ULTRASOUND TISSUE CHARACTERIZATION USING NAKAGAMI MODEL WITH TEMPORAL AVERAGING

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Abstract: We present a new application of Nakagami distribution in medical ultrasonographic (USG) imaging. The parameter *m* from this distribution is used for parametric imaging and shows an alternatively ultrasound image. The application is in USG image analysis or segmentation. Our method is based on three dimensional sliding window (2 spatial and 1 temporal dimension) and can be used for static objects only. We use the envelope of the radiofrequency (RF) signal for estimation. Both, the simulated and real RF data are used for testing of our estimator.

Introduction

Ultrasound tissue modeling can provide an important information that can be used for diagnosis, image segmentation, interpretation or visualization. This paper describes a statistically based approach for ultrasound image representation. Because the radiofrequency (RF) signal can be considered as a random signal arising from some probability density function (PDF), one can estimate the parameters of this PDF in order to characterize the underlying tissue. There are many models based on various kinds of PDF and describing tissue in a more or less complex way, for example, Rayliegh or Ricean distribution, K-distribution, Log-normal distribution [6]. Here, we use Nakagami-*m* distribution because of its complexity and versatility [1].

The Nakagami-*m* distribution has found many applications in technical sciences. It has been also shown by extensive empirical measurements that this distribution is an appropriate model for radio links [5]. A further growing area of Nakagami-*m* distribution application is the ultrasound tissue characterization [2] and adaptive filtering [4]. The envelope of the ultrasound radiofrequency (RF) signal could be described by this distribution and the parameters can then be used to distinguish between various kinds of tissues, e.g. detection and identification of abnormalities in breast, liver or kidney [1,2].

The general problem in estimation of the PDF parameters is a low number of samples. In this article we use the temporal averaging to increase the number of samples. We tested our estimator on simulated and real data. The method and some results are described below and some suggestions for future research are given at the end of this article.

Method

The echo signal can be considered as a sum of backscattered and backreflected single echoes from a number of scattering points and strong reflectors in the tissue [6]. We can express this echo signal (in one point/time) with the help of phasors notation. Each scatter reflects x_k amount of signal with the phase shift θ_k (due to the random location)

$$X = \sum_{i=0}^{N-1} x_i . e^{j\theta_i} \quad . \qquad (1)$$

In most cases, the amplitude x_i can be considered deterministic and we can rewrite (1) as

$$X = \frac{1}{\sqrt{N}} \sum_{i=0}^{N-1} \alpha_i . e^{j\theta_i} \quad , \qquad (2)$$

where $\alpha_i = x_i / \sqrt{N}$ are normalized by $\sqrt{N}$. We can express the radiofrequency signal as a time signal by involving the instantaneous frequency ω_0:

$$s(t) = X_r(t).\cos(\omega_0 t) + j.X_i(t).\sin(\omega_0 t) \quad . \qquad (3)$$

With the clinical scanner, we can obtain only the *inphase* (first) component. For envelope detection we assume the analytical nature of this signal and the *quadrature* (second) component is obtained by the virtue of the Hilbert transform (*HT*). The envelope is simply obtained by

$$S(t) = \sqrt{X^2{}_r(t) + HT\{X^2{}_r(t)\}} \quad . \qquad (4)$$

The PDF, *f(S)*, of the envelope of RF signal, under the Nakagami model is given by [1]:

$$f(S) = \frac{2m^m S^{2m-1}}{\Gamma(m)\Omega(m)} e^{-\frac{m}{\Omega}S^2} \quad , \qquad (5)$$

where *m* is the Nakagami parameter and Ω is the scaling parameter.

There is simple estimator for Ω parameter [4]. It represents the average power reflected back from tissue. There are many methods for estimation of the parameter

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m [4], for example, Tolparev-Polyakov (T-P), Lorenz, Greenwood-Duran (G-D), Bowman, Cheng-Beaulieu or inverse estimators. We have shown in our previous work [4,5] that G-D and T-P estimators are good estimators for our purpose. In this work we will use only the T-P estimator.

