ESTIMATION OF *IN VIVO* PULSES IN MEDICAL ULTRASOUND

Jørgen Arendt Jensen

Electronics Institute, bldg. 349
Technical University of Denmark
DK-2800 Lyngby
Denmark

An algorithm for the estimation of one-dimensional *in-vivo* ultrasound pulses is derived. The routine estimates a set of ARMA parameters describing the pulse and uses data from a number of adjacent rf lines. Using multiple lines results in a decrease in variance on the estimated parameters and significantly reduces the risk of terminating the algorithm at a local minimum. Examples from use on synthetic data confirms the reduction in variance and increased chance of successful minimization termination. Simulations are also reported indicating the relation between the one-dimensional pulse and the three-dimensional, attenuated ultrasound field for a concave transducer. Pulses are estimated from *in-vivo* liver data showing good resemblance to a pulse measured as the response from a planar reflector and then properly attenuated. The main application for the algorithm is to function as a preprocessing stage for deconvolution algorithms using parametric pulses.

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1. INTRODUCTION

An image of soft tissue structures is generated in medical ultrasound by emitting a three-dimensional pulsed field into the region of interest. Although the pressure field is rather complex, it can be predicted quite accurately by using modern acoustic methods [1-5]. The field is calculated as a convolution between a term accounting for the spatial extent of the field and a one-dimensional pulse. This pulse accounts for transducer excitation and for the electro-mechanical pulse-echo impulse response. In the case of an attenuating medium, the pulse can also include attenuation.

The spatial spread of the field can be quite accurately predicted from *a priori* knowledge of the transducer geometry. The one-dimensional pulse shape does depend on the attenuation of the pulse from the intervening tissue and can, thus, not be known before the actual patient measurement. It is, therefore, of interest to estimate the one-dimensional pulse from the signal received by the transducer. An estimate will make it possible to calculate the three-dimensional field and to get information about the attenuation in the tissue. A prime application of this algorithm is to function as a preprocessing step for deconvolution algorithms. It supplies a parametrized one-dimensional pulse that includes attenuation. Such a pulse is necessary in order to perform proper deconvolution of ultrasound images to compensate for the extent of the ultrasound pulse. Previous attempts to improve the resolution has not had much success. One

reason for this might be that the pulse used in the deconvolution process was not known with a sufficient precision. This algorithm attempts to increase this precision and it has successfully been applied as a preprocessing stage for *in-vivo* deconvolution, thus obtaining a factor 2.4 increase in resolution [6].

Several authors have investigated pulse estimation using various models. A number of authors used an AR (AutoRegressive) model for the pulse [7–9]. The pulse estimation was here used as an intermediate step to obtain the attenuation coefficient of the tissue. An ARMA (AutoRegressive Moving Average) model was used in [10] to get a close correspondence to the actual pulse shape. The results indicated that the first major oscillations in the pulse were predicted accurately, but the tail of the pulse was not reliably resolved. The problem is caused by the limited amount of data employed. The number of samples used from one A-line is limited by the assumption of stationarity of the pulse. If a long segment is used, the pulse will change significantly due to the attenuation, and a better estimate will not be obtained. One solution to this problem is to employ adjacent A-lines, as the one-dimensional pulse will be the same for all the lines at the same depth. This method was used in [11], where a cepstral technique was used to obtain non-parametric pulses. A number of A-lines could be used to significantly decrease the variance on the results.

This paper derives a multi-channel algorithm that estimates a set of ARMA parameters for the pulse. The advantage of the approach is that a large amount of data can be used for which the pulse can be assumed stationary. Further, the algorithm estimates a parametric pulse that is suited for use in today's advanced deconvolution algorithms [12, 16], which can handle position varying pulses.

