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Abstract. We have previously proposed an intersection profile method for reconstructing four-dimensional (4-D) magnetic resonance imaging (MRI) consisting of one breathing cycle of the thoracoabdominal region. This method captures a set of temporal sequence images in a proper sagittal plane and sets of temporal sequence images in continuous coronal slices. The former set is used as a navigator slice and the latter sets are used as data slices. A 4-D MRI is reconstructed by synchronizing the respiratory pattern found in the navigator slice and the data slices. We propose a prospective method to reduce the acquisition time for data slices. During data slice acquisition, the synchronization process between the respiratory pattern found in the navigator slice and one data slice is monitored in real time. Data acquisition will be terminated and moved to the next data slice based on a threshold value. We used 14 data sets (seven patients with certain pulmonary disease and seven healthy volunteers) previously obtained for the original intersection profile method for a simulation using the proposed method to evaluate the time reduction and impact on image quality. Each of the data set was tested using three different threshold values and the acquisition time can be reduced up to 75%. Although the quantitative evaluation of image quality was slightly worse than that by the conventional method, the difference based on the visual inspection was subtle to human eyes. © 2015 Society of Photo-Optical Instrumentation Engineers (SPIE) [DOI: 10.1117/1.JMI.2.2.024008]

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1 Introduction

In recent years, four-dimensional (4-D) medical imaging of thoracoabdominal organs has been increasingly applied in radiotherapy treatment planning and analyzing diaphragm motion.^{1–3} One of the advantages of 4-D medical imaging over three-dimensional (3-D) medical imaging is that the anatomic motion and organ deformation caused by respiratory motion can be clearly observed. This leads to better understanding of pulmonary function diseases of the lung, such as chronic obstructive pulmonary disease (COPD). The most commonly used imaging modality to reconstruct 4-D medical imaging is computed tomography (CT). Early reports on using 4-D CT acquisition may be found in the literature.^{4–6} There are two standard ways to carry out 4-D CT: prospective gating and retrospective gating.^{4–8} Prospective gating requires a predetermined gating window in specific breathing phases. Images are taken only when the respiratory phase is within the gating window. The process is repeated until volume of interest in a certain respiratory phase is fully covered. On the other hand, retrospective gating 4-D CT requires obtaining images in all breathing phases

without a gating window and covering the volume of interest. Those images are then synchronized according to their respective respiratory phases and locations using a separate signal that represents its breathing phase.

Another common imaging modality used to reconstruct 4-D medical imaging of thoracoabdominal organs is magnetic resonance imaging (MRI). Reconstruction of 4-D MR images has been less investigated compared to 4-D CT, which is well-established. Several studies have proposed reconstruction of 4-D MR images using time-sequential two-dimensional (2-D) MR images.^{9–13} A common approach for reconstruction of 4-D MR images is using 2-D MR images to cover both the volume of the respiratory organ and the volume of the respiratory phases from the inhalation to exhalation phases. The 2-D MR images are then retrospectively sorted based on the obtained respiratory phase to reconstruct the 4-D MR images (i.e., retrospective 4-D MRI).

Although the results of the reconstruction usually have good image quality, retrospective 4-D MRI requires long acquisition times because a large number of 2-D images must be acquired for the purposes of sorting and volume construction. Consequently, such retrospective 4-D MRI consists

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of many breathing cycles and captures the irregularity of respiration as well.⁹

One navigator-based method that is used for 4-D MRI reconstruction was proposed by Tokuda et al.¹⁰ This method was designed to acquire a series of 3-D images that cover the whole range of respiratory organs by using the gating method. Instead of using one gating window, Tokuda et al. used several bins (gating windows) to segment respiratory signals into several partitions. Since the purpose of this method is to obtain real-time tracking of 4-D MRI, complex hardware integration that used an analog-to-digital converter, a radio frequency pulse, and a personal computer with an MR scanner is required.

We have developed a hardware-independent method to reconstruct a robust and high-quality 4-D MR image consisting of one breathing cycle from a temporal sequence of 2-D MR images.¹⁴ This is a navigator-based method called the intersection profile method. Time sequential 2-D MR images in the sagittal plane, which functions as the navigator slice (NS), are obtained first for a long time so as to include many respiration cycles, typically 3 min. Data slices (DSs) (time sequential 2-D MR images in the coronal plane) are then obtained from the front (anterior) to back (posterior) body positions for 1 min for each slice position. Several spatiotemporal (ST) patterns from both the NS and DS are extracted at their intersection location to obtain the respiratory patterns. The 4-D MRI reconstruction is done by combining a proper respiratory pattern from each DS that has the highest similarity to the corresponding NS.

One of the drawbacks of this method is that it requires 20 to 30 min to obtain a full data set. In this paper, we modify the method so as to shorten the acquisition time of MRI data. For this purpose, a prospective technique during 2-D MR image acquisition is introduced. In the modified method, a reference respiratory pattern is determined from the NS. Then, during the DS image acquisition, each respiratory pattern is compared with the reference respiratory pattern in real time and a similarity measure between them is calculated. Once the similarity measure reaches the threshold, the image acquisition for the current DS will be halted and the acquisition proceeds to the next position. In order to implement this idea to real MRI equipment, the manufacturer must change the image acquisition system. Currently it is not realized yet. On the other hand, we have much raw data collected from the previous method. Consequently, we can simulate how the prospective method works using those images.