Our aim is to estimate the parameter *m* from the envelope of the RF data, which are not usually available in conventional scanners. We've used the GE Vingmed System5 for data acquisition that enables recording of RF data (or IQ data) in off-line mode [9]. We also tested the ability of our estimator on simulated data. The simulation model is based on 1-D convolution (in axial direction) as was described in [4] and is simply extended to 2D model by convolution in lateral direction (based on the supposed separability of the point spread function - PSF). As a convolution sequence, a simple approximation of the PSF in lateral direction was used [7].

The flow chart of our approach is depicted on Figure. 1. We use the RF data after the envelope detection and therefore no data reduction is used. This fact increases the number of samples in our estimator.

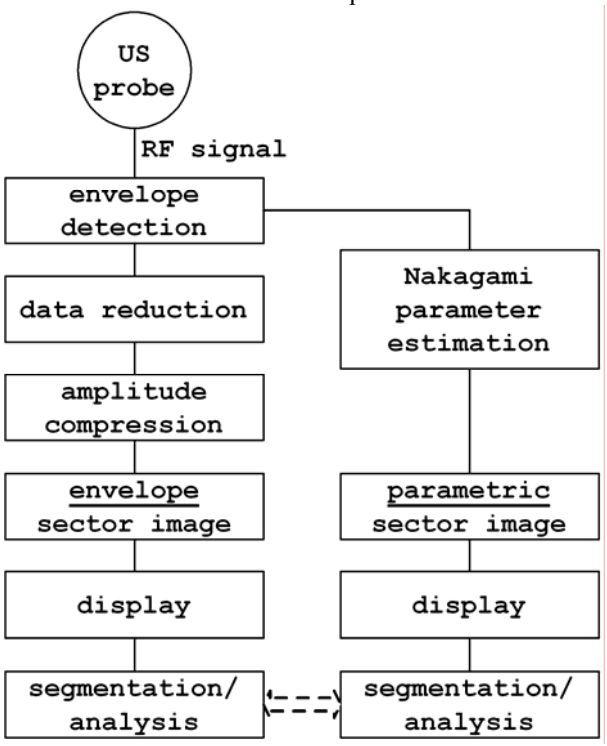

Figure 1. Flow chart of our approach - after envelope detection the estimation is performed.

First, we've tested our estimator on the *simulated RF data*. As the value of parameter *m* depends on the number of scatters [8] within the resolution cell, we performed simulations with three regions with various scatters density. Figure 2a shows the simulated ultrasound envelope image. There are 3 regions with 1.5, 3.8 and 9.6 scatters per resolution cell. Figure 2b shows the distribution of parameter *m*. The estimation was performed within a sliding window sized [61x5] pixels. The window is rectangular, because the axial resolution in USG is higher than lateral. Therefore the size in axial direction can be larger (61 rows). The 5 columns contain 5 A-scans. Figure 2c shows the profile through all columns and center row. The borders between regions are more clearly visible, particularly between the 1st and 2nd region, in comparison with the original image.

