Velocity estimation using recursive ultrasound imaging

In Chapter 12 a way to estimate the velocity and to perform motion compensation was given. The method relies on the fact, that using long data sequences from the practically uninterrupted data flux, the velocity can be estimated with a lower bias and standard deviation. Precise velocity estimation leads to precise motion compensation, which on its turn leads to precise velocity estimation. Breaking this circle, however, would lead to the opposite effect: bad motion estimation leads to bad motion compensation, which on its turn worsens the motion estimation. Thus, the method is not robust\(^1\).

This chapter introduces a modified cross-correlation estimator making it possible to estimate the velocity out of the non motion-compensated high-resolution images. First the rationale behind the method is given and then the results of the velocity estimation with the new method are compared with the existing methods.

### 13.1 Derivation of the method.

#### 13.1.1 Measurement principle

Consider the simple experiment simulated in Field II and shown in Figure 13.1. A single scatterer moves towards the transducer. The image is formed using four transmissions. Initially the scatterer is centered at 55 millimeters away from the transducer. Between two emissions it moves at a distance \( \Delta z = -\lambda/4 \). The simulated transducer has 64 elements, a center frequency of 5 MHz and a pitch of \( \lambda \), with assumed speed of sound 1540 m/s. The left and right images are formed transmitting sequentially with elements \{1, 22, 43, 64\} and \{22, 43, 64, 1\}, respectively. In both cases the scatterer starts from the same position. The middle row of images in Figure 13.1 show 50 dB B-mode images of the obtained point-spread-functions. They are not symmetric and differ in shape. Comparing the two RF lines (given in yellow on the B-mode images) reveals that the echoes are shifted and different in shape. Because of the change in shape the cross-correlation is low and the velocity cannot be estimated with a high precision. If the synthetic aperture is to be used for velocity estimation of blood flow, one must consider the velocity gradient present in the flow, which decreases the correlation between the consecutive RF signals even more. The conclusion is that the consecutive high-resolution non-motion-compensated RF lines are not suited for velocity estimations.

\(^1\)For me a robust method is a method not sensitive to small errors, and without memory of previous errors.
Chapter 13. Velocity estimation using recursive ultrasound imaging

The reason for this is that the motion artifacts are caused by the change of position of both, the scatterer and the transmitting element as discussed in the end of Chapter 11. This is confirmed by Figure 13.1 which shows that for the same displacement of the scatterer, and different transmit sequence the motion artifacts differ.

The velocity estimation [132] using conventional beamformation methods, in essence, compares RF signals from the same range (depth). Because the sound travels through the same tissue layers, the data samples taken at the same spatial position have undergone the same distortions (phase aberration, refraction, shift in mean frequency, attenuation, etc.). The estimation of blood is based on comparing the changes (phase shifts) in the signal at the particular point, from which the velocity is estimated. The same principle can be applied to estimating the velocity using synthetic aperture imaging.

Consider Figure 13.2 which shows the creation of 3 high resolution images using two emissions per image. The transmit sequence is illustrated in the top left part of the figure. In the right side of the figure the B-mode images of the created point-spread-functions are given. It can be clearly seen that they have different geometries. The bottom plot shows a single RF line from
13.1. Derivation of the method.

Each of the images (the line is indicated with yellow on the B-mode images). The RF lines from the first and the third images are time shifted versions of each other, while the RF line from the second image has a different appearance.

Using the notation used in Chapter 11 the point spread-function of a high-resolution image \( P(x, z; \vec{x}_f) \) is obtained from the point-spread-functions of the low resolution images \( p_i(x, z; \vec{x}_f) \) as:

\[
P(x, z; \vec{x}_f) = \sum_i R[\beta_i]p_0(x, z; \vec{x}_f),
\]

where \( \vec{x}_f = (x_f, z_f) \) is the position of the point scatterer, and \( \beta_i \) is the angle, at which the point spread function of the low resolution image is inclined, and the subscript 0 of \( p_0 \) means that
Chapter 13. Velocity estimation using recursive ultrasound imaging

this point-spread-function is parallel to the transducer surface. The angle \( \beta_i \) is related to the transmitting element \( i \) with the relation:

\[
\beta_i = \arctan \left( \frac{i - \frac{N_{\text{sec}} + 1}{2}}{2z_f} \right),
\]

where \( d_x \) is the pitch of the transducer and \( N_{\text{sec}} \) is the number of transducer elements. The same approximations as in Chapter 11 will be used:

\[
p_0(x, z; \tilde{x}_f + \Delta \tilde{x}) = T'[\Delta \tilde{x}] \{ p_0(x, z; \tilde{x}_f) \}
\]

