Blood Velocity Estimation
Using Compressive Sensing

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Abstract

Duplex ultrasonography is a mode of medical ultrasonography that allows one to visualize, at the same time, the inner structure of the body (B-mode) and the blood flow at a particular point in the body (Doppler mode). This mode requires a strategy for alternating B-mode and flow emissions. Traditional strategies either halve the maximum measurable velocity or introduce gaps in the flow data. The objective of this article is to propose a completely original method based on compressive sensing for reconstructing the Doppler signal segment by segment. Our approach is based on randomly alternating B-mode and flow emissions. The influence of the different parameters on the reconstruction quality is studied in detail. The technique is evaluated and its feasibility is validated in simulation and from experimental in vivo data. It is also compared to the only method from the literature, proposed by Jensen, that reconstructs blood velocity estimates from sparse data sets.

Index Terms

Ultrasound, compressive sensing, Doppler, blood flow
I. INTRODUCTION

Medical ultrasound (US) is an imaging modality that can produce images at very high frame rates thanks to the quick propagation of ultrasound waves in human tissue (typically around 1500 m.s\(^{-1}\)). The pulse repetition frequency (PRF) is in a range of several kHz depending on the depth of investigation. As a result, US is extremely well adapted as soon as tissue motion is involved, for example in echocardiography [1] [2], elastography [3] and blood flow imaging [4]. However, in some situations where many RF signals need to be acquired, the physical limits imposed by the ultrasound velocity are reached, for example in 3D ultrasound [5]. This can also occur in some specific situations when imaging blood flow as detailed herunder.

There are mainly two ways to show blood velocity in vessels: i) either one point is selected in the B-mode image, and the evolution of the velocity at that given point is shown as a function of time on a so-called pulsed Doppler spectrogram (referred to later on as pw-spectrogram), or ii) the spatial distribution of the velocities in a region of interest is superimposed on the B-mode image in a so-called color flow mapping mode (CFM). As the two representations do not show the same information, one might be interested in showing both modes as a complement to the B-mode image in a triplex mode. One could even show a pw-spectrogram at two different positions in the vessel (before and after a stenosis, for example) which would lead to a quadroplex mode. Note that the Doppler signal used to construct the pw-spectrogram lies in the audible frequency band. As a consequence most of the Doppler systems are equipped with an audio system that enables to listen to the Doppler signal. This provides the doctors with an intuitive way to evaluate the flow.

The type of ultrasound pulses (sometimes also called ultrasound burst) that are sent out by the probe when B-mode imaging is done is different from the one sent out for flow imaging. In particular for B-mode imaging it is important to have short wide-band pulses that will lead to short echoes and consequently to a better resolution in the images. Whereas, for blood flow imaging it is necessary to use narrow-band pulses in order to increase the precision of the estimation of Doppler shift. As a consequence, if both modes need to be done in the same imaging sequence, the time must be shared between the two types of acquisition. This study will simply focus on a duplex mode where B-mode and pw-spectrogram radiofrequency (RF) signals need to be acquired. In a typical situation there are two solutions. The first one consists in interleaving the two kinds of acquisition. This, however, lowers the pw-spectrogram pulse repetition frequency (FPRF) by a factor of two, while dividing the maximum possible velocity estimate by a factor of two. Another possibility is to acquire all signals for the B-mode image in a row, and then the signals for the pw-spectrogram. This leads to pw-spectrograms with missing parts of the signal and makes the interpretation of the corresponding audio signals very difficult. The gaps could be artificially filled by several methods, such as those described by Kristoffersen and Angelsen [6] or Klebæk et al. [7]. However, these methods assume that the flow is stable or roughly predictable, which leads to inaccurate reconstructions in case of abrupt variations. Therefore, strategies that take the instantaneous frequency content into account should be considered.

In this context, Jensen developed in [8] a technique based on sparse data sets. Both regular (or deterministic) and completely random sequences were tested. The same group further investigated this technique in [9].
best of our knowledge, these are the only studies related to spectral velocity estimation from sparse data sets.

On the other hand, the recently introduced compressive sensing (CS) technique is able, under certain conditions, to reconstruct with high accuracy a signal from a limited number of randomly selected samples pushing the limit far below the limits of the Shannon theorem. The use of CS in medical ultrasound is extremely recent [10] [11] [12] [13] [14] [15].

