OPTIMIZING SINGLE COMPONENT DESPOT USING A CRAMER-RAO LOWER BOUND FRAMEWORK

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Target Audience: Reseachers interested in quantitive MR imaging and protocol optimization frameworks.

Purpose: T1 and T2 relaxometry is increasingly being used for assessing brain changes in disorders such as Parkinson's or Alzheimer's diseases and in developmental processes, particularly myelination. Capabilities to map T1 and T2 efficiently and at high resolution are valuable in this context. One candidate method is Driven Equilibrium Single Pulse Observation of T1 and T2 (DESPOT), which uses Spoiled Gradient Echo (SPGR) and balanced Steady-State Free Precession (bSSFP) sequences over a range of varying Flip Angles (FA) to estimate T1 and T2. Although, multicomponent signal models have been proposed[1] no extensive evaluation has been done of the performance of the single compartment model to optimize performance and efficiency for the range of relaxation times found in the human brain. We hypothesized that improved performance could be achieved by optimizing the parameters used and conjectured that there would be different optima for neonatal and adult brains. We have explored the use of the Cramér-Rao Lower bound (CRLB – Eq.1), a statistical tool that predicts the minimum possible variance that can be obtained when estimating parameters given a set of independent noisy measurements. Our work was inspired by Lankford and Does[2], who used the CRLB framework to evaluate the multicomponent models. Here, we propose a way of using the CRLB as an optimization tool to guarantee a low estimation standard deviation over a grid of different relaxation times in order to design optimal DESPOT acquisitions.

$$\Sigma_{\hat{\theta}} \geq \frac{\partial E[\hat{\theta}]}{\partial \theta} F^{-1} \frac{\partial E[\hat{\theta}]}{\partial \theta}^{T} \quad \text{Eq.1}$$

$$CF = \max_{i,j} \left\{ \sqrt{\frac{CRLB_{T_{1,i}}}{T_{1,i}^2} + \frac{CRLB_{T_{2,j}}}{T_{2j}^2}} \right\} \quad \text{Eq.2}$$

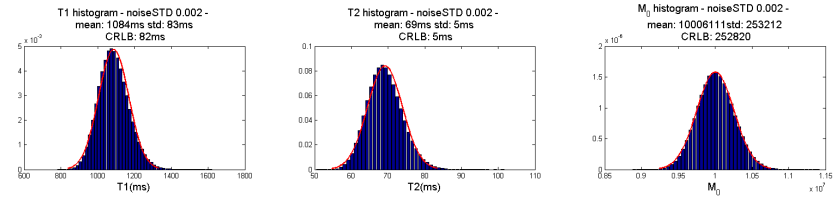

Fig.1

Methods: The CRLB provides an estimate of the minimum variance of estimated parameter values (e.g. T_1 and T_2) and is constructed from a product of the inverse of the Fisher information matrix, constructed from the curvature values of the parameter space log-likelihood surface, and the estimator gradient matrix of the parameters (theta), which accounts for bias introduced by estimation procedure[2]. To construct the CRLB we employ signal models for the imaging sequences concerned, in this case SPGR and bSSFP. Following Alexander[3] we formulate a cost function (CF, Eq.2) for optimizing estimation of T_1 and T_2 as a function of scan parameters (Flip angle (FA) and SPGR repetition time (TR_{SPGR}), TR_{SSFP} was maintained fix to avoid increased banding artifacts) by calculating CRLB at a grid of values ($T_{1,i}$, $T_{2,j}$) at intervals of 4ms for T_1 and 1ms for T_2. On each evaluation, the CRLB for each parameter is divided by the square of that parameter, so that equal relative precision for each degree of freedom is guaranteed. CF is conservative in that it always selects the worst-case bounds detected. We seek the min value of CF using the simulated annealing routine implemented in the MatLab 2012b optimization toolbox. Total examination time is a key design consideration. We adopted the original acquisition scheme of 2xSPGR+2xbSSFP proposed by Deoni et al.[4,5] as a base line and sought optimized solutions that would enhance performance in the same acquisition time. For adult brain the ranges of relaxation times were[6]: $T1_{WM}$=1039-1129ms, $T2_{WM}$=61-72ms; and $T1_{GM}$=1706-1934ms and $T2_{GM}$=92m-106ms. For neonates[7]: $T1_{WM}$=2500-3000ms, $T2_{WM}$=209-347ms and $T1_{GM}$=1885-2283ms and $T2_{GM}$=138-154ms. Validation of the CRLB was performed with Monte Carlo simulation of 10^6 sets of 2 SPGR (FA=3°,12°) and 2 SSFP signals (FA=20°,80°), with TR_{SPGR}=TR_{bSSFP}=3.4ms[4,5] (Fig.1) and true tissue values of M_0=1, T1=1084ms and T2=69ms. Gaussian distributed noise was added to both the real and imaginary part of each signal with a standard deviation of σ=0.002M_0 (Estimated from previously available in-house exams). Knowledge of B_0 and B_1^+ inhomogeneities was assumed. On each trial SPGR and bSSFP curves were simultaneously fitted using MatLab 2012b simplex algorithm fminsearch.