The considerations for the velocity estimations will be made for a single point scatterer as was done in Chapter 10. The signals for a number of emissions from the same scatterer will be needed. The superscript \( (n) \) will be used to denote the current emission. The point spread function at emission \( n \) will be denoted with \( P^{(n)}(x, z; \tilde{x}_f^{(n)}) \), where \( \tilde{x}_f = (x_f^{(n)}, z_f^{(n)}) \) is the current position of the scatterer. The considerations will be restricted only to the axial motion and the \( x_f \) coordinate will be skipped in the notation further. At position \( n \), the formation of the current point spread function is expressed as:

\[
P^{(n)}(x, z; \tilde{x}_f^{(n)}) \sum_{k=n-N}^{n} R[\beta_i; z_f^{(k)}] p_0(x, z; z_f^{(k)})
\]

Let for the time span from \( (n-2N)T_{prf} \) to \( nT_{prf} \)\(^2 \) the point scatterer has a constant mean axial velocity \( v_z \). The distance traveled by the scatterer between two emissions is constant \( \Delta z = v_z T_{prf} \). Using the aforementioned assumptions one gets:

\[
P^{(n)}(x, z; \tilde{x}_f^{(n)}) = \sum_{k=n-N+1}^{n} T[0, (k - (n - N + 1)) \Delta z] R[\beta_i; z_f^{(n-N+1)}] \{ p_0(x, z; z_f^{(n-N+1)}) \}
\]

Considering the point spread function obtained at time instance \( n - N \) one gets:

\[
P^{(n-N)}(x, z; \tilde{x}_f^{(n-N)}) = \sum_{k=n-2N+1}^{n-N} T[0, (k - (n - 2N + 1)) \Delta z] R[\beta_i; z_f^{(n-2N)}] \{ p_0(x, z; z_f^{(n-2N)}) \}
\]

Realizing that:

\[
p_0(x, z; z_f^{(n-N)}) = T[0, N \Delta z] p_0(x, z; z_f^{(n-2N)})
\]

and

\[
R[\beta_i, (x, z)] T[\Delta z, \Delta x] \equiv T[\Delta x, \Delta z] R[\beta_i; (x - \Delta x, z - \Delta z)]
\]

\(^2\)\( N \) is used instead of \( N_{\text{tot}} \) in this chapter. The reason is that the subscript “\( xmt \)” is too long and the equations cannot fit on a single line.
13.1. Derivation of the method.

\[ P^{(n)}(x, z; z_f^{(n)}) = \]
\[ = \sum_{k=n-N+1}^{n} T[0, (k - (n - N + 1))\Delta z] R[\beta_i; z_f^{(n-N+1)}] \{p_0(x, z; z_f^{(n-N+1)})} \]
\[ = \sum_{k=n-2N+1}^{n-N} T[0, N\Delta z] T[0, (k - (n - 2N + 1))\Delta z] R[\beta_i; z_f^{(n-N)}] \{p_0(x, z; z_f^{(n-2N+1)})} \] (13.8)
\[ = T[0, N\Delta z] \sum_{k=n-2N+1}^{n-N} T[0, (k - (n - 2N))\Delta z] R[\beta_i; z_f^{(n-N+1)}] \{p_0(x, z; z_f^{(n-2N+1)})} \]
\[ = T[0, N\Delta z] P^{(n-N)}(x, z; z_f^{(n-N)}) \]

The above equation might look somewhat overwhelming but it can be summarized as follows. Let a scatterer move at a constant speed. Using the same order of emissions, but starting at different initial moments, one can obtain images that have the same shape but at different spatial positions. This process is illustrated in Figure 13.3.

The two-dimensional point spread function \( P(x, z; z_f) \) is obtained by range-gating the beamformed RF lines from the high-resolution image around the time instance \( t \) corresponding to the image depth \( z_f \). Equation (13.8) means that for small distances (up to several wavelengths) there is a segment in the high-resolution line \( H^{(n)}(t) \), which is a time-shifted version of a segment from the high-resolution line \( H^{(n-N)}(t) \):

\[ H^{(n)}(t) = H^{(n-N)}(t - t_s). \] (13.9)

The two scan lines are beamformed in the same direction and the motion is along the scan line itself. There is a limit, however, on the time elapsed between the two scan-lines due to the

Figure 13.3: Illustration of the fact that images of a moving scatterer acquired at different time instances but using the same transmit order are translated versions of each other.
Table 13.1: Typical velocities in the human vascular system (data taken from [132], originally published in [151]).

<table>
<thead>
<tr>
<th>Vessel</th>
<th>Peak velocity cm/s</th>
<th>Mean velocity cm/s</th>
</tr>
</thead>
<tbody>
<tr>
<td>Ascending aorta</td>
<td>20 - 290</td>
<td>10 - 40</td>
</tr>
<tr>
<td>Descending aorta</td>
<td>25 - 250</td>
<td>10 - 40</td>
</tr>
<tr>
<td>Abdominal aorta</td>
<td>50 - 60</td>
<td>8 - 20</td>
</tr>
<tr>
<td>Femoral artery</td>
<td>100 - 120</td>
<td>10 - 15</td>
</tr>
<tr>
<td>Arteriole</td>
<td>0.5 - 1.0</td>
<td></td>
</tr>
<tr>
<td>Capillary</td>
<td>0.02 - 0.17</td>
<td></td>
</tr>
<tr>
<td>Inferior vena cava</td>
<td>15 - 40</td>
<td></td>
</tr>
</tbody>
</table>

