

Noise estimation for averaged DW MR images

Nikolaos Dikaos¹, Valentin Hamy¹, Shonit Punwani¹, and David Atkinson¹

¹Centre for Medical Imaging, University College London, London, Greater London, United Kingdom

Purpose: Diffusion weighted (DW) imaging can aid discrimination between benign and metastatic lymph nodes of patients with head and neck squamous cell carcinoma [1], but have inherently low SNR. DW uses modulus images, which at the absence of averaging and with single coil acquisition follow Rician distributed noise. Otherwise the expected noise distribution will depend on the number of receiver coils used during the acquisition, the way images from different coils are combined [2] and whether images are averaged. The scope of this project was to estimate the noise using an adaptation of the median-absolute-deviation (MAD) in the wavelet domain for the expected noise distribution, and calculate the diffusion coefficient (ADC) with a non linear regression (NR) algorithm that accounts for underlying noise.

Theory: Donoho [3] suggested a MAD estimator in the wavelet domain for Gaussian noise σ_G . Briefly the 2D magnitude DW images were decomposed using Haar wavelet decomposition into 4 subbands (LL, HL, LH, HH, L= low and H=high frequencies). The lowest subband (LL) mainly corresponds to the object, hence the LL subband is used to segment (using the K-means algorithm) the object. Having segmented the object the noise is estimated from the wavelet coefficients (y_i) corresponding to its HH subband, hence $\sigma_G = \text{median}(|y_i|)/0.6745$. Coupe [4] adapted the method for Rician noise. In this work MAD estimator was adapted for noise from averaged magnitude images. To estimate σ for the expected probability density function (pdf) the iterative method suggested by Koay and Basset was followed that uses the update formula $\sigma = \sqrt{\sigma_G^2 / \zeta(\theta)}$, where $\zeta(\theta)$ is a correction factor based on the SNR θ . The pdf of averaged magnitude MR images (i.e. sum of RVs) is given by the convolution of their pdfs and can be approximated by a formula similar to the one suggested by [5],

$$p_{\text{aver}}(M_b | S_b, \sigma) = \frac{c_2 M_b}{\sigma^2} \cdot \left(\frac{c_2 M_b}{c_1 S_b} \right)^{N_{AV}-1} \cdot e^{-(c_2 M_b^2 + c_1 S_b^2) / 2\sigma^2} \cdot I_{N_{AV}-1} \left(\frac{c_2 M_b c_1 S_b}{\sigma^2} \right) \quad \text{Equation 1}$$

where c_1, c_2 are constants, and N_{AV} is the number of averages. To optimize the value of the c_1, c_2 , eq 1 was fitted with a NR algorithm to the convolved Rice pdfs. In accordance with the results shown in [5] the closed form approximation fits the convolved Rice pdfs accurately. Consequently $\zeta(\theta)$ will be

$$\zeta(\theta) = 2 \cdot N_{AV} + (c_1 \cdot \theta)^2 - \beta^2 \left[{}_1F_1(-0.5, L, -\frac{(c_1 \cdot \theta)^2}{2}) \right]^2 \quad \text{Equation 2}$$

Where ${}_1F_1$ is the confluent hypergeometric function, and β_L is a factor depending on the number of coils. To avoid the bias induced during the calculation of the diffusion coefficients due to non Gaussian noise NR fitting was employed to fit the centre of the expected pdf to the measured DW signal [6]. To measure the centre of the pdf, the maximum probability (MP) was used.

Methods: Simulated DW image ($N_{AV}=4$) was generated at $b=1000 \text{ s/mm}^2$ consisting of two regions; one corresponding to normal tissue and another that corresponds to malignant tissue. The values for the normal and malignant tissue were taken from our clinical data. Different noise levels were applied at the generated images (corresponding to SNR values from 30 to 2).

Axial DW images of the neck were acquired using a DWI spin echo sequence on a Philips Achieva 3T MRI scanner. Trace DW images were derived at $b=0, 50, 100, 300, 600, 1000 \text{ s/mm}^2$. Sixteen single averages were acquired for each bvalue using 5mm thick slices for one subject, and 2.5mm for another (reduced SNR). To measure noise after parallel imaging reconstruction, the $b=1000 \text{ s/mm}^2$ acquisition was repeated using the same reconstruction parameters but without radiofrequency (RF) pulses. This noise-only method was repeated for a scan with $N_{AV}=4$. Sixteen ADC values were calculated from the DW images ($N_{AV}=1$) with the NR and MP method.

