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Analysis of speckle in ultrasound images using fractional order statistics and the homodyned *k*-distribution

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Abstract

It is necessary to identify speckled regions in ultrasound images to control adaptive speckle suppression algorithms, for tissue characterisation, and to estimate the elevational separation of B-scans by speckle decorrelation. Previous authors have proposed classification techniques based on second order powers of the homodyned *k*-distribution, or lower order powers of the more limited *k*-distribution. In this paper we explore the speckle discrimination properties of statistics based on arbitrary powers of the ultrasound echo envelope signal using a combination of simulations and theoretical results from the homodyned *k*-distribution. We conclude that statistics based on powers less than one are surprisingly less effective than some higher powers. A simple discriminant function for speckle is evaluated quantitatively in simulation and qualitatively on sample B-scan images.

Keywords: Homodyned *k*-distribution; Speckle; Fractional-order statistics

1. Introduction

Ultrasound B-scan images represent the back-scattering of an ultrasound beam from structures inside the body. There are two main types of scattering: diffuse scattering which leads to speckle in the image, and coherent scattering that creates clear light and dark features. Diffuse scattering arises when there are a large number of scatterers with random phase within the resolution cell of the ultrasound beam. Coherent scattering results when the scatterers in the resolution cell are in phase.

It is possible to parameterise regions of ultrasound B-scan images in terms of the number of scatterers in a resolution cell and the proportion of coherent, as opposed to diffuse, scattering. Let s^2 be the coherent signal energy and $2\sigma^2$ the diffuse signal energy. We use $k = s/\sigma$ as an indication of the proportion of coherent to diffuse reflectors, and μ as the effective number of scatterers per resolution cell.

If we can find k and μ for a patch in an ultrasound image, then we can use this information for speckle identification, to aid segmentation, and for tissue characterisation. The speckle identification is particularly useful as this is required for adaptive speckle suppression algorithms and for use in decorrelation algorithms to estimate the elevational distance between neighbouring B-scans.

Dutt and Greenleaf [1] describe a method for finding k and μ using the statistics of the ultrasound signal intensity, and a model based on the homodyned *k*-distribution. Data samples of over a thousand pixels are required to obtain stable statistics for these techniques. There have therefore been attempts to use lower order statistics (e.g., fractional order moments) in the hope that these measures will require smaller samples. Presumably because of the analytic inconvenience of the homodyned *k*-distribution, these approaches have been based on the *k*-distribution which is only a valid model in the absence of any coherent scattering [2,3]. Preliminary experiments were performed in which the statistics used in [2,3] were calculated to a variety of powers in the range 0.25–2, both using the homodyned *k*-distribution and using simulations. In all cases the statistics had a strong dependency on k and a weak variation with μ. In real B-scan images, where $k \neq 0$ cannot be ruled out, it is therefore impossible to use the *k*-distribution to find the

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effective number of scatterers, μ, without the results being severely corrupted by any coherent scattering present.

In this paper we extend Dutt and Greenleaf's original approach for inferring k and μ from sample statistics by exploring the performance of statistics that make use of data raised to different powers.

2. Choice of statistic for speckle discrimination

To find k and μ we need two statistics. Having found k and μ we can then label as speckle patches with high μ and low k. Following [1] we choose the ratio of the mean to the standard deviation, and based on [2,3] we calculate these statistics on arbitrary powers v of the data values A.

$$R = \frac{\text{mean}}{\text{standard deviation}} = \frac{\langle A^v \rangle}{\sqrt{\langle A^{2v} \rangle - \langle A^v \rangle^2}} = \frac{1}{\sqrt{\langle J^{2v} \rangle - 1}} \tag{1}$$

$$S = \text{skewness} = \frac{\langle (A^v - \langle A^v \rangle)^3 \rangle}{(\langle A^{2v} \rangle - \langle A^v \rangle^2)^{\frac{3}{2}}} = \frac{\langle J^{3v} \rangle - 3\langle J^{2v} \rangle + 2}{(\langle J^{2v} \rangle - 1)^{\frac{3}{2}}} \quad \text{where } \langle J^v \rangle = \langle A^v \rangle / \langle A \rangle^v \tag{2}$$

Based on the results in [2,3], we are expecting values of v less than one to perform well. We therefore perform simulations to select the value of v for which R and S have maximum variation to discriminate speckle from non-speckle, and the lowest possible noise variance.

