Optimally discriminant moments for speckle detection in real B-scan images

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Abstract

The paper presents and evaluates a speckle detection method for B-scan images. This is a fully automatic method and does not require information about the sensor parameters, which is often missing in retrospective studies.

The characterization and posterior detection of speckle noise in ultrasound (US) has been regarded as an important research topic in US imaging, for improving signal-to-noise ratio by removing speckle noise and for exploiting speckle correlation information. Most of the existing methods require either manual intervention, the need to know sensor parameters or are based on statistical models which often do not generalize well to B-scans of different imaging areas. The proposed method aims to overcome those limitations.

The main novelty of this work is to show that speckle detection can be improved based on finding optimally discriminant low order speckle statistics. In addition, and in contrast with other approaches the presented method is fully automatic and can be efficiently implemented to B-scan images.

The method detects speckle patches using an ellipsoid discriminant function which classifies patches based on features extracted from optimally discriminant low order moments of the uncompressed intensity B-scan information. In addition, if the uncompressed signal is not available, we propose and evaluate a method the estimation of this factor.

The computation of low order moments using an optimality criteria, the decompression factor estimation and other key aspects of the method are quantitatively evaluated using both simulated and real (phantom and in vivo) data. Speckle detection results are obtained using again phantom and in vivo studies which show the validity of our approach. In addition, speckle probability images (SPI) are presented which provide valuable information about the distribution of speckle and non-speckle areas in an image.

The presented evaluation and results show the effectiveness of our approach. In particular, the need for using discriminant analysis to determine the optimal discriminant power of the statistical moments and that this optimal value strongly depends on the characteristics and imaged tissues in the B-scan data.

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1. Background and motivation

Ultrasound (US) imaging is based on capturing differential tissue scatter or reflection of sonic pulses. Reflection and scattering are closely related concepts, and the basic difference lies in the particle size at the point of interaction. One tends to refer to scattering if the particle size is much smaller than the wavelength, while reflection happens when...
the particle size is larger than this wavelength. Scattering or reflection mainly occurs at boundaries caused by variations in homogeneity and/or compressibility. Assuming a spatially randomly distributed population of sub-resolution scatterers, one can talk about incoherent or diffuse scattering which gives rise to speckle noise or fully developed speckle. If the distribution of sub-resolution scatterers follows a given pattern, a coherent component is introduced.

Speckle noise has been shown to follow a Rayleigh probability distribution function (PDF) [5,2], whereas the adaptive coherent component commonly is regarded as a Rician PDF [5,2]. A Rician PDF is characterized by a parameter \( k \), which is the ratio between the coherent and diffuse components of the signal.

In terms of simulating speckle patterns, the echo envelope can be modeled as a sum of backscatter signals emitted from a given number of points in the imaged area. This summation can be expressed, using phasor notation, as

\[
A = s + \sum_{i=1}^{\mu} a_i
\]

where \( A \) is a single amplitude sample (which is related to the gray-level intensity of a B-scan). The parameter \( s \) represents the coherent signal and \( a_i \), the random (also referred to as diffuse) component. A single sample \( A \) can be simulated using the above equation: a single vector \( s \) with zero phase and amplitude \( k \) (the coherent signal) is added to the sum of \( \mu \) vectors of length \( \sqrt{2/\mu} \) and random phase which forms the diffuse component [17]. Samples with different values of \( k \) and \( \mu \) can be classified as being either speckle or non-speckle. In line with other authors [18], a sample is regarded as speckle when there are a high number of scatters per resolution cell (large \( \mu \), typically \( \mu > 10 \)) and the coherent component is not dominant \( (k < 1) \). Non-speckle samples will have a larger variability in terms of \( k \) and \( \mu \), but commonly will have either a small number of scatters or a dominant coherent signal \( (k \geq 1) \). Histograms for simulated speckle and non-speckle examples are shown in Fig. 1, which includes Rayleigh and Rician distributions fitted to those speckle and non-speckle distributions, respectively.

One should note that this simulation does not aim to provide realistic ultrasound data, nevertheless this is not the aim here. The aim is to obtain synthetic (as opposed to realistic) data which will contain the main statistical features in order to differentiate between speckle and non-speckle patterns. The simulation approach results in typical echo envelopes of speckle and non-speckle which might not be realistic but will contain the main statistical features of such signals. The method is based on the statistical analysis of the echo envelope, as shown by many authors [6,18,25,19], this envelope can be described by a random walk phasor summation in the complex plane. This random walk will generate the envelope distribution from which we extract the statistical features, is simulated with Eq. (1).

