

## Determination of the optimal set of b-values for ADC mapping under a Rician noise assumption

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**Synopsis(100/100 words):** Mapping of the apparent diffusion coefficient (ADC), estimated from a set of diffusion-weighted (DW) images acquired with different b-values, often suffers from low SNR, which can introduce large variance in ADC maps. Unfortunately, there is no consensus on the optimal b-values to maximize the noise performance of ADC map. In this work, we determine the optimal b-values to maximize the noise performance of ADC mapping by using a Cramér-Rao Lower Bound (CRLB) approach under realistic noise assumptions. The strong agreement between the CRLB-based analysis, Monte-Carlo simulations, and ADC phantom experiment, suggests the utility of this approach to optimize DW-MRI acquisitions.

**Purpose (731/750 words):** Mapping of the apparent diffusion coefficient (ADC) from a set of diffusion-weighted (DW) images acquired with different b-values, often suffers from low SNR, which can introduce large variance in ADC maps. Unfortunately, there is currently no consensus on the optimal set of b-values to maximize the noise performance (ie: minimize the variance) of ADC mapping. The purpose of this work is to optimize the set of b-values for ADC mapping, using Cramér-Rao Lower Bound<sup>1</sup> (CRLB) analysis under the assumption of realistic Rician distributed data, noise distribution commonly present in MRI<sup>2</sup>.

### Methods:

Determination of optimal b-values: The ADC mapping signal model is described by  $S(b) = S_0 e^{-bADC}$ . In order to maximize the noise performance of ADC estimation we optimize the set of b-values via the CRLB approach. Such an approach was previously employed, in related contexts, in Refs<sup>3,4</sup> under Gaussian noise assumptions, and by Ref<sup>5</sup> for the Kurtosis model under a Rician assumption. Given a set of independent Rician distributed observations of the ADC signal model,  $S_k$  where  $k \in [1, \dots, K]$ , with the same noise level, the CRLB of the ADC (CRLB<sub>ADC</sub>) is given by the element (2,2) of the inverse of the Fisher Information Matrix<sup>1</sup> (Eq. 2), where  $I_n$  is described in Ref<sup>6</sup>. Therefore, for a given target ADC, noise level, and number of b-values (K), the determination of the set of K b-values that optimizes the noise performance of the ADC estimation is performed by an iterative brute force algorithm. The iterative algorithm starts from a set of b-values composed only of b-value=0 s/mm<sup>2</sup> and iteratively adds to the set the b-value that achieves minimum CRLB<sub>ADC</sub> among a large set of b-value candidates. The proposed algorithm iterates until a set of K b-values is completed. Table 1 shows the pool of candidate b-values and other parameters employed.

Eq. 2:

$$FIM = \begin{bmatrix} \sum_{k=1}^K e^{-2b_k ADC} I_n(S_k, \sigma) & \sum_{k=1}^K S_0 b_k e^{-2b_k ADC} I_n(S_k, \sigma) \\ -\sum_{k=1}^K S_0 b_k e^{-2b_k ADC} I_n(S_k, \sigma) & \sum_{k=1}^K S_0^2 b_k^2 e^{-2b_k ADC} I_n(S_k, \sigma) \end{bmatrix}$$

Validation of optimal b-values: The sets of b-values obtained with the proposed CRLB-based approach are compared to those obtained experimentally from:

- 1) Monte-Carlo simulations, which included 13 different target ADCs (400 simulated pixels each) with a Rician distribution and parameters from Table 1.
- 2) An ADC phantom<sup>6</sup> experiment consisting of 13 vials with different ADCs at room temperature. The DW-MRI acquisition was performed at 1.5T (GE Healthcare, Waukesha, WI) using a standard single shot EPI sequence with the following parameters: slice thickness of 5 mm, FOV=24cm x 24cm, matrix size of 144x144, TE=111 ms, and 41 b-values uniformly distributed between 0-2000 s/mm<sup>2</sup>. Further, this acquisition was repeated 16 consecutive times (discarding the first three repetitions to avoid steady-state effects) to enable voxel-wise determination of ADC estimation statistics.