To generate a simulated sample, the sum of μ vectors of length $\sqrt{2/\mu}$ and random phase is added to a single vector with (arbitrarily) zero phase and length k. The amplitude of the total provides a single sample A, with $\sigma = 1$. We represent speckle using data with no coherent scattering component ($k = 0$), and enough scatterers per resolution cell so that the central limit theorem will be valid ($\mu = 50$). To represent non-speckle we either introduce coherent scattering of equal amplitude to the diffuse scattering ($k = 1$, $\mu = 50$), or we severely reduce the number of scatterers per resolution cell ($k = 0$, $\mu = 2$), or we do both these things ($k = 1$, $\mu = 2$). This gives us a total of four different classes of simulated data.

Five thousand sets of 500 random samples were generated for each of the four combinations of k and μ. For each value of v, the standard deviation among the R values for the four (k, μ) combinations was divided by the standard deviation among the 5000 different times the R statistic was calculated. This gave a measure of the meaningful variation in R divided by the noise in measuring R for each of the (k, μ) combinations. This measure is shown, as a function of v, in Fig. 1(a). The same measure is shown for S in Fig. 1(b).

Fig. 1(c) shows the minimum value of all of the graphs in Fig. 1(a) and (b) for each value of v. Surprisingly, values of v less than 1 are not necessarily the most effective for speckle discrimination. The values close to $v = 1$ appear unattractive, and values close to $v = 2$ seem, on the basis of this simulation, to perform well. Using $v = 2$ results in Dutt and Greenleaf's algorithm for speckle detection [1] which has an efficient closed form solution derived in [4].

For this paper we take the peak of the graph in Fig. 1(c) and choose $v = 1.8$. Using Eqs. (1) and (2) together with this value of v, we have complete definitions of the statistics, R and S, to be used.

3. Discriminant function for speckle

We now have to design a discriminant function in (R, S) space to separate speckle from non-speckle based on the B-scan echo envelope amplitude. We do this by exploring the regions of (R, S) space occupied by speckle, first using the homodyned k-distribution, and then with simulations.

The homodyned k-distribution models the amplitude signal from μ weak scatterers with $\langle A^2 \rangle = 2\sigma^2$, and coherent scattering amplitude s [5]. The moments can be calculated by numerical integration of (corrected) equation B.15 in [6].

$$\langle A^v \rangle = \int_0^\infty \left(\frac{2\sigma^2}{\mu}\right)^{\frac{v}{2}} \times \frac{\Gamma\left(1+\frac{v}{2}\right)}{\Gamma(\mu)} x^{\left(\frac{v}{2}+\mu-1\right)} e^{-x} {}_1F_1\left(\frac{-v}{2}; 1; \frac{-\mu s^2}{2\sigma^2 x}\right) dx \tag{3}$$

Numerical integration of the confluent hypergeometric function ${}_1F_1$ was performed using the Maple (Waterloo Maple Software) and Matlab (The Mathworks Inc.) programs to produce the graph in Fig. 2(a). In theory, speckle with $\mu > 10$ and $k < 1$ corresponds to the triangular area between the lines.

For the simulations, data was generated as in the previous section, but this time using samples of size 4000 rather than 500. Fig. 2(b) shows (R, S) space with a variety of samples based on $\mu \geqslant 10$, $k < 1$ plotted in as dots and samples with $\mu < 10$, $k \geqslant 1$ plotted as circles. Fully developed speckle with $k = 0$ and $\mu > 50$ comes out in the same place for the theory and the simulations. The shape of the area corresponding to speckle statistics is however different, particularly for low values of μ. This is because of the difference between the way μ is used to determine the effective number of scatterers in the homodyned k-distribution and the direct use of μ to determine the number of weak scatterer vectors in the simulation.