The objective of this study is to investigate in detail the feasibility of compressive sensing blood flow estimation. In a recent conference paper, we provided preliminary results [16]. The only study in the literature that might be compared to our work is reported in [17]. However, the technique that we propose is quite different as we propose to reconstruct the Doppler signal segment by segment from data sets where flow and B-mode emissions are randomly interleaved. The influence of several parameters such as the window length, the sample selection rate, the overlapping coefficient, the windowing technique or the decomposition basis are studied. Moreover, our method has been tested on simulated data and experimental data. Finally, it is also compared to the results given by the method proposed by Jensen in [8].

The paper is organized as follows. Compressed sensing (CS) theory is first presented in section II. In section III, the application of CS to blood flow estimation is presented. In section IV, details on the simulations and reconstruction are given. Then in section V, the simulation results are given. In section VI, our CS-based technique is compared to the method proposed in [8]. Finally, the experimental feasibility is presented in section VII. A conclusion is given in section VIII.

II. COMPRESSIVE SENSING THEORY

Compressive sensing allows the reconstruction of a signal $f \in \mathbb{C}^n$ from a small number of random measurements $b \in \mathbb{C}^m$, $m < n$. Mathematically, the measurements $b$ are samples of the representation $y$ of $f$ in a so-called sensing orthobasis $\Phi$. Thus we have:

$$f = \Phi y$$

$$b = Ry = R\Phi^H f$$

where $R$ is an $m \times n$ full rank matrix, composed of $m$ randomly selected rows of the identity matrix. The sensing basis $\Phi$ depends on the acquisition device. For example, in MRI, $\Phi$ is the Fourier basis. For the proposed application in duplex ultrasonography, $\Phi$ will be the identity matrix.

At the heart of CS lies the assumption that $f$ has a sparse representation in a model orthonormal basis $\Psi$, i.e.:

$$f = \Psi x$$

where $x$ only has $s < m < n$ nonzero coefficients. The signal $x$ is then called $s$-sparse. CS theory [18] shows that this sparsity, combined with certain conditions on $R$, $\Phi$ and $\Psi$, allows the exact recovery of $x$ with overwhelming probability. To be more precise, the samples should be selected uniformly at random, and bases $\Phi$ and $\Psi$ should be mutually incoherent [19]. From (1), (2) and (3) we can write

$$b = Ax$$
where $A = R\Phi^H\Psi$ is an $m \times n$ full rank matrix (i.e. the $m$ rows of $A$ are independent). In these settings, the CS problem amounts to solving the underdetermined system (4) for $x$, under the constraint that $x$ is sparse. Once $x$ is estimated, the signal $f$ can be computed from (3).

For matrices $A$ satisfying the so-called restricted isometry property (RIP), Candès et al. [20] showed that the CS problem may be solved through the following $\ell_0$-minimization problem

$$P_0 : \quad \text{minimize } \|x\|_0 \quad \text{subject to } b = Ax$$

where $\|x\|_0$ counts the number of nonzero entries in $x$. Problem $P_0$ means that from all the possible solutions of (4), we seek the sparsest one. In general, solving $P_0$ is NP-hard. Suboptimal greedy algorithms attempt to solve this problem by successively adding non-zero components to a sparse approximation of $x$ (see [21]).

However, by imposing a more restrictive bound on the isometry constant, the sparsest solution of (4) can also be found by solving the following basis pursuit (BP) problem [22], [23]:

$$\text{BP}_0 : \quad \text{minimize } \|x\|_1 \quad \text{subject to } b = Ax$$

where $\|x\|_1 = \sum_{i=1}^n |x(i)|$ is the $\ell_1$-norm of $x$. The $\ell_0$-$\ell_1$ equivalence, using the RIP, was presented by Candès in [22].

The framework described above assumes that we are given exact samples of the signal to be recovered. This is seldom the case in practice, since the measurements are usually corrupted by noise, i.e.:

$$b = Ax + e$$

where $e$ represents a noise term of bounded energy $\|e\|_2 \leq \epsilon$. The original basis pursuit problem can then be recast [22] as the following basis pursuit denoising problem:

$$\text{BP}_\epsilon : \quad \text{minimize } \|x\|_1 \quad \text{subject to } \|b - Ax\|_2 \leq \epsilon$$

In practice, the signal is generally not exactly sparse but most of its coefficients in (3) are small. When most of the energy of $f$ is contained in a few coefficients of $x$, the signal is called compressible, and an approximate solution can still be found by $\text{BP}_0$ (6) or $\text{BP}_\epsilon$ (8).