The optimal sets of b-values for the Monte-Carlo simulations and the ADC phantom experiment were obtained iteratively. At each iteration, the b-value that minimizes the variance of the ADC estimation among all candidate b-values is added to the selected set. The procedure is analogous to the one employed in the CRLB-based optimization, but using the experimental variance instead of the  $CRLB_{ADC}$  (note that 13 repetitions are available for each of the Monte-Carlo simulations and the ADC phantom experiment). Each ADC estimation was performed pixel-wise via a Maximum Likelihood<sup>7</sup> estimator (ML).

**Results:** Table 2 shows the optimal sets of b-values obtained from the CRLB-based theoretical analysis, Monte-Carlo simulations, and ADC phantom experiment for one of the vials ( $ADC=2.1 \cdot 10^{-3} \text{mm}^2/\text{s}$ ). Further, Figure 1 shows, for the same vial, the evolution of the  $CRLB_{ADC}$  and experimental variances with respect to the number of b-values employed. Figure 2 shows a color-coded comparison of the optimal sets of b-values for all the vials in Table 1.

**Discussion:** Results indicate a strong agreement between optimal sets of b-values obtained using the proposed CRLB-based theoretical analysis and those found experimentally both by the Monte-Carlo simulations and by the ADC phantom experiment. This illustrates the potential of the proposed CRLB-based approach to maximize the noise performance (minimize the variance) of ADC mapping by optimizing the choice of acquired b-values. In order to achieve a procedure that is suitable for the selection of the set of b-values in clinical settings, further validation is still required, considering realistic distributions of target ADCs, the effect of T<sub>2</sub> relaxation, and *in-vivo* results.

**Conclusion:** The optimization of the set of b-values is critical to maximize the noise performance (ie: minimize variance) of the ADC estimation in DW-MRI. The proposed approach may help optimize and standardize DW-MRI acquisitions by computing the optimal set of b-values for a target ADC.

#### References:

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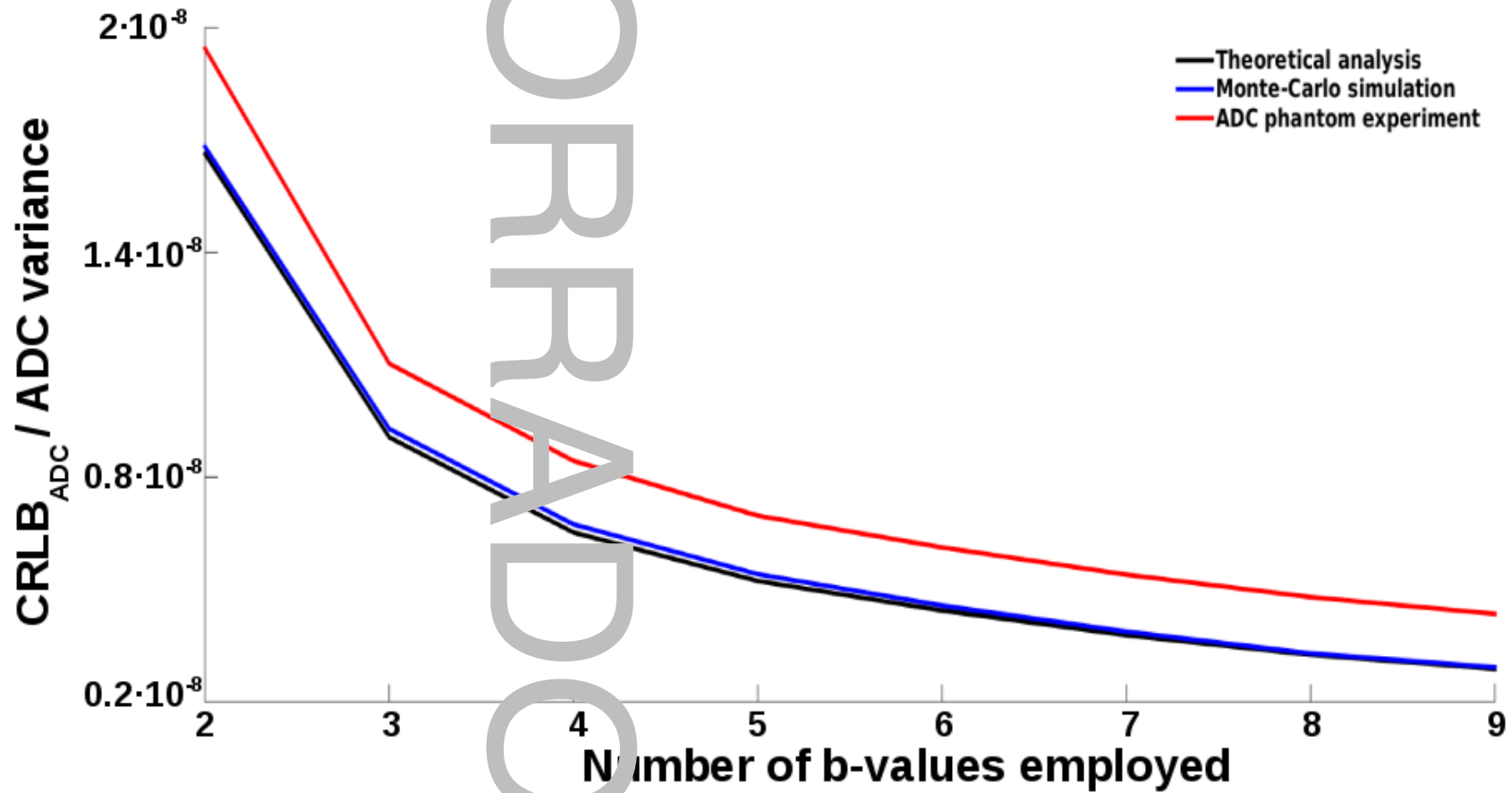
**Table 1:** Parameters of interest obtained from the ADC phantom experiment. These values were also applied for CRLB-based optimization as well as in the Monte-Carlo simulations.