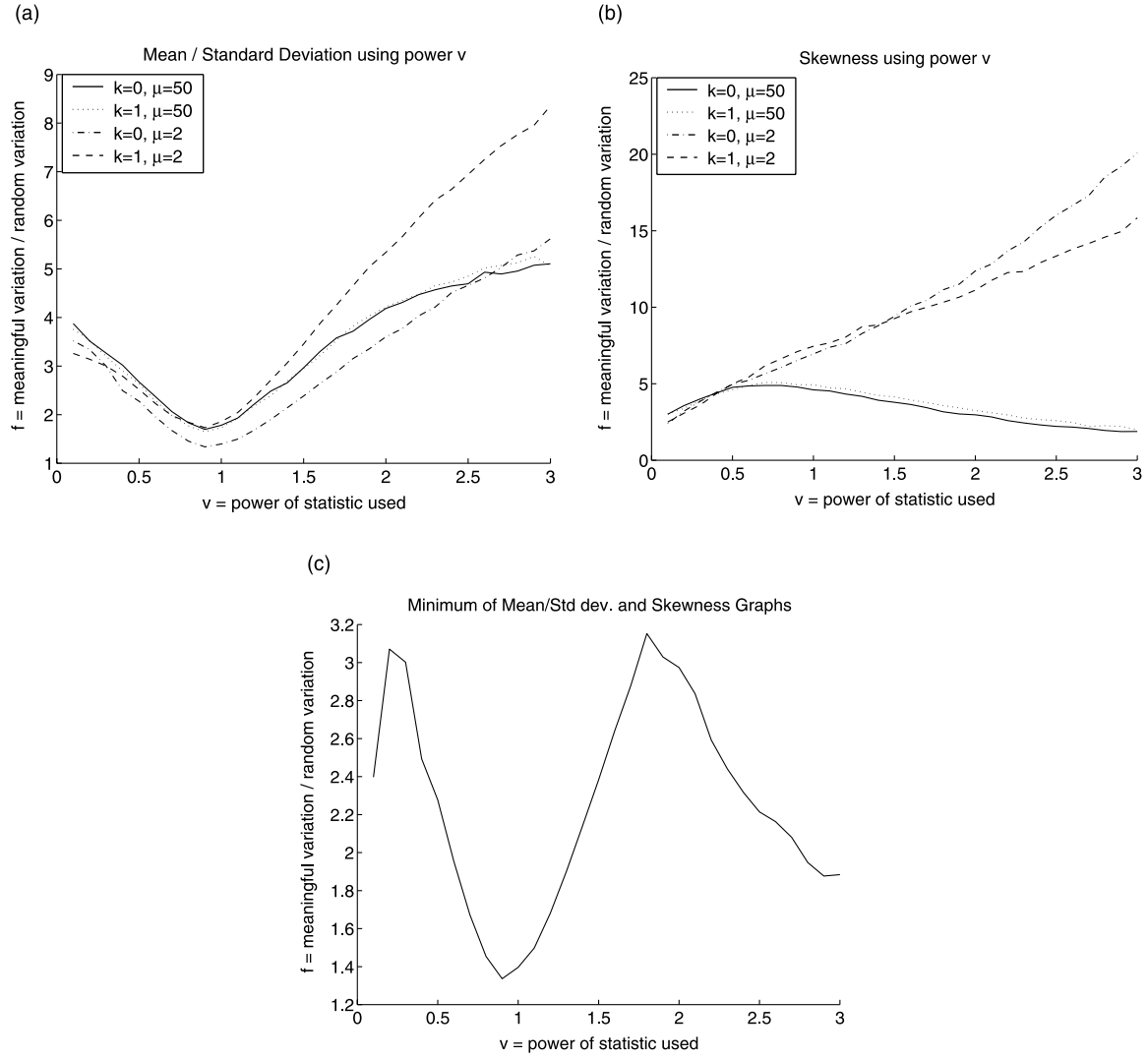

Fig. 1. In (a), the statistic R (see Eq. (1)) is computed 5000 times on samples of size 500 for the four cases shown in the legend. The value f plotted is the standard deviation between the four cases, divided by the standard deviation within each case. Each line is labelled with the case used in the denominator. k is the ratio of coherent to diffuse scattering. μ is the effective number of scatterers per resolution cell. v is the power used in calculating the statistic R. (b) Shows the same graphs for the statistic S (see Eq. (2)). (c) Shows the minimum of the eight graphs in (a) and (b) for each value of v.

Based on these initial experiments, an elliptical discriminant function was chosen for systematic evaluation by simulation. This is shown in Fig. 2(b). For all combinations of $0 < k < 3$ and $2 < \mu < 50$ a hundred values of R and S were generated using samples of size 4000. The 100 values were used to estimate the probability that simulated data with each combination of k and μ parameters would fall inside the ellipse and thus be classified as speckle. These probabilities are shown in Fig. 3(a). The figure shows pleasingly clear discriminant boundaries at $k = 1.1$ and $\mu = 6$, which are plausible values for a simple speckle detector.

The experiment was repeated using samples of 1000 rather than 4000 data values. The results are shown in Fig. 3(b). Note the considerable degradation in performance. Very few combinations of μ and k that we would expect to correspond to speckle result in a 90% probability of correct classification, and none of these are over 95%. We therefore conclude that large sample sizes are required for this classification strategy.

4. Evaluation on B-scans

Ultrasound images were decompressed to yield the approximate echo envelope amplitude using the technique described in [4], adapted to use R and S (with $v = 1.8$) as the target statistics. The mean values for R and S for labelled speckle in the resulting images were then used as the centre point of the elliptical discriminant function. The rule for speckle detection was thus very simple and fast to implement: calculate R and