### III. Application to Blood Velocity Estimation

The original Doppler signal is denoted by $y \in \mathbb{C}^N$, and its sampling frequency is $f_{prf}$. The sample selection rate, $r$, is the ratio of the number of Doppler samples retained to the total number of samples, $N$. The time saved by ignoring the other samples is used for B-mode imaging. The Doppler signal is assumed to be available in real time, which led us to this segment-by-segment reconstruction strategy, whose principle is summarized in Fig. 1.

The segments are indexed by $k$, and each segment $y_k$ has the same length $n$. The overlapping rate between two consecutive segments is called $r_{ol}$, and therefore the shift between two consecutive segments can be defined by $\delta = (1 - r_{ol})n$. The practical significance of these parameters is summarized in Fig. 2.
The efficiency of CS depends to a large extent on the way samples are selected, which must be as random as possible. Let \( s \) be a random \([rN]\)-element subset of \([1, N]\). For all \( k \in [0, k_{\text{max}}] \) where \( k_{\text{max}} \) is the maximum number of segments -1, we define
\[
\sigma_k = [k\delta + 1, k\delta + n]
\]
\[
y_k = y(\sigma_k)
\]
\[
s_k = s \cap \sigma_k
\]
\[
R_k = \left( \delta_{s_k(i), j} \right)_{i \in [1, |s_k|], j \in [1, n]} \in \mathcal{M}_{|s_k| \times n}(\{0, 1\})
\]
\[
b_k = R_k y_k
\]
where \( \delta_{\cdot, \cdot} \) is Kronecker’s delta, \(|s_k|\) is the number of elements in \( s_k \) and \( \mathcal{M}_{|s_k| \times n}(\{0, 1\}) \) is the set of \(|s_k| \times n\) matrices in \([0, 1]\). For a given \( k \), the set \( \sigma_k \) corresponds to the position in \( y \) of the samples in \( y_k \), whereas \( s_k \) corresponds to the position in \( y \) of the samples in \( b_k \). \( R_k \) is the restriction matrix such that \( b_k = R_k y_k \).

From there, we can use basis pursuit algorithms to reconstruct \( y_k \):
\[
\hat{x}_k = \arg \min_x \|x\|_1 \quad \text{s.t.} \quad R_k \Psi x = b_k
\]
\[
\hat{y}_k = \Psi \hat{x}_k
\]

After obtaining all the \( \hat{y}_k \) comes the recombination step, which consists in reconstructing the full complex signal \( y \) out of the reconstructed segments. To do so, each \( \hat{y}_k \) is first multiplied by a window function \( w \in \mathbb{R}^n \), then shifted by \( k\delta \) samples to the right. The full reconstructed signal \( \hat{y} \) is obtained by adding all the shifted, windowed \( \hat{y}_k \) and demodulating the result, i.e. compensating for the modulation caused by the windowing and overlapping of the \( \hat{y}_k \).

Thus, for all \( i \in [1, N] \) we have
\[
\mu(i) = \sum_{k=0}^{k_{\text{max}}} w(i - k\delta)
\]
\[
\hat{y}(i) = \frac{1}{\mu(i)} \sum_{k=0}^{k_{\text{max}}} \hat{y}_k(i - k\delta) \cdot w(i - k\delta)
\]
The windowing can help prevent the appearance of discontinuities at the beginning and end of each segment in the reconstructed signal, which, in the audio domain, corresponds to regularly spaced small clicks and generally to a lower SNR (see section V-D).

IV. EXPERIMENTAL SETTINGS

A. Simulated Doppler data

Using the FIELD II program [24], and the example given at [25] we simulated the blood flow in a femoral artery. First the scatterers contained in an artery of radius 4.2 mm are generated. It consists of a list of random coordinates spatially uniformly distributed and a list of random amplitudes following a Gaussian distribution. Then, the scatterers are moved in order to obtain their position at each time instance according to the Womersley model.
The PRF was set to 5 kHz for a mean velocity of 0.15 m/s and a beam/flow angle of 60°. The 128-element probe had a centre frequency of 3.5 MHz. The complete setup of the simulation as well as the complete simulation code can be found at [25]. We focus on the reconstruction of a Doppler signal that corresponds to a complete cardiac cycle of about 1 s. The resulting pw-spectrogram is presented in Figure 3.