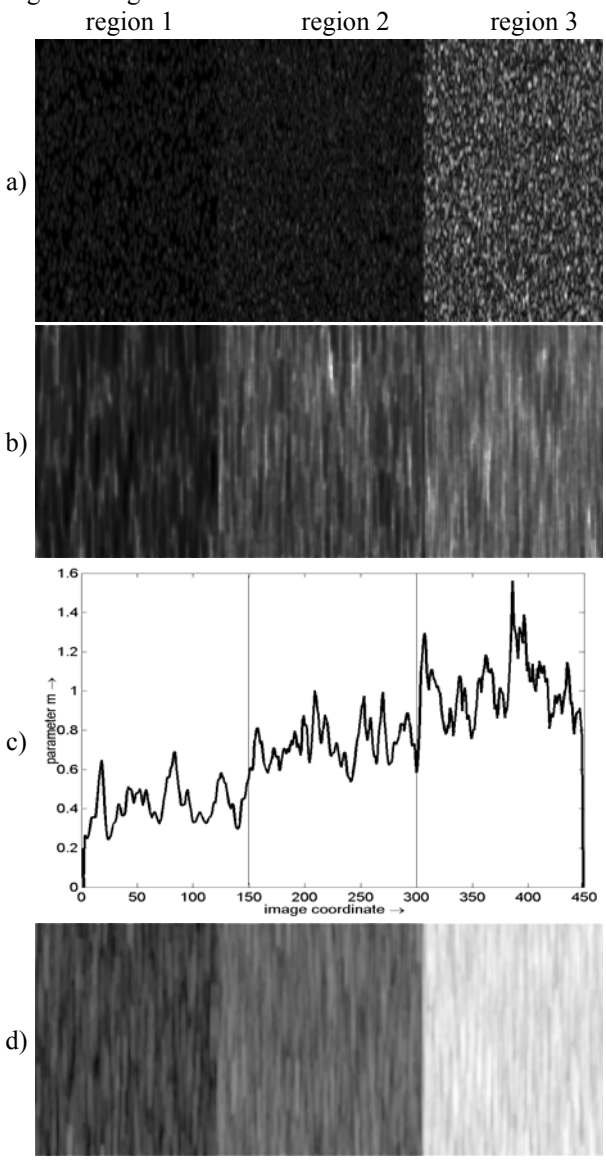

Figure 2. a) The simulated image of three regions with different number of scatters; b) distribution of *m* parameter; c) profile through all columns and center row; d) distribution of Ω (the size of the sliding window was [61x5])

Table 1: Evaluation of parameter *m* in simulated regions: mean ± standard deviation

window size / region	**1**	**2**	**3**
31x5 (155)	0.47 ± 0.19	0.90 ± 0.27	1.16 ± 0.40
61x5 (305)	0.43 ± 0.13	0.83 ± 0.18	1.08 ± 0.20
91x5 (455)	0.41 ± 0.10	0.79 ± 0.16	1.04 ± 017
121x5 (605)	0.39 ± 0.09	0.75 ± 0.16	1,00 ± 0.19
whole region	0.38 ± 0.09	0.75 ± 0.14	1,00 ± 0.18

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Figure 2d shows the Ω parameter distribution, which characterizes the backreflected and backscattered power; it is presented only for completeness.

Ideally, the brightness (value) within each region should be the same, but because of the randomness of ultrasound reflections, the value is changing. We can evaluate this fact with the help of the *mean* and *standard deviation* from each region. Table 1 shows these values for different window sizes; total number of samples is in the parenthesis. One can see that the standard deviation decreases with the larger window. As the number of samples used for estimation increases, the mean value is approaching the 'true' value that was obtained from the whole region and is shown on the last row. From this table we can infer the minimum number of samples needed for estimation.

Farther, we tested our estimator on *real RF data*. As we have seen on simulated data, there is a problem with the window size, which determines the number N of samples needed for the parameter estimation. When increasing N in a homogeneous region, the estimation accuracy increases too. But real tissues are highly inhomogeneous that requires a small window to preserve a reasonable spatial resolution. Essentially, there are two possibilities to ensure sufficient samples N.

The real objects are 3D and we can collect the adjoining scans to create a 3D moving window. This requires (ideally) the position information of each scan and algorithm for scan matching (aligning) to eliminate blurring by different position of objects in the individual scans. This solution is quite computationally demanding.

A simpler solution consists of using a time window over several B-scans without scan matching (Figure 3). This means that we use values from several consecutive scans to increase number of samples for the estimator irrespective of tissue structure. It is clear that this method is convenient only for static objects and requires a high frame rate. There is a further requirement – the physician should move the probe slowly to minimize blurring in the estimation process.

