PERFORMANCE EVALUATION OF CARDIAC MRI IMAGE DE NOISING TECHNIQUES

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Abstract—Black-blood cardiac Magnetic Resonance Imaging (MRI) plays an important role in diagnosing a number of heart diseases. The technique suffers inherently from low contrast-to-noise ratio between the myocardium and the blood. In this work, we examined the performance of different classification techniques that can be used. The three techniques successfully removed the noise with different performance. Numerical simulation has been done to quantitatively evaluate the performance of each technique.

Keywords - MRI, Image denoising, black blood contrast, Bayes classifier.

I. INTRODUCTION

Black-blood cardiac Magnetic Resonance Imaging (MRI) plays an important role in diagnosing a number of heart diseases. In black-blood MRI imaging, the blood signal is nullled in order to increase the myocardium versus the background contrast-to-noise ratio (CNR) and also to avoid the flow artifacts generated by the blood. Aletras et al [1] proposed an acquisition technique for acquiring cardiac images with black-blood contrast. Nevertheless, the technique could null the blood signal only at one specific time instance during the cardiac cycle and thus cannot produce cine sequences. This limitation prohibits using the technique in the assessment of the heart motion. Another technique that can be used to produce cine sequence with black-blood contrast was proposed by Frahm et al and known as STEAM [2]. Unfortunately, the use of STEAM was hindered by severe deformation-dependent artifact that has been reported by many researchers [2, 3]. To overcome these limitations, Fahmy et al proposed a modified STEAM based technique that successfully: 1) corrects the STEAM artifacts; 2) produces cardiac cine sequences with black blood contrast [4]. Low contrast-to-noise ratio (CNR) is a limitation of this technique [5], all feature vectors are then classified into two background regions in the reconstructed sequence, as mentioned above, it is required to identify the background regions in the reconstructed sequence, p (x, y) and suppress their signal. In this work, a feature vector \( \bar{v} = [S_1(x, y), S_2(x, y)] \) is used to represent the information available for each pixel (x, y) in the sequence p(x, y). Based on the Bayes classifier technique [5], all feature vectors are then classified into two classes (background and tissues) as follows. First, a Bayes discriminant function is built using the joint probability function in Eq. (2.a) and (2.b),

\[
(f_{S_1S_2}(S_1S_2|\text{tissue}) = f_{S_1}(S_1|\text{tissue}) \cdot f_{S_2}(S_2|\text{tissue}) = \frac{s_1s_2}{\sigma^2} \cdot e^{-\frac{p\sin(\delta\omega)s_1^2}{\sigma^2}} \cdot I_0\left(\frac{p\sin(\delta\omega)s_1}{\sigma}\right)
\]

\[
(f_{S_1S_2}(S_1S_2|\text{bgkgrnd}) = f_{S_1}(S_1|\text{bgkgrnd}) \cdot f_{S_2}(S_2|\text{bgkgrnd}) = \frac{s_1s_2}{\sigma^2} \cdot e^{-\frac{\frac{s_1s_2}{2} + \frac{s_1s_2}{2x\sigma^2}}{2x\sigma^2}}.
\]

II. THEORY

A. Black-blood cardiac MRI: Noise-free mode

The basic idea behind the modified STEAM technique is to acquire two black-blood STEAM image sequences with complementary image intensity. That is, one sequence captures static and low contracting tissues while the other captures highly contracting tissues. Then the two sequences are processed to get rid of this deformation-dependency. In the noise-free case, given a time frame t, the signal intensities in pixel (x, y) in the acquired images was shown [4] to be given by,

\[
S_1(x, y, t) = \frac{1}{2}p(x, y)\sin(\delta\omega(x, y, t)),
\]

\[
S_2(x, y, t) = \frac{1}{2}p(x, y)\sin(1 - \delta\omega(x, y, t)),
\]

where p(x, y) is the signal component representing the nuclear properties of the tissues at pixel p(x, y) and e\(\delta\omega(x, y, t)\) is a deformation-dependent term that is related to the tissue strain, e(x, y, t). These parameters can be easily estimated as described in references [2] and [6].
\[
\text{pixel}(x,y) = \begin{cases} 
\text{e backgrnd}, & d(\bar{v}) < 0 \\
\text{e tissue}, & d(\bar{v}) > 0
\end{cases} \tag{4}
\]

