Respiratory Motion Correction in Dynamic-MRI: Application to Small Bowel Motility Quantification during Free Breathing

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Abstract. This study introduces a combination of two registration techniques for respiratory motion removal and the quantification of small bowel motility from free breathing cine MRI. The use of robust data decomposition registration (RDDR) allows for exclusive correction of respiratory motion in order to avoid errors in further analysis of motility due to the effects of breathing. The proposed method is assessed using regions of interest (ROIs) contoured in dynamic MRI of six healthy volunteers. The use of RDDR prior to motility quantification results in reduced errors on motility scores in ROIs, with respect to breath-holds.

Keywords: respiratory motion, registration, Robust PCA, small bowel, gastrointestinal motility.

1 Introduction

Evaluation of bowel motility using dynamic MRI is of growing interest both in terms of its use as a biomarker and as an investigational tool for a number of diseases affecting both the enteric and autonomic nervous systems. The principle difficulties pertaining to quantification of this system are functional complexity of the organ and deep anatomical location, prohibiting assessment through conventional instrumentation. Advances in rapid MRI techniques allow rapid cine acquisition of small bowel peristalsis and have presented a partial solution to this challenging aspect of human physiology. In addition, registration has permitted the quantitative analysis of these image series and the results have provided novel biomarkers for inflammatory activity in Crohns disease, validated against a histopathological reference standard [1][2]. Small bowel motility studies using registration have however been limited to breath-hold data sets allowing the algorithm to quantify the local deformations caused by peristalsis. Often, patients are unable to perform a breath hold and respiratory motion is added to that generated by peristalsis. The amplitude and nature of this respiratory motion can confound the analysis of peristaltic motility. In this study we propose to pre-process dynamic (cine) MR datasets using a robust data decomposition

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(RDDR) technique [3] to correct for the breathing component of motion, while leaving the motility component unchanged. We then process the data using the existing, validated small bowel registration technique to derive a motility metric in six healthy volunteers, comparing their free breathing motility score to a breath-hold gold standard.

2 Theory

2.1 Registration and Quantification of Small Bowel Motility

Odille et al. introduced a modified optical flow registration technique for the quantification of small bowel motility [1]. This technique uses a joint non-rigid transformation and modeling of intensity changes within a time-series. Following a multi-resolution approach, a dense representation of the deformations is obtained. Intensity changes that are not related to in-plane motion are modelled via an additional parameter in the algorithm cost function. The cost function is formulated as follows:

$$C(u_x, u_y, I_{map}) = \|I_{src}(T_{u_x,u_y}) + I_{map} - I_{ref}\|^2 + R(u_x, u_y, I_{map}) \qquad (1)$$

The operator $\|\cdot\|$ in (1) represents the Euclidean norm, and respectively denote the reference and the source images for registration, is the intensity correction field and is the displacement field in the two directions of the 2D image space represented by the vectors and . An additional regularization parameter is added to enforce spatial smoothness on , and based on their second order derivatives. A Gauss-Newton optimisation is chosen to iteratively minimize the cost function. The technique described above is referred to as 'optical flow registration' throughout this paper. Quantitative assessment of motility can be computed from the Jacobian determinants of the displacement fields obtained after registration. For each pixel the standard deviation of the Jacobian determinant through time provides a surrogate measure of local bowel contraction and expansion.

2.2 Robust Data Decomposition Registration

Hamy et al. developed a registration technique named robust data decomposition registration (RDDR) [3] based on iterative decomposition of a time-series using robust PCA (RPCA). RPCA relies on the idea that a given dataset can be decomposed into a low rank component (e.g. smooth and slower variations) and a sparse component (e.g. rapid and local changes). Let M be Casorati matrix with each column being formed from all the pixels of a 2D time-frame. RPCA splits such a matrix into a low rank L component and a sparse component S. This is achieved under the constraint that the sum of L and S must correspond exactly to the initial dataset M. It was shown that such decomposition can be formulated as an optimization problem [4]:

$$\begin{aligned} &\text{minimize: } \|L\|_* + \lambda\|S\|_1 \\ &\text{subject to: } L + S = M \end{aligned} \qquad (2)$$

where $\|\cdot\|_*$ and $\|\cdot\|_1$ respectively represent the nuclear norm (i.e. the sum of the matrix singular values) and the l1-norm (i.e. the sum of the absolute values of the matrix elements). The parameter λ appearing in (2) is a trade-off parameter: for high values all the information will appear in L while S will be empty, and vice-versa. The optimal setting of λ may depend on the application and the nature of the data. We hypothesize that RPCA applied to dynamic MRI of the small bowel will separate pseudo-periodical respiratory motion from sparse peristaltic motion.

