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# Motion compensation for the estimation of high-resolution blood flow in ultrafast ultrasound imaging

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## ABSTRACT

In this paper, we address the problem of tissue motion compensation in blood flow estimation from ultrafast Doppler sequences. The goal is to improve the estimation of tumor contours, offering neurosurgeons better visualization and thereby leading them to make better decisions while performing brain surgery. Estimating these contours can be done by solving the problem of separation of blood flow and tissue in ultrasound images. To solve this problem, we focus on a recently developed variant of the Robust Principal Component Analysis (RPCA)-based method by embedding a deconvolution step into the algorithm in order to improve the resolution of the reconstructed blood flow. However, this approach is prone to failure in the presence of tissue motion. In this work, we propose to overcome this limitation by incorporating a motion compensation step into the above RPCA-based method. We implement and quantitatively compare motion compensation algorithms based on the Lucas-Kanade and Demon registration methods on simulation data. In addition, preliminary results are obtained on *in vivo* data. We show that a motion compensation step allows to improve the perception of thin vascular vessels and to reduce the amount of noise on the estimated flow.

**Keywords:** Ultrafast ultrasound, Doppler, Robust PCA, Blood flow, Demon registration, Lucas Kanade, Motion compensation

## 1. INTRODUCTION

Brain surgery is the systemic treatment of brain cancers. To remove tumor more efficiently, one of the most widely used methods is to determine the boundary between the tumor and other healthy tissues. We rely on the fact that tumors induce a strong vascularization in their environment which leads to a strong presence of blood flow around the tumor. Thus, a common approach is to evaluate the tumor area by estimating the blood flow on the ultrasound images. In this work, we propose a high sensitivity and high resolution blood flow extraction technique from ultrafast ultrasound sequences.

To obtain an estimate of blood flow, we must separate the flow from the surrounding tissues. For this purpose, the SVD technique has been widely used [1]. It consists in decomposing the acquired spatio-temporal matrix of the ultrasound slices into singular values and vectors. The singular values are then sorted and thresholded to separate the blood flow from the surrounding tissues and noise. This is a fast and efficient technique, but it requires empirical adjustment of some parameters. This often leads to insufficient separation results which make this technique difficult to use in practice.

To address these shortcomings of the SVD, the RPCA method (or its variants), which allows to consider a physical model of the data, has been investigated (see in e.g. [2,3] and references therein). These methods have been reformulated as an inverse problem which is solved by using the alternating direction method of multipliers (ADMM) framework. Subsequently, a deconvolution step was integrated based on the knowledge of the system point spread function (PSF), that is experimentally measured or estimated jointly with the blood flow (non-blind or blind-deconvolved respectively), to improve the resolution of the reconstructed blood flows [2,3].

Despite their interest, all these methods rely on the assumption that the tissue surrounding the blood is motionless. Thus, tissue movements induced by cardiac pulsatility, patient breathing, ultrasound probe, etc. during the data acquisition are not considered by these algorithms. This consequently leads to an inaccurate estimation in many cases. In this work, we propose to take into account the tissue motion by adding a motion compensation step to the RPCA-based algorithm. The desired result is a precise visualization of underlying vascular networks with a level of flow detection that allows the identification of tumor contours.

## 2. BACKGROUND

### 2.1 Robust Principal Component Analysis (RPCA)

To estimate the blood flow, an ultrafast in phase and quadrature (IQ) Doppler sequence is acquired. It consists of  $N_t$  frames of size  $N_x \times N_z$ , with  $N_z$  the depth,  $N_x$  the probe width and  $N_t$  the acquisition time. The first step is to reshape the ultrafast Doppler acquisition into a 2D space-time matrix, known as the Casorati matrix [3, 4]. The model for the separation between the blood flow and the surrounding tissues is the following:

$$C = S + T + N, \quad (1)$$

where  $C$  is the Casorati matrix and where  $S$ ,  $T$  and  $N$  are the Doppler blood flow, tissue and noise matrices respectively. In the general case where the tissue is assumed to be motionless,  $T$  is of low rank and is thus caught by the nuclear norm. The blood is considered to be present in relatively thin, limited in number vessels,  $S$  is thus sparse and is promoted by the l1 norm.  $N$  is assumed to be an additive Gaussian noise.