B. Identifying and removing background noise using thresholding techniques

In this work two types of classifiers are used based on simple thresholding and we will refer to these classifiers with Quadratic Classifier and Rectangular Classifier. We will compare the efficiency between them and the proposed technique. In the thresholding techniques it is important to properly determine the threshold value. In this work, the threshold value was determined according to the following equation,

\[
\text{Threshold} = \beta \frac{\mu_{\text{tissue}} + \mu_{\text{background}}}{2} \tag{5}
\]

where \(\mu_{\text{tissue}}\) is the mean value of the tissue signals averaged over the entire range of deformations, \(\mu_{\text{background}}\) is the mean value of the background signals and \(\beta\) is a preset factor that is used to improve the segmentation results. It is worth noting that the threshold value obtained when \(\beta = 1\) corresponds to the optimal threshold value described in [10] assuming additive Gaussian noise. However, this value did not give good results in our simulation because of the violation of the Gaussianity assumption. Classifying a pixel as background noise is decided according to the following formulas for Quadratic and Rectangular Classifiers in the formulas (6) and (7) respectively.

\[
\sqrt{(S_1^2 + S_2^2)} < \text{Threshold} \tag{6}
\]

\[
S_1 < \text{Threshold AND } S_2 < \text{Threshold} \tag{7}
\]

c. Numerical simulation

Numerical simulations were done to illustrate the feasibility of using the proposed method for differentiating the background and the tissue regions. Two cases have been considered for simulation.

Case 1: Simulation of background signal

The background signal in images \(S_1\) and \(S_2\) was generated using a Rayleigh number generator. A range of standard deviation \(\sigma\) from 10 to 70 (with step = 10) was used to generate 100,000 pair of signal intensity samples at different SNR and the vector \(\bar{v} = [S_1, S_2]\) was created for each sample. This set of vectors was created for each value of \(\sigma\). Figure 2.a shows a plot of the joint probability density function of \(S_1, S_2\) for the generated samples at each value of \(\sigma\).

Case 2: Simulation of tissue signal

In order to simulate the signal intensities of the tissues, Rician random variables were generated on the form:

\[
S_1 = \sqrt{(n)^2 + (n + p \cdot \text{sinc}(\delta\omega))^2} \tag{8.a}
\]

\[
S_2 = \sqrt{(m)^2 + (m' + p \cdot \text{sinc}(1 - \delta\omega))^2} \tag{8.b}
\]

where \(p\) was set to 255 and the variables \(n, m, m'\) are independent Gaussian random variables with zero mean and a range of standard deviation \(\sigma\) from 10 to 70. This simulation corresponds to different signal to noise ratios of 20 log \((255/\sigma)\) (which is the SNR value of the MRI data set, as will be shown later). The variable \(\delta\omega\) was varied from 0 to 1 to simulate different levels of tissue deformation. As in the above case, 100,000 pair of signal intensity samples and the vector \(\bar{v} = [S_1, S_2]\) was created for each sample. Figure 2.b shows a plot of the joint probability density function of \(S_1\) versus \(S_2\) for the generated samples.

d. Removing background noise

For each two vectors of background & tissue which generated with each different values of \(\sigma\) & \(\delta\omega\) over the predefined range was tested by application of the proposed method to classify each generated vector \(\bar{v}\) either as background or tissue based on equation (4) and using Quadratic and Rectangular techniques based on formulas in equations (6) and (7). All the samples that were identified as background were excluded and the joint probability density function of \(S_1\) versus \(S_2\) for the remaining samples was re-calculated. Images in Figure 2.c, 2.d shows the resulting joint probability density functions using Bayesian classifier. Figure 2.e, 2.f shows the resulting joint probability density functions using Quadratic classifier. Images in Figure 2.g, 2.h show the resulting joint probability density functions using Rectangular classifier. Evidently from the figure, it can be shown that the method was successful in suppressing most of the background signal. Also it shows that some background samples still exist while some tissue signal intensities were mistakenly suppressed. Nevertheless, this type of errors is natural in any classification process (usually referred to as type-I and type-II errors). It is shown that by increasing \(\sigma\) value during generation of the two vectors that type-II error increase and type-I error still fixed. The Bayes classification keeps these errors at their minimal value. It is worth noting that the edges of the suppressed areas in images 2.e and 2.d represent the Bayes decision boundary given by setting Eq. (3) to zero and solving for \(S_1\) and \(S_2\).
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In Figure (3) shows the result of applying bayes classifier to real MRI images.