\*The CRLB-based optimization is under the assumption of NEX=13.

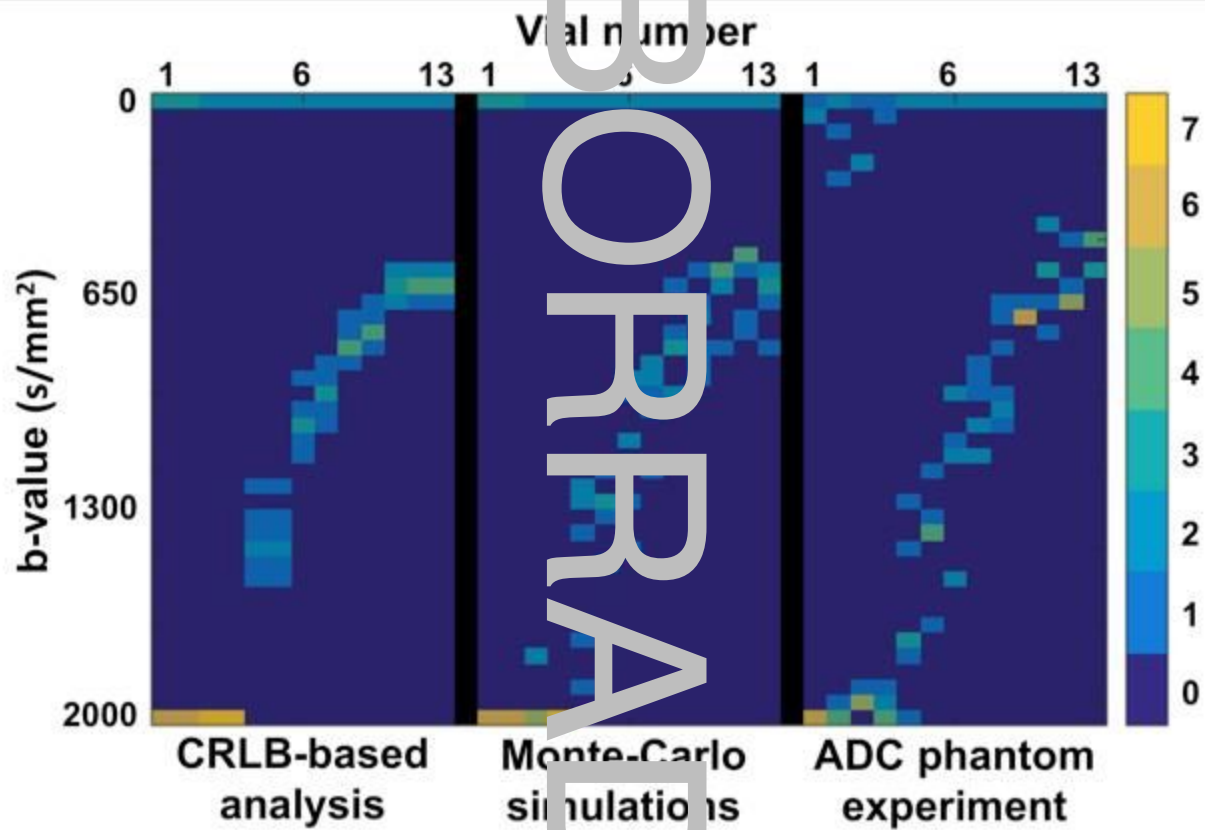
	VIAL 1	VIAL 2	VIAL 3	VIAL 4	VIAL 5	VIAL 6	VIAL 7	VIAL 8	VIAL 9	VIAL 10	VIAL 11	VIAL 12	VIAL 13
ADC ( $\cdot 10^{-3}$ mm <sup>2</sup> /s)	0.3	0.32	0.54	0.54	0.7	0.7	1.2	1.3	1.6	1.7	2.1	2.1	2.1
SNR of b <sub>0</sub> image	42	53	35	49	29	23	40	25	51	53	58	47	40
NEX*	13												
b-values (s/mm <sup>2</sup> )	0, 50, 100, 150, 200, 250, 300, 350, 400, 450, 500, 550, 600, 650, 700, 750, 800, 850, 900, 950, 1000, 1050, 1100, 1150, 1200, 1250, 1300, 1350, 1400, 1450, 1500, 1550, 1600, 1650, 1700, 1750, 1800, 1850, 1900, 1950, 2000												

**Table 2.** Results of the b-value optimization for vial 1 ( $ADC = 2.1 \cdot 10^{-3} \text{ mm}^2/\text{s}$ ). b-values appear in the same order they were included in the optimal sets.

Number of b-values (K)	Optimal set of b-values (s/mm <sup>2</sup> ) (CRLB-based analysis, Monte-Carlo simulations, ADC phantom experiment)
K=2	0 500 0 450
K=3	0 550 550 0 500 500 0 450 500
K=4	0 550 500 600 0 500 500 550 0 450 600 650
K=5	0 550 500 600 600 0 500 500 550 500 0 450 600 550 650
K=6	0 550 550 600 600 650 0 500 500 550 750 700 0 450 600 650 650 650
K=7	0 550 550 600 600 650 0 0 500 500 550 750 700 0 0 450 600 650 650 650 0
K=8	0 550 550 600 600 650 0 600 0 500 500 550 750 700 0 500 0 450 600 650 650 650 0 650
K=9	0 550 550 600 600 650 600 600 0 500 500 550 750 700 500 500 0 450 600 650 650 650 650 650



**Figure 1:** Evolution of the minimum  $CRLB_{ADC}$  of the  $CRLB$ -based analysis and minimum variance of the Monte-Carlo simulations and the ADC phantom experiment for vial 12 as the number of employed b-values increases ( $ADC = 2.1 \cdot 10^{-3} \text{ mm}^2/\text{s}$ ,  $SNR=47$ ).



**Figure 2:** Optimized set of K=9 b-values for the 13 vials of the theoretical, Monte-Carlo simulations, and ADC phantom experiments. Each column shows the optimal set of b-values found for a vial, where the color code indicates how many times a certain b-value was included in the optimal set.