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DERIVING ATTENUATION PROFILES FROM RAW DIGITAL ULTRASONOGRAPHIC DATA

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The objective of the paper is to estimate automatically one-dimensional attenuation profiles on isolated "rays" forming ultrasonic images. The estimates are entirely based on raw digital ultrasonographic data, without reference to any a-priori knowledge on the tissue character. Using a common model of ultrasound propagation in homogeneous media, the presented "layered" formulation allowed for simplified, thus manageable estimation of the attenuation profiles. The derived model has been discretised and the least squares method used for computing vectors of unknown coefficients of attenuation and dispersion. The results of analysing real ultrasonographic data, as presented on included figures, are rather promising, in spite of the mentioned simplifications.

K e y w o r d s: ultrasonography, image processing, raw ultrasound data, attenuation map, ultrasound attenuation estimation

1 INTRODUCTION

Ultrasonic medical imaging, based on similar imaging principle as radar scanning — providing the image as a "fan" of individual "rays", uses the ultrasonic impulses that are attenuated due to several physical phenomena when travelling through the tissue. The attenuation, which is thus dependent on the physical properties of the diagnosed tissue, is rather high and must be compensated for by increasing the amplification of the reflected signal the more the longer is the path travelled by the impulse on the "ray". Imaging, as provided by commercial ultrasonic scanners, commonly uses the so called time-gain compensation (TGC) – an adjustable, but for all rays fixed, curve of the image-depth dependent amplification. The operator (usually medical staff) looking at the resulting image adjusts the curve manually. To create the image this way is simple technically but it causes some artefacts, namely shadows appearing behind objects with greater absorption differing from the expected constant. Some papers, *eg* [3–5], have been published on the automatic gain compensation which relies on estimates of the attenuation profiles on the path of the impulse but these estimates themselves present still a challenging problem. They may either be based on the known tissue properties, *eg* spatial distribution of the attenuation coefficient when the types of tissues in the range of the image are known, or the attenuation distribution may be estimated automatically by analysing the received (reflected) ultrasonic impulse, utilising knowledge on the properties of ultrasound propagation. The present paper is devoted to a simplifying approach allowing to determine the attenuation profile from the measured data automatically.

2 ANALYSIS OF THE PROBLEM

Mathematical model

The propagation of an ultrasound impulse is a rather complicated phenomenon encompassing attenuation, possibly multiple reflections and scattering. We will consider a simplified view of it in one-dimensional representation that will lead to a reasonably tractable formulation.

Let us suppose that the ultrasonic probe transmits a wide-band ultrasonic impulse that travels along the straight path considered as the so-called ultrasonic "ray". The attenuation causes the wave-amplitude decrease as given by

$$A(z, f) = A(0, f)e^{-\mu(f,z)z}\,, \tag{1}$$

where $A(z, f)$ is the amplitude of the ultrasound wave component of frequency f in distance z from the transducer and $\mu(f, z)$ is the variable attenuation coefficient. When $\mu(f, z)$ can be supposed independent of z, *eg* $\mu(f)$ as in a homogeneous material, the situation is rather simple. Nevertheless, we will have to use a more complex model as stated below.

Let us consider the frequency range of the signal from 2.5 up to 7.5 MHz, simple propagation with only single reflection or scattering on each inhomogeneity on the path, with negligible secondary reflections. Absorption is then the most important cause of signal suppression for these frequencies. The common model as described in [6] describes the ultrasound absorption coefficient $\mu(f)$ as linearly dependent on frequency — we can therefore write $\mu(f) = \mu f$. We will also assume a constant velocity of ultrasound propagation in the tissue independent of attenuation so that the correspondence between time and depth of forward propagation is linear, $z = ct$.