### B. Reconstruction frames

As mentioned in section II, the quality of the reconstruction depends on the sparsity of its representation in the model basis $\Psi$. Doppler signals raise a specific challenge, since they do not easily lend themselves to a sparse
representation. We compare herein two models that have already been applied to CS in ultrasound images: the Fourier basis and the directional wave atoms tight frame [10] (see Figure 4). Wave atoms can be seen as an extension of the standard wavelets. We have experimentally verified the ability of these two transforms to make the corresponding Doppler signal sparse. From a simulation of blood flow in a femoral artery, Figure 5 illustrates the sparse property of the resulting Doppler signal expressed both in the Fourier and wave atom domain. It was noted that in this particular case, wave atoms appeared to be a slightly better model than the Fourier basis.

C. Test protocol

Our objective is to evaluate the performance of the method by acting on the following parameters:

![Sorted DFT (dashed line) and Wave atoms (solid line) coefficients' normalized magnitude computed from a doppler signal corresponding to a simulation of blood flow in a femoral artery](image)
<table>
<thead>
<tr>
<th>Default value</th>
<th>Tested values</th>
</tr>
</thead>
<tbody>
<tr>
<td>$r$</td>
<td>0.6</td>
</tr>
<tr>
<td>$n$</td>
<td>$2^8$</td>
</tr>
<tr>
<td>$r_{ol}$</td>
<td>0.5</td>
</tr>
<tr>
<td>$w$</td>
<td>Hanning</td>
</tr>
<tr>
<td>$\Psi$</td>
<td>DFT</td>
</tr>
</tbody>
</table>

We measure the influence of the first three parameters separately, by making one of them vary within the range specified in the “Tested values” column, while the other two other are set to their default value.

As CS is based on random sampling, the reconstruction quality may vary depending on the sample set retained from the original data. To allow statistical analysis, for each parameter setting, the simulation is repeated using $n_{rep} = 50$ independent random sampling sets.

**D. Measurements**

To measure the quality of the reconstructions for a given parameter set $(r, n, r_{ol}, \Psi, w)$, we use the average SNR, defined as

$$\text{SNR} = -20 \cdot \log \left( \frac{\|\hat{y} - y\|_2}{\|y\|_2} \right)$$

where $\langle \cdot \rangle$ represents an averaging over the $n_{rep}$ repetitions.

Pw-spectrograms and direct listening of the reconstructed signals are also used to determine the quality of our method. For a given parameter setting, the reconstructed signal that is chosen among the $n_{rep}$ results to compute the pw-spectrogram is the one that corresponds to the median SNR.

**E. Reconstruction algorithm**

The calculation of each $\hat{x}_k$ by solving (14) is carried out by an iterative algorithm taken from YALL1, a solver developed by Zhang et al. [26], [27] based on the alternating direction method.

As the Doppler signal should be available to the diagnostician in real time, the computational time required by YALL1 to reconstruct each segment needs to be controlled. Using the default stopping criteria unfortunately leads to very heterogeneous computational times depending on the parameters we use. Therefore, we decided to implement the real-time calculation constraint by modifying the reconstructing algorithm. Thus, for each segment reconstruction, the maximum time allowed in the main loop of the algorithm is set to $\delta/f_{prf}$.

The drawback of our method is that for the most demanding cases, i.e. for high values of either $r$, $n$, or $r_{ol}$, the segment reconstruction algorithm may be interrupted before it converges to the solution. In general, the SNR stabilizes after 10 to 20 iterations.

The calculations were performed with Matlab running on a single core of an Intel xeon quad-core L5430 at 2.66 GHz.
V. SIMULATION RESULTS

A. Influence of the sample selection rate

We first evaluate the influence of the sample selection rate $r$ on performance by making it vary from 0.1 to 0.9, while the other parameters are set to their default values. As shown in Figures 6, 7 and 8, $r$ is a determining factor for the quality of the reconstruction. Figure 6 shows typical variations of the SNR for each value of $r$. Figure 7(a) displays the SNR and Figure 7(b) gives the average number of iterations per segment, both as a function of $r$. Figure 7(a) shows that the SNR logically increases with the number of samples $r$ whatever the selected signal representation and that the DFT applied with a Hanning window provides a slightly higher SNR at higher $r$. Figure 7(b) indicates that the number of iterations decreases with $r$ while remaining above the 10 to 20 limit mentioned in section IV-E, so it is not a limiting factor here. The decay of the number of iterations per segment comes from the fact that the average number of rows in $R_k$ is directly proportional to $r$, which means each iteration requires more computing time. Lastly, the pw-spectrograms shown in Figure 8 confirm that the less sparse portions of the signal require more samples to be recovered accurately. Indeed, whereas the last two-thirds of the cardiac cycle are still accurately recovered for $r = 0.2$, the first third, which has a much broader spectrum, becomes seriously corrupted by reconstruction noise at $r = 0.4$ and is hardly legible at $r = 0.2$.

