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Simulation study of changes in ultrasound speckle statistics with the system point spread function

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The intensity point signal-to-noise ratio, SNR_I , characterizing the ultrasound speckle statistics, depends on the tissue scattering microstructure and the imaging systems point spread function. Both should be described in three-dimensional space. Therefore, a three-dimensional simulation model is used in this paper to generate a rf signal and study the variations in SNR_I with the transducer center frequency and bandwidth. Results are in agreement with existing theoretical predictions. A possible method to analyze the SNR_I data is also presented that can produce a straight line slope as a feature value that depends on the tissue scattering microstructure only. Such a feature may prove to be more useful than SNR_I values in tissue characterization problems.

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INTRODUCTION

Interaction of an acoustic wave with an inhomogeneous medium, such as tissue, results in backscattered signals that exhibit random fluctuations. There has been a renewed interest lately in developing methods to extract information from the signal and relate it to the scattering microstructure. Stochastic models for the scattering process have been proposed.¹ Various different moments (first-order statistics)¹⁻³ and autocorrelation functions⁴ (second-order statistics) of the radio frequency and envelope-detected intensity signal have been used as features for structure characterization. One important understanding that has emerged from this work is that, N_e , the "effective" number of scatters in the resolution cell volume determines the statistics of the echo signal, not the number of scatterers per unit volume of the medium (number density n). Guided by the theoretical predictions,⁵ a major objective of this simulation study was to examine the variations in the statistics of the envelope-detected intensity signal with cell volume for different scatterer number densities n (or mean scatterer spacings). It is also shown that analysis of this multi-cell volume data can lead to a feature that is inversely proportional to n , and therefore useful as a tissue signature. Sleefe and Lele¹ have used the cell volume information to estimate n from kurtosis of the radio frequency signal in medical ultrasound. Similarly Denbigh and Smith⁶ have also used such information to calculate fish number density from the first and second moments of the intensity signal in underwater acoustics. However, the statistical estimator for n has been shown to be unstable with very large variance in the Rayleigh limit (large N_e).⁷ This has also been observed by the authors of Ref. 1 and 6. Therefore we decided to use the inverse of n as a feature to be estimated from the data since it does not have the instability mentioned above.⁷

The point intensity signal-to-noise ratio SNR_I is de-

fined as the ratio of the statistical mean to the standard deviation of the intensity signal. Following Jakeman,⁵ SNR_I can be related to N_e as follows:

$$\text{SNR}_I^{-2} = 1 + (1/N_e), \quad N_e = nV_eA, \quad (1)$$

where N_e is the "effective" number of scatterers in a given resolution cell volume V_e and is assumed to be a Poisson-distributed random variable in the medium. Through the term A , N_e also depends on the statistical distribution of scattering strengths w_n . The term A can be estimated from the second and fourth moments of the distribution function as $A = \langle w^2 \rangle^2 / \langle w^4 \rangle$, where $\langle \cdot \rangle$ stands for the expectation value. Here, A is the inverse of kurtosis.² In medical ultrasound, the resolution cell volume can be estimated from the knowledge of the three-dimensional intensity point spread function $P(\vec{r})$ as⁸

$$V_e = \frac{[\int P(\vec{r}) d\vec{r}]^2}{\int P^2(\vec{r}) d\vec{r}} = \frac{c}{2} \frac{[\int B(r) 2\pi r dr \int \bar{h}(t) dt]^2}{[\int B^2(r) 2\pi r dr \int \bar{h}^2(t) dt]}, \quad (2)$$

where c is the speed of sound in tissue. Note that we have approximated $P(\vec{r})$ in the far field or in the focal zone of a circular disk transducer as a product of two functions: (i) the circularly symmetric intensity beam pattern $B(r)$ and (ii) $\bar{h}(t)$, the square of the envelope-detected interrogating pulse. If the beam pattern is represented by the diffraction pattern of a circular disk [Eq. (6)] then the full width at half-maximum (FWHM) beamwidth can be shown to be inversely proportional to f_0 , the center frequency of pulse excitation. Similarly, assuming a Gaussian pulse envelope, the FWHM of $\bar{h}(t)$ becomes inversely proportional to Δf , the FWHM bandwidth of the pulse excitation.

