A Min-Max CRLB Optimization Approach to Scan Selection for Relaxometry

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Target audience: Researchers interested in quantitative MRI, T_1/T_2 relaxometry, methods for scan design, and/or steady-state pulse sequences.

Introduction and Motivation

Many MR quantification methods require multiple scans with different scan parameters, to enable estimation of object parameters by per-voxel fitting. For such techniques, it is desirable to design fast scan protocols that provide maximal "information" about underlying parameters of interest. This "information" has previously been measured using contrast-to-noise ratio [1, 2] and variations [3, 4]. In this work, we instead contend that in relaxometry, estimator precision is a more natural benchmark for scan optimality. Specifically, we explore a min-max optimization approach for guiding scan design. At the heart of our method lies the Cramér-Rao Lower Bound (CRLB), a statistical metric useful for bounding the variance of an unbiased estimator. Though it has found success in optimizing scans for other applications [5, 6], to our knowledge the CRLB has not been used to guide scan design for relaxometry. Using this min-max CRLB approach, we optimized dual-echo steady state (DESS) [7] scans for T_2 estimation in the brain.

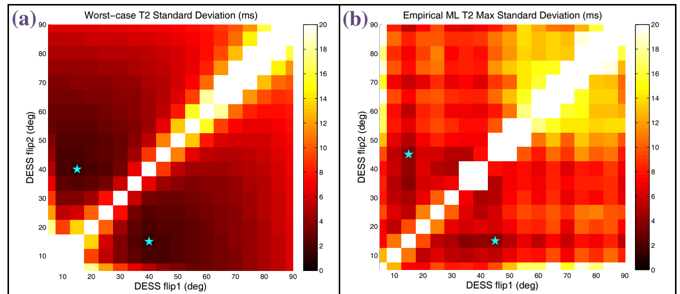

Figure 1: Comparison of *(a)* predicted and *(b)* observed $\hat{T}_2$ standard deviations. *(a)* Theoretical worst-case $\hat{T}_2$ standard deviations, over a T_1, T_2, κ range relevant in brain imaging. *(b)* Empirical ML $\hat{T}_2$ standard deviations; for each flip angle pair, the max over (separately computed) WM and GM ROIs is shown. All values (ms) are plotted as $\boldsymbol{\alpha}$ is varied for 2 DESS scans. Predicted and empirical global minima (starred) occur at similar flip angle pairs *(a)* (15,40)° and *(b)* (15,45)°, respectively.

Theory and Problem Formulation

A broad class of pulse sequences produce signals that can be described with the general model $y_m = f_m(\boldsymbol{\theta};\, \alpha_m, T_{R,m}, T_{E,m}) + \epsilon_m$, where f_m models the noiseless signal for a voxel in the mth dataset; $\boldsymbol{\theta} := [M_0^*, T_1, T_2, \kappa]^T$ denotes the unknown object parameters; $\alpha_m, T_{R,m}, T_{E,m}$ are the mth choice of flip angle, repetition time, and echo time; and $\epsilon_m \sim \mathbb{C}\mathcal{N}(0, \sigma^2)$ is complex white Gaussian noise. Here $M_0^* := M_0 e^{-T_E/T_2^*}$ accounts for T_2^* relaxation; T_1 and T_2 are the spin-lattice and spin-spin relaxation parameters of typical interest; and κ captures spatial variation in the nominal flip angle. A complete scan profile contains a total M datasets and defines length-M vector extensions $\boldsymbol{y}, \boldsymbol{f}(\boldsymbol{\theta};\, \boldsymbol{\alpha}, \boldsymbol{T_R}, \boldsymbol{T_E})$, and $\boldsymbol{\epsilon}$ of the corresponding scalar variables and functions.

The matrix CRLB states that the covariance of any unbiased estimator of $\boldsymbol{\theta}$ is bounded as $\operatorname{cov}(\boldsymbol{\theta};\, \boldsymbol{\alpha}, \boldsymbol{T_R}, \boldsymbol{T_E}) \succeq \mathbf{F}^{-1}(\boldsymbol{\theta};\, \boldsymbol{\alpha}, \boldsymbol{T_R}, \boldsymbol{T_E})$, where Fisher information $\boldsymbol{F}$ takes the form $\boldsymbol{F}(\boldsymbol{\theta};\, \boldsymbol{\alpha}, \boldsymbol{T_R}, \boldsymbol{T_E}) = \frac{1}{\sigma^2}[\nabla \boldsymbol{f}(\boldsymbol{\theta};\, \boldsymbol{\alpha}, \boldsymbol{T_R}, \boldsymbol{T_E})]^T [\nabla \boldsymbol{f}(\boldsymbol{\theta};\, \boldsymbol{\alpha}, \boldsymbol{T_R}, \boldsymbol{T_E})]$. In relaxometry, we are interested in precise T_1 and T_2 estimation. To optimize scan parameters, a reasonable objective function to minimize is thus given by: $\Psi(\sigma_{T_1}, \sigma_{T_2}) := c\sigma_{T_1} + \sigma_{T_2}$, where

$$\sigma_{T_1} := \sqrt{\left[\mathbf{F}^{-1}(\boldsymbol{\theta};\, \boldsymbol{\alpha}, \boldsymbol{T_R}, \boldsymbol{T_E})\right]_{(2,2)}} \text{ and } \sigma_{T_2} := \sqrt{\left[\mathbf{F}^{-1}(\boldsymbol{\theta};\, \boldsymbol{\alpha}, \boldsymbol{T_R}, \boldsymbol{T_E})\right]_{(3,3)}}$$