The RDDR motion correction process can be described as follows: a given time series (with NT time frames) is represented as a Casorati matrix with NT columns and each column being made from all the Np pixels in one frame. Following RPCA decomposition, the low-rank time-frames are then registered. The resulting deformation fields are applied to the initial time-series so that a part of the motion can be removed. The process is then repeated for increasing values of the trade-off parameter (see figure 1). The process is stopped when the sparsity of the sparse component first falls below a threshold: in this case when the percentage of non-zero elements in S is less than 20%. If a lower threshold is used, peristaltic motion may start appearing in the low rank component. Additionally a maximum number of 10 iterations is set.

The registration algorithm in RDDR utilizes a similarity metric named residual complexity (RC) [5] which also incorporates an intensity correction field that brings the source and the target images into agreement in the intensity space. RC favors the transformation that leads to the minimum complexity of the residual difference image. This is achieved by measuring the sparseness of the residual in terms of the discrete cosine transform basis functions. B-spline based FFD [6] is used as a transformation with a gradient descent optimization scheme. Considering two (low-rank) time-frames I_{ref} and I_{src} to be registered by the unknown transformation T_{FFD}, and the intensity correction field I_{corr} (also unknown). Registration can be achieved by minimizing the following cost function:

$$C_{RC}(T_{FFD}, I_{corr}) = \|I_{ref} - I_{src}(T_{FFD})\|^2 + \beta\|PI_{corr}\|^2 \tag{3}$$

P and β respectively are the regularization operator and the regularization parameter. I_{corr} can be analytically solved by equating the derivative of the objective function to zero. If the identity matrix is denoted by Id, and the residual image by r:

$$\begin{aligned} I_{corr} &= (Id + \beta P^T P)^{-1} r \\ r &= I_{ref} - I_{src}(T_{FFD}) \end{aligned} \tag{4}$$

By substituting this new expression in (4) and applying eigen-decomposition to $P^T P$, it yields:

$$\begin{aligned} C_{RC}(T_{FFD}) &= r^T (Id + \beta P^T P)^{-1} r \\ C_{RC}(T_{FFD}) &= r^T Q d \left(1 - \frac{1}{1 + \beta\delta_i}\right) Q^T r = (Q^T r)^T \Delta Q^T r \end{aligned} \tag{5}$$

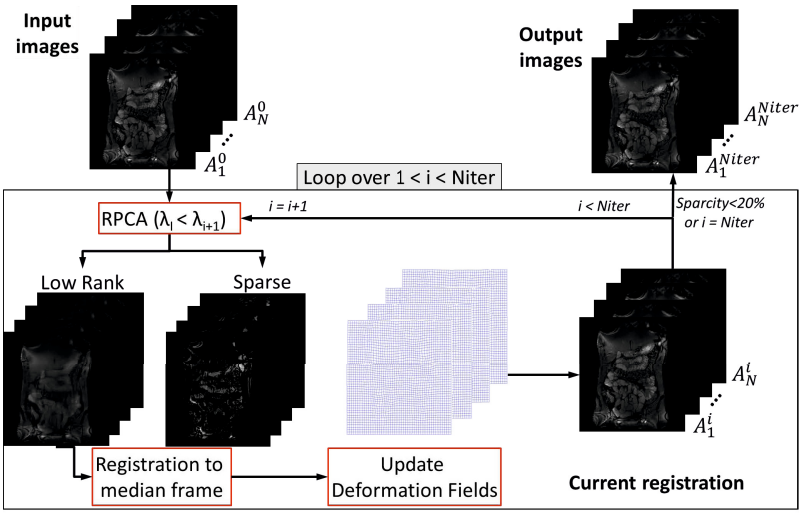

Fig. 1. Flow chart illustrating the process of RDDR (The parameter λ is gradually increased to let more information appear in the Low rank component over iterations)

$d(\cdot)$ denotes a diagonal matrix and the δ_is and Q respectively are the eigenvalues and the eigenvector matrix of $P_T P$. The objective function minimization is made possible by choosing a particular form for the eigenvectors Q and solving for the (diagonal) matrix Δ within the regularization. The discrete cosine transform (DCT) basis function is chosen for the eigenvectors. Thus RC is minimized when the residual image can be represented using the smallest possible number of function basis, corresponding to alignment of the input images.

RDDR has been successfully applied to dynamic contrast enhanced (DCE) MRI time series registration using the ability of RPCA to separate low rank respiratory motion from sparse changes induced by an injected contrast agent [3].