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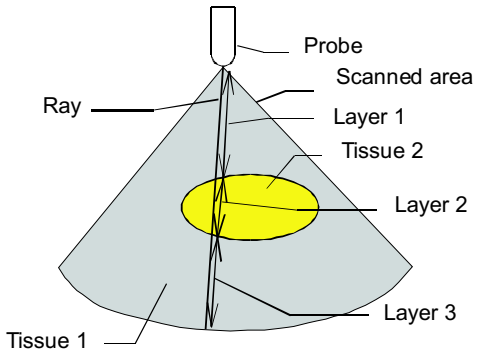

Fig. 1. Basic model (simplified to 3 layers)

Our model of the imaged tissue will be formed as a composition of M homogeneous layers (Fig. 1) along the ray. (Naturally, the composition of layers will be dependent on the ray position thus being variable in the frame of the whole fan or image). Every layer has its attenuation constant coefficient μ_i, its depth Δ_i and its local signal-return-ratio σ_i, produced both by specular reflection and/or backscattering in the layer. If there are some specular reflections on acoustical impedance steps on the trace of the ray, the corresponding thin areas are treated as separate layers.

The transducer emits a short impulse in time $t = 0$ and then it scans the returning impulse reflections. The signal received in time t_1 was reflected/scattered in the tissue in time $\frac{1}{2}t_1$ and it has passed $M(t_1)$ layers, each of them two times (forth and back). The $M(t_1)$-th layer has been passed only to the depth $\frac{1}{2}t_1c - \sum_{i=1}^{M(t_1)-1}\Delta_i$, where c is the speed of ultrasound propagation.

Let $\Delta_{M(t)} = \frac{1}{2}tc - \sum_{i=1}^{M(t)-1}\Delta_i$ and $\widetilde{\Delta}_i = 2\Delta_i$; then the total travelled way of the signal received at time t may be expressed as $2z = \sum_{i=1}^{M(t)}\widetilde{\Delta}_i$. The amplitude of its component of frequency f is (taking into account the model (1) for individual layers and also the relation $t = 2z/c$)

$$A(z,f) = A(ct/2,f) = A(0,f)\exp\Big(-f\sum_{i=1}^{M(t)}\mu_i\widetilde{\Delta}_i\Big)\sigma_{M(t)}\,.$$

It may be (on the first look) argued that this expression does not take into account the interference phenomena among individual returned components of the wave as their phase relations are not respected. Nevertheless, following the problem definition, this is not to be reflected because we are not trying to compensate for the interference causing the speckles but exclusively for the differing attenuation of the signal at different time instants.

Transformed and simplified formulation

In order to simplify the formulation of the problem, logarithmic transform will be applied to both sides of equation (1), which is always possible as all its components are positive: really, the function e^x is positive for all $x \in R$ while the return-ratio σ_i is non-negative by definition and nonzero for real tissue materials; thus we can write $\sigma_i = e^{s_i}$. The amplitude of the emitted signal $A(0,f)$ is positive in the frequency band $f \in (f_1, f_2)$, where f_1 and f_2 are dependent on the used probe and its input (transmitted) signal; although it is supposed $A(0,f)$ elsewhere, this is out of the range of the equation use.

We can therefore write

$$\ln A(z,f) = \ln A(0,f) - f\sum_{i=1}^{M(t)}\mu_i\widetilde{\Delta}_i + s_{M(t)} \qquad (2)$$

for the interval (f_1, f_2). Here, s_i can be interpreted as a logarithmic measure of the local signal-return-ratio. The primary aim of the analysis is to determine vector μ but as the only quantity accessible to the measurement is (if at all) $A(z,f)$, all other quantities on the right hand side of (2) must be determined or estimated as well.

When measuring the video signal, *ie* the envelope of the received wide-band radio-frequency signal, we obtain only the information on the resulting integral amplitude of the echo, which can be regarded approximately proportional to the mean value with respect to frequency. Therefore, in equation (2) we do not know the quantity $A(z,f)$ but only this integral value, for simplicity denoted as $A(z)$. Under these circumstances, we decided to simplify the problem by removing the dependence on f. Although this approximation may seem to ignore one important aspect, it makes the problem immediately tractable and the results support it as probably a sound simplification. We can remove the frequency dependence when considering the mean values with respect to frequency, obtained by integrating the equation from f_1 to f_2 and dividing by the length of the interval,

$$\frac{1}{f_2-f_1}\int_{f_1}^{f_2}\ln A(z,f)\mathrm{d}f = \frac{1}{f_2-f_1}\int_{f_1}^{f_2}\Big(\ln A(0,f) - f\sum_{i=1}^{M(t)}\mu_i\widetilde{\Delta}_i + s_{M(t)}\Big)\mathrm{d}f\,.$$

