

# Rician Noise Reduction in MR images via Non-Local Maximum Likelihood Estimation

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## INTRODUCTION

Post-acquisition denoising of MR images is of importance for clinical diagnosis and computerized analysis, such as tissue classification and segmentation. It has been shown that the noise in MR magnitude images follows a Rician distribution, which is signal-dependent when SNR is low. It is particularly difficult to remove the random fluctuations and bias introduced by Rician noise. The objective of this paper is to estimate the noise free signal from MR magnitude images. We model images as random fields and present a Non-Local Maximum Likelihood (NLML) method for Rician noise reduction in the spirit of Non-Local (NL) means filtering [1]. Our method yields an optimal estimation result [2][3] such that it is more accurate in recovering the true signal from Rician noise than NL means in the sense of root mean square (RMS) error as well as preserving/enhancing contrast between tissues, especially when SNR is very low. It also performs better than conventional Local Maximum Likelihood (LML) in reserving and defining sharp tissue boundaries.

## THEORY

In MRI, the raw data measured through a quadrature detector are intrinsically complex valued and corrupted by zero mean Gaussian-distributed noise. The real and the imaginary images are reconstructed by an inverse Fourier transform, which will preserve the Gaussian characteristics of the noise, since it is a linear and orthogonal transform. However, the noise is no longer Gaussian for magnitude images: the nonlinear mapping changes it from Gaussian to Rician. Let us consider a region of constant noise free signal amplitude  $A$ . For  $N$  independent measured magnitude pixels  $m_1, m_2, \dots, m_n$ , which are degraded by a zero-mean Gaussian noise of standard deviation  $\sigma$ , the joint PDF is  $p_m = \prod_i (M_i/\sigma^2) \cdot \exp[-(M_i^2 + A^2)/2\sigma^2] \cdot I_0(AM_i/\sigma^2)$ , where  $M_i$  is the magnitude variable corresponding to the observation  $m_i$ ; and  $I_0$  is the zeroth order modified Bessel function of the first kind. By maximizing the log likelihood function  $\log L = \sum_i \log(m_i/\sigma^2) - \sum_i (m_i^2 + A^2)/2\sigma^2 + \sum_i \log I_0(AM_i/\sigma^2)$ , we have  $A_{est} = \arg\{\max_A(\log L)\}$  if  $\sigma^2$  can be considered known. When  $A \ll \sigma$ , the Rician PDF approaches the Rayleigh,  $p_m = \prod_i (M_i/\sigma^2) \cdot \exp[-M_i^2/2\sigma^2]$ . ML estimation of  $\sigma^2$  is  $\sigma_{est}^2 = (1/2N) \sum_i m_i^2$ . Indeed, typical MR images usually include an empty region of air outside the tissue of interest, so noise variance  $\sigma^2$  can be well estimated from the background region.

## METHODS

The key part of ML estimation is how to identify regions containing constant  $A$ . The most straightforward strategy, referred as LML, is to draw a window around one pixel, just like most commonly used smoothing filters, and claim that if the window is small enough, the underlying amplitude can be considered as a constant. However, this conventional approach usually makes restored images look blurred or unfocused near the edges. Inspired by the NL means approach [1], we assume that pixels which have similar neighborhoods come from the same distribution. In other words, the intensity of pixel  $i$  is predicted by using its non-local neighborhood, which is any set of pixels  $j$  in the image such that the window around  $j$  is similar to the window around  $i$ . To better adapt to the image, the similarity windows can have different shapes and sizes. For a given pixel  $i$ , we consider a square window  $\omega_i$  of fixed size around it, for the simplicity. We denote all pixels within  $\omega_i$  as a vector  $v(\omega_i)$ . The distances between  $i$  and any other pixel  $j$  in the image is measured by  $d_{ij} = \|v(\omega_i) - v(\omega_j)\|$ . Finally, we define the nearest  $k$  neighbors of  $i$  as its non-local neighborhood  $N_i$ , which is used to predict noise free amplitude via ML. Three criteria are taken into account in the comparison of denoising methods: 1. RMS error, which is defined as  $\sqrt{(|A - A_{est}|)/N}$ ; the better denoising technique will produce the smaller RMS, that is, the denoised image is closer to the true image; 2. Contrast, which is defined as  $\text{abs}[\text{mean}(m_{\text{tissue1}}) - \text{mean}(m_{\text{tissue2}})] / [\text{mean}(m_{\text{tissue1}}) + \text{mean}(m_{\text{tissue2}})]$ . The bias introduced by Rician noise tends to reduce the contrast between tissues, and a good denoising method should have the ability of improving the contrast; 3. Display, by which the denoising methods can be compared visually.