Figures 9 and 10 show the pw-spectrograms obtained from linear interpolation of downsampled data as well as
Figure 8. Typical pw-spectrograms of DFT-based reconstructions for various values of \( r \). \( (n = 256, r_{ol} = 0.5, w = \text{Hanning}) \)

Figure 9. Pw-spectrograms obtained from linear interpolation of randomly downsampled data.

Figure 10. Comparison of the average SNR obtained from compressive sensing and linear interpolation.

the comparison in terms of SNR between this approach and the compressive sensing based approach proposed. The great benefit of compressive sensing in terms of pw-spectrograms and SNR is clearly highlighted.
Figure 11. Influence of $n$ on (a) the SNR and (b) the number of iterations per segment.

B. Influence of the segment length

The choice of the segment length when using the DFT essentially amounts to finding a compromise between time and frequency resolution. If $n$ is too large, the blood flow may vary too much within the time frame corresponding to one segment, thus leading to a less sparse spectra and therefore to more reconstruction noise. On the other hand, if the segments contain too few samples, the frequency components of the signal cannot be recovered accurately. Figure 11 shows that 256 is the optimal value for $n$ when using the DFT. The SNR is affected by our real-time constraint only for $n \geq 1024$, so poor time resolution is the only factor explaining the SNR drop at $n = 512$.

The situation is different for wave atoms, since they are already localized in both frequency and time. The only factor that affects the SNR for large values of $n$ is the number of iterations per segment, which is smaller due to the fact that $\Psi$ is $n \times 2n$ for wave atoms, when it is only $n \times n$ for the DFT. The larger computation time needed for each iteration using wave atoms leads to a reduced allowed number of iterations per segment in order to meet the real time conditions. With segments lengths greater than or equal to 512 the number of iterations per segments drops dramatically and so does the SNR. As a consequence, the optimal segment length for real-time reconstruction on our computing platform is $n = 256$ for wave atoms as well as for the DFT.

C. Influence of the overlapping rate

A higher overlapping rate means that more segments $\hat{y}_k$ contribute to the determination of the same sample, which statistically leads to a lower reconstruction error. Figure 12 shows that using overlapping segments can bring up to a 4 dB increase in the SNR.

However, the overlapping rate should not be too close to 1, as the time allowed for each segment reconstruction, and therefore the number of iterations per segment is directly proportional to $1 - r_{ol}$ (see Fig. 12.b).

D. Influence of windowing

As explained in section III, windowing the $\hat{y}_k$ with a Hanning window before recombining them helps minimize the overall reconstruction noise. Figure 7.a reveals that while the gain brought by windowing remains marginal in
most cases, it can become quite significant for high values of \( r \). This is particularly the case with wave atoms, with a 1 to 10 dB increase in the SNR when \( 0.6 \leq r \leq 0.9 \). This can also be observed in Figure 12 which shows that, especially in the case of wave atoms, for \( r = 0.6 \) and \( n = 256 \), there is a difference around 1 dB for most \( r_{\text{col}} \) values. There is no reason not to use windowing since its computational cost is virtually nonexistent.

### E. Influence of the transform choice

Figure 7 shows that from our default setting \((n = 256, r_{\text{col}} = 0.5, w = \text{Hanning})\), the use of wave atoms brings an additional 1 to 10 dB to the SNR, the gain being greater when \( r \) is high. As a consequence, the amount of noise in the pw-spectrograms shown in Figure 13 is lower than the one observed in Figure 8. Note that the reconstruction noise is of a different nature: a single miscalculated wave atom coefficient affects a broader range of frequencies but only a few samples of the segment in the time domain.

While wave atoms yield a better SNR, Figures 7.b, 11.b and 12.b show that the number of iterations per segment is always significantly higher with the DFT, because wave atoms form a redundant frame with redundancy 2, which means that \( \Psi \) has twice as many columns as when the DFT is used, thus increasing the computing time needed by each iteration. Therefore, reconstruction using wave atoms is more prone to limitations due to the real-time constraint when using high values of \( r, n, r_{\text{col}} \) or any combination of these.