We denote $y(z) = \int_{f_1}^{f_2}\ln A(z,f)\mathrm{d}f$ and approximate it by the measured value $\ln\big(A(z)\big)$. After a few simplifying steps and integration we get

$$y(z) = y(0) - \frac{1}{2}\big(f_2^2 - f_1^2\big)\sum_{i=1}^{M(t)}\mu_i\widetilde{\Delta}_i + (f_2-f_1)s_{M(t)}\,, \quad (3)$$

where $y(0) = \int_{f_1}^{f_2}\ln A(0,f)\mathrm{d}f$ is the integral of logarithmic amplitude of emitted signal.

Our aim is to compute μ_i and s_i by least squares method while choosing a suitable tissue model, *ie* the

layer thicknesses $\widetilde{\Delta}_i$ (though also unknown at the beginning). If we know some initial estimates $\mu_{0,i}$ and $s_{0,i}$ of coefficients μ_i and s_i, we can write

$$\mu_i = \mu_{0,i} + \partial\mu_i\,, \quad s_i = s_{0,i} + \partial s_i\,, \tag{4}$$

where $\partial\mu_i$ and ∂s_i are corrections leading to proper values. When we denote $f_3 = \frac{1}{2}\left(f_2^2 - f_1^2\right)$ and $f_4 = f_2 - f_1$, and substitute (4) into (3) and then transfer the known terms to the left-hand side (on the choice of a concrete value of $y(0)$ see the paragraph on practical aspects), we get

$$y(z) - y(0) + f_3 \sum_{i=1}^{M(t)} \mu_{0,i}\widetilde{\Delta}_i - f_4 s_{0,M(t)} = - f_3 \sum_{i=1}^{M(t)} \partial\mu_i\widetilde{\Delta}_i + f_4\partial s_{M(t)}\,. \tag{5}$$

3 DISCRETISED SOLUTION BY LEAST SQUARES METHOD

The next step is equidistant discretisation in z with the period of sampling $\Delta z = cT$, where the time period of sampling T is given by the A/D converter used in the ultrasonic scanner. The total number N of samples on the ray is therefore fixed while the number M of layers approximating the tissue structure can be initially chosen arbitrarily as far as the problem remains sufficiently determined (see below). We will use the notation $x_j = x(cjT)$.

After discretisation, equation (5) acquires the matrix form

$$\mathbf{X}\overline{\boldsymbol{u}} = \overline{\mathbf{l}}\,, \tag{6}$$

where

$$\overline{\mathbf{l}} = \begin{bmatrix} y_1 - y_0 + f_3 \sum_{i=1}^{M(1)} \mu_{0,i}\widetilde{\Delta}_i - f_4 s_{0,M(1)} \\ \vdots \\ y_n - y_0 + f_3 \sum_{i=1}^{M(N)} \mu_{0,i}\widetilde{\Delta}_i - f_4 s_{0,M(N)} \end{bmatrix},$$

$$\overline{\boldsymbol{u}} = \begin{bmatrix} f_4\partial\overline{\boldsymbol{s}} \\ f_3\partial\overline{\boldsymbol{\mu}} \end{bmatrix},$$

$$\mathbf{X} = \left[\begin{array}{cccc|cccc|c} 1 & 0 & \dots & 0 & -1 & 0 & \dots & 0 & \\ 1 & 0 & \dots & 0 & -2 & 0 & \dots & 0 & \\ \vdots & \vdots & \ddots & \vdots & \vdots & \vdots & \ddots & \vdots & * \\ 1 & 0 & \dots & 0 & -\widetilde{\Delta}_1 & 0 & \dots & 0 & \\ \hline 0 & 1 & \dots & 0 & -\widetilde{\Delta}_1 & -1 & \dots & 0 & \\ 0 & 1 & \dots & 0 & -\widetilde{\Delta}_1 & -2 & \dots & 0 & \\ \vdots & \vdots & \ddots & \vdots & \vdots & \vdots & \ddots & \vdots & ** \\ 0 & 1 & \dots & 0 & -\widetilde{\Delta}_1 & -\widetilde{\Delta}_2 & \dots & 0 & \\ \hline \vdots & \vdots & \ddots & \vdots & \vdots & \vdots & \ddots & \vdots & \\ 0 & 0 & \dots & 1 & -\widetilde{\Delta}_1 & -\widetilde{\Delta}_2 & -\widetilde{\Delta}_3 & \dots & -\widetilde{\Delta}_{M(N)} \end{array}\right] \begin{array}{l} \\ \\ \\ \\ \\ \\ \\ \\ \\ *** \end{array}$$