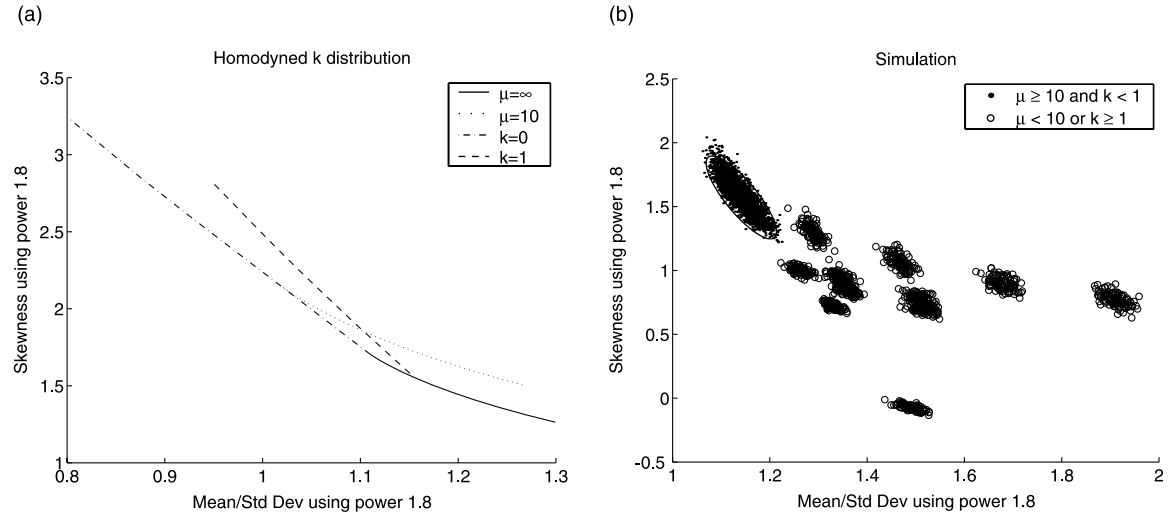

Fig. 2. (a) Shows the statistics R and S (see Eqs. (1) and (2)), computed from the moments of the homodyned k-distribution to the power of 1.8. The (R, S) values inside the triangular shaped region correspond to speckle. (b) Shows the same statistics computed on samples of 4000 simulated speckle values as described in Section 3. The dots correspond to speckle and the circles to non-speckle. The ellipse drawn around the group of dots is the chosen discriminant function. k is the ratio of coherent to diffuse scattering. μ is the effective number of scatterers per resolution cell.

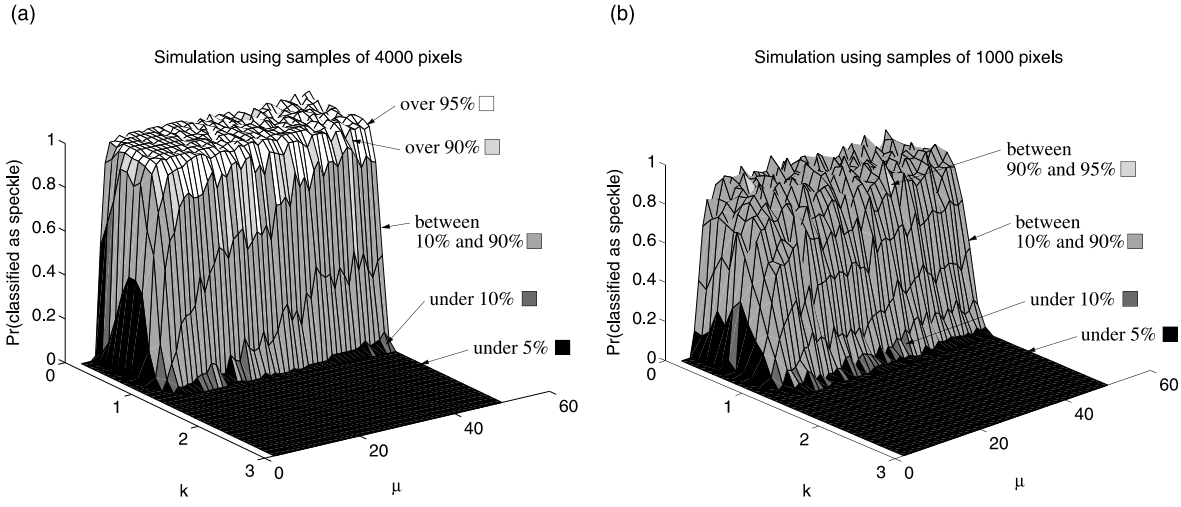

Fig. 3. (a) Shows the result of a simulation to evaluate the elliptical discriminant function for speckle selection. 100 sets of 4000 data points were evaluated for each combination of k, the ratio of coherent to diffuse scattering, and μ, the effective number of scatterers per resolution cell. The probability of each (k, μ) combination being classified as speckle was estimated. The diagram shows clear thresholds at $k = 1.1$ and $\mu = 6$. (b) Shows the same diagram, only using samples of 1000 rather than 4000 data values. Notice that there are no probabilities above 95%, and the general performance is degraded.

S and if the values lie in the ellipse call the patch 'speckle'. Based on the results of the previous section we should aim for a sample size close to 4000 to use for estimating the R and S statistics. We choose circular patches of radius of 32.2 pixels containing 3249 samples.

Fig. 4(a) shows an image from an ultrasound scan of a liver. Fig. 4(b) shows the patches in this B-scan classified as speckle by the algorithm above. Although a large sample size is required to work effectively, which prohibits fine-grained analysis, the technique does appear to be successful at picking patches with a relatively uniform speckled appearance.