## RESULTS AND DISCUSSIONS

To evaluate proposed technique quantitatively according to RMS and Contrast, a simulated image of  $150 \times 150$  was used, which contained 2 tissues with original contrast of 0.33. Rician noises with different  $\sigma^2$  were added to the original image to generate noisy images with SNR of 7, 5, 3.5, 2.33, 1.75, 1.4 and 1.17, respectively. The SNR is defined as  $A/\sigma$ . Fig.1 shows that our NLML produces lowest RMS when SNR is less than 5, which means NLML performs better than the other two methods in recovering true signal when SNR is very small; while when SNR is large, the Rician distribution tends to be Gaussian, so RMS produced by the three methods are almost the same. In addition, Fig.1 also shows that the restored image by NLML presents the highest contrast, which means NLML is more effective in preserving the contrast of the noiseless image. Moreover, qualitatively or visually, we compared three methods using simulated MR data obtained via BrainWeb[4], as shown in Fig.2. Restored images via NLML appear clearer and boundaries are much better defined. On the contrary, detailed structures tend to be lost and contrast between tissues is reduced in restored image via NLmeans, and LML makes denoised image look blur and unfocused. In summary, our NLML yields more accurate result in MR image denoising, especially when the SNR is very small. It also has ability of preserving the original contrast between different tissues as well as of preserving and better defining tissue boundaries.

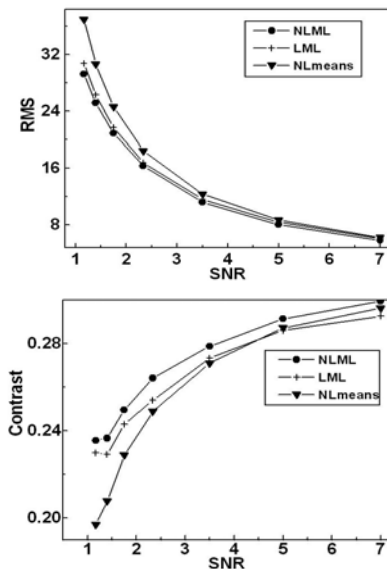


Fig. 1 Performance comparison of NLML to LML and NLmeans.

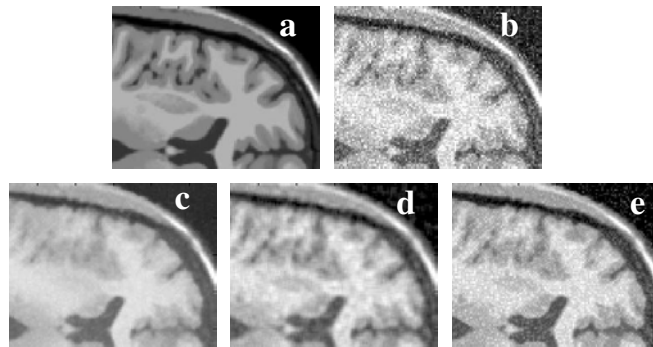


Fig.2. Effects of various denoising methods. (a) Noiseless T1 image; (b) Noisy image (Gray matter SNR is about 3.3); (c) Denoised image by NLmeans; (d) Denoised image by LML; (e) Denoised image by NLML.

## REFERENCE:

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