* first layer thickness — $\widetilde{\Delta}_1$, ** second layer thickness — $\widetilde{\Delta}_2$
*** last row of the last layer

Then, because $\mathbf{X}$ is a matrix of type $N \times 2M$, the equation system is over-determined as far as the chosen number of layers M fulfils $N \geq 2M$ (with respect to the special structure of the matrix $\mathbf{X}$, $\widetilde{\Delta}_i \geq 2, \forall i$). Therefore, it can only be solved in the sense of least square error minimisation. The unique least squares solution $\hat{\overline{\boldsymbol{u}}}$ is equal, according to [8],

$$\hat{\overline{\boldsymbol{u}}} = \left(\mathbf{X}^\top\mathbf{X}\right)^{-1}\mathbf{X}^\top\,\overline{\mathbf{l}}\,. \tag{6}$$

Note: Another way to compute the least squares solution is via pseudoinverse of $\mathbf{X}$, but we have a full rank matrix and the used way is better from the computational point of view.

Now, we will discuss some practical problems, having the numerical solution point of view in mind, *eg* how to choose the initial estimation of the thicknesses $\widetilde{\Delta}_i$, the attenuation coefficients and signal local return-ratios.

We do not know the amplitude of the transmitted signal y_0 but its value must be somehow determined to ascertain the value of $\overline{\mathbf{l}}$. It can be shown that the choice of y_0 has a direct effect on the computed values of the local signal-return-ratio but it has no effect on the determined attenuation coefficients (because y_0 is only a constant shift of $\overline{\mathbf{l}}$). As we do not need values of the local signal return-ratio, y_0 can be chosen arbitrarily, for example $y_0 = 0$ (*ie* unitary initial amplitude) or $y_0 = y_1$.

Initial estimates of the unknown values can be set as follows: the initial local signal-return-ratios $s_{0,i} = 1$ and the initial attenuation coefficients

$$\mu_{0,i} = \frac{y(N)}{N y(1)}\,. \tag{7}$$

This choice makes the first element y_1 of the measured data equal to the last one (*ie* y_N) after restoration based on this zero-approximation model.

We use the following strategy for choosing M and the set of Δ_i:

1. choose the number of layers $M = 1$, the depth of layer is equal to the number of samples $\Delta_1 = N$, $y_0 = y_1$, $s_{0,i} = 1$ and $\mu_{0,i}$ in compliance with (7),
2. compute the attenuation coefficients from the current model and restore the data by means of it (result is in $y_{1,i}$),
3. compute the standard deviation q and the mean value e of the restored data (*ie* $y_{1,i}$) and test the restored data on statistically significant over-crossings of the limit $|y-e| \geq 3.3q$. We find $i_{1,k}$ and $i_{2,k}$, $i_{1,1} < i_{2,1} < i_{1,2} < i_{2,2} < \dots < i_{1,m} < i_{2,m}$ so that $|y_{1,i} - e| \geq 3.3q$ for $i \in [i_{1,k}, i_{2,k}]$. The new set of Δ_i is used then such that $\Delta_1 = i_{11}$, $\Delta_2 = i_{21} - i_{11}$, $\dots$, $\Delta_{2m-1} = i_{1,m-1} - i_{2,m-1}$, $\Delta_{2m} = i_{2,m} - i_{1,m}$, $\Delta_{2m+1} = N - i_{2,m}$ while observing the constraint $\Delta_i \geq 10$ (to ensure