### F. Delay between signal acquisition and reconstruction

Consider a segment \( y_k \) whose first and last sample correspond to Doppler emissions. Before even starting its reconstruction, all Doppler samples within the segment must be acquired. This means that the first sample of the reconstructed segment \( \hat{y}_k \) cannot be obtained before the last sample of \( y_k \) is acquired. This implies an incompressible delay between the acquisition and the reconstruction of the Doppler signal that is equal to \((n - 1)/f_{\text{prf}}\). In our default setting, this corresponds to a 50 ms delay, which is barely perceptible in real time, but we should keep this issue in mind when \( f_{\text{prf}} \) is low or when considering increasing \( n \).

In addition to the delay due to the acquisition, we must also take into account the time needed for the reconstruction
Figure 13. Typical pw-spectrograms of wave-atom-based reconstructions for various values of \( r \). \( n = 256, r_{ol} = 0.5, w = \text{Hanning} \)

itself, which equals \( \delta/f_{prf} \) in the case of real-time reconstruction. In our default setting, this corresponds to an additional delay of 25.6 ms.

G. Dynamic adaptation of the sample selection rate

As can be seen in Figures 8 and 13, the quality of the reconstructed signal is not uniform over the entire cardiac cycle. Less compressible segments, i.e. segments that have a broad spectrum, require more samples to be recovered with a certain level of accuracy. The idea we develop in this section is to dynamically adapt the sample selection rate \( r \) in order to equalize the reconstruction noise over the whole cycle. This involves predicting the sparsity of the segment being acquired, which could be done, for example, by using information from the last reconstructed segment, assuming the blood flow can be considered stationary over a period of time equal to \( \delta/f_{prf} \). However, our goal in this section is not to define how to adapt \( r \) in concrete terms, but to evaluate the potential gain that could result from this adaptation.

To do so, we first compute the mean squared error of the reconstructed signal as a function of \( r \) and time (the resulting plot is given in Figure 14). This is done by running our reconstruction algorithm for \( r = 0.01, 0.02, \ldots, 0.99 \) with \( n = 256, r_{ol} = 0.5, w = \text{Hanning}, \Psi = \text{DFT}, n_{rep} = 50 \). The mean squared error (MSE) at sample \( i \) is computed as follows:

\[
\text{MSE}(r, i) = \frac{1}{1 + j_{\text{max}}(i) - j_{\text{min}}(i)} \sum_{j = j_{\text{min}}(i)}^{j_{\text{max}}(i)} (\hat{y}(r, j) - y(j))^2/n_{rep}
\]

with \( j_{\text{min}}(i) = \max(0, i - n/4) \) and \( j_{\text{max}}(i) = \min(N, i + n/4) \).

Since the error decreases as \( r \) increases, we can easily compute the isoline of the MSE that corresponds to the desired average sample selection rate \( \bar{r} \). We represent this isoline by the function \( \rho_{\bar{r}}(i) \). Figure 15 shows these isolines for \( \bar{r} = 0.1, 0.2, \ldots, 0.9 \). Then we update our random sampling function so that for all \( i \), sample \( i \) has probability \( \rho_{\bar{r}}(i) \) of being a Doppler emission.

Figure 16 shows pw-spectrograms resulting from reconstructions based on this new sampling function. The reconstruction noise is now more uniformly distributed over time, thus leading to a much better average SNR, as shown in Figure 17, with a gain close to 10 dB for a wide range of sample selection rates.
The drawback of this method is that the framerate for the B-mode might be significantly different between diastole and systole. For example to maintain the isoline $\bar{r} = 0.5$ the instantaneous $r$ varies between 0.3 and 0.8. However, the method could easily be modified to take into account the specification of a minimum framerate, at the cost of more noise in the reconstructed Doppler signal.

Figure 14. Mean squared error as a function of $r$ and $i$ ($n = 256$, $r_{ol} = 0.5$, $w = \text{Hanning}$, $\Psi = \text{DFT}$).

Figure 15. Isolines of the MSE for $\bar{r} \in 0.1, 0.2, \ldots, 0.9$ ($n = 256$, $r_{ol} = 0.5$, $w = \text{Hanning}$, $\Psi = \text{DFT}$).

Figure 16. Typical pw-spectrograms obtained with adaptive sample selection rates ($n = 256$, $r_{ol} = 0.5$, $w = \text{Hanning}$, $\Psi = \text{DFT}$).
VI. COMPARISON WITH OTHER STUDIES

An additional study reporting spectral velocity estimation from sparse data sets is given in [8]. In this study, two kinds of sparse data sequences are used, regular (or deterministic) and fully random sequences. In both approaches, the aim is to spare some time to be able, for example, to interleave B-mode acquisitions between the velocity emissions. This leads to different sample selection rates.