2. THE ALGORITHM

The purpose of the procedure is to estimate the one-dimensional *in-vivo* pulse. This pulse accounts for the basic pulse-echo impulse response of the transducer and for the attenuation of the intervening tissue between the transducer and the region of interest [10, 11, 13] as described in section 5. The pulse is parametrized by using an ARMA model [14]:

$$\begin{aligned} A(q)y_s(k) &= C(q)e_s(k) \\ A(q) &= 1 + a_1q^{-1} + a_2q^{-2} \dots + a_{n_a}q^{-n_a} \\ C(q) &= 1 + c_1q^{-1} + c_2q^{-2} \dots + c_{n_c}q^{-n_c} \end{aligned} \quad (1)$$

$y_s(k)$ is the received signal and $e_s(k)$ is the equivalent, one-dimensional scattering signal. a_x are the autoregressive coefficients, c_x the moving average coefficients and q^{-1} the unit backwards shift operator. The polynomial orders are n_a and n_c , respectively, so this is an ARMA(n_a, n_c) model.

The parameters are estimated by minimizing the variance of the prediction error, given by:

$$V_s = \frac{1}{2N} \sum_{k=1}^N \hat{e}_s(k, \Theta) \hat{e}_s(k, \Theta) \quad (2)$$

for a single measured signal $y_s(k)$, where $\hat{e}_s(k, \Theta)$ is the estimated prediction error based on the set of parameters in Θ^1 . N is the number of samples in the segment used for the estimation.

¹ Boldface letters denote that the variable is a vector or matrix.

Generally the set is:

$$\Theta^t = (a_1, a_2, \dots, a_{n_a}, c_1, c_2, \dots, c_{n_c}). \quad (3)$$

$\bullet^t$ denotes transposed.

The one-dimensional pulse is changing down through the tissue due to dispersive attenuation. This makes the selection of N somewhat difficult. A large N decreases the variance of the coefficients, if the pulse has the same shape throughout the data segment. This will not be the case in medical ultrasound for long segments spanning a number of centimeters due to dispersive attenuation. A short segment ensures a stationary pulse, but also yields parameters with a large variance. One method for decreasing the variance is to use a number of input signals e_s , that are uncorrelated, but where the output signals are generated by process with the same statistical properties. This can be done in medical ultrasound by employing adjacent A-lines from a B-scan image. Such lines will, for most images, experience the same attenuation of the pulse, as the same tissue type is penetrated. The scattering from the tissue emanates from numerous independent sources like individual cells, tissue fibers, connective tissue etc. These structures have a small spatial extent, so the lateral correlation between adjacent A-lines is solely determined by the extent of the ultrasound field for a fully developed speckle signal. The correlation between the lines, thus, decreases with lateral displacement, so using a number of lines will introduce significant, new information. Short segments containing a quasi-stationary pulse can be employed using this approach, and a sufficient amount of data is still present to ensure a low variance of the parameters.

The new criterion is:

$$V_N = \frac{1}{2N} \sum_{k=1}^N \hat{\mathbf{e}}^t(k, \Theta) \mathbf{W} \hat{\mathbf{e}}(k, \Theta) \quad (4)$$

$\hat{\mathbf{e}}(k, \Theta)$ is a column vector of order M holding samples for all A-lines entering the estimation. M is the number of A-lines used. $\mathbf{W}$ is a weight matrix of size $M \times M$ giving the weight assigned to each line relative to other lines. In this algorithm $\mathbf{W}$ is diagonal, so no cross products between channels are introduced. The matrix can be used to reflect the confidence or importance of individual lines. Note also that keeping this matrix diagonal eliminates the need for keeping the individual lines coherent. It is sufficient to ensure that data are taken at the same depth in tissue, and, thus, is representative of pulses with the same shape.

The parameters are found by minimizing V_N . This is an iterative task, as $\hat{\mathbf{e}}(k, \Theta)$ must be estimated along with Θ . The prediction error is found from the prediction of $\mathbf{y}$.

$$\begin{aligned} A(q)\mathbf{y}(k) &= C(q)\mathbf{e}(k) \\ \Updownarrow \\ \mathbf{y}(k) &= [1 - A(q)]\mathbf{y}(k) + [C(q) - 1]\mathbf{e}(k) + \mathbf{e}(k) \end{aligned} \quad (5)$$

Assuming the mean value of $\mathbf{e}(k)$ to be zero, the best possible prediction of $\mathbf{y}(k)$, based on previous observations, is:

$$\hat{\mathbf{y}}(k|\Theta) = [1 - A(q)]\mathbf{y}(k) + [C(q) - 1]\hat{\mathbf{e}}(k, \Theta) \quad (6)$$