Discussion and Results

Figure 4 shows ultrasound images of the kidney – 5 consecutive frames are shown. The physician was asked to move slowly through whole kidney. The framerate was only 14 frames / second thus the sampling time is about 70ms. The original size of one frame (before scan conversion) is 2856 rows and 107 A-scans. The center ultrasound frequency was 1.7 MHz and the sampling frequency 20 MHz. This corresponds to 11 samples per wavelength. The axial resolution depends on the properties of the ultrasound probe; it is inversely proportional to the transducer bandwidth [8]. Typically, it is several wavelengths and we can set the size of window in the range of tens of rows (with respect to the sampling frequency). The number of columns was set to 3 only, because of poor lateral resolution.

The various sizes of 3D moving window were tested. It was empirically found that maximum useful number of B-scans is 5, because of increasing blurring. This corresponds to the acquisition time 357ms.

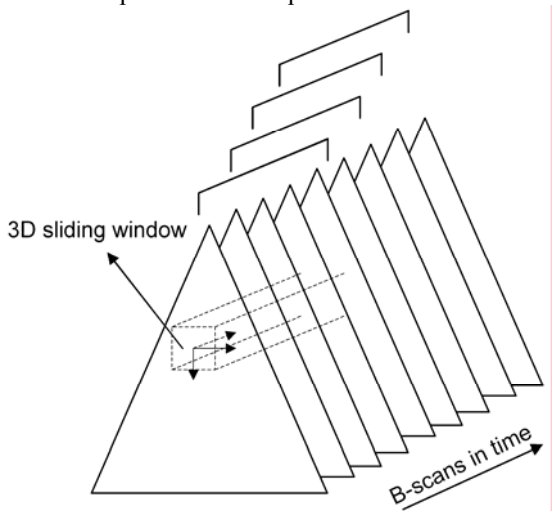

Figure 3. 3D sliding window for estimation of m parameter.

Figure 6 shows two parametric images with various window sizes; *31x3x5* and *61x3x5*. The number of samples is *465* and *915*, respectively. One can see that smaller window leads to a parametric image with higher resolution. We can visually compare these images with the envelope image on Figure 4 that was obtained as an average of five corresponding B-scans.

We can see that the m-parametric image can show the strong reflections from tissues with different acoustic impedance and these borders are more clearly visible in comparison with traditional envelope B-scans.

Conclusion

A new method of parametric ultrasound imaging was presented. It is based on the spatial and temporal sample collection for the parameter estimator. We've shown the correspondence between the original ultrasound image and the corresponding parametric m-image on simulated RF data. The capabilities of estimator were also shown on real RF data.

As mentioned above, there is another possibility to estimate the parameter, which takes into account the spatial tissue distribution. This will be a focus of our interest in near future.

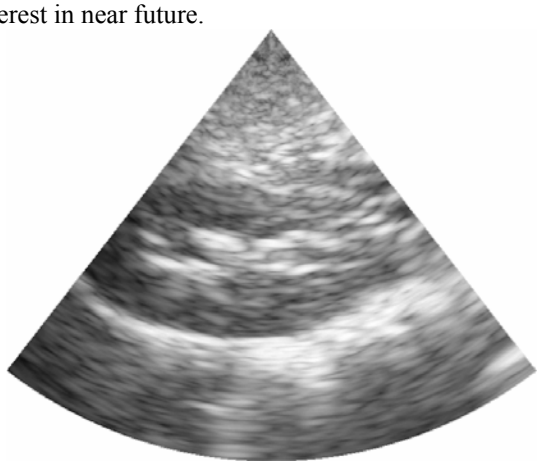

Figure 4. Result of averaging of 5 consecutive B-scans that are shown below on Figure 5.