Equation (1) indicates that SNR_I approaches the limiting value of 1 as N_e becomes large. This can happen as $n \rightarrow$ large (high scatterer density) or as $V_e \rightarrow$ large. It is the latter behavior that we have studied and demonstrated with our simulation experiments. We have varied the res-

FIG. 1. Microbeam geometry used for the model simulation. The diameter of the microbeams is equal to S , the mean scatterer spacing. Here, r_k is the radial distance of k th annulus from the central axis. The maximum beam radius was set at 2 mm, corresponding to the first minimum of the diffraction pattern at the lowest frequency of 1.0 MHz.

olution cell volume V_e by changing f_0 , the center frequency, and Δf , the bandwidth of pulse excitation. Due to the bandwidth limitations of clinical PZT transducers, it may not be possible, in practice, to generate all seven different pulses used in this study with a single transducer (Table I). We are currently investigating the use of PVDF broadband transducers driven by a frequency-modulated pulse. The details of the technique have been published elsewhere⁹ and will not be presented here. With such a technique, it is possible to generate pulses with different f_0 and Δf .¹⁰

I. THEORETICAL SIMULATION

We have used a computer model described by Kuc *et al.*¹¹ for simulating reflected signals from a three-dimensional random medium. Multiple scattering is ignored and the total reflected radio frequency signal is considered to be a superposition of the reflected signal from all scatterers. The region of interest is assumed to be in the focal zone of the transducer, centered at a distance z_0 . The field of the transducer is partitioned into a set of cylinders or microbeams arranged in concentric annular regions that lie parallel to the transducer axis (Fig. 1). Such a partitioning scheme allows one to incorporate the effect of change in beam pattern into the simulation process in a straightforward manner. The diameter of the microbeam is determined by the mean spacing of the scatterers S . The tissue is modeled as a set of scatterers that have random scattering strengths and are randomly located within each microbeam. A Gaussian distribution function with a zero mean and standard deviation of 0.5 was used to model the scattering strengths w_n . Within each microbeam the round trip propagation times were random variables but in accordance with a Poisson process. The average time separation between scatterers in a given segment was the controllable parameter of the Poisson distribution and was set equal to $2S/c$. Governed by these two probability laws, we generate the reflector sequence from the j th microbeam in the k th annulus, denoted by $m_{k,j}(t)$:

$$m_{k,j}(t) = \sum_n w_n \delta(t - t_n). \quad (3)$$

The total reflected signal is equal to the sum of the contributions from each microbeam. Since the microbeams within a given annulus are equidistant from the axis (the

TABLE I. Imaging pulse parameters.

Symbol	Center frequency f_0 (MHz)	Bandwidth Δf (MHz)	Cell volume (mm ³)	$(f_0^2 \Delta f)^{-1}$
A	1.00	0.50	2.48	2.0
B	2.00	1.02	0.32	0.24
C	3.00	1.57	0.09	0.07
D	4.00	2.12	0.04	0.03
E	2.00	0.50	0.67	0.5
F	3.00	1.02	0.15	0.11
G	4.00	1.57	0.05	0.04

distance given by r_k in Fig. 1), their reflector sequences can first be added and then the annular sum can be convolved with the point spread function of the transducer appropriate for the given annulus and depth z_0 . The composite reflection sequence $m_T(t, z_0)$ is then equal to

$$m_T(t, z_0) = \sum_{k=1}^{N_a} \left(h(r_k, z_0, t) * \sum_{j=1}^{N_m} m_{k,j}(t) \right), \quad (4)$$

where $*$ stands for convolution with respect to t . Here, N_a and N_m are the number of annuli and number of microbeams in each annulus, respectively. Because of the radial symmetry and the approximation in the focal zone, we can write the point spread function $h(r_k, z_0, t)$ as $B(r_k, z_0)h(t)$, where $B(r_k, z_0)$ is the relative value of the beam pattern at radius r_k and $h(t)$ is the interrogating pulse:

$$m_T(t, z_0) = h(t) * \sum_{k=1}^{N_a} B(r_k, z_0) \sum_{j=1}^{N_m} m_{k,j}(t). \quad (5)$$