The detection of speckle can be regarded as an important research topic in different imaging modalities such as ultrasound and laser imaging. In this work, we focus on medical ultrasound, where speckle analysis has been commonly investigated focusing on two (often complementary) goals. A first aim is to minimize the effects of speckle noise in images, which is often characterized by areas of low-contrast and highly corrupted by non-homogeneous noise. This is commonly approached using adaptive noise suppression [13], or spatial compounding [21,22] algorithms. A second (complementary) goal is to regard speckle patches as important sources of information. In this case, the aim is not to minimize its effects, but extract information from speckle: the spatial correlation information provided by close speckle image patches can be exploited to determine spatial relationships between them and used for freehand 3D reconstruction [11], flow-based ultrasound imaging techniques [4] or for other novel imaging techniques such as elastography [20].

![Fig. 1. Histograms of simulated (a) speckle \((k = 0, \mu = 50)\) and (b) non-speckle \((k = 3, \mu = 8)\). In addition, (a) Rayleigh \((D_{\text{Rayleigh}}(x) = \frac{1}{\sigma_{\text{Rayleigh}}^2} \exp \left( -\frac{x^2}{2\sigma_{\text{Rayleigh}}^2} \right)\)), with \( \sigma_{\text{Rayleigh}} = 0.9855 \) and (b) Rician \((D_{\text{Rician}}(x) = \frac{1}{\sigma_{\text{Rician}}^2} \exp \left( -\frac{x^2}{2\sigma_{\text{Rician}}^2} \right) I_0\left(\frac{2sx}{\sigma_{\text{Rician}}^2}\right)\)), with \( s = 2.922 \), \( \sigma_{\text{Rician}} = 1.0588 \), and \( I_0() \) the zeroth order modified Bessel function of the first kind) distributions fitted to speckle and non-speckle histograms, respectively.](https://doi.org/10.1016/j.ultras.2007.11.010)
The main aim of this work is to provide an automatic method for the detection of fully developed speckle patterns in B-scan images. One common approach to this is to describe speckle using a known statistical model. Various models have been proposed for speckle characterization, Rayleigh and Rician models were originally proposed but more general models such as the Nakagami [9], Generalized Gamma [19], K [3,24], Generalized K and Homodyned K distributions [7,10,25] have been shown to account for better speckle description at the expense of a more complex formulation. The aim of those methods is to obtain an initial estimate of the model parameters based on extracting statistical features from the experimental data, commonly moments of different orders. Using those features, a maximum likelihood estimation (MLE) or a maximum a posteriori (MAP) approach is applied to obtain the final model parameters. An accurate estimation of model parameters strongly depends on knowing the acquisition parameters and imaged tissue characteristics. Using typical (commonly retrospective) data from clinical practices it is often difficult to obtain this acquisition information. Hence, the above mentioned statistical distributions become empirical approximate models. An interesting paper discussing the suitability of four different models for cardiac US images is given in Ref. [23].

Instead of using a specific statistical distribution, an alternative approach, which is adopted here, is to describe speckle based on statistical features directly computed from the amplitude distribution. These features are typically extracted from the amplitude moments of the US image (or B-scan). A classification model, typically based on clustering techniques [12,14] or application-specific discriminant functions [16] is trained on known speckle and non-speckle data, and is subsequently used for classifying new features as being speckle or non-speckle. In other words, speckle detection becomes a two-class pattern recognition problem.

To increase image contrast, usually the final gray-level intensity of a B-scan is given by a logarithmic compression of the original amplitude signal. Hence, to be able to obtain a good characterization of the speckle in ultrasound images, B-scan information needs to be decompressed. Several authors [6,18] have suggested a mapping of the form \( I = D \ln(A) + G \), where \( I \) is the final B-scan intensity, \( D \) a compression factor, \( G \) an offset value and \( A \) the original amplitude signal. The offset value is often disregarded as it does not affect the statistics of the speckle, hence \( D \) being the important factor to be determined in order to obtain good speckle detection.