The audio files corresponding to the study in [8] are available online [28]. From these audio files it is possible to reconstruct the corresponding pw-spectrograms. In Figure 18, the pw-spectrogram corresponding to the reference audio signal is given as well as the ones corresponding to one fully random and two deterministic sequences from [8]. These pw-spectrograms are compared to the ones given by our compressive sensing-based technique with the same sampling rates.

The settings for our technique were \( n = 256, r_{ol} = 0.5, w = \text{Hanning}, \Psi = \text{DFT} \). From this figure we can conclude that depending on the situation, the results of our technique are at least equivalent or even better, for example, in the comparison between the fully random sequence at a sample selection rate of 0.6.

VII. RESULTS FROM AN IN VIVO EXPERIMENTAL DATA SET

Finally, we propose to test this technique on experimental in vivo data acquisitions. This experimental validation has been conducted in two steps. First, the acquisition was performed using a conventional approach, i.e. all Doppler RF lines were acquired in a row at a sufficient PRF. Then, samples were removed randomly at different sample selection rate in order to imitate the CS acquisition. This was done in order to have a reference signal to compare our reconstruction with and evaluate quantitatively our technique as described in section VII-A. Second an acquisition performing the described CS scheme, i.e. doing randomly Doppler or B-mode acquisitions has been performed. The objective of this second experiment was to test if the random interleaving of B-mode and Doppler acquisition influences our technique as described in section VII-B.

The data were acquired using the advanced open platform for ultrasound research, Ula-Op, described by Tortoli et al. in [29]. For the second series of acquisitions the system needed to be configured in a very specific manner
Figure 18. Comparison between Jensen’s results and the reconstructions using compressive sensing at an equivalent sample selection rate. The first top pw-spectrogram is the reference. And then in the left column auto_bd_3_3 means 3 B-mode acquisitions followed by 3 Doppler acquisitions. auto_bd_1_2 means 1 B-mode acquisition followed by 2 Doppler acquisitions. auto_random_pb_0_4 means a random distribution of Doppler and B-mode acquisitions in which 40% of the acquisition are B-mode acquisitions. The right column represents the results obtained with our proposed technique.

in order to enable to switch randomly between Doppler and B-mode as described in VII-B.

A. First in vivo experimental data set with ground truth

The femoral artery of a 23 year old male healthy volunteer was scanned at $f_{prf} = 5$ kHz using a L523 linear array from Esaote (Esaote Spa, Genoa, Italy).

Figure 19 shows the original pw-spectrogram as well as a study of the influence of the different parameters on the SNR. Figure 19(b) shows the SNR as a function of $r$ values for the different reconstruction bases and windowing strategies. Obviously, the SNR increases for higher $r$ values. The four different combinations of reconstruction bases and windowing give equivalent results. Figure 19(c) shows the influence of the window length $n$. Consistent with the simulations, an optimum is found around $n = 256$. Figure 19(d) shows the influence of the window overlapping $r_{ol}$. As in the simulations, higher $r_{ol}$ values increase the SNR slightly. However, the range of SNR values does not vary much (between 11 and 12.5). Moreover, it is important to keep this parameter not too high in order to allow enough time for each segment reconstruction.

Figure 20 shows the pw-spectrograms obtained for different $r$ values (0.8, 0.6, 0.4 and 0.2). The other parameters are set to $n = 256$, $r_{ol} = 0.5$, $w$ = Hanning, $\Psi$ = DFT. The degradation of the visual aspect of the pw-spectrogram...
Figure 19. In vivo results from a femoral artery acquired with the Ula-Op system. Influence of the different parameters on the SNR. (a) Original pw-spectrogram (b) SNR as a function of $r$, (c) SNR as a function of $n$, and (d) SNR as a function of $r_{ol}$

is obvious for decreasing values of $r$. Nevertheless, the ability of the compressed sensing technique proposed to reconstruct experimental pw-spectrograms is demonstrated. Indeed, the shape of the pw-spectrograms, both in terms of maximum frequency value and spectrum broadening, can be recovered down to $r=0.4$ with an SNR higher than 8.5 dB. Again, the parts of the pw-spectrogram where the spectrum is the widest show the strongest deviation compared to the original pw-spectrogram. This is the place where the signal has a less sparse representation in the transform domain, hence the poor reconstruction. The technique would benefit from an adaptive sampling rate in order to further optimize it, as illustrated on simulated data in section V-G.