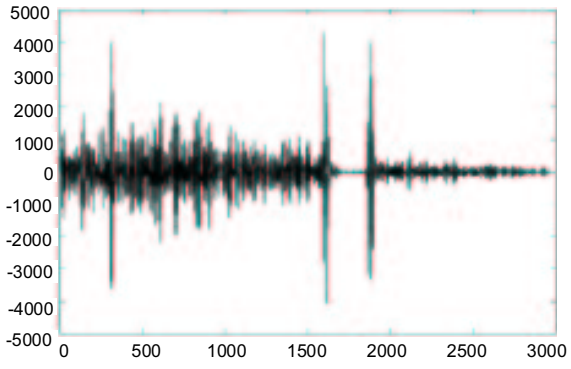

Fig. 2. Measured signal

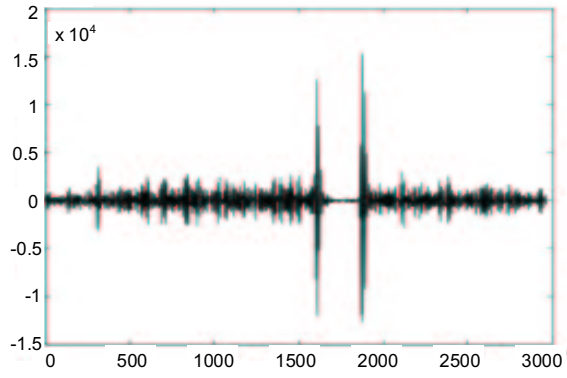

Fig. 3. Restored signal after Step 2

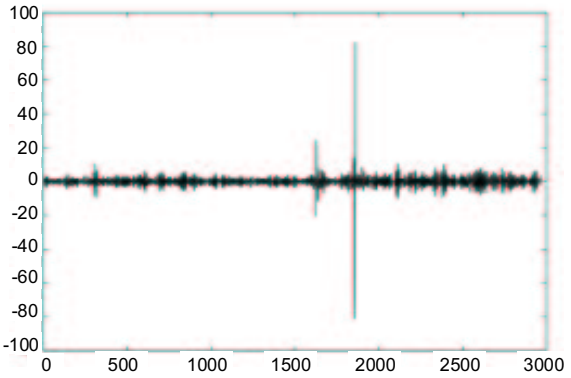

Fig. 4. Residual vector after Step 2

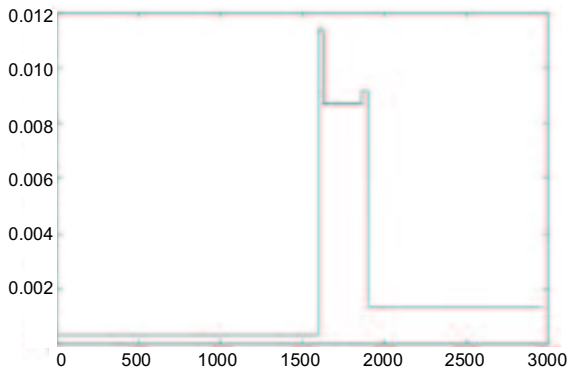

Fig. 5. Estimated attenuation profile $\mu(z)$

stability of the algorithm — a layer cannot be too thin),then $M = 2m + 1$,

4. if the previous step gave no changes or if the number of iterations is greater then $iter_{\max}$ or if the number of layers is greater then $M_{\max}$ then stop the algorithm, else go to step 2.

In this way, a reasonable structure of layers with respect to the structure of tissues to be modelled is gradually approached to.

Under the given iterative scheme, a good estimation of solution error of equation (6) is the norm of the correction vector $\hat{\overline{\boldsymbol{u}}}$, which must "converge to zero"[1]. A further criterion is the norm of the residual vector

$$\overline{\boldsymbol{v}} = \overline{\mathbf{l}} - \mathbf{X}\hat{\overline{\boldsymbol{u}}}$$

that measures the quality of the choice of M and $\widetilde{\Delta}_i$.

4 TESTS AND DISCUSSION

We have tested the designed algorithm on the ultrasonographic data provided by the Catholic University, Leuven (Belgium) — see acknowledgement, measured on both a well identifiable professional tissue-phantom with a series of intense "point" targets on the central axis and several "lesions" as areas of different acoustical impedance and attenuation, and a biological in-vivo specimen. The data are scanned with 36.3125 frames per second, the number of radio-frequency samples on a "ray" is 2964 and the number of rays in one frame ("fan") is 78. The envelope (video) signal used in this project has been derived by discrete Hilbert transform from these radio-frequency data.