change in the relative position of the scatterers, the change in the shape and size of the point-spread-function etc. Friemel and colleagues [148] have studied the decorrelation in speckle and found that for the velocities present in the body the peak cross-correlation value falls to 0.9, if the translation in elevation direction is $\Delta z_{\text{max}}$ 0.37 mm. The maximum axial speed that can be measured in this case is:

$$v_{\text{max}} = \frac{\Delta z_{\text{max}} f_{\text{prf}}}{N}.$$  \hfill (13.10)

Assuming $N = 4$ and $f_{\text{prf}} = 7000$ Hz, one gets $v_{\text{max}} \approx 0.65$ m/s. The value for the lateral shift $\Delta x_{\text{max}}$ for which the correlation value falls to 0.9 is reported to be 2.8 mm. Measuring at 45 degrees the maximum velocity which results in a peak correlation value of 0.87 – 0.9 is 0.9 m/s. Table 13.1 shows some typical values of velocities in the human circulatory system. Most of the velocities given are within the range, for which the peak of the cross-correlation function is around 0.9.

The shift in position of the high-resolution images can be found from their cross-correlation:

$$R_{n-N,n}(\tau) = \frac{1}{2T} \int_{T} H^{(n-N)}(t)H^{(n)}(t+\tau) \, dt$$
$$= \frac{1}{2T} \int_{T} H^{(n-N)}(t)H^{(n-N)}(t+\tau-t_s) \, dt$$
$$= R_{n-N,n-N}(\tau-t_s).$$ \hfill (13.11)

The peak of the cross-correlation function is located at $\tau = t_s$. The velocity can be found from the time shift:

$$v = \frac{c}{2NT_{\text{prf}}} t_s.$$ \hfill (13.12)

As a summary: the measurement principle is to estimate the time shifts between two high-resolution scan lines. The images from which the time shifts can be estimated must be acquired using the same transmit sequence, so they experience the same motion artifacts.
13.1. Derivation of the method.

Figure 13.4: Estimation of the cross-correlation function from a number of high-resolution RF lines.

13.1.2 Estimation of the cross-correlation function

Figure 13.4 shows the process of estimating the cross-correlation function. Only a single RF line (along the same direction) from consecutive high-resolution images is shown. Two adjacent RF lines have decreased correlation due to motion artifacts caused by different transmit sequences. The same transmit sequence is used for RF lines that are separated by $N - 1$ emissions. The estimation of the cross-correlation is like the standard procedure described in Chapter 10. The RF lines are divided into segments and the segments from the same depth are cross-correlated. The discrete version of the cross-correlation is:

$$
\hat{R}_{1N}[n, i_{seg}] = \frac{1}{N_s} \sum_{k=0}^{N_i-1} H^{(1)}[k + i_{seg}N_s]H^{(N)}[k + i_{seg}N_s + n],
$$

(13.13)

where $N_s$ is the number of samples in the segment and $i_{seg}$ is the number of the segment. To improve the estimate, some averaging must be done. Assuming that the velocity does not change significantly, the time shift $t_s$ estimated from $\hat{R}_{1N}$ should be the same as the time shift $t_s$.

$^3$Remember that the higher the peak cross-correlation, the bigger the accuracy and the smaller the standard deviation of the estimates are.
of the peak of the cross-correlation function $R_{\Delta 2,N+1}$ as shown in Figure 13.4. The averaging can be expressed as:

$$\hat{R}_{1Nd}[n,i_{\text{seg}}] = \frac{1}{N_s(N_c - 1)} \sum_{i=0}^{N_c-2} \sum_{k=0}^{N_c-1} H(i)[k + i_{\text{seg}}N_s]H(i+N)[k + i_{\text{seg}}N_s + n], \quad (13.14)$$

where $N_c$ is the number of lines over which the averaging is done. The span of $\hat{R}_{12d}$ determines the maximum detectable velocity. In order to detect the same velocity range as the “conventional” cross-correlation estimator, the length of the interval in which the peak is searched must be $N$ times bigger. If the search length is within the interval $[-N_s,N_s]$, then the largest detectable velocity becomes:

$$v_{\text{max}} = \frac{c}{2N} f_{prf} f_s,$$

(13.15)

The minimum velocity is:

$$v_{\text{min}} = \frac{c}{2N} f_{prf} f_s,$$

(13.16)

which is $N$ times smaller than the minimum detectable velocity in the conventional cross-correlation estimators. In order to improve the estimates a second order polynomial is fitted to the three point around the peak of the cross-correlation function.