This work describes a speckle detection methodology based on extracting optimally discriminant low order speckle statistics and simultaneously estimating the decompresion factor of the data. The paper is structured as follows: Section 2 describes a fully automatic approach for speckle detection in B-scan data and Section 3 shows real and simulated results. The paper finishes with conclusions and future work.

2. Materials and methods

As previously stated, our work builds on the speckle detection methodology proposed by Prager et al. [17,18], but incorporates novel aspects such as the optimal selection of the power statistics applied to real B-scans and moreover, removes the need of manual intervention, aspects which we believe make the method more robust.

2.1. Speckle characterization

Speckle in ultrasound images is commonly characterized by using three parameters: the coherent signal energy \( s^2 \), the diffuse signal energy \( 2 \sigma^2 \) and the number of scatterers per resolution cell \( \mu \). The coherent and diffuse signals are also commonly expressed as the ratio \( k = s/\sigma \), the proportion of coherent to diffuse signal. As demonstrated by different authors [6,18], speckle can be characterized by two low order moments: the ratio between the mean and the standard deviation (\( R \)) and the skewness (\( S \)), which are defined by

\[
R = \frac{E(A)}{\sqrt{E(A^2) - E^2(A)}}, \quad S = \frac{E((A - E(A))^3)}{(E(A^2) - E^2(A))^{3/2}} \tag{2}
\]

where \( A \) is the signal amplitude, and \( v \) the power of the statistical moment. Effectively, \( R \) and \( S \) can be computed using \( v \) values different from one. This issue is important as the use of a specific value of \( v \) could lead to a better discrimination between speckle and non-speckle signals. For instance, in all experiments described by Prager et al. [18] a value of \( v = 1.8 \) was used. This value was qualitatively obtained using simulated data. As noted in [12], this assertion may not be always valid, they showed that an analysis of the discriminant power of the \( R-S \) features should be carried out to determine the optimal order of the statistics.

2.2. Speckle detection

The proposal by Prager et al. is based on a simultaneous method for estimating B-scan decompression parameters and subsequently detect speckle regions based on the ellipsoid discriminant function obtained from the \( R-S \) statistical features from the data. For the sake of completeness their algorithm is described below.

(1) Obtain an ellipsoidal discriminant function using simulated speckle data.
(2) Choose an initial compression value \( D \).
(3) Manually label speckle patches in the real B-scan images (in their experiments 40 patches are used).
(4) For each patch:
   (a) Decompress the patch intensity using \( I = \exp(p/D) \).
   (b) Compute \( R-S \) features from \( I \), using a \( v \) value arbitrarily set equal to unity.

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(c) Using the elliptical discriminant function, compute feature error values. If the error is large, use an optimization algorithm to minimize the error with respect to $D$, obtaining the estimation of the decompression factor ($D$).

(5) Adapt the elliptical center parameters using the mean $R$-$S$ features from the manually labeled patches.

(6) Decompress all patches in the image, using the $D$ value, obtain $R$-$S$ features and use the elliptical discriminant function to assert if it is a speckle patch (i.e. inside the ellipse).

The above approach presents some drawbacks. A first problem is the need for manually detecting initial speckle regions in order to extract sample statistics. Manual intervention is also needed for the definition of the discriminant ellipse parameters. Another important drawback is the fact that $R$-$S$ are computed using an arbitrarily order ($\nu = 1.8$ for simulated data and $\nu = 1$ for real B-scans). Our proposal tackles the above problems, proposing a novel method for automatically detecting initial speckle patches (referred to as core patches) and selecting the most discriminant features for speckle detection. The method is described by the following steps,

1. Obtain an elliptical discriminant function from speckle simulated data for different $\nu$ values ranging from 0 to 3.
2. Automatically detect core speckle and core non-speckle regions and decompression factor $D$ from real B-scan data (see the following section).
3. Using core speckle and core non-speckle, compute $R$-$S$ statistics and find $v_{opt}$, the $v$ value where those statistics are optimally discriminant.
4. Modify the parameters of the elliptical discriminant function, as in step 5 of the original method.
5. For all patches in the image, decompress and test if it is speckle, as in step 6 of the original method.

Different key aspects of the proposed method need to be described and evaluated in detail. Core speckle detection (step 2) and the optimally discriminant statistics (step 3) are described in the following sections.