Then:

$$\begin{aligned} \hat{\mathbf{e}}(k, \Theta) &= \mathbf{y}(k) - \hat{\mathbf{y}}(k|\Theta) = A(q)\mathbf{y}(k) - [C(q) - 1](\mathbf{y}(k) - \hat{\mathbf{y}}(k|\Theta)) \\ &= [A(q) - C(q) + 1]\mathbf{y}(k) - [C(q) - 1]\hat{\mathbf{y}}(k|\Theta) \end{aligned} \quad (7)$$

Thus:

$$C(q)\hat{\mathbf{y}}(k|\Theta) = [C(q) - A(q)]\mathbf{y}(k) \quad (8)$$

Note that both $\mathbf{y}$ and $\hat{\mathbf{y}}$ are column vectors of order M , and that the polynomial filters are the same for each channel.

The minimum variance is found by using a Newton-Raphson algorithm [14] properly changed to accommodate for multiple lines. The parameter estimate is updated by:

$$\Theta^{(i+1)} = \Theta^{(i)} + \alpha \mathbf{g}^{(i)} \quad (9)$$

where the gradient is:

$$\mathbf{g}^{(i)} = -[\mathbf{V}_N'']^{-1} \mathbf{V}_N' \quad (10)$$

$$\mathbf{V}_N' = \frac{dV_N}{d\Theta} \quad (11)$$

$$\mathbf{V}_N'' = \frac{d^2V_N}{d\Theta^2} \quad (12)$$

α is a constant multiplied onto the gradient. Calculation of the derivatives is done by:

$$\begin{aligned} \frac{dV_N}{d\Theta} &= \frac{\frac{1}{2N} \sum_{k=1}^N \hat{\mathbf{e}}^t(k, \Theta) \mathbf{W} \hat{\mathbf{e}}(k, \Theta)}{d\Theta} \\ &= \frac{1}{N} \sum_{k=1}^N \frac{d\hat{\mathbf{e}}^t(k, \Theta)}{d\Theta} \mathbf{W} \hat{\mathbf{e}}(k, \Theta) \\ &= -\frac{1}{N} \sum_{k=1}^N \Psi^t(k, \Theta) \mathbf{W} \hat{\mathbf{e}}(k, \Theta) \end{aligned} \quad (13)$$

$$\Psi(k, \Theta) = \frac{d\hat{\mathbf{y}}(k|\Theta)}{d\Theta} = -\frac{d\hat{\mathbf{e}}(k, \Theta)}{d\Theta} \quad (14)$$

$\Psi(k, \Theta)$ is a matrix of dimension $M \times (n_a + n_c)$ holding the derivative of the prediction with respect to the parameters. The derivatives are calculated by using (8):

$$q^{-i} \hat{\mathbf{y}}(k|\Theta) + C(q) \frac{d\hat{\mathbf{y}}(k|\Theta)}{dc_i} = q^{-i} \mathbf{y}(k)$$

$\Updownarrow$

$$C(q) \frac{d\hat{\mathbf{y}}(k|\Theta)}{dc_i} = q^{-i} (\mathbf{y}(k) - \hat{\mathbf{y}}(k|\Theta)) = q^{-i} \hat{\mathbf{e}}(k, \Theta) \quad (15)$$

$$C(q) \frac{d\hat{\mathbf{y}}(k|\Theta)}{da_i} = -q^{-i} \mathbf{y}(k) \quad (16)$$

The second derivative, $\mathbf{V}_N''$, is approximated by the pseudo Hessian [14]:

$$\mathbf{V}_N'' = \frac{1}{N} \sum_{k=1}^N \Psi^t(k, \Theta) \mathbf{W} \Psi(k, \Theta) \quad (17)$$

Using this approximation to the Hessian the term $\frac{1}{N} \sum_{k=1}^N \frac{d\Psi^t(k, \Theta)}{d\Theta} \hat{\mathbf{e}}(k, \Theta)$ is neglected. If Θ is close to the true value, then $\hat{\mathbf{e}}(k, \Theta)$ is nearly white and consequently the term is close to zero. Far away from the minimum, when the function values between the current value and the minimum can not be well approximated by a quadratic function, the effect of the Hessian is not so important. Neglecting the term also assures that (17) is positive semidefinite, and, thus, guarantees convergence to a stationary point [14].