### 13.1.3 Stationary echo canceling

Usually the echo canceling is done by subtracting the adjacent lines [132, 143] or by using a high-pass filter with a very short impulse response. This way of processing is chosen because of the short data sequences available for the motion, typically $N_c \sim 8, 10$. Using a synthetic aperture imaging with recursive beamformation gives an uninterrupted data stream and filters with long impulse responses can be used. In this thesis the stationary echo canceling was done by subtracting the mean from the signal at a given depth:

$$H^{(k)}(t) = H^{(k)}(t) - \frac{1}{N_c + 1} \sum_{i=-\frac{N_c}{2}}^{\frac{N_c}{2}} H^{(i)}(t) \quad (13.17)$$

When the cross-correlated lines are not obtained in successive emissions, only every $N$th line is used:

$$H^{(k)}(t) = H^{(k)}(t) - \frac{1}{N_c + 1} \sum_{i=-\frac{N_c}{2}}^{\frac{N_c}{2}} H^{(k+iN)}(t). \quad (13.18)$$

### 13.2 Results

The performance of the suggested approach was tested for a flow with constant velocity as was done in Chapter 12 and for a flow which has a parabolic profile.
13.2. Results

<table>
<thead>
<tr>
<th>Parameter</th>
<th>Value</th>
<th>Unit</th>
</tr>
</thead>
<tbody>
<tr>
<td>Transducer center frequency</td>
<td>7.5</td>
<td>MHz</td>
</tr>
<tr>
<td>Relative transducer bandwidth</td>
<td>66</td>
<td>%</td>
</tr>
<tr>
<td>Number of elements</td>
<td>64</td>
<td></td>
</tr>
<tr>
<td>Excitation center frequency</td>
<td>5</td>
<td>MHz</td>
</tr>
<tr>
<td>Pulse repetition frequency</td>
<td>7000</td>
<td>Hz</td>
</tr>
<tr>
<td>Propagation velocity</td>
<td>1540</td>
<td>m/s</td>
</tr>
<tr>
<td>Center wavelength</td>
<td>308</td>
<td>µm</td>
</tr>
<tr>
<td>Excitation length</td>
<td>468</td>
<td>µm</td>
</tr>
<tr>
<td>Lines for one estimate</td>
<td>20</td>
<td></td>
</tr>
<tr>
<td>Correlation length</td>
<td>3.1</td>
<td>mm</td>
</tr>
<tr>
<td>Search length</td>
<td>±468</td>
<td>µm</td>
</tr>
<tr>
<td>Step between two estimates</td>
<td>1</td>
<td>mm</td>
</tr>
<tr>
<td>Velocity</td>
<td>0.495</td>
<td>m/s</td>
</tr>
</tbody>
</table>

Table 13.2: Relevant parameters for the experimental verification of the new method.

13.2.1 Constant velocity

The performance of the method was tested on data measured using the XTRA system (see Appendix J for description of the system). The measurement setup was described in Section 12.4.1. The velocity estimation was applied on the very same data set. Only four transmit elements evenly distributed across the receive aperture \((N = 4)\) were used in transmit. Two cases were investigated: (1) the standard cross-correlation estimation when the cross-correlation is done between successive lines, and (2) the new cross-correlation scheme in which the cross-correlation is done between lines that are separated by 3 emissions.

The parameters used in the velocity estimation are summarized in Table 13.2. These parameters were used for both cases of velocity estimation.

Figure 13.5 shows the values of the estimates as a function of emission number and depth. As it can be seen it completely misses the true estimates. The estimates very about the zero in both positive and negative directions. Figure 13.6 shows that the standard deviation is relatively small, which shows that the errors are due to the motion artifacts which are not random in nature. Figures 13.7 and 13.8 show the results from the velocity estimation using the modified cross-correlation estimation procedure. There are two relatively large errors in the beginning of the profile (between 15 and 20 mm) and at 60 mm. Looking at the reference image shown in Figure 12.9 on page 174 one can see that these two regions correspond to the strong wire scatterers that are placed along a line parallel to the transducer surface. As discussed in Chapter 10 the dominating source of error in the absence of noise, when all of the scatterers move with the same velocity is the error associated with the beam width modulation. When the scattering is diffused as in the case of speckle this phenomenon is less pronounced compared to the case when a single strong scatterer enters and exits the beam. The relative standard deviation is around 1 %, which is less even than the standard deviation of the reference velocity estimation in Chapter 12. The reasons for this are: (1) the time delay \(t_s\) is 4 times larger for the modified cross-correlation procedure and can be determined with a higher precision (see Figure 10.5), (2) the correlation interval is larger giving a better estimate of the cross-correlation function, and (3) more lines are used to average the estimated cross-correlation function. Having successfully
Figure 13.5: The result of velocity estimation using non-motion-compensated high-resolution images and a standard cross-correlation velocity estimation procedure. The estimated velocity as a function of emission number and depth is shown.

Figure 13.6: The result of velocity estimation using non-motion-compensated high-resolution images and a standard cross-correlation velocity estimation procedure. The figure shows the mean velocity and the region of ± one standard deviation.

estimated the velocity of a constant flow, the ability of the modified cross-correlation estimation procedure using synthetic aperture imaging for laminar flow with parabolic profile was tested.