2.3. Core speckle and non-speckle

To estimate the B-scan decompression factor, a number of speckle patches need to be detected. However, speckle patches cannot be successfully detected if no decompression estimation is obtained. This is clearly an optimization problem where decompression and speckle patches need to be simultaneously estimated. In the original work [18], this was approached by manually detecting fully developed speckle patches. Here, this is solved using a RANSAC based approach [8]. The RANSAC algorithm is based on finding the points (or patches in this work), obtained from randomly sampled data that best describe a given model (here based on a stability criteria, see algorithm below).

The idea behind the detection of speckle and non-speckle patches is based on the assumption that the decompression values $D$ found after optimization (step 4c of Prager et al.’s proposal) are stable as a function of $v$ for speckle patches. For the case of non-speckle patches, $D$ values will present high variability as a function of $v$, explained by the fact that optimization will be unable to find a meaningful $D$ value. This assumption has been confirmed by a number of simulated and empirical experiments, some of them shown in the evaluation section.

The final estimate of the compression factor will be obtained analyzing the most stable values (i.e. the median value computed from values with the smallest fluctuation). In addition, the patches closest to this estimation will be regarded as the core speckle patches. The RANSAC based method for core speckle and simultaneous decompression estimation is described using the following steps:

1. Choose an initial compression value $D$.
2. Extract $N$ random patches from the B-scan data.
3. For each patch $p$
   (a) Decompress the patch intensity using $I_p = \exp(p/D)$
   (b) Compute $R$-$S$ features from $I_p$, for a range of $v$ values from 0 to 3 ($F_{\nu_p}$).
   (c) For each $F_{\nu_p}$ use an optimization algorithm to estimate the decompression value ($D_{\nu_p}$).
4. Extract the most stable $D_{\nu_p}$ values as a function of $v$ ($D_{\nu_p}$). Stability is defined by the values with minimal standard deviation.
5. Compute the median of all $D_{\nu_p}$ providing a final estimation of the compression factor as a function of $v$: $D_v$ (see Section 3.2). This will form the RANSAC estimated model.
6. Core speckle patches are defined as the $N_{sp}$ patches with $D_{\nu_p}$ smallest squared error compared to $D_v$. Using the RANSAC terminology, this error metric becomes the measure of the model fit. Core non-speckle patches will be randomly sampled ($N_{ns}$) from the patches with the largest error.

This algorithm iterates until a minimal error is obtained or when the magnitude of the error remains constant.

It should be noted that if no core speckle patches are present in the data, the developed approach will find the most similar patches to speckle (although this might not be pure speckle). This makes the method more robust in the sense that if no speckle is found, it finds the most sensible answer, the patches most similar to pure speckle.

In addition to the log compressed image, some ultrasound machines already provide the uncompressed echo amplitude signal or in some cases, the information about the decompression factor used. In those cases, the method would not need to estimate the decompression parameter, making the core speckle and non-speckle step less compu-
tionally costly, avoiding the use of the optimization algorithm in order to obtain the estimation of the decompression factor $D$. The aim of the proposed method, however, is to provide an estimation of the acquisition parameters (i.e. decompression factor) even if the transducer parameters are unknown, as still happens in many ultrasound data analyzed, mainly because of their retrospective nature (where non-compressed images are unavailable) or due to limitations of the ultrasound scanner.

2.4. Discriminant analysis

Other authors have already justified the need of finding optimal discriminant statistics for speckle detection (see [12]). However, in their work they applied the discriminant analysis only to speckle simulated data, not to real B-scan images. In addition, a different speckle detection approach is adopted here.

The $R-S$ statistics can be regarded as features for a classic pattern recognition problem [26]: given a set of feature values classify them as being speckle or non-speckle. As a set of $R-S$ features is obtained for each sampled $v$ value, one could assume that the most appropriate features are those which maximize a specific measure of discriminating power. The most accurate classification is likely to occur when the data is well separated for each class (maximizing interclass variability) and the data within each class is heavily clustered (minimizing intra-class variability). Different criteria have been proposed as a measure of this discrimination. The aim is to use the value of $v$ which maximizes this criteria for computing the $R-S$ features.