The RPCA algorithm consists in resolving an inverse problem in which the estimate of  $S$  and  $T$ , i.e.  $(\hat{S}, \hat{T})$  can be formulated as:

$$[\hat{S}, \hat{T}] = \arg \min_{S, T} \|C - S - T\|_F^2 + \lambda \|S\|_1 + \rho \|T\|_* , \quad (2)$$

where  $\lambda, \rho > 0$  are two hyperparameters balancing the trade-off between blood sparsity and tissue low rank.  $\|\cdot\|_F^2$  is the Frobenius norm,  $\|\cdot\|_1$  is the l1 norm and  $\|\cdot\|_*$  is the nuclear norm.

### 2.2 Bind-Deconvolved Robust Principal Component Analysis (BD-RPCA)

The Bind-Deconvolved Robust Principal Component Analysis (BD-RPCA) algorithm integrates a deconvolution step using the point spread function (PSF) which is estimated using a 2D blind convolution method in [5], concurrently with the high-resolution blood flow [3]. Within this method, in order to improve the computational speed, we assume that the PSF is a block circulant with circulant block (BCCB) matrix. More precisely, for an ultrasound image degraded by a PSF:

$$S = HX, \quad (3)$$

where the low-resolution blood flow  $S$  is the matrix product between  $H$  - the matrix in BCCB form of the measured PSF and  $X$  - the high-resolution blood component to be estimated. So far,  $X$  has been estimated under the assumption that the tissue is motionless. Thus, to further improve the resolution of the blood estimation, we propose to take into account the movements of the tissue. This problem was also considered in [4] and [6] with either inaccurate or complex methods. Let  $M$  be the joint movement of tissue and blood, the new proposed model, more realistic, is the following:

$$C = M(HX + T) + N. \quad (4)$$

## 3. PROPOSED METHOD

### 3.1 Motion compensation

The standard procedure for estimating the movement is to have a separate processing phase dedicated to motion correction. There are two strategies to take into account the tissue motion. The first one is to estimate the apparent motion. The second one is to consider the motion compensation as a problem of non-rigid image registration. This paper is a preliminary work which folds in the later strategy. We embed a classical registration (Demon registration) [7] step in the RPCA-based method. We compare this method to techniques folding in the first strategy, namely an explicit motion estimation prior to the blood separation. For this purpose, we consider a motion estimation based on an optical flow approach, namely the Pyramidal Lucas-Kanade algorithm [8]. Finally,

we also compare these approaches to the algorithm proposed in [6], which includes a background-foreground separation of the estimated motion using a stable principal component pursuit (SPCP) algorithm.

Demon registration is an image registration algorithm in which the estimated motion field is regularized by Gaussian filtering in order to find a smooth solution. Each iteration of the Demon registration algorithm start by computing a displacement field  $V$  which is calculated based on the optical flow equations:

$$V_x = \frac{-(I_{\text{ref}} - I_{\text{mov}})\nabla_x I_{\text{ref}}}{[(\nabla_x I_{\text{ref}})^2 + (\nabla_y I_{\text{ref}})^2] + (I_{\text{ref}} - I_{\text{mov}})^2 + \epsilon}, \quad (5)$$

$$V_y = \frac{-(I_{\text{ref}} - I_{\text{mov}})\nabla_y I_{\text{ref}}}{[(\nabla_x I_{\text{ref}})^2 + (\nabla_y I_{\text{ref}})^2] + (I_{\text{ref}} - I_{\text{mov}})^2 + \epsilon}, \quad (6)$$

where  $V_x$  and  $V_y$  represent respectively the horizontal and vertical components of the displacement field  $V$ ,  $I_{\text{ref}}$  is the reference image,  $I_{\text{mov}}$  is the image whose motion is to be compensated,  $\nabla$  corresponds to the matrix gradient operator ( $\nabla_x$  thus refers to the horizontal component of the gradient),  $\epsilon$  is a term that prevents divisions by zero. At each iteration, an inter-images displacement field is computed, this field is regularized and then the image is registered. The final displacement field between two images is thus the sum of the displacement fields found at each iteration. This is a very fast algorithm, but it works on an empirical basis, there is no guarantee of convergence. In this study we used the pyramidal version (multi-scale registration) of Demon registration.

### 3.2 Simulation data

To evaluate these motion compensation algorithms, we use realistic simulation data mimicking typical speckle patterns (See Fig. 1). The use of a simulation is motivated by the accessibility to the ground truth of the motion fields. A flow is simulated in two rectangles of size  $12 \times 70$  and  $10 \times 35$  pixels respectively. The motion in these two rectangles is generated using the circshift function of Matlab which produces a uniform and constant movement in the chosen direction. Finally, the resulting image sequence is convoluted with an experimentally measured PSF. This results in 400 images of size  $451 \times 161$  pixels that have the same static tissue and two rectangles of blood flow animated with motion. For all the images except the first one, a homogeneous, B-spline displacement field is applied. This represents a weak displacement field with random directions. The amplitude of the displacements does not exceed one pixel. This is a realistic movement for the tissue (in the context of an inter-frame difference for ultra-fast imaging) that can be appraised visually but which does not represent in an exhaustive way the movements that can occur (in particular the large movements).