13.2.2 Parabolic velocity profile

Developing a full model of the blood flow in the human circulatory system is beyond the scope of the thesis. Most articles on this subject assume a parabolic velocity profile and a steady flow
13.2. Results

Figure 13.7: The result of velocity estimation using non-motion-compensated high-resolution images and the modified cross-correlation velocity estimation procedure. The estimated velocity as a function of emission number and depth is shown.

Figure 13.8: The result of velocity estimation using non-motion-compensated high-resolution images and the modified standard cross-correlation velocity estimation procedure. The figure shows the mean velocity and the region of ± one standard deviation.

(i.e. $\partial v/\partial t = 0$ at one particular position). This type of blood flow will be investigated here. Such velocity profile is developed in long and in narrow (with small radius) tubes. A comprehensive treatment of the subject can be found in Chapter 3, “Flow physics”, in Estimation of blood velocities using ultrasound. A signal processing approach by Jensen [132]. Figure 13.9 shows a typical measurement situation for measuring blood flow. A vessel with radius $R$ is placed in front of a transducer. The angle between the vessel and the normal vector to the transducer surface is $\beta$. In this case the normal to the transducer surface coincides with the $z$
Chapter 13. Velocity estimation using recursive ultrasound imaging

axis of the coordinate system. The blood flow is measured along a scan line that is defined by an azimuth angle $\theta$ (this is the angle between the scan line and the normal vector to the transducer surface). The velocity has a parabolic profile:

$$v(r) = v_{\text{max}} \left( 1 - \left( \frac{r}{R} \right)^2 \right), \quad (13.19)$$

where $r$ is the distance to the center of the vessel and $v_{\text{max}}$ is the maximum velocity in the center of the vessel. The distribution of the magnitude of the velocity is depicted in Figure 13.9 with arrows. The estimation procedure (13.12) gives only the velocity component along the scan line. The true velocity is found by:

$$\hat{v}_{\text{true}} = \frac{\hat{v}}{\cos \gamma}, \quad (13.20)$$

where $\gamma$ is the angle between the scan line and blood vessel. The angle can be determined by using simple geometric relations as:

$$\gamma = \beta - \theta. \quad (13.21)$$

One must be careful with the definition of the angles. In the case shown in Figure 13.9 the positive angles are defined in the direction from the $z$ axis towards the $x$ axis.

Table 13.3 shows typical sizes of the larger vessels in human’s vascular system. Their diameter $2R$ is close to 1 cm, and this is the size of the vessel simulated using Field II.

The vessel that was simulated had a diameter of 1 cm and a length of 5 cm. It closed an angle $\beta$ of 45° with the $z$ axis. The center of the vessel was positioned on the $z$ axis ($x = 0, y = 0$) 50 mm away from the transducer. To simulate the interaction with the blood 10 scatterers per cell of size $1 \times 1 \times 0.5$ mm were generated giving a total of 78549 scatterers. The positions of the scatterers were randomly selected with an uniform (white) distribution within the boundaries of the vessel. Their amplitudes had a Gaussian distribution with a zero mean [132]. Each
### Table 13.3: Typical dimensions of some vessels in the human vascular system (data taken from [132], originally published in [151]).

<table>
<thead>
<tr>
<th>Vessel</th>
<th>Internal diameter [cm]</th>
<th>Wall thickness [cm]</th>
<th>Length [cm]</th>
</tr>
</thead>
<tbody>
<tr>
<td>Ascending aorta</td>
<td>1.0 - 2.4</td>
<td>0.05 - 0.08</td>
<td>5</td>
</tr>
<tr>
<td>Descending aorta</td>
<td>0.8 - 1.8</td>
<td>0.05 - 0.08</td>
<td>20</td>
</tr>
<tr>
<td>Abdominal aorta</td>
<td>0.5 - 1.2</td>
<td>0.04 - 0.06</td>
<td>15</td>
</tr>
<tr>
<td>Femoral artery</td>
<td>0.2 - 0.8</td>
<td>0.02 - 0.06</td>
<td>10</td>
</tr>
<tr>
<td>Carotid artery</td>
<td>0.2 - 0.8</td>
<td>0.02 - 0.04</td>
<td>10-20</td>
</tr>
</tbody>
</table>