One of the most commonly used methods is the analysis of the within class ($S_w$) and the between class ($S_b$) scatter matrices [26]. The within class scatter matrix, $S_w$, assuming equally probable classes is defined as

$$S_w = \frac{1}{c} \sum_{i=1}^{c} E\{(X - m_i)(X - m_i)^T\}$$ (3)

where $c$ is the total number of classes, $X$ is the feature vector (i.e. $N$ features derived from $R-S$ values) and $m_i$ is the mean feature vector for class $i$. The between class scatter matrix, $S_b$, is related to the mean differences of each class compared to the total mean for all classes ($M$), and is defined as

$$S_b = \frac{1}{c} \sum_{i=1}^{c} E\{(m_i - M)(m_i - M)^T\}$$ (4)

Defining the total scatter matrix $S_m$ as the sum of the $S_w$ and $S_b$ scatter matrices, different measures of discrimination power can be computed. To follow a consistent notation with [12], those measures are referred to as $J_1$, $J_2$ and $J_3$ and are defined as follows:

$$J_1 = \text{trace}(S_m)/\text{trace}(S_w), \quad J_2 = \text{det}(S_m)/\text{det}(S_w), \quad J_3 = \text{trace}(S_w^{-1} * S_b)$$ (5)

For all cases a higher value denotes higher class separability, although this criteria does not always coincide for all measures, which, empirically determined from the experiments, is especially true for the $J_1$ measure. With respect to the problem of speckle detection, $R-S$ features used for speckle detection will be those computed using the value of $v$ which maximizes class separability (referred to as the $v_{opt}$ value) based on the $J_{1,...,3}$ measures.

3. Results

3.1. Simulated data

As an initial evaluation, different experiments have been carried out to validate the speckle detection framework using simulated data. As stated above, Eq. (1) simulates a single random sample. In order to be able to statistically characterize a speckle pattern a larger number of samples is needed, this will be referred to as the sample size and is related to the size of the image patches used for speckle detection in B-scan images. Therefore the significance of the computed feature will depend on the number of samples used. A single feature vector is obtained for each simulation. In order to be able to characterize speckle and non-speckle patterns a large number of feature vectors must be computed, this will be referred to as the set size, which is equal to the number of image patches used.

3.1.1. Experiment 1: discriminant analysis

A total of four different speckle and non-speckle patterns have been simulated using different $k$ and $\mu$ parameters, namely $I_s = (0.50)$ as fully developed speckle and $I_s = (1.50)$, $I_s = (0.2)$, $I_s = (1.2)$ as non-speckle patterns. For each pattern a total of 1000 sets have been simulated (each set contains a 1000 samples, which is equivalent to a 1D representation of an image patch of, e.g. $25 \times 40$ pixels) and subsequently $R-S$ features have been computed as a function of $v$. Fig. 2a shows class separability for the 2-class problem as a function of $v$. The maximum value for $J_1$ is around 3 (which is the extrema of the used $v$ range), whereas $J_2$ and $J_3$ are consistent in finding an optimal $v$ value around 0.5. For this latter value, Fig. 2b shows the scatter plot of the $R-S$ features where a clear discrimination can be seen between the data except for $I_2$ and $I_3$ (and to a lesser extend $I_1$). This overlap is explained by the similar parameters used, related to fully developed speckle and speckle with an small amount of coherent scattering. It can be seen, as pointed out previously, that $J_2$ and $J_3$ values corresponds to similar discrimination criteria. Therefore, and similarly to [12], $J_3$ measures will be used as discriminant criteria ($J_2$ could also be used). In conclusion, these results suggest that class separability is not optimal for a fixed value as suggested in [18].

A similar experiment, but using a different set of speckle and non-speckle patterns (using different $k$ and $\mu$ parameters) is presented see Table 1 for the parameters used.

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From a total of eight different sets (4000 samples each) simulating speckle and non-speckle data, \( R - S \) features have been computed as a function of \( v \). Fig. 3a shows the discriminant analysis using the \( J_1, \ldots, J_3 \) measures for this data. Clearly, both \( J_2 \) and \( J_3 \) coincide, resulting in an optimal \( v \) value \((v_{\text{opt}} = 1.6)\); a different value from the previous simulated experiment, which illustrates the need for the discriminant analysis step. Fig. 3b shows a scatter plot of these features labeled as being speckle (+) and non-speckle (−). The scatter plot in Fig. 3b is obtained using the \( v_{\text{opt}} \) value. Fully developed speckle data, although simulated using four different parameters is mainly clustered, while some of the non-speckle data overlaps with the speckle due to its similar parameters. This figure also shows the ellipse discriminant function, automatically obtained from the speckle data, which provides a robust and computationally efficient method for speckle detection. Using this ellipsoid function, the figure also shows detection results, where black samples depict detection errors (black dots are false negatives and black crosses are false positives) and gray samples are correctly classified samples (dots are true positives and crosses true negatives). This experiment provides information about the usefulness of the ellipsoid function and the suitability of performing the discriminant analysis. For the \( v_{\text{opt}} \) value, we obtain 91% of correct classification, with a lower accuracy for the other \( v \) values, which again suggests that the use of optimal discriminant analysis has a positive impact in the detection of speckle. A justification for the use of the discriminant analysis for improving speckle detection rates is investigated in the next experiment.