5. Conclusions

Contrary to the authors' expectations when starting this work, we have demonstrated that statistics based on powers of the ultrasound echo envelope amplitude less than one are not necessarily better for speckle discrimination than statistics based on higher powers.

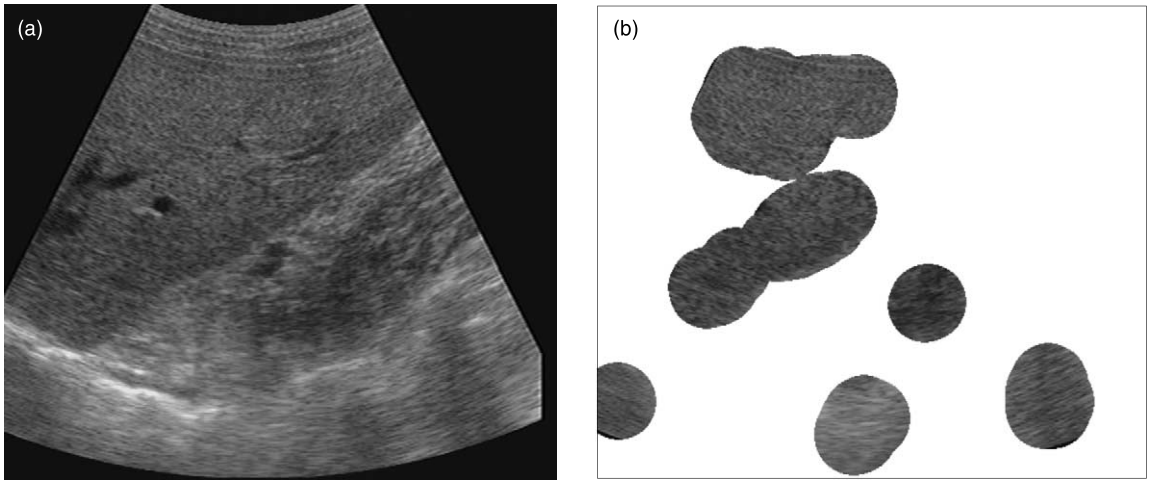

Fig. 4. (a) shows an image from an ultrasound scan of a liver, and (b) shows the regions classified as speckle in this image using the elliptical discriminant function in (R, S) space from Fig. 2 (b).

We have demonstrated that, in simulation, a simple elliptical discriminant function in (R, S) space provides a very efficient way of selecting speckled regions based on thresholds in (k, μ) space. This technique produces plausible results on approximately decompressed B-scan images. Unfortunately, large samples are required to obtain reliable estimates of R and S which limits the resolution of the speckle discrimination procedure.

References

[1] V. Dutt, J.F. Greenleaf, Ultrasound echo envelope analysis using a homodyned k distribution signal model, Ultrasonic Imaging 16 (1994) 265–287.

[2] V. Dutt, J.F. Greenleaf, Speckle analysis using signal to noise ratios based on fractional order moments, Ultrasonic Imaging 17 (1995) 251–268.

[3] F. Ossant, F. Patat, M. Lebertre, M.-L. Teriierooiterai, L. Pourcelot, Effective density estimators based on the k distribution: interest of low and fractional order moments, Ultrasonic Imaging 20 (1998) 243–259.

[4] R.W. Prager, A.H. Gee, G.M. Treece, L.H. Berman, Decompression and speckle detection for ultrasound images using the homodyned k-distribution, Technical Report CUED/F-INFENG/TR.397, Cambridge University Engineering Department, November 2000.

[5] E. Jakeman, R.J.A. Tough, Generalized k distribution: a statistical model for weak scattering, Journal of the Optical Society of America A 4 (9) (1987) 1764–1772.

[6] V. Dutt. Statistical analysis of ultrasound echo envelope, Ph.D. Thesis, Mayo Graduate School, August 1995.