### Table 13.4: Relevant parameters for the simulation of the parabolic flow.

<table>
<thead>
<tr>
<th>Parameter</th>
<th>Value</th>
<th>Unit</th>
</tr>
</thead>
<tbody>
<tr>
<td>Transducer center frequency</td>
<td>7.5</td>
<td>MHz</td>
</tr>
<tr>
<td>Relative transducer bandwidth</td>
<td>66</td>
<td>%</td>
</tr>
<tr>
<td>Number of elements</td>
<td>64</td>
<td></td>
</tr>
<tr>
<td>Transducer pitch</td>
<td>205</td>
<td>μm</td>
</tr>
<tr>
<td>Transducer height</td>
<td>4</td>
<td>mm</td>
</tr>
<tr>
<td>Excitation type</td>
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<td></td>
</tr>
<tr>
<td>Excitation start frequency</td>
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<td></td>
</tr>
<tr>
<td>Excitation end frequency</td>
<td>17</td>
<td>MHz</td>
</tr>
<tr>
<td>Excitation duration</td>
<td>20</td>
<td>μs</td>
</tr>
<tr>
<td>Sampling frequency</td>
<td>100</td>
<td>MHz</td>
</tr>
<tr>
<td>Pulse repetition frequency</td>
<td>7000</td>
<td>Hz</td>
</tr>
<tr>
<td>Propagation velocity</td>
<td>1540</td>
<td>m/s</td>
</tr>
<tr>
<td>Maximum velocity</td>
<td>0.18</td>
<td>m/s</td>
</tr>
</tbody>
</table>

The scatterer had a velocity associated with its radial position (relative to the central axis of the vessel). Between every two emissions the scatterers were translated in a direction parallel to the walls of the transducer. Every scatterer was displaced at a distance corresponding to its velocity. The scatterers that “fell out” of the vessel were put in again from the opposite side (cyclically moved).

The most important parameters of the simulation are listed in Table 13.4.

One of the serious problems in synthetic aperture imaging is the poor signal to noise ratio. This makes it almost imperative to use coded excitation, and that is why such an excitation was used in the simulations. The excitation was a linear FM chirp, sweeping the frequency range from 0 to 17 MHz in 20 μs. Such a chirp cannot pass unaltered through the transducer. The applied filter is not the matched filter, but is rather a filter optimized with respect to minimizing the range side-lobe level [119]. The chirp, the filter, and the logarithmically compressed envelope of the output of the filter are given in Figure 13.10. The output of the filter was created by convolving the excitation with the impulse response of the transducer twice, and then convolving it with the impulse response of the filter. The low level of the range side lobes guarantees that there will be a minimum influence on the estimates from signals coming from the stationary echoes.
and from other segments of the blood vessel.

The estimates using cross-correlation can be improved by two means: (1) using longer data segments (in depth, or equivalently fast time) and (2) using more lines to average the cross-correlation estimate. In the former case the correlation length was set to $5\lambda$, where $\lambda$ is the wavelength at the center frequency of the transducer. In the simulation $\lambda$ is equal to 205 $\mu$m. The number of lines over which the cross-correlation function is averaged is $N_c = 4$. The interval in which the maximum of the cross-correlation function is sought is restricted to $\pm 2.5\lambda$. In the latter case, when $N_c = 24$, the correlation length is $2.5\lambda$ and the search interval is set to $\pm 1.7\lambda$.

The high-resolution images were obtained using only four transmit elements evenly distributed.
13.2. Results

Figure 13.11: Velocity profile at $\gamma = 45^\circ$ using the traditional cross-correlation velocity estimation. The number of lines per estimate is $N_c = 24$, and the segment length is $2.5\lambda$.

Figure 13.12: Velocity profile at $\gamma = 45^\circ$ using the traditional cross-correlation velocity estimation. The number of lines per estimate is $N_c = 4$, and the segment length is $5\lambda$.

across the aperture. The modified cross-correlation velocity estimation was compared to the traditional approach, the results of which are given in Figures 13.11 and 13.12. The thin black lines outline the true velocity profile. The thick blue lines give the mean of the estimate, and the thin blue dotted lines show enclose the region of plus/minus one standard deviations.

Figures 13.11 and 13.12 show the cases in which the number of lines are $N_c = 24$ and $N_c = 4$, respectively. In order for the results to be comparable to the results when using the modified cross-correlation approach, the search length was 4 times smaller (the scatterers travel 4 times shorter distance). It can be seen that for small velocities, the motion artifacts do not distort the signal significantly, the correlation between successive high-resolution images is relatively high, and the velocity can be determined. For higher velocities, however, the effect of the mo-
Figure 13.13: Velocity profile at $\gamma = 45^\circ$ using the modified cross-correlation velocity estimation. The number of lines per estimate is $N_c = 24$, and the segment length is $2.5\lambda$.

Figure 13.14: Velocity profile at $\gamma = 45^\circ$ using the modified cross-correlation velocity estimation. The number of lines per estimate is $N_c = 4$ and the segment length is $5\lambda$.

motion artifacts dominates the estimated velocity (like a negative profile around a certain pedestal). The standard deviation is also large. The mean values of the estimated velocity profiles are similar showing that the velocity estimation is influenced mainly by the motion artifacts which have deterministic character.