### 3.1.2. Experiment 2: correct classification

Another experiment is presented to assess if the use of the discriminant criteria for \( v \) corresponds to an optimal speckle...
detection rate. Characteristic speckle and non-speckle data has been simulated using the parameters described in the last experiment the four speckle and four non-speckle patches in Table 1. An ellipsoid discriminant function has been fitted using the $R-S$ features from speckle data for different $v$ values. The experiment is based on selecting a number of random samples from the simulated data and test if they belong to speckle using the ellipsoid function. The aim is to evaluate if the optimally discriminant $v$ value ($v_{opt}$) improves speckle detection results.

Fig. 4 shows the results (mean and standard deviation) for two different simulations (500 and 1000 sample sizes) in terms of correct classification rate (CCR), sensitivity and specificity. In each graph, circles show the position of the $v_{opt}$ value for both sample sizes. It can be seen that in both simulations the $v_{opt}$ value is closely in line with the best classification, sensitivity and specificity rates. Although the maximum rates are not obtained at $v_{opt}$, it provides a close value to these maximum for all criteria, and globally, it can be regarded as an optimal trade-off.

![Fig. 4. Speckle detection: (a) mean and (b) standard deviation for simulated data using different sample sizes: 500 and 1000 samples. In all graphs a circle corresponds to the $v_{opt}$ value for each sample size.](image-url)
value. Note, for instance, that a high CCR value is obtained while also obtaining high specificity and sensitivity. Results with different simulated data (not included here) also corroborate these findings.

In terms of sample size, 500 sample size data results gives slightly worst results, specially for the lower order moment in CCR and specificity. This is due to the fact that statistics are drawn from smaller sample sizes making those features less significative. However, for the $v_{\text{opt}}$ value, both sample sizes obtain similar results corresponding to the best detection rates. In that sense, selecting the $v_{\text{opt}}$ value minimizes the inconvenient effects of having small sample size.

One should also notice the high specificity rates. Recalling that specificity measures the proportion of true negatives of all non-class (i.e. true negative and false positive) cases, in this particular case, non-speckle data have a minimum overlap with the speckle discriminant function, hence the small number of false positives. Those rates increase when dealing with non-speckle patches with parameters close to speckle (experienced in real data or simulated data with $k$ and $\mu$ similar to speckle). However, in all cases the ellipsoid discriminant function ensures a good fitting of the speckle data keeping the number of false positives relatively low. In conclusion, this experiment shows that the use of $v_{\text{opt}}$ value provides an optimal value for computing the feature statistics taking accuracy, sensitivity and specificity into account.

### 3.2. Detection of core speckle and non-speckle in real images

Evaluation of the core speckle and non-speckle detection algorithm described above is presented in this section. Different simulated and experimental results have been obtained in order to empirically show the validity of the assumption that speckle patches provide a more reliable decompression estimation compared to non-speckle patches.

#### 3.2.1. Decompression estimation

The first experiment is based on manually selecting a set of speckle and non-speckle patches from a B-scan (results shown here are for the prostatic phantom image of Fig. 7, top). Subsequently, for each patch in the same B-scan, the decompression factor is estimated (step 3 described in Section 2.3) in order to obtain the behavior of $D$ for both speckle and non-speckle patches as a function of $v$. Fig. 5 shows these estimations, mean and standard deviation values for a total of 10 speckle and 10 non-speckle manually chosen patches. It is clear that non-speckle regions give a highly variable $D$ estimation, whereas speckle patches are relatively stable. This fact is used in our method for automatically obtaining the decompression factor as a function of $v$. This estimation, $D_{\text{v}}$, is also shown in Fig. 5a (square in the plot) and it is computed as the median of the most stable decompression values obtained after applying the optimization process in a set of randomly sampled patches (as explained in Section 2.3). Hence, at the same time, we are detecting speckle patches as those stable results are likely to be related to speckle patches (see section below on core speckle detection). Although the true decompression factor was not available from the data, the estimation obtained by the proposed method is in line with the values manually obtained (+) in Fig. 5a.