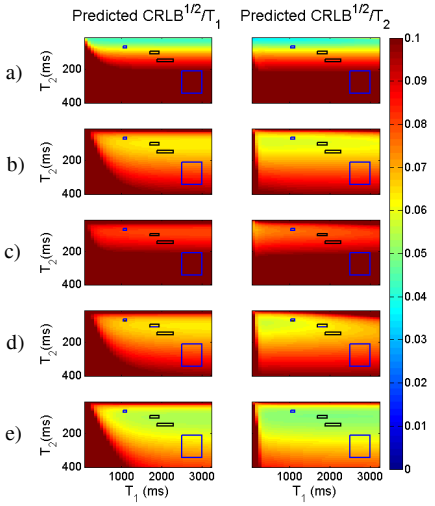

Fig.2

Figure 2	FA_{SPGR} (°)	FA_{bSSFP} (°)	TR_{SPGR} (ms)
a)	3.00, 12.00	20.00, 80.00	3.40
b)	5.49, 5.56	21.01, 55.96	3.40
c)	5.96	14.10, 40.15, 51.22	3.40
d)	7.87	21.29, 43.29	6.80
e)	9.25	23.49, 68.61	10.18

Table 1

Results: Fig.1 confirms that the √CRLB is in agreement with the standard deviation obtained directly from Monte Carlo simulation. A small bias in the predicted distribution can be observed relative to the histogram, which results from the CRLB being calculated using a Gaussian noise model whereas the simulated magnitude images display Rician noise statistics. Table 1 presents the original (a) and optimized (b-e) parameter sets for adult brain. The results for neonatal brain were virtually identical with performance differences of < 0.5%, so are not presented. Fig.2 shows the estimation precisions, √CRLB/T_1 and √CRLB/T_2, in each case plotted over a range of (T_1, T_2) parameter space that encompasses both subject groups. In this figure, blue and black rectangles indicate WM and GM ranges respectively. It is striking that when using 2xSPGR, the optimization results in two virtually identical flip angles (Table 1b) and in fact these are close to the Ernst angle for the smallest T_1 in the range used. Removing this apparent redundancy and using only 1 SPGR while adding an extra bSSFP to keep exam time constant (Fig 2c) damages performance, presumably because of the low signal-to-noise ratio of the lone SPGR. Returning to 2xbSSFP but doubling the TR_{SPGR} (Fig 2d) restores performance. A further increase in TR_{SPGR} (Fig 2e) gives better results still, but at the cost of increased acquisition time.

Conclusion: We have shown that the CRLB allows reliable and systematic determination of how DESPOT estimation precision varies under different protocol conditions for a range of expected T_1 and T_2 values. By building the CRLB into an optimization tool it is possible to achieve rational designs for examinations intended to quantify these important relaxation parameters. Contrary to expectations, a single set of parameters was found to be effective for all brain T_1 and T_2 values, making for a single unified protocol. The result is an examination that allows both relaxation times to be estimated to a precision of better than +/- 7% under realistic SNR conditions. Parallel imaging and other acceleration strategies could decrease examination time, although reduced SNR and changing noise distributions would lead to different optimality tradeoffs.

References: 1.Deoni, S. C. L. et al., MRM 147 (2012);2.Lankford, C. L. et al., MRM 69,127(2013);3.Cercignani, M. et al., MRM 56,803(2006);4.Deoni, S. C. L. et al., MRM 49,515(2003);5.Deoni, S. C. L. et al., MRM 51,194(2004);6.Stanisz, G. J. et al. MRM 54,507(2005);7.Williams, L.-A. et al. Radiology 235,595(2005);