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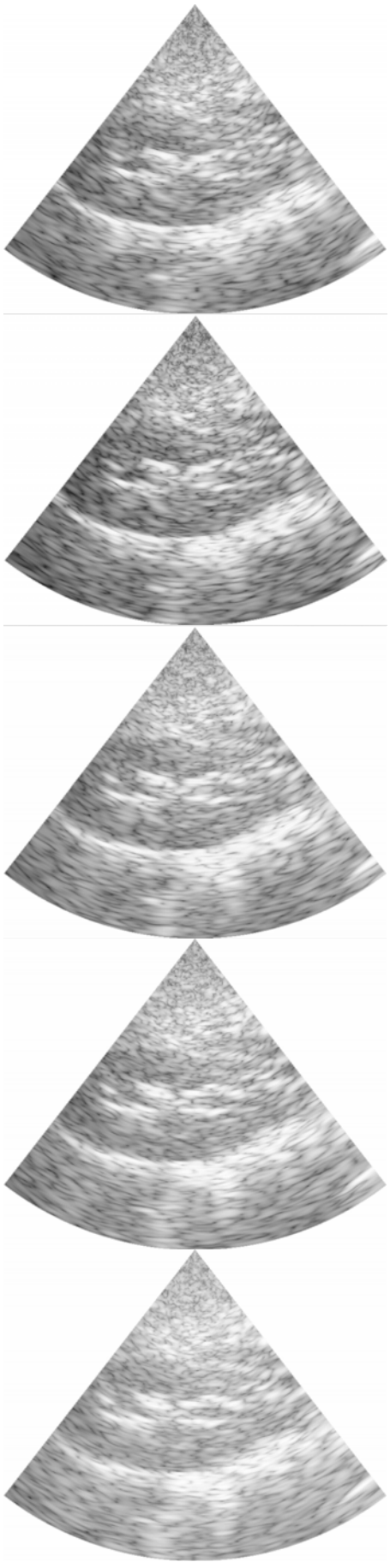

Figure 5. a) to e) five consecutive B-scans of kidney.

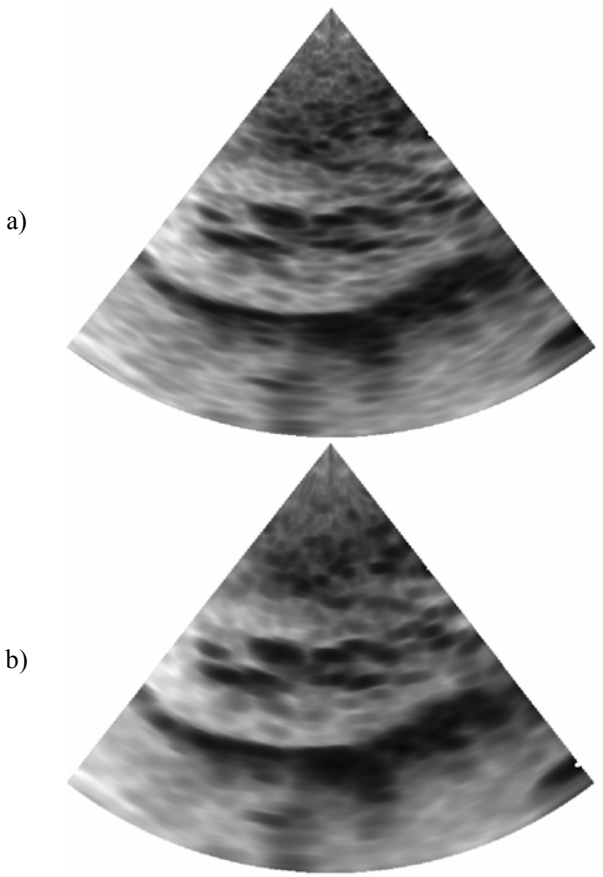

Figure 6. Distribution of parameter *m* obtained by 3D sliding window method. 5 frames was used in temporal dimension. 2D window was: a) 31x3, b) 61x3.

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