#### 3.2.2. Detection of core speckle and non-speckle

Automatically extracting the most stable estimations of the decompression value will provide the core speckle patches, whereas the most unstable results will be defined as the non-speckle patches. Both speckle and non-speckle patches will be used for obtaining the $R-S$ features used for computing the optimally discriminant $v_{\text{opt}}$ value. Fig. 6 shows core speckle and non-speckle detection results in real B-scan data for prostatic phantom and in vivo liver images. The number of patches (the $N_{\text{sp}}$ and $N_{\text{nsp}}$ values) is set to 20, which is not a particularly critical value. Note

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**Fig. 5.** Decompression estimation experiment: (a) mean and (b) standard deviation of the $D$ estimation as a function of $v$ using manually labeled speckle and non-speckle patches. It can be seen that speckle patches obtain a stable estimation compared to non-speckle patches. In addition, in (a) the decompression estimation ($D_v$) obtained with the proposed method is shown (square).

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565 that those patches might overlap with each other, hence it
566 might be difficult to visually appreciate the total number of
567 patches found. In both cases, core speckle clearly shows
568 typical low intensity fully developed speckle patches,
569 whereas core non-speckle are characterized by high-con-
570 trast regions with important coherent signal components.
571 To obtain these results, and the results shown in the follow-
572 ing sections, square patches of 25 \times 25 pixels, a total of 625
573 samples, have been used. This is motivated by the need of
574 detecting sufficiently small speckle patches, but also having
575 statistically significant features. This trade-off is given by
576 this sample size of 625.
577 As shown in the simulated experiments (Section 3.1.2)
578 using small sample sizes (500) classification results using
579 the $v_{opt}$ value are in line with much larger sample sizes.
580 Other sample sizes have been tested, obtaining similar
581 trends: a larger sample size (i.e. 1000) tends to obtain a
582 slightly better discrimination of speckle (commonly less
583 false positives) but at the expense of finding less speckle
584 patches (patches are larger, therefore patches with purely
585 speckle noise are less likely to be found). On the other
586 hand, a smaller sample size obtains less detection accuracy,
587 as statistics from those patches are less significant. One
588 should note that this evaluation has been qualitatively per-
589 formed as no ground truth was available in the real B-scan
590 data. Nevertheless, the findings are in line with the simu-
591 lated results previously obtained (Section 3.1.2).

3.3. Speckle detection results

The proposed algorithm has been tested using a prost-
592 tatic phantom and in vivo liver US images. The phantom
593 images were acquired using a tissue equivalent ultrasound
594 prostate phantom from CIRS with a Siemens Antares
595 ultrasound machine (7.5 MHz probe). The phantom is a
596 simplification of the tissue characteristics of a real prostate.
597 For the liver images a 3.5 MHz probe on a Toshiba Pow-
598 ervision was used in a normal adult. Although a single
599

Fig. 6. Results for core speckle detection in (a) prostatic phantom and (b) liver images. Original B-scan (top), core speckle (middle) and core non-speckle
patches (bottom).
image was used for the core speckle detection for each data set, (the ones shown in Fig. 6), detection results are qualitatively satisfactory as shown in Fig. 7 and Fig. 8.

For the prostatic phantom (Fig. 7), two different non-consecutive scans have been tested. In both B-scans the method interestingly detects regions not only with dark

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Fig. 7. Speckle detection results for prostatic phantom images. (a) Original and (b) speckle detection.

Fig. 8. Speckle detection results for liver images. (a) Original and (b) speckle detection.
speckle patches (similar to the core speckle) but also lighter speckle areas inside the prostate area. It should be noted that these lighter areas were not detected as core speckle (see Fig. 6), which is explained by the fact that those patches were not the best core speckle candidates as they presented a slightly higher variation when estimating the decompression factor $D$. Based on our experiments, some detected speckle patches (see Section 2.3) can show a slightly larger variation in $D$ estimation than found for the core speckle patches detection (see Section 2.2). However, the opposite has not been observed: non-speckle is never stable when estimating the decompression factor.