In the focal zone, $B(r_k, z_0)$ can be approximated by

$$B(r_k, z_0) = \left(\frac{2J_1(x)}{x} \right)^2, \quad \text{where } x = \left(\frac{2\pi f_0 d r_k}{c z_0} \right), \quad (6)$$

d is the radius of the transducer, and $J_1(x)$ is the first-order Bessel function of the first kind. Finally, we compute the intensity signal $I(t)$ as $I(t) = [m_T^2(t) + \bar{m}_T^2(t)]$, where $\bar{m}_T(t)$ is the Hilbert transform of $m_T(t)$. The SNR_I value was calculated from the time samples of the signal $I(t)$. More details on the simulation procedure can be found elsewhere.¹²

II. INTERROGATING PULSE AND TISSUE MODEL PARAMETERS

The interrogating pulse waveform $h(t)$ was modeled as a sinusoidal function at frequency f_0 modulated by a Gaussian envelope. The center frequency f_0 and the FWHM bandwidth Δf were determined from the Fourier transform. The sampling period for all the $h(t)$ and the random reflector sequences $m_{k,j}(t)$ was $\Delta t = 0.05 \mu s$. The parameters of the interrogating pulses used in the simulations are summarized in Table I. Seven different combinations of center frequency f_0 and bandwidth Δf were used. Each pulse has been labeled by a symbol A through G. The lengths of reflector sequences corresponded to a 2-cm-deep tissue segment. Ultrasound speed was $c = 1560$ m/s. The

FIG. 2. Plot of SNR_I as a function of $(f_0^2 \Delta f)$ for three different tissue models with different mean scatterer spacing. The interrogating pulse that was used is designated by a symbol A through G.

beam pattern for every pulse used in the simulation was calculated using Eq. (6) with $d=2.4$ cm, $z_0=5$ cm, and the center frequency f_0 of the pulse.

An estimate of the resolution cell volume V_e is also reported in Table I for each case. This was done by calculating the volume of an equivalent cylinder whose diameter was given by a FWHM beamwidth of $B^2(r, z_0)$ from Eq. (6) and whose height was given by $c/2$ times the FWHM pulse width calculated from $\bar{h}(t)$, the squared enveloped of the pulse. Three different tissues models were considered. In each model, the scattering strength w_n was a random variable with a zero mean Gaussian distribution and a standard deviation of 0.5. The mean scatterer spacing S was fixed at 0.23, 0.3, and 0.55 mm for tissue model 1, 2,

and 3, respectively. All three tissue models were probed with seven different interrogating pulses listed in Table I. In each case, 20 different statistically independent simulations were performed. Ergodicity was assumed and therefore both time and ensemble averaging was used. Reported SNR_I values are averages of 20 A-line simulations.