The parameters are updated by (9) with α initially set to one. The new prediction error variance is calculated, and, if lower than the previous value, the new set of parameters is used for calculating a new gradient. α is divided by two if the variance is not lower, and a new update is done. The procedure is stopped if the norm of the search gradient becomes less than a prescribed limit, or if α is bisected ten times without an improvement in variance. A stable model is ensured by finding the roots of the two polynomials and projecting poles and zeros outside the unit circle into the unit circle at each iteration step. A flow chart of the algorithm is shown in figure 1.

Fig. 1 Flow chart for the multi-channel pulse estimation algorithm.

3. IMPLEMENTATION DETAILS

A set of initial parameters is needed in order to start the iterative procedure. This is done by first fitting an AR model of order $n_a + n_c$, filtering the data to obtain $\hat{\mathbf{e}}(k, \Theta_{AR})$ and then estimating an ARX(n_a, n_c) model [14] with $\hat{\mathbf{e}}$ as the external input. The multi-channel formulation of these estimators is:

$$\begin{aligned}
 \hat{\mathbf{y}}(k|\Theta) &= \Phi^t(k)\Theta \\
 \Phi^t(k) &= (-\mathbf{y}(k-1), -\mathbf{y}(k-2), \dots, -\mathbf{y}(k-n_a), \hat{\mathbf{e}}(k-1, \Theta), \dots, \hat{\mathbf{e}}(k-n_c, \Theta)) \\
 \Theta^t &= (a_1, a_2, \dots, a_{n_a}, c_1, c_2, \dots, c_{n_c}) \\
 \hat{\Theta} &= \left[\frac{1}{N} \sum_{k=1}^N \Phi^t(k) \mathbf{W} \Phi(k) \right]^{-1} \frac{1}{N} \sum_{k=1}^N \Phi^t(k) \mathbf{W} \mathbf{y}(k)
 \end{aligned} \tag{18}$$

The initial parameters are used for obtaining the initial prediction error and derivatives.

The algorithm uses a segment of data from tissue at a particular depth for estimating the pulse. Reflectors are found both before and after the segment, and energy emanating from these reflectors will leak into the data segment due to the length of the pulse. The calculated prediction error will, therefore, initially be corrupted. To remedy this, the summation for finding the prediction error variance and the derivatives is started one pulse length after the segment start. This gives a much more correct estimate of the prediction error and, thereby, the derivatives.

The resulting variance of the estimated parameters is [14]:

$$\begin{aligned} \text{Var}[\hat{\Theta}] &= \text{diag} \left\{ \frac{1}{N S_w} \sum_{k=1}^N \hat{\mathbf{e}}^t(k, \Theta) \mathbf{W} \hat{\mathbf{e}}(k, \Theta) \left[\frac{1}{N S_w} \sum_{k=1}^N \Psi^t(k, \Theta) \mathbf{W} \Psi(k, \Theta) \right]^{-1} \right\} \quad (19) \\ S_w &= \sum_{i=1}^M \mathbf{W}_{ii} \end{aligned}$$

$\text{diag}\{\cdot\}$ denotes a column vector found by taking the diagonal elements of the matrix. S_w is the sum of the elements in the weight matrix. Note that the variance is easily calculated from the matrices used in the algorithm.

4. SIMULATED DATA

Simulated data was used to verify the function of the algorithm and the expression for the variance. A set of 200 independent A-lines was generated by convolving an ARMA(5,6) model given by:

$$\begin{aligned} A(q) &= 1.0000 - 3.1641q^{-1} + 4.6059q^{-2} - 3.6337q^{-3} \\ &\quad + 1.5553q^{-4} - 0.2737q^{-5} \quad (20) \\ C(q) &= 1.0000 - 1.4797q^{-1} + 0.2141q^{-2} - 0.1639q^{-3} \\ &\quad + 0.5689q^{-4} + 0.2437q^{-5} - 0.3538q^{-6} \end{aligned}$$

with a white, random Gaussian signal. The ARMA model was determined from a measured ultrasound pulse impinging on a planar reflector. White, Gaussian noise was then added to obtain an RMS signal-to-noise ratio of 40. Two experiments were conducted. One using a single line containing 700 samples, and one using 10 lines also containing 700 samples each. Both experiments were repeated 20 times. $\mathbf{W}$ was selected to be the identity matrix.