Fig. 8 shows speckle detection results for two different B-scans of a liver. In this case, images show less obvious structured patterns compared to the prostatic phantom images. The method successfully detects a large number of speckle patterns avoiding the small darker structures (i.e. vessels) and the brightest areas with larger coherent components.

Similarly to the simulated case, the discriminant analysis of the phantom results of Fig. 7 is shown in Fig. 9a. In this case, although this is not simulated data, a clear maximum is observed, specially for the $J_2$ and $J_3$ measures at $v_{opt} = 1.8$. This value was used for obtaining the results shown in Fig. 7. Fig. 9b shows discriminant analysis for speckle detection for the liver images shown in Fig. 8. For this particular case, the $v_{opt} = 0.3$, a value different from the phantom case, illustrating the need for the discriminant analysis step for an optimal speckle detection.

In addition, Fig. 10 shows the estimation of the decompression factor, with a similar and stable plot for both cases, although a slightly higher value is observed for the liver images. This illustrates that although a large variation is shown in the $v_{opt}$ estimation (Fig. 9), this does not imply a variation on the decompression factor, which in both cases are in line with typical ultrasound values.

3.3.1. Speckle probability images

The information obtained from the proposed speckle detection methodology can be used to obtain speckle probability images (SPI). Taking into account that a patch is classified as being speckle if it lies inside the ellipse discriminant function, a SPI can be generated plotting the results of this function for all pixels in the image. This image provides information about the distribution of fully developed speckle areas, but also about the position and amount of coherent noise areas, given by the difference from the core speckle data. Fig. 11 shows two examples of SPI images for the prostatic phantom and liver cases where a lighter gray-level indicates a higher speckle probability. It is clear that results are in line with the findings obtained for the core speckle and core non-speckle and for speckle detection where areas with an important amount of coherent scattering (i.e. region boundaries, high impulse noise) are clearly denoted as low probability regions of fully developed speckle. Resolution of the speckle probability images strongly depends on the quality of the acquired data. This is illustrated by the two results shown in Fig. 11. The prostate phantom is a clear example of retrospective data where no acquisition information is available and the image quality has been degraded due to lossy compression (i.e. frames are extracted from an avi file), which typically presents blocky effects. It should be noted that the SPI images for
the prostatic case show lower resolution (blocky and discontinuous regions), especially when compared to the liver images. This illustrates the fact that speckle characterization is obviously dependent on image quality. Nevertheless, it should be emphasized that the results using the proposed methodology are robust enough and obtained good speckle discrimination even with lower quality images. Although lossy formats should be avoided, these are still typically found in clinical practice, especially when analyzing retrospective cases or with equipment which does not conform to current imaging standards such as DICOM.

4. Discussion and conclusions

A methodology for the detection of speckle patterns in B-scan ultrasound images has been presented. The proposed method stems from a previously published proposal based on the computation of low order statistics from the raw envelope signal. Nevertheless, important novel aspects are introduced such as optimally discriminant features and the suppression of the need of manual intervention. Various quantitative and qualitative evaluation results using both simulated and real data have been provided which show the effectiveness of our approach. In particular, it has indicated the need for using discriminant analysis to determine the optimal discriminant power of the statistical moments and that the optimal value strongly depends on the characteristics and imaged tissues found in the B-scan data. This has been made specially clear as different optimal values have been obtained for simulated data and prostatic phantom and liver images. The detected speckle patches obtained with the proposed method can be used in other algorithms in terms of adaptive speckle suppression [13], segmentation [15] and speckle de-correlation approaches for freehand 3D reconstruction [11], elastography [20] or flow estimation [4] using ultrasound image sequences.

The use of SPI information for subsequent processing steps such as non-linear anisotropic diffusion techniques [1] or other adaptive noise suppression algorithms opens an interesting application area of the speckle detection methodology presented in this paper. However, this applicability and the development and evaluation of those methods are beyond the scope of this paper, and will be part of future research.

Future work will incorporate a large scale evaluation of the speckle detection using both simulated and real data. In addition, the applicability of the speckle information to the signal-to-noise improvement in B-scan data will be investigated.

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References


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