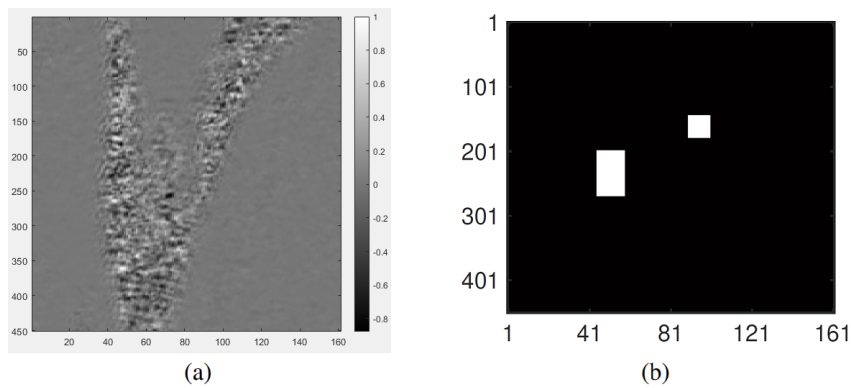


Figure 1. (a) B mode of simulated data and (b) blood flow ground truth.

### 3.3 Performance assessment

We chose to use the endpoint error (EE) to assess the different algorithms. This error has an interesting physical meaning for our problem, as it can be seen as an approximation of the percentage of the motion that has not been compensated. The EE corresponds to the Euclidean distance between the estimated displacement and its ground truth. In order to be able to compare the EE for different pairs of images, the EE is normalized by the ground truth of the displacement, then the normalized EE is averaged over all displacements in the motion field. Thus, we define the average value of the normalized endpoint error (Avg. nEE) as :

$$\text{Avg. nEE} = \frac{1}{N_i N_j} \sum_{i,j=1}^{N_i, N_j} \frac{[(U_{\text{GT}}(i, j) - \hat{U}(i, j))^2 + (V_{\text{GT}}(i, j) - \hat{V}(i, j))^2]^{\frac{1}{2}}}{[U_{\text{GT}}(i, j)^2 + V_{\text{GT}}(i, j)^2]^{\frac{1}{2}}}, \quad (7)$$

where  $U_{\text{GT}}$  and  $V_{\text{GT}}$  are respectively the matrices of ground truth for the horizontal and vertical parts of the motion field,  $\hat{U}$  and  $\hat{V}$  are respectively the matrices of the horizontal and vertical part of the estimated motion field,  $N_i$  and  $N_j$  are respectively the numbers of rows and columns of the considered matrices. In the following, to compare the motion compensation algorithms, we use the average value of Avg. nEE computed on the sequence of images. More precisely, the first image of the sequence will serve as the reference image, the other images of the sequence will have their motion compensated with respect to the first image. We will compare each estimated displacement field with the corresponding ground truth by calculating the value of Avg. nEE. In order to eliminate the statistical variance of the result, we will take the average of all Avg. nEE. It is this average value that will quantify the quality of the motion compensation obtained by the algorithm considered. From this point, when we speak of Avg. nEE it is implied that it is the average Avg. nEE calculated on all the computed motion fields for the simulated sequence.

## 4. RESULTS

### 4.1 Simulation results

#### 4.1.1 Movement estimation

There is a major challenge in the compensation of the joint movement of the tissue and the blood flow. In addition to this joint motion, the blood flow possesses its own motion and it is partly this motion that allows the separation of blood flow from tissues by the PCA methods. Indeed, the motion of the blood will reduce its spatio-temporal coherence thus reducing the chances of the flow being classified as tissues by the algorithm. Assuming that the motion compensation step has compensated for both the joint motion and the motion of the flow, then it is likely to have damaged the separability between the tissue and the blood flow. Thus, the objective will be to only compensate the joint motion which is represented by  $M$  in the equation (4). Therefore, the ground truth of the motion does not include the motion of the simulated flow but only contains the homogeneous motion field added after the convolution.