are bounds on the standard deviations of unbiased T_1, T_2 estimates; and $c \in [0,1]$ controls the relative importance of T_1 versus T_2 estimation. This optimization cannot be performed directly over scan parameters $\boldsymbol{\alpha}, \boldsymbol{T_R}, \boldsymbol{T_E}$ because of an implicit dependence on the unknown $\boldsymbol{\theta}$. We instead solve the following min-max optimization problem:

$$(\boldsymbol{\alpha}^*, \boldsymbol{T_R^*}, \boldsymbol{T_E^*}) \in \arg \min_{\boldsymbol{\alpha}, \boldsymbol{T_R}, \boldsymbol{T_E}} \max_{T_1, T_2, \kappa} \Psi(\sigma_{T_1}, \sigma_{T_2}) \; s.t. \; \|\boldsymbol{T_R}\|_1 \le T_{tot},$$

where T_{tot} defines a scan time constraint. This optimization *minimizes* over $(\boldsymbol{\alpha}, \boldsymbol{T_R}, \boldsymbol{T_E})$ the *worst-case* cost, viewed over an application-specific range of T_1, T_2, κ values.

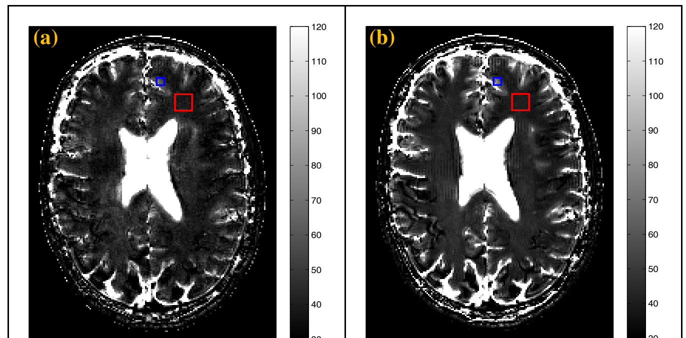

Figure 2: Regularized T_2 estimates from DESS data, for *(a)* two optimized flip angles (15,40)°, and *(b)* all 18 flip angles (5, 10, …, 90)°. WM and GM ROIs are indicated. T_2 estimates from two optimized DESS scans versus many are qualitatively similar.

Experimentation and Results

We applied this min-max scan design method to joint T_1, T_2 estimation from DESS data. DESS has recently been proposed as a fast technique for T_2 relaxometry [8] because it provides two datasets with widely different T_2 contrasts per acquisition. With four unknowns, a minimum of two scans are required to yield $M = 4$ datasets. As a simple example, we selected $c = 0$ and optimized two DESS scans for precise T_2 estimation. We constrained unknown parameter T_1, T_2, κ ranges [500, 900]ms, [50, 90]ms, and $[2^{-0.5}, 2^{0.5}]$, respectively, to encourage precise estimation in the brain. We selected our search space to keep scans as short as possible, fixing $\boldsymbol{T_R}$ and $\boldsymbol{T_E}$ to the minimum possible values and varying only $\boldsymbol{\alpha}$ over [5, 90]°. For $M = 4$ datasets from two DESS scans, we found the minimizer to be at $\boldsymbol{\alpha}^* = (15, 40)°$ (Fig. 1a).

We evaluated our method by comparing our scan design against all possible two-scan combinations, within 5° resolution. We collected *in vivo* DESS data (α = 5:5:90°; T_R/T_E = 17.3/4.7ms; 240x240x6 matrix size; 24x24x1.8cm^3 FOV; 2 cycles of gradient dephasing along the slice-selective direction) from a 32-channel Nova receive head array in a 3T GE scanner and combined the coil data using coil sensitivity estimates [9]. For each flip angle combination, we estimated parameter maps by solving a nonlinear least-squares maximum-likelihood (ML) problem using the Variable Projection Method [10]. We then computed empirical $\hat{T}_2$ standard deviations (Fig. 1b) within white matter (WM) and grey matter (GM) regions of interest (ROIs). Predicted and empirical $\hat{T}_2$ standard deviations were minimized for similar choices of flip angles.

	$\boldsymbol{\alpha}^* = (15, 40)°$	$\boldsymbol{\alpha} = (5, \ldots, 90)°$
WM	39.1 ± 2.6	40.4 ± 1.3
GM	59.7 ± 9.8	66.6 ± 7.2

Table 1: T_2 means $\pm$ standard deviations in the WM and GM ROIs marked in Fig. 2. Much T_2 content in DESS can be accurately and precisely captured with just two well-chosen scans.

Table 1 compares T_2 estimates from the optimized flip angles $\boldsymbol{\alpha}^* = (15, 40)°$ (Fig. 2a) against a T_2 estimate from all (2 echoes)(18 flip angles) = 36 datasets (Fig. 2b). We obtained these images by adding modest edge-preserving regularization (through an optimization problem similar to the one proposed in [11]) to the unbiased T_2 maps. These numbers emphasize that, beyond two well-chosen acquisitions, collecting additional DESS data does not substantially change T_2 estimates.

Conclusions

We have described a CRLB-inspired min-max optimization problem for guiding scan design in relaxometry. As an illustration, we optimized a scan protocol consisting of two fast DESS acquisitions for T_2 relaxometry in the brain. Our results showed that predicted and empirical $\hat{T}_2$ standard deviations over WM/GM regions of interest recommend similar combinations of scan parameters. We then compared a regularized T_2 estimate from our suggested scan protocol against one from many acquisitions and found that much of the T_2 content in DESS data is well captured with only two scans.

Acknowledgments

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