3 Materials and Methods

3.1 Data

Six healthy volunteer were scanned for this study. Volunteers fasted for 4 hours prior to the scan and consumed 1 litre of 2% mannitol solution to distend the bowel and provide contrast. Volunteers lay prone in a Philips Achieva 3T scanner and were imaged using the following parameters: manufacturers torso coil, balanced gradient echo sequence ($2.5x2.5x10mm$), FA 20 degrees, TE/TR=$1.7/3.5ms$), 1 volume per second temporal resolution. Each subject was scanned in breath hold ($20s$) immediately followed by free-breathing ($60s$) in the same anatomical position with no more than a 30 second gap between the commencement of the breath hold and free breathing scan.

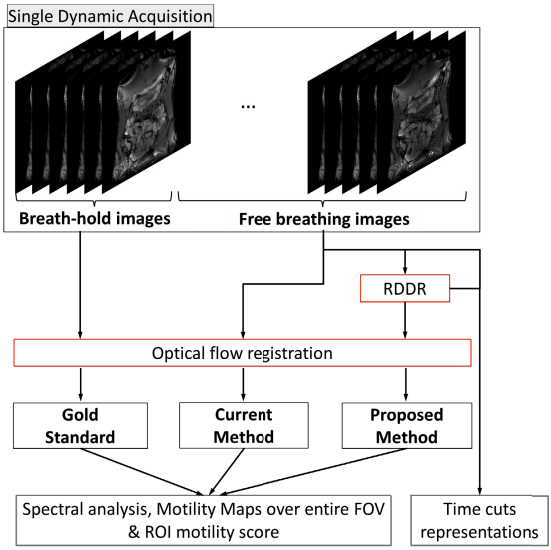

Fig. 2. Flow chart illustrating the proposed method and validation. The gold standard is based on images acquired during breath-hold immediately before the acquisition during free-breathing

3.2 Validation

Each free-breathing data set was registered using optical flow alone, and RDDR followed by optical flow registration. The results were compared to that of optical flow applied to data acquired during breath-hold which was used as gold standard for this study (see figure 2). Immediately after RDDR the effect of respiratory motion correction was qualitatively assessed by generating time-cut images representing the temporal evolution of a pixel-wide line across all time-frames. For each subject, motility maps were computed based on the Jacobian determinant obtained after optical flow registration for each pixel in the field of view.Frequency analysis of the effect of RDDR was run for each subject. Spectra of intensity changes for each pixel in the field of view were summed to provide information on the relative spectral power of the different types of motion [7].A radiologist with five years experience in small bowel enterography placed a region of interest (ROI) around the small bowel in a single anatomical slice of each of the 6 dynamic data sets. Each ROI was propagated automatically through the time series based on the optical flow registration results. The motility metric is presented as the standard deviation of the Jacobian determinant of pixels under the ROI.

4 Results

Example images of time cuts and motility maps obtained after registration are presented (see figures 3 and 5). The time cut representation shows an accurate

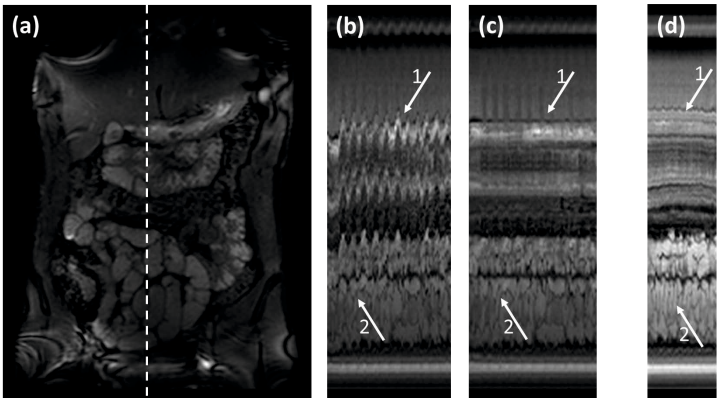

Fig. 3. Time cut representation of dynamic time-series of the small bowel in a healthy volunteer: the location of the time cuts is indicated by a white dashed line in (a), time cuts before (b) and after registration with RDDR (c) are presented. Breath-hold data is shown as reference (d). Important displacements due to respiratory motion are accurately corrected by RDDR (arrow 1) whereas bowel motility remains unchanged (arrow 2)

correction of breathing motion after RDDR while peristaltic motion is left unchanged. This effect was confirmed by the spectral analysis of pixel intensity changes before and after RDDR. In all cases the peak observed for frequencies between 0.3 and 0.5 Hz was largely attenuated by RDDR and the rest of the spectrum was similar to that of non registered data. This is consistent with the results in [7] where the interval $0.3 - 0.5$ Hz is defined as the breathing band. An example is shown in figure 4.