Figures 13.13 and 13.14 show the velocity profiles using the modified cross-correlation estimation procedure. The maximum bias (at the top of the profile) of the profile in Figure 13.13 is -3.05 % and the maximum standard deviation is 2.7 %. The exciting part is that velocity profile in Figure 13.14 has a similar performance, but is obtained only with 8 emissions (if $N_c = 4$ then RF lines from the images $H^{(1)}$ to $H^{(4)}$ are cross-correlated with RF lines in images $H^{(5)}$ to $H^{(8)}$). The bias of the maximum of the estimated profile with respect to the maximum of
13.2. Results

Figure 13.15: Velocity profile at $\gamma = 35^\circ$ using the modified cross-correlation velocity estimation. The number of lines per estimate is $N_c = 4$, and the segment length is $5\lambda$.

Figure 13.16: Velocity profile at $\gamma = 55^\circ$ using the modified cross-correlation velocity estimation. The number of lines per estimate is $N_c = 4$, and the segment length is $5\lambda$. The signal was range gated too-early and the estimates do not cover the whole vessel.

The true profile is -2.5 %. The standard deviation varies between 1.2 % at 50th mm and 5 % at 42d mm. The high value of 12.1 % of the standard deviation at depth of 48 mm is caused by a single false peak detection - magnitude of -0.17 m/s. If this peak is removed the standard deviation at this point becomes 2.15 %.

The fact that the velocity can be estimated from synthetic aperture imaging using only 8 emissions gives the foundations to develop velocity estimations for real-time 3D scanners. Scanning the volume plane by plane, one could use 8 emissions per plane. In such a way velocity estimates as well as B-mode data will be available for the whole volume. The performance of the
velocity estimation using only 8 emissions for angles $\gamma = 35^\circ$ and $\gamma = 55^\circ$ is shown in Figures 13.15 and 13.16, respectively.

In Figure 13.16 the estimated velocity profile is not complete because the received raw RF signals by the individual elements were range gated.

13.3 Discussion and prospectives of the velocity estimation with synthetic aperture imaging

In order to estimate the velocity in conventional ultrasound scanners, the pulse is transmitted several times in the same direction. This leads inevitably to a decrease in the frame rate. Because of its nature, synthetic transmit aperture ultrasound imaging, or more precisely its variation recursive ultrasound imaging generates high-resolution RF lines at every emission. This gives practically uninterrupted flow of data. The estimates can be based on larger data segments thus improving the precision of the estimates. It was also shown that the estimates can be made with only a few emissions as they are normally done in conventional systems. This opens up for the possibility to have real-time velocity estimates in real-time 3D systems, thus making these systems full-featured ultrasound scanners, not only baby face renderers as they are in the present moment.

This chapter showed that in order to work with synthetic aperture imaging, the velocity estimation algorithms must be altered. The class of time-shift measurement systems is suitable for the purpose. In the following a brief overview of some of the most promising approaches will be treated.

13.3.1 Velocity estimation using cross-correlation along the blood vessel

The estimation of the velocity using cross-correlation of transverse beams was first suggested by Bonnefous [152]. It was further developed and perfected by Jensen and Lacasa [153, 154]. Figure 13.17 shows the measurement principle. The beam is focused along lines parallel to the axis of the vessel. Each of these lines from emission $n$ is cross-correlated with the line from emission $n + 1$. The offset of the peak of the cross-correlation function is a measure of the movement of the scatterers. The traditional cross-correlation approach traces the signals towards and away from the transducer. Therefore only the axial velocity components can be found. With this method the signal is traced along the blood vessel, and velocity components parallel to the transducer surface can be measured. In the initial work [153] a broad beam was sent in the tissue and in receive the delays were set to focus along the axis of the vessel. The method has two problems: (1) it is not equally sensitive in the axial and lateral directions, and (2) the beam profile changes as a function of space, thus affecting the accuracy of the estimates. The latter of the problems was addressed by Jensen and Gori [46] by using matched filters. The filters have different impulse responses depending on the varying spatial impulse response (which can be numerically found), thus compensating for the fixed focus in transmit. This approach can be extended to synthetic aperture imaging in a straight-forward manner.

The beams are perfectly focused in transmit and receive. As seen from Figure 11.8 on page 163 a lateral translation of the scatterer causes a lateral translation of the low-resolution image. If one considers a laminar flow, then all the scatterers located at a radial distance $r$ from the center of the vessel move with a constant velocity $v$. The distance which they travel for the time $T_{prf}$...
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![Diagram of blood vessel and beams along the vessel]

Figure 13.17: The data used to find the velocity is taken from lines along the vessel.