All of the pulses estimated are shown in figure 2, with the results from the single channel algorithm shown at the top. The true pulse, the mean of the estimated pulses and ± 3 standard deviations calculated from the estimates are shown in figure 3. The mean pulse quite closely resembles the true pulse, and the expected drop of a factor $\sqrt{10}$ in standard deviation (SD) is obtained, when the multi-channel algorithm is employed. This makes it possible to get a realistic estimate of the whole pulse shape, not just the main oscillations as in [10].

The variance of the parameters is shown in table 1. The calculated columns are computed from the actual parameters estimated. The single channel algorithms calculated variance has

Fig. 2 Pulses estimated from synthetic data. One line of data is used for the top graph and 10 lines for the bottom.

Fig. 3 True pulse (—), mean of pulses (---) and ± 3 standard deviations (- · -) of the pulses in figure 2.

Table 1 Estimated and calculated variances for simulated data

Parameters	True	Standard deviation (single)			SD (multi)	
		Estimated	Calculated	Corrected	Estimated	Calculated
a_0	1.0000	0	0	0	0	0
a_1	-3.1641	0.1341	0.6540	0.1211	0.0374	0.0378
a_2	4.6059	0.3763	1.5889	0.3247	0.1056	0.1100
a_3	-3.6337	0.5001	1.8911	0.4306	0.1410	0.1514
a_4	1.5553	0.3373	1.1309	0.2927	0.0954	0.1057
a_5	-0.2737	0.1077	0.3436	0.0993	0.0305	0.0350
c_0	1.0000	0	0	0	0	0
c_1	-1.4797	0.1295	0.6768	0.1020	0.0360	0.0365
c_2	0.2141	0.1602	0.4944	0.1020	0.0461	0.0491
c_3	-0.1639	0.0680	0.1884	0.0577	0.0216	0.0192
c_4	0.5689	0.0736	0.2876	0.0619	0.0227	0.0218
c_5	0.2437	0.0908	0.1445	0.0662	0.0286	0.0251
c_6	-0.3538	0.0478	0.2596	0.0470	0.0148	0.0110

also an adjacent corrected variance. When using the algorithm, the initial parameters are supplied by the AR/ARX algorithm described in the previous section. As noise is present and a limited number of data is used, different initial parameters are found for each realization. Due to the non-linear search local minima exist, and it is quite possible that the algorithm is terminated at a local minimum, when a small amount of data is used or a low signal-to-noise ratio encountered. This has happened in 7 out of 20 cases for the single channel algorithm. Taking out these seven cases and then calculating the standard deviation gives the corrected column. A close correspondence between estimated and calculated standard deviation is then obtained.

The multi-channel algorithm avoids the local minima problem for all trials since much more data is employed. Thus, the calculated and estimated standard deviations are similar, and it is a factor of $\sqrt{10}$ less than for the single channel algorithm.

The false-minima problem demonstrates why it is not appropriate to just average parameters obtained from a number of single channel estimates. That would be trying to average solutions from different areas of the search space, and in general would not lead to a $1/M$ reduction in variance (and quite possibly even a worse result), as the multi-channel algorithm does.