EXAMPLE 1. This test presents an example of the estimation of an attenuation profile on a single ray.

Step 1: Given $N = 2964$, we choose initially $M = 1$, $\widetilde{\Delta}_1 = N$, initial estimation $y_0 = y_1$, $\mu_{0,1} = 0.0002083$ and $s_{0,1} = 1$.

Step 2: By computation according to eq. (6), we obtain $\mu_1 = 0.00094097$, $s_1 = 0.4263$, norm of residual vector is 1701.2. We compute the restored signal by using the equation

$$A_{rest}(z, f) = A_{original}(z, f) \exp\Big(f \sum_{i=1}^{M(t)} \mu_i \widetilde{\Delta}_i - s_{M(t)}\Big).$$

[1] This is correct only for the exact solution, on the computer it is convergence to "(approximate) digital zero".

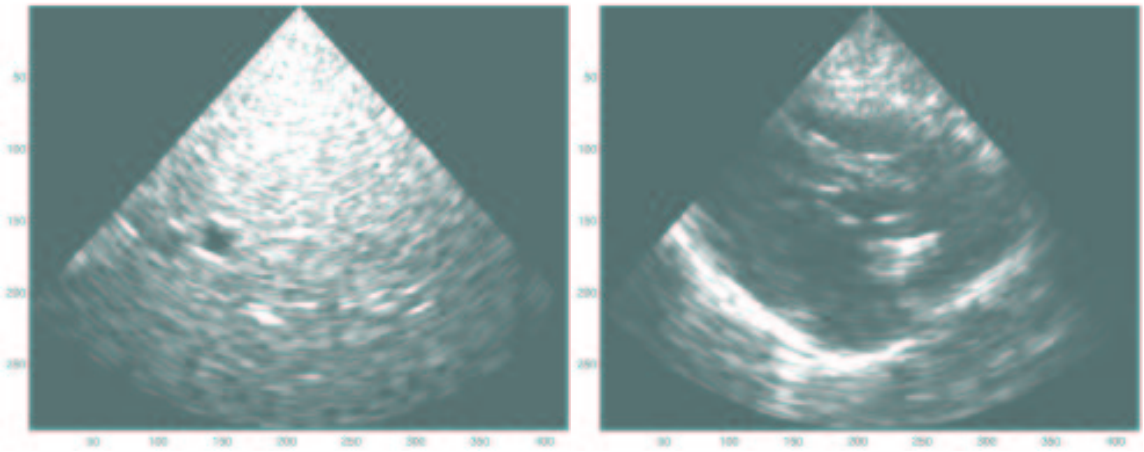

Fig. 6. Ultrasonic images of a) phantom, b) a pig's heart

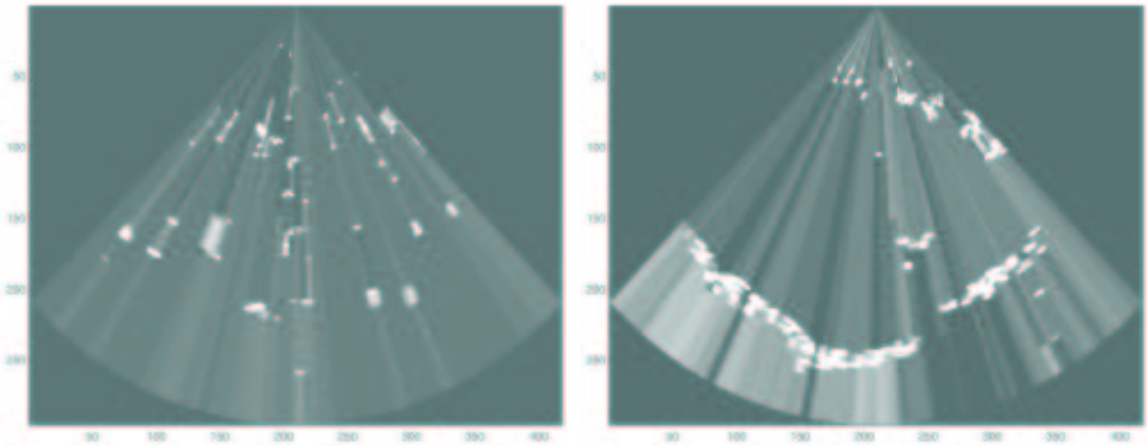

Fig. 7. Fig. 7a. Attenuation map of a) phantom, b) a pig's heart

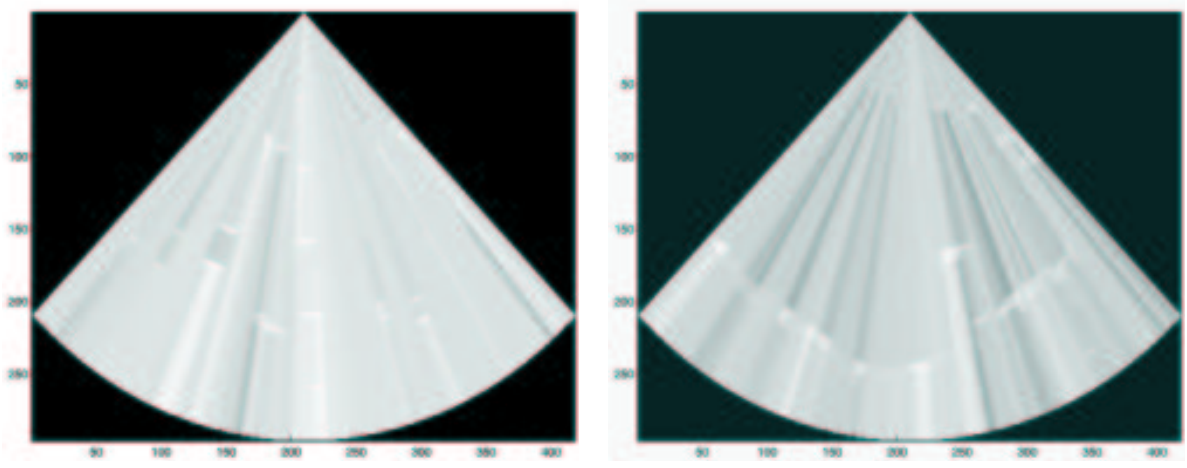

Fig. 8. Fig. 8a. Local signal return-ratio of a) phantom, b) a pig's heart

Step 3: We compute the standard deviation q and derive a new set of Δ_i and consequently $M = 5$ (see the algorithm description, step 3) and solve again the equation (6).

Examples 2 and 3. In these two examples we can see practical results of the algorithm as applied to real ultrasonographic data. Case (a) is the image of a well-defined tissue phantom, case (b) is the image of a pig's heart. Though the results, as presented in Figures 7 and 8 are well acceptable, a problem of the present algorithm is also illustrated there. The independent analysis of individual A-mode scans, which does not take into account the lateral correlation among data, produces some artefacts in

the derived maps thus making them partly inconsistent at places: the large differences appearing between near areas in neighbouring A-mode scans are in some cases rather unrealistic. This will hopefully be improved by using basically the same approach in two dimensions, *ie* analysing a group of neighbouring rays simultaneously, which is planned as the next step.

5 CONCLUSION

A novel method to estimate automatically the ultrasound attenuation map from the measured video (envelope) ultrasonographic data, *ie* without any reference to the prior knowledge of the scanned tissues, has been suggested, providing an approximate solution to a so far unsolved problem. The approach thus may represent an important step on the way to fully automatic attenuation correction in ultrasonography.

The used model of ultrasound propagation has been simplified by averaging the frequency dependence, then discretised and the solution sought by the least squares method. The simplification includes also neglecting of the noise effects. In spite of the mentioned simplifications, the method has proved to work reasonably well for available sets of test data.

The treatment of the problem as a two-dimensional one, taking into account mutual dependences between neighbouring "rays", which may be expected to improve the accuracy, may be the next step. Inclusion of frequency dependencies of ultrasound propagation, so far unfeasible with the presently available means, might be considered as a next higher level in approaching the problem of attenuation estimation in future.

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