Between every two emissions is

\[ \Delta l = |\vec{v}| T_{prf}. \]  \hspace{1cm} (13.22)

The traveled distance can be decomposed into an axial and lateral components (see: Figure 13.17):

\[ \Delta x = \Delta l \sin \beta \]
\[ \Delta z = \Delta l \cos \beta \]  \hspace{1cm} (13.23)

Using the arguments from Section 13.1.1 which are illustrated for the case of pure axial motion in Figure 13.3 one gets that:

\[ \frac{1}{2} P^{(n)}(x, z; (x_f^{(n)}, z_f^{(n)})) = T[N \Delta x, N \Delta z] P^{(n-N)}(x, z; (x_f^{(n-N)}, z_f^{(n-N)})) \]  \hspace{1cm} (13.24)

In this case it is straightforward to show that a line \( s^{(n)}(x, y) \) at emission \( n \), defined along the beam:

\[ x = x_f + l \sin \beta \]
\[ z = z_f + l \cos \beta \]  \hspace{1cm} (13.25)

is a shifted version of the line \( s^{(n-N)}(x, y) \) :

\[ s^{(n)}(x, y) = s^{(n)}(x - N \Delta x, y - N \Delta y). \]  \hspace{1cm} (13.26)

It is convenient to express the line in terms of \( l \), which in this case is distance from the focal point \( x_f, z_f \) along the direction defined by the angle \( \beta \). The relation becomes:

\[ s^{(n)}(l) = s^{(n-N)}(l - N \Delta l). \]  \hspace{1cm} (13.27)

Cross-correlation the two lines gives:

\[ R_{1N}(\tau) = R_{11}(\tau - \Delta l), \]  \hspace{1cm} (13.28)
where $R_{11}$ is the auto-correlation function of the signal, and $\tau$ is a lag in space. The velocity is then:

$$\hat{v} = \frac{\Delta l}{NT_{prf}}.$$  \hfill (13.29)

The minimum detectable velocity is dependent on the spacing between the samples comprising the scan line $s(i)$. This approach solves partly the problem with decorrelation due to migration of scatterers. More information on the subject can be found in [154].

### 13.3.2 Velocity estimation using speckle tracking

Estimating the blood velocities by tracking the speckle produced by moving blood has been suggested by Trahey and colleagues in 1987 [155, 156]. The idea is that the current random distribution of blood cells creates certain speckle patterns (two dimensional image). For the distance that the blood cells travel for the time of a few (usually 5 to 10) emissions these patterns remain intact and the change in their position can be traced by using a two dimensional convolution. The two-dimensional cross-correlation procedure has been simplified in subsequent papers [157], and made more robust by tracking the speckle pattern within smaller regions and using parallel beamforming [158, 159, 160].

The velocity estimation using speckle tracking (called in the recent papers “ensemble tracking” [160]) is illustrated in Figure 13.18. Several acquisitions are done in the same direction. In receive several lines within the boundaries of the transmit beam are formed in parallel. To improve the performance the RF data from the receive beams are rescaled to compensate for the lateral transmit beam profile. A small 2D kernel is chosen and a match for it is sought in a larger bounding 2D region. The pattern matching algorithm that was used in [160] is based on the so-called sum absolute difference (SAD) [157]:

$$\varepsilon(\eta, \xi, n) = \sum_{i=1}^{j} \sum_{j=1}^{k} |B_0(i, j)| - |B_n(i + \eta, j + \xi)|,$$ \hfill (13.30)

where $\varepsilon$ is the SAD coefficient, $n$ is the acquisition number, $B_n(i, j)$ is the brightness of the
pixel at location \((i, j)\) in the \(n\)th image, \(l\) is the lateral dimension of the kernel in pixels, \(k\) is the axial dimension of the kernel in pixels, and \(\eta\) and \(\xi\) are lateral and axial pixel offsets of a prospective matching region within the search region. The best match is found at the smallest value of the difference. The result of the process is interpolated in a fashion similar to the curve fitting shown in Figure 10.4, and the interpolated offsets \((\hat{\eta}_m, \hat{\xi}_m)\) at which the maximum occurs are found. The magnitude of the velocity is given by:

\[
|\vec{v}| = \sqrt{\left(\frac{\hat{\eta}_m \Delta x}{n T_{prf}}\right)^2 + \left(\frac{\hat{\xi}_m \Delta z}{n T_{prf}}\right)^2}
\]

(13.31)

where \(\gamma\) is the angle between the beam axis and the velocity vector, \(\Delta x\) and \(\Delta z\) are the lateral and axial spatial sampling intervals respectively, and \(T_{prf}\) is the pulse repetition interval.

This approach can be modified for use with synthetic aperture imaging in the same way as the cross-correlation velocity estimators. The speckle patterns from emissions \(0\) and \(N\), \(1\) and \(N + 1\), \(N - 1\) and \(2N - 1\) can be tracked and then the estimates can be averaged for higher accuracy.

In conclusion, this chapter showed that images obtained with the same sequence of transmissions over a short time period (\(\approx 1\) ms) exhibit high correlation. Many of the time-domain velocity estimation algorithms can be modified for use with synthetic aperture imaging. This chapter showed how to modify the velocity estimator using time shift measurement (aka cross-correlation velocity estimation) and through simulations showed that the amount of emissions per color flow map can be reduced to eight. If a 3D scan is performed plane by plane using 8 emissions per plane, a color flow map for each of the planes can be created and combined in a color flow map for the whole volume.