5. RELATION TO THE THREE-DIMENSIONAL ULTRASOUND FIELD

The pulse estimated in this work is related to the one-dimensional electro-mechanical pulse used in describing the three-dimensional pulsed field generated and received by an ultrasound transducer. In general the voltage trace from a transducer insonifying point scatterers can be described by [3]:

$$p_r(\vec{r}_2, t) = v_p(t) \star_t f_m(\vec{r}_1) \star_r h(\vec{r}_1, \vec{r}_2, t) \star_t h(\vec{r}_1, \vec{r}_2, t) \quad (21)$$

where $\star_t$ denotes a temporal and $\star_r$ a spatial convolution. h is the spatial impulse response of the particular transducer geometry. $\vec{r}_1$ denotes the position of the scatterer and $\vec{r}_2$ the

position of the transducer. $f_m(\vec{r}_1)$ denotes the spatial distribution of scatterers and $v_p(t)$ is the one-dimensional pulse accounting for the transducer pulse excitation and for the pulse-echo electro-mechanical impulse response. The attenuation of the ultrasound by the tissue between the transducer and the scatterers can, to a good approximation, be lumped into this pulse, which then is written as $v_{pa}(t, |\vec{r}_1 - \vec{r}_2|)$ [5]. The full three-dimensional field can, thus, be calculated if $v_p(t)$ is known, as h can be calculated from knowledge of the transducer geometry.

Simulations were performed for a concave transducer in order to establish the relationship between v_p and the pulse estimated in this work. The program described in [4] was used for evaluating (21). Scatterers with a density of 10 scatterers per resolution cell was generated with a Gaussian scattering strength and random position within a $4 \times 2 \times 5$ cm (width, height, depth) cube starting 6 cm from the transducer surface. The received voltage response from a 8.1 mm diameter concave transducer focused at 100 mm was then calculated by the program by using a 3 MHz measured pulse and summing the response from all the scatterers. Translating the block of scatterers 20 mm laterally in front of the transducer yielded 20 simulated rf A-lines. The pulse estimation algorithm was then applied on 20 different runs and a set of pulses estimated.

The scattered waves emanates from a large collection of independent scatterers when insonifying inhomogeneous tissue, and the received rf A-line is a summation of the responses from all these scatterers. The pulse estimation algorithm applied to such rf A-lines determines the mean pulse for the region under investigation. A signal equivalent to that received from a large collection of scatterers is generated by an infinitely large plane reflector simulating that contributions arrive from all different spatial locations, although they for the plane reflector are summed coherently. The properties of this signal is thus equivalent to that received from the scatterers, and properties can be derived from the equivalent signal.

Fig. 4 Impulse response received from a 10×10 cm plane reflector.

Fig. 5 The top graph shows the differentiated pulses estimated from simulated data generated by the field program. The bottom graph shows the mean of the differentiated estimated pulses (---) and ± 3 standard deviations (- · -) along with the correct pulse as the solid line.

The impulse response received from a 10×10 cm plane reflector placed 8 cm from the transducer is shown in figure 4. The response starts abruptly and slowly decreases as the distance to the sections of the wall that contributes to the response increases. Differentiating this impulse yields a response very close to a dirac function, and the received response from a wall is, thus, $v_p(t)$ integrated over time. A differentiation of the received signal thus yields v_p . The same argument can be applied to the collection of independent scatterers, and a differentiation of the estimated pulse uncovers $v_p(t)$. The distance to the reflector is of little importance. Roughly the same response is received independent of the reflector distance to the transducer, and the estimation procedure is thus applicable over the whole image.

Differentiating the estimated pulses with respect to time yields the results shown in figure 5 along with $v_p(t)$ shown as the dashed line. Very little difference between the true and differentiated estimated pulses are seen supporting the previous argument, and making it possible to construct the full three-dimensional field from the estimated pulse.

6. IN-VIVO DATA

In-vivo data was obtained at Herlev University Hospital, Denmark using our dedicated sampling system [15]. It uses a sampling frequency of 20 MHz and has a resolution of 12 bits. A Brüel & Kjær 1846 real-time scanner was employed. The transducer was a concave, round ($R=8.1$ mm) 3 MHz, Brüel & Kjær 8529 mechanical sector scan probe with a focus at 10 cm. The image used here is a longitudinal scan of the right liver lobe with the right kidney.

A part of the liver with a homogeneous speckle pattern was selected for the pulse estimation. Ten lines were used for each estimate and data was taken between 2.9 and 5.8 cm from the transducer surface. The angle between the lines was 0.88° , so the region had a size of roughly 2.9×0.6 cm and contained 7000 sample points in all.