III. RESULTS

Values for $(f_0^2 \Delta f)^{-1}$ for different pulses are listed in Table I along with the estimates of the cell volume V_e . A strong proportionality was found between V_e and $(f_0^2 \Delta f)^{-1}$. This is not just empirical because by using Eq. (6) for $B(r)$ and a Gaussian function for $\bar{h}(t)$ in the integrals for V_e in Eq. (2), this proportionality can be proved. The constants of proportionality depend on c , z_0 , and d . Therefore, if the experiments are designed to ensure that these constants do not change and to the extent that Eq. (6) represents the beam pattern, $(f_0^2 \Delta f)^{-1}$ could be used as a measure of V_e . Otherwise some independent measurement or *a priori* knowledge of V_e is necessary for the analysis of the data. With that caveat we will use $(f_0^2 \Delta f)$ as a measure of $(1/V_e)$. The estimates of SNR_I are plotted as a function of $(f_0^2 \Delta f)$ in Fig. 2 for all three different tissue models. The abscissa therefore represents the inverse of cell volume V_e . Data points corresponding to the largest cell volume are near the zero of the abscissa. The nonlinear drop in SNR_I with decreasing V_e is consistent with theoretical predictions [Eq. (1)]. The number density n , calculated as S^{-3} , turns out to be approximately 82, 37, and 6 per mm^3 for model 1, 2, and 3, respectively. Here, w_n are Gaussian distributed for our model, therefore, kurtosis=3 and $A=1/3$ in all cases for our simulations.² Therefore, for the largest cell volume case (points labeled as A), the "effective" number of scatterers N_e within the cell volume (from Table I) comes out to be 68, 31, and 5 for model 1, 2, and 3, respectively. Similarly for the smallest cell volume case (points labeled as D) N_e is 1, 0.6, and 0.1, respectively. Even though the statistical moments used in Refs. 1 and 6 for the direct estimation of n are different from ours, the associated error is expected to show similar behavior, especially the instability⁷ as $N_e > 3$. Given the error bars in our SNR_I estimates, we can expect very large error in the direct estimation of n at most of our data points. Indeed reasonable estimates for n could only be obtained after throwing away all data points except the ones for the three smallest cell volume cases. Therefore, as suggested by Wagner *et al.*⁷ we have examined the estimator for $(1/n)$ by plotting $(\text{SNR}_I^{-2} - 1)$ as a function of the inverse of cell volume represented by $(f_0^2 \Delta f)$ in Fig. 3. As predicted by theory [Eq. (1)] we do observe a linear trend for all three models. Straight lines are linear fit to the data points. The slope of these lines should be proportional to $(nA)^{-1}$, and therefore is a signature of the tissue scattering microstructure. To avoid crowding the graph, the standard deviations are shown only for the points corresponding to the lowest and highest cell volume. Unlike the estimator for n , the standard deviations do not diverge as N_e becomes large ($N_e > 3$ or so).^{1,6,7} The data points at a large cell volume in fact help to establish the intercept of the line,

FIG. 3. Plot of $(\text{SNR}_T^{-2} - 1)$ as a function of $(f_0^2 \Delta f)$ for three different tissue models. The interrogating pulse used is designated by a symbol A through G. Straight lines are least-square fit to each model data.

which for our model should be zero. The small nonzero intercept value seen in our data is probably due to a small positive bias in SNR_T estimates resulting from insufficient averaging of independent sample points.¹³ Using the slope values of straight line fits in Fig. 3 and a constant of proportionality = 0.7657, between the estimates of $(1/V_e)$ and $(f_0^2 \Delta f)$ determined from the values in Table I, and assuming $A = 1/3$, it is possible to estimate n and calculate the mean scatterer spacing for the three models. We obtain values of 0.31, 0.28, and 0.23 mm for model 1, 2, and 3, respectively. The largest error is for the lowest density case ($S = 0.55$ mm). This estimate improves to about 0.4 mm if we calculate the slope after dropping the two points that correspond to the smallest cell volume cases. Indeed, our preliminary theoretical analysis of the error associated with this type of estimator indicates that the error may in fact increase as N_e become smaller, quite opposite of what is observed in direct estimation of n .

IV. CONCLUSIONS

In this paper we have examined the role played by the ultrasound imaging system's point spread function in controlling and changing the speckle statistics. We observe deviation from the limiting value of 1 for intensity SNR_T , as a function of decreasing cell volume. The functional behavior of the observed deviations is in agreement with the existing theoretical predictions that incorporate the ef-

fect of point spread function on SNR_T . A possible method to analyze the data is also presented that circumvents the problem of the strong increase in the error as N_e increases, for the usual estimator for n . The mean scatterer spacings considered in this simulation are 3 to 5 times smaller than the spacings that are considered relevant for tissue characterization in medical ultrasound.¹ Therefore the scatterer number densities are perhaps one to two orders of magnitude larger here. However, the cell volumes considered in this study are typically smaller by the same order of magnitude compared to the medical ultrasound case. Since the important parameter that governs the speckle statistics, i.e., N_e , is about the same, the results presented in this paper have relevance to medical ultrasound. We do recognize that attenuation and frequency-dependent scattering effects have not been considered in this study. Therefore, the actual results on real tissue might be more complex. Further work is needed to expand this model.

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