Table 1. Assessment of the studied motion compensation algorithms

	Avg. nEE	Time (s)
Demon registration	0.42	40
Pyramidal Lucas-Kanade + SPCP	0.57	189
Pyramidal Lucas-Kanade	0.68	26

The results of movement compensation are presented in Tab. 1. The Time corresponds to the execution time of the motion estimation algorithm is seconds for the whole simulation sequence (399 images). The observation of the motion fields generated by the Pyramidal Lucas-Kanade algorithm shows that it suffers from the defect of compensating the motion of the blood flow. The solution presented in the literature is to add a foreground/background separation step on the motion field (we refer to the complete algorithm as Pyramidal

Lucas-Kanade + SPCP) in order to avoid compensating for the proper motion of the flow. Pyramidal Lucas-Kanade + SPCP gives significantly better results by obtaining an Avg. nEE of 0.57 but at the same time this change significantly increases the execution time of the algorithm. The most interesting result is obtained by the Demon registration algorithm with an Avg. nEE equal to 0.42 obtained after only 40 seconds of computation. Almost 60% of the motion has been compensated which is rather satisfactory. Note that we tried to add foreground/background separation technique to Demon registration, but we did not see any improvement in the Avg. NEE.

#### 4.1.2 Blood flow estimation

We compare the BD-RPCA and registration to the other techniques. The results of Power Doppler estimation (PD) are depicted in Fig. 2. Fig. 2(a) is the PD obtained by BD-RPCA without motion correction; Fig. 2(b) is the PD by Pyramidal Lucas-Kanade; Fig. 2(c) is the PD by Pyramidal Lucas-Kanade with SPCP [6]; Fig. 2(d) is the PD by BD-RPCA with Demon registration.

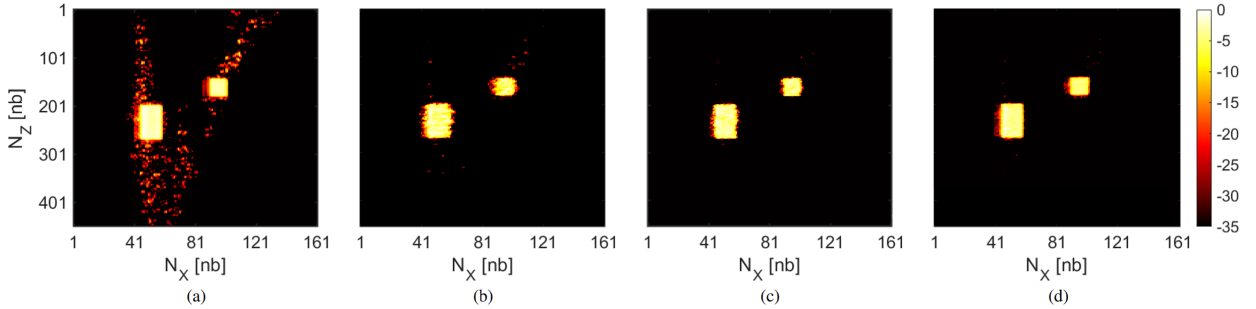


Figure 2. Power Doppler estimated by BD-RPCA: without motion correction (a); with Pyramidal Lucas-Kanade (b); with Pyramidal Lucas-Kanade and SPCP (c); with Demon registration (d).

One can see that the three motion compensation methods significantly reduce the number of false positives (resulting from the tissue motion) in the flow estimation. However, there are still residual, and the estimated flow still has significant blurs at its edges. Although the three methods give similar noise reduction, the blood flow estimated with Demon registration presents considerably sharper edges. From this point of view, the result obtained with the method presented in [6] is also better than the one estimated by Pyramidal Lucas-Kanade.

Table 2. Assessment of the flow estimation

	NRMSE	PSNR (dB)
No correction (control sample)	0.0755	22.4436
Demon registration	0.0512	25.8122
Pyramidal Lucas-Kanade + SPCP	0.0639	23.9261
Pyramidal Lucas-Kanade	0.0658	23.6408

The ground truth allows us to quantitatively compare the results using the normalized root mean square error (NRMSE) and the peak signal-to-noise ratio (PSNR) as defined in [3]. The results reported in Tab. 2 are very consistent with what we have observed above. Demon registration gives the smallest NRMSE and the highest PSNR while having a reasonable computation time.

PD results show that registration algorithms are probably preferable to motion estimation algorithms because the former will correct for small inter-image differences (even if they do not always estimate a very realistic motion). This will remove false positives related to the moving tissue to a greater extent than in the case where one estimates the optical flow.