Eight different estimates could be made for the homogeneous liver region. The mean pulse along with ± 3 standard deviation limits are shown in figure 6. The low variance on the responses attest to the procedure's ability to estimate the main features of the pulse. A measured pulse is also shown as the solid line. It is the response measured from a planar reflector placed at the focal point of the transducer. This measured pulse was attenuated to yield the prediction shown in figure 6. The attenuation coefficient was 1 dB/[MHz cm] and the mean depth in the tissue sample (4.35 cm) was used. The attenuation value was chosen so the oscillations in the pulse had the same zero crossings. The attenuation was assumed to be minimum phase.

Fig. 6 Mean of estimated *in-vivo* pulses (---) and ± 3 standard deviations (- · -). A measured and attenuation corrected pulse is shown as the solid line.

Table 2 Estimated and calculated variances for *in-vivo* data

	Parameters		Standard deviation (single)		
	Mean	Corrected	Estimated	Calculated	Corrected
a_0	1.0000	1.0000	0	0	0
a_1	-2.7942	-2.9156	0.0409	0.3520	0.0836
a_2	4.6414	4.9104	0.1100	0.7920	0.2374
a_3	-4.6535	-5.0057	0.1715	1.0521	0.3654
a_4	3.3193	3.5564	0.1630	0.7347	0.3246
a_5	-1.4497	-1.5490	0.0950	0.3242	0.1749
a_6	0.4095	0.4175	0.0316	0.0481	0.0458
c_0	1.0000	1.0000	0	0	0
c_1	-1.4688	-1.5938	0.0417	0.3636	0.0916
c_2	1.2716	1.4024	0.0636	0.4050	0.1778
c_3	-1.0013	-1.0721	0.0535	0.2465	0.1554
c_4	0.4700	0.5362	0.0374	0.2163	0.1171
c_5	-0.0804	-0.0828	0.0303	0.0673	0.0723
c_6	0.2921	0.2830	0.0283	0.0354	0.0265
c_7	-0.1099	-0.1485	0.0215	0.1144	0.0369

The overall shape of the mean pulse seems to correspond well with the prediction although there are significant deviations beyond the 3 standard deviations limits. The main part of the pulse seems to be in accordance with the predicted pulse and the length also corresponds well to that predictioned. It should here also be remembered that it is a predicted pulse, as the true pulse cannot be measured *in-vivo*.

The estimated and calculated standard deviation for the parameters are shown in table 2. Due to the lower signal-to-noise ratio than for the simulated data, one set of parameters are significantly different from the other seven implying that a local minimum was found. Neglecting this parameter set yields the corrected column for the standard deviation. The estimated standard deviation is then, in the mean, a factor of 2.1 less than the calculated standard deviation. This indicates that the lines used are not uncorrelated, and the factor of 2.1 suggests correlation over roughly four lines. An estimated autocorrelation in the lateral direction averaged over all the samples used is shown in figure 7. The autocorrelation indicates a correlation over roughly four lines explaining the higher calculated variance.

7. CONCLUSION

We have here presented an algorithm for the estimation of one-dimensional ultrasound pulses using a number of A-lines. Results from simulated data were shown indicating the superiority to the single channel algorithm in its ability to elude local minima and reduce the variance on the parameters with a factor of $1/M$, where M is the number of independent lines employed. Tested on *in-vivo* data the algorithm also showed a satisfactory performance, when the results were compared to a measured and synthetically attenuated pulse. The usefulness of this pulse for deconvolution purposes has been demonstrated in [6], where an increase in resolution of 2.4 was obtained by using this pulse estimation algorithm in combination with Mendel's deconvolution algorithm.

Fig. 7 Estimated lateral autocorrelation of *in-vivo* data.

The algorithm has the ability of using previously estimated parameters by skipping the initial AR/ARX step. This can be used for making an efficient approach to track the changing pulse shape down through the tissue. Segments should then be overlapping and parameters from the previous segment used for initializing the current estimation. It would then be possible to make an adaptive deconvolution down through the tissue by the algorithm suggested in [16], thereby properly taking into account the dispersive attenuation of tissue.

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