B. Second in vivo experimental data set with real random acquisitions interleaving

In this second series of acquisitions, the objective was to validate qualitatively that the random switching between Doppler and B-mode acquisitions does not influence too much our technique. Indeed, in a conventional Doppler acquisition, the received echo signal will contain clutter from vessel wall and other structures with multiple reflections. These echoes will have a long reverberation time after each pulse transmission; usually much longer than the time between each pulse transmission. The range Doppler signal will therefore pick up clutter from several consecutive pulses. This is not a problem when the pulses are transmitted with a constant time interval; after a few pulses, the clutter signal will become stationary, and can be removed by a high pass filter. However, if one pulse is left out, the clutter signal will suddenly change, giving a wideband clutter noise which can not be removed by the highpass filter.
To test this, it has been necessary to modify the acquisition procedure of the Ula-Op scanner. Unfortunately it is not possible to have complete random acquisitions. The Ula-Op can be configured with random pattern of interleaved B-mode and Doppler acquisitions that is 32 pulse repetitions (32 x 1/PRF) long. This pattern is then repeated again and again. As a result we have generated a random pattern using Matlab corresponding to a 0.6 sample selection rate. 19 random Doppler acquisitions were interleaved with 13 B-mode acquisitions. It can be reasonably considered that after 32 pulse repetitions the reverberation of the first pulse does not influence the new pulse anymore and this scheme reproduces fairly the proposed scanning procedure.

The experiment was conducted on a 34 years-old healthy male volunteer at a basis PRF of 7 kHz. The reconstructed pw-spectrogram using parameters is given in Figure 21. Here the quantitative evaluation of the result is not possible, but the visual inspection let us believe that our technique is not significantly affected by a real random acquisition scheme.

In order to give the reader an idea of the level of signal from blood, clutter and noise, the data from the acquisition presented in Figure 21, denoted $s_{21}(t)$ as well as an acquisition done with the probe in the air, denoted $s_{air}(t)$, were used as follows. The signal $s_{air}(t)$ was used to calculate the power of thermal noise $P_{noise}$. As most of the clutter signal is lying in the low frequencies a "clutter signal" $s_{clut}(t)$ was obtained from $s_{21}(t)$ as the output of a second order lowpass Butterworth filter of cutoff frequency 60 Hz. The mean power of $s_{clut}(t)$ was denoted $P_{clut}$. The mean power of the blood signal $P_{blood}$ was obtained as the difference between the power of the complete signal minus $P_{clut}$. The clutter-to-blood ratio calculated from those signals was equal to 22.6 dB and the signal-to-noise ratio was equal to 7.1 dB. A more rigorous experimental investigation of clutter could be performed using the method given in [30].

**VIII. DISCUSSION AND CONCLUSION**

In this paper, we have proposed an ultrasound technique for blood flow estimation based on compressive sensing. The technique proposed has potential application in duplex, triplex or quadroplex modes, where the acquisition time...
Figure 21. Pw-spectrogram obtained with real random acquisition scheme

needs to be shared for the different modes. The proposed technique shows improved results compared to linear interpolation. With this approach, at least equivalent results (or even better depending on the configuration) to the method proposed in [8] are also achievable.

As the compressive sensing technique relies on the assumption that the signal is sparse in a given decomposition basis, the situations where this assumption is respected provide the best estimation. This is one reason why the pw-spectrograms are better reconstructed with the Fourier basis when the velocity range is narrow. Whereas when the velocities are distributed over a wide band of values, the error is greater. In the simulations, this makes the last two-thirds of the pw-spectrogram well reconstructed for \( r \) values down to 0.2, whereas the first third of the pw-spectrogram is strongly corrupted by reconstruction noise for values lower than 0.4. Also, in our experimental measurements the wave atoms tight frame and the Fourier basis lead to equivalent results since the quantity of significant coefficients in the decomposition basis is very similar.

In practice, we have shown that there is an optimal segment length. In our configuration, this length was equal to 256 samples, for both the simulations and the experimental data sets. Concerning the sample rate selection, the optimal value is a compromise between quality of reconstruction and time that must be saved for B-mode or CFM acquisitions. As shown in section V-G the method would greatly benefit from an automatic calculation of the sample selection rate. The development of such a technique is not within the scope of this paper and will be the subject of future research. Other future developments will also attempt to find a decomposition basis where the data have a sparser representation than in the two tested bases, namely Fourier and wave atoms. Finally we will need to investigate more quantitatively the influence of the clutter level doing for example simulations as proposed in [31].

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