated by the number of isochromats included in the analysis, which also greatly increases the computation time. Requiring just 0.25% of the computation time, the EPG approach provides a flexible and efficient alternative to calculating the exact signal amplitudes. This rapid calculation of spoiling characteristics allows for identifying optimal sequence parameters for minimal bias and developing bias correction methods for acquired datasets, potentially even in real-time and on the scanner console. Given the somewhat higher bias predicted by the EPG approach, future work will look at experimentally assessing the accuracy of the two approaches across a wider range of parameters.

<u>Acknowledgement:</u> This work was supported by the Wellcome Trust.

<u>References:</u> 1. Preibisch, C. & Deichmann, R. *Magn. Reson. Med.* **61,** 125–35 (2009). 2. Torrey, H. *Phys. Rev.* **104,** 563–565 (1956). 3. Yarnykh, V. L. *Magn. Reson. Med.* **63,** 1610–26 (2010). 4. Kiselev, V. G. *J. Magn. Reson.* **164,** 205–211 (2003). 5. Weigel, M., Schwenk, S., Kiselev, V. G., Scheffler, K. & Hennig, J. *J. Magn. Reson.* **205,** 276–85 (2010). 6. Weiskopf, N. *et al. Front. Neurosci.* **7,** 1–11 (2013).