Across all ROIs, the median motility score for data acquired during breath-hold was 0.292. For the same contoured feature in data acquired during free breathing median motility scores were 0.346 (i.e. 18.3% error with respect to breath-hold) for optical flow registration only and 0.288 (i.e. 1.2% error) for RDDR followed by optical flow. The details of the different scores per ROI are presented in table 1. Overall the effect of RDDR was more important for ROIs located in the upper abdomen, and thus more affected by free breathing (see figure 5).

5 Discussion

For this study we collected volunteer breath hold and free breathing data and used the breath hold as a reference in the analysis of the motion correction with RDDR. A limitation of this reference lies in the time delay between acquisitions which permits subtle changes to occur within the bowel either slowing or increasing peristalsis. Although negligible, said changes make the two data sets an imperfect match and thus not a true gold standard. An alternative approach might have been to develop a phantom that simulates both respiration

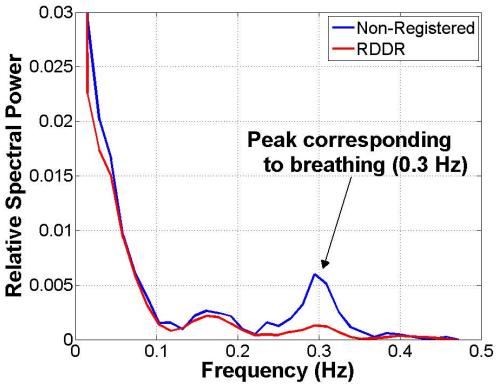

Fig. 4. Spectral analysis before and after registration with RDDR. The peak corresponding to breathing is attenuated by RDDR whereas the rest of the spectrum remains similar

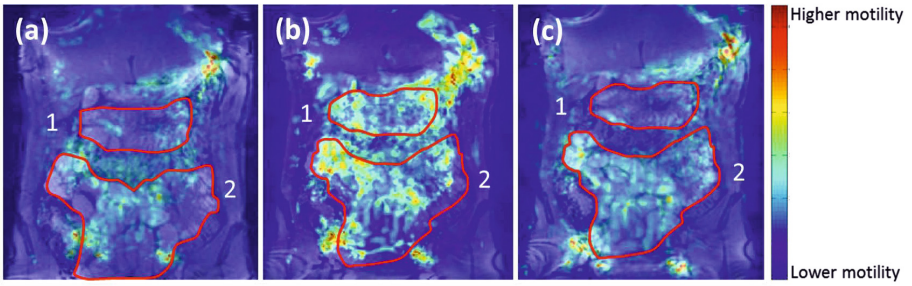

Fig. 5. Example of motility maps. Breath-hold gold standard (a), free breathing optical flow registration alone (b) and RDDR followed by optical flow (c). Respiratory motion compensation is visible in the upper bowel (ROI 1). The effect of RDDR is less important in the lower bowel(ROI 2) further from the diaphragm.

Table 1. Motility scores obtained for ROIs in all the 6 subjects. When more than one ROI had been contoured for a given subject, the average score was taken

Subject	Gold Standard	Optical Flow	RDDR&Optical Flow
1	0.328	0.42	0.244
2	0.316	0.333	0.29
3	0.231	0.295	0.153
4	0.268	0.358	0.287
5	0.369	0.45	0.35
6	0.2	0.295	0.2

and peristaltic motion, however this would be complex and fail to negate the necessity for validation in patient data sets. Based on the results presented here and the visual inspection of cine series, RDDR provided good respiratory motion correction enabling motility quantification with values similar to a 20s breath hold scan.Both optical flow registration and RDDR were initially developed for separate applications. Optical flow registration has been successfully applied in the past to quantify motility in time-series acquired during breath-hold, while RDDR has been used for registration of dynamic contrast enhanced MRI. Since the physiological mechanism studied here differs from contrast enhancement, the use of RDDR with no further modification might be not be optimal. Future work will include a more elegant stopping criterion for the iterative process, e.g. using a sparsity threshold based on a larger cohort of subjects.

6 Conclusion

RDDR can be used for selective motion correction in the context of small bowel motility quantification. In this study we showed, based on the analysis of dynamic MRI time-series of six healthy volunteers, that RDDR can be successfully applied to correct for respiratory motion while preserving small bowel peristalsis. This could allow a robust extension of motility quantification to free-breathing acquisition and longer scanning times. This could provide more complete observation of peristaltic waves, and lead to a better understanding of motility in disease.

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