## 4.2 *in vivo* results

Preliminary results using demon registration were obtained on *in vivo* ultrafast Doppler sequences acquired during open brain surgery on human patient. The selected region contains a glioma. The size of this dataset is  $260 \times 192 \times 1000$  pixels. An important characteristic of living tissue is that the motion is continuous, the total movement accumulates from slice to slice. To take this information into account, for each image of the ultrasound sequence except the first, the Demon registration algorithm is initialized with a displacement field that is a fraction of the displacement field found for the registration of the previous image in the ultrasound sequence. Moreover, the displacement computed at each iteration of motion field computation can now be penalized (the convergence speed is reduced by computing proportionally smaller displacements) in the case where the motion computed at the previous iteration has increased the inter-frame difference between the two images. This addition limits the risks of divergence of the algorithm on large data sets.

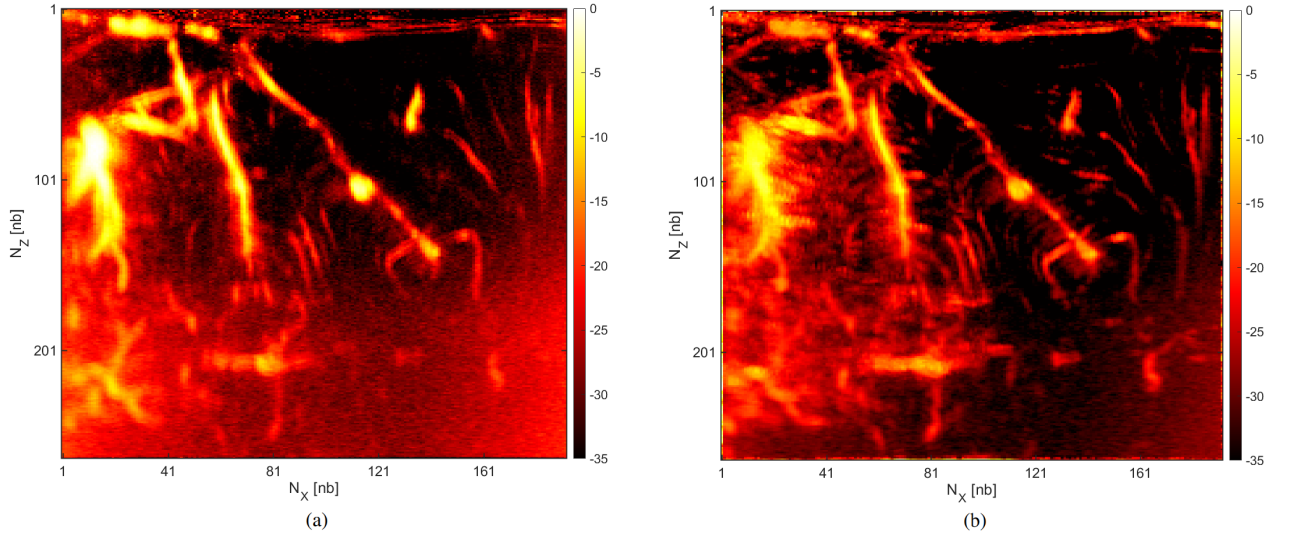


Figure 3. (a) Power Doppler estimated on non-registered *in vivo* images; (b) Power Doppler estimated on *in vivo* images registered with Demon registration.

It is difficult to evaluate in a relevant manner the results on the *in vivo* data as we do not possess the ground truth. Ideally, we want to obtain a good contrast while keeping a maximum of blood vessels visible. Visually examining the Fig. 3, one may remark that on the Power Doppler image estimated with Demon registration, we can see the small vessels derived from the three main vertical vessels. One can also notice that this image has much less noise on the right side. This is an area with little movement where it is easy to achieve a good quality registration. However, one can see that in the Fig. 3 the maximum intensity of the power Doppler is lower. It is likely that as for the simulation data, the motion related to the flow is also compensated which reduces the contribution of the motion compensation.

## 5. CONCLUSION

In this paper, we have investigated the problem of motion compensation while estimating the blood flow. We show that the compensated movements lead to a more precise estimation of the blood and thus could potentially lead to a better brain cancer surgery. On the *in vivo* data we obtain an effective elimination of false positives. We can also detect thin vessels that are normally not detectable. However, the image registration prior to the BD-RPCA algorithm shows limitations when the motion is too important, which may happen for long ultrasound sequences. Future work will be dedicated to estimate jointly the motion  $M$  with the high-resolution flow  $X$  by means of an iterative approach.

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## ETHICS

The data acquisition was done with a clinical research protocol (ELASTOGLI) approved by the institutional review board (CCP: ‘Comite de Protection des Personnes’, No 123748) and local ethical committee. It strictly complies with the ethical principles for medical research involving human subjects of the World Medical Association Declaration of Helsinki.