Fig.3. One time frame of cardiac cine sequence: (a) before removing noise (b) after noise removal using bayes classifier.

E. Comparison of Noise Removal techniques

Sensitivity, Specificity and Precision as defined in [10] are statistical measures of the performance of this binary classification test. So these three parameters have been calculated for each method with different cases. Sensitivity in our case is the ability of the classifier to identify the background signals and has the formula,

\[
\text{Sensitivity} = \frac{TP}{(TP + FN)} \tag{9}
\]

where TP (true positive) is the number of vectors that have been identified as background signal by the classifier and it is really background signal. FN (false negative) is the number of the vectors that have been identified as tissue signal by the classifier and it is really background signal. Specificity is the ability of the classifier to identify the tissue signals and has the formula,

\[
\text{Specificity} = \frac{TN}{(TN + FP)} \tag{10}
\]

where TN (true negative) is the number of vectors that have been identified as tissue signal by the classifier and it is really tissue signal so it can be called true tissue. FP (false positive) is the number of the vectors that have been identified as background signal by the classifier and it is really tissue signal. Precision has the formula,

\[
\text{Precision} = \frac{TP}{(TP + FP)} = \frac{\text{Sens}}{(1 - \text{Spec} + \text{Sens})} \tag{11}
\]

So for each two sets of vectors generated from different values of \(\sigma\), \(\partial\omega\) sensitivity and specificity was computed. For each of Bayesian, Quadratic and Rectangular Classifiers' results Sensitivity, Specificity and Precision are computed to show the difference between all the used classifiers. Figure (4) shows the Sensitivity value for each classifier where the vertical axis represents sensitivity and the horizontal axis represents the noise standard deviation. Figure (5) shows the Specificity value for each classifier where the vertical axis represents specificity and the horizontal axis represents the noise standard deviation. Figure (6) shows the Precision value for each classifier where the vertical axis represents precision and the horizontal axis represents the noise standard deviation.

IV. DISCUSSION

In this work it was shown that the overall performance of the Bayesian classifier is better in terms of sensitivity, specificity and precision as shown in figures (4), (5) and (6). Although the Rectangular classifier has better sensitivity than the Bayesian classifier as shown in figure (4), it has the worst specificity and precision in figures (5) and (6) especially in the high range of the SNR values. In addition, although the
Quadratic classifier’s sensitivity, specificity and precision is not much lower than the Bayesian classifier, it has the lowest sensitivity as shown in figure (4). From Table (1) it can be observed that Bayesian classifier requires more computation time than the other two techniques. However as discussed above the Bayesian classifier is much better than the Quadratic and Rectangular classifiers in the performance of denoising but in case of the speed need we can sacrifice the performance.

TABLE I
RELATIVE COMPUTATION TIME FOR EACH TECHNIQUE

<table>
<thead>
<tr>
<th>Classifier Type</th>
<th>Relative Computation Time</th>
</tr>
</thead>
<tbody>
<tr>
<td>Bayesian Classifier</td>
<td>2.387</td>
</tr>
<tr>
<td>Quadratic Classifier</td>
<td>1.085</td>
</tr>
<tr>
<td>Rectangular Classifier</td>
<td>1.000</td>
</tr>
</tbody>
</table>

Fig.4. The Sensitivity (Ability of detecting Background) signals using the three methods for generated signals with different $\sigma$ as a function of applied field.

Fig.5. The Specificity (Ability of detecting Tissue) signals using the three methods for generated signals with different $\sigma$.

Fig.6. The Precision using the three methods for generated signals with different $\sigma$.

V. CONCLUSION

In this work, the performance and the efficiency of the three different classifiers have been calculated that can be used to identify the background noise in the Black Blood Cardiac MR images. It was shown that the Bayes classifier is the best among the three techniques in terms of sensitivity, specificity and precision. Nevertheless, the Bayes Classifier takes longer computation time than the other techniques; we can sacrifice with the time factor to get better performance. That is, the computation time is the price paid for optimal noise removal.

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VI. REFERENCES