Results: The proposed MAD method predicted the different applied noise levels of the simulated DW $b=1000 \text{ s/mm}^2$ image ($N_{AV}=4$) with an $R^2=0.95$.

Noise was estimated with the proposed MAD method (σ_R) for the two subjects for $N_{AV}=1$ and 4, the real noise was estimated by fitting the expected pdf to the histogram from the noise-only data with an expectation-maximization (EM) algorithm (fig 1 & 2). A summary of the results is shown in table 1. Sixteen ADC values are calculated separately with the NR and the MP method from the single averages DWI. The median value of the ADC populations ($N_{AV}=1$) is 0.94 for the NR, and $1.03 \text{ mm}^2/\text{s}$ for the MP respectively ($p < 10^{-4}$). Four well aligned $N_{AV}=1$ DWI were selected, and averaged. The ADC from the $N_{AV}=4$ DWI was 0.98 for the NR, and $1.04 \text{ mm}^2/\text{s}$ for the MP. To conclude the proposed MAD accurately predicted the noise levels of simulated DWI and noise scans. Accounting for noise lead to ADC values 10% higher for $N_{AV}=1$, and 6% for $N_{AV}=4$.

Table 1: Noise estimates with proposed MAD (σ_R), and with EM fit (σ_T) on measured noise distribution.

	Slice Thick 5mm Subject 1	Slice Thick 2.5mm Subject 2
$N_{AV}=1$	$\sigma_R=45$ ($\sigma_T=48$)	$\sigma_R=154$ ($\sigma_T=162$)
$N_{AV}=4$	$\sigma_R=29$ ($\sigma_T=30$)	$\sigma_R=76$ ($\sigma_T=97$)

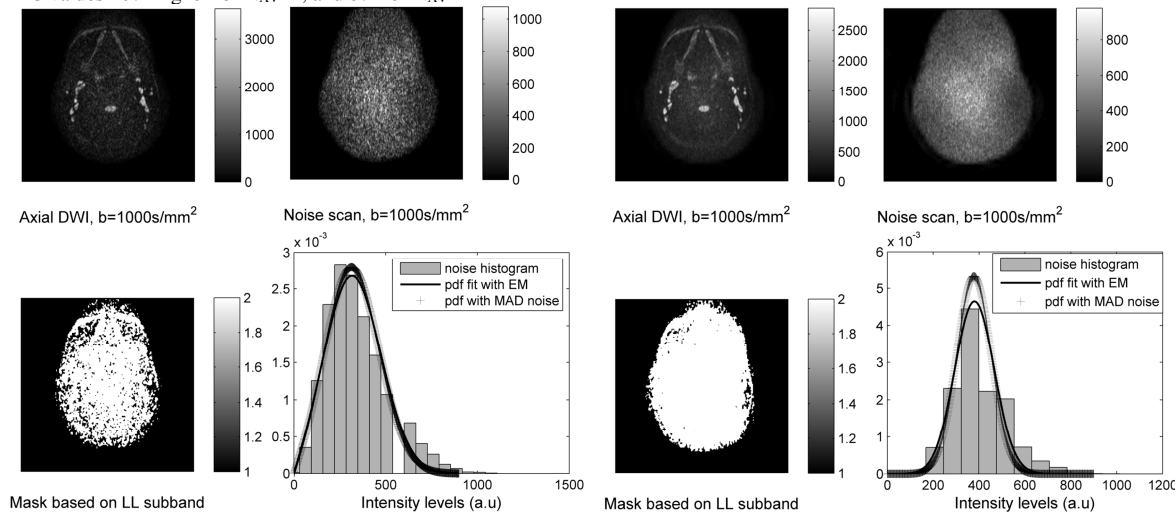


Figure 1: The expected pdf fitted to the noise histogram ($N_{AV}=1$, subject 2) with EM, and with MAD noise estimate.

Figure 2: The expected pdf fitted to the noise histogram ($N_{AV}=4$, subject 2) with EM, and with MAD noise estimate.

Acknowledgements: The study was partially funded by UK EPSRC grants EP/I018700/1 and EP/H046410/1.

References: [1] Perrone A et al Eur J Radiol 2011; 77:281-286. [2] Dietrich O et al MRI 2008; 26: 754-62 [3] Donoho et al Biometrika 1994; 81: 425-455. [4] Coupe P et al MIA 2010;14:483-93 [5] Hu J IEEE 2005; 9:133-6 [6] Kristoffersen A JMRI 2007;187:293-305.