In the following sections, we first review our previous method and describe how we modified it to reduce the acquisition time. We then present the experimental results using 14 data sets. The time reduction and image quality are evaluated and discussed.

2 Methods

2.1 Coordinate System and Image Acquisition

In this section, we define a coordinate system and variables and then describe the method for image acquisition. We show specific values for some parameters to clarify the process and provide a practical situation for readers.

We first define a 3-D coordinate system as shown in Fig. 1. Two types of 2-D MR images are used: the NS and the DS. The NS is a temporal sequence of 2-D MR images in the sagittal plane, which consists of several hundred frames. Those MR images are obtained at a constant X axis position and consist of several respiratory patterns in all acquisition data. We

Fig. 1 Coordinate system of the proposed method. A navigator slice (NS) intersects with data slices (DSs) at the location (X_s, y_i) .

formally denote the signal intensity of a frame in NS as $f_{\text{navi}}(X_s, y, z, t_{\text{navi}})$ where t_{navi} represents the t_{navi} th frame in NS. Here, X_s represents the X axis position where the NS is located and (y, z) represents the position in the NS.

The DS is the temporal sequence of 2-D MR images in the coronal plane. One set of DS consists of DSs along the Y axis (anterior-posterior) to cover the thoracic volume. Each of the DS in the DS set also consists of several hundred frames and has some respiratory patterns in all breathing phases. The signal intensity in the DS is denoted as $f_{\text{data}}(x, y_i, z, t_{\text{data}})$, $i \in 1, 2, 3, \dots, n$. Here y_i represents the Y axis position where the i 'th DS is located, (x, z) represents the pixel position in the DS, and n represents the number of DSs.

When the NS and DS are at the same respiratory phase, they should share the same signal intensity at (X_s, y_i) along the Z axis and ideally the following expression should be satisfied:

$$f_{\text{navi}}(X_s, y_i, z, t_{\text{navi}}) = f_{\text{data}}(X_s, y_i, z, t_{\text{data}}). \quad (1)$$

Although the NS and DS intersect at the location (X_s, y_i) , they are not obtained at the same time. The NS is obtained first at X_s and sequentially followed by DS acquisition at the location y_i , $i = 1, 2, 3, \dots, n$. The total time of image acquisition for one subject is equal to 3 min for NS acquisition and n min to obtain n slices for the DS. Normally, ~ 10 to 25 slices are obtained for the DS set. Thus, the total acquisition time to obtain a complete data set ranges from 13 to 28 min.

2.2 Description of Intersection Profile Method

Before describing our proposed method in detail, we first give an overview of our previous 4-D MRI reconstruction using the intersection profile method. Figure 2 shows a schematic illustration of the original intersection profile method.

Because the DS and NS intersect at y_i , $i = 1, 2, 3, \dots, n$, n ST patterns can be generated from both the NS and DS at the intersection location. These ST patterns represent breathing cycles at a location (X_s, y_i) over time. Several respiratory patterns can be extracted from ST patterns generated from the NS.

Fig. 2 Schematic illustration of the original intersection profile method. The procedure to find a respiratory pattern from DS, which is similar to that of the NS, is shown.

The idea of the intersection profile method is to employ the similarity of respiratory patterns found in ST patterns from the NS and ST patterns from the DS. The respiratory patterns found in the NS are used as references and compared with the ST patterns from the DS. A similarity measure using the normalized cross-correlation (NCC) is used to find the best matching respiratory pattern between the reference and ST patterns from the DS. A 4-D MR image can be reconstructed once the best matching respiratory patterns are found for each intersection location, y_i . The detailed procedure to reconstruct 4-D MR images using the intersection profile method is as follows:

1. Determine the intersection location of NS and each DS, denoted as y_i , where $i = 1, 2, 3, \dots, n$ and n is the number of DSs.
2. Manually set a region of interest (ROI) around the diaphragm boundary of the NS.
3. Generate n ST patterns from the ROI of the NS.
4. Extract respiratory patterns from the NS. One respiratory pattern is denoted as $A_{k,i}(z, t)$, $k = 1, 2, 3, \dots, m$, where k denotes the k 'th respiratory pattern and m is the number of respiratory patterns extracted from the ST pattern. The period of the k 'th respiratory pattern is denoted by w_k .
5. Set ROI around the diaphragm boundary of the DSs and generate n ST patterns from each DS. Denote the ST patterns from DS as $B_i(z, t_{data})$.

6. For each $A_{k,i}$, $k = 1, 2, 3, \dots, m$ and $i = 1, 2, 3, \dots, n$, find the best NCC value between $A_{k,i}$ and B_i . The best NCC value from the k 'th pattern at y_i is denoted as $C_{k,i}$. The time at the DS where C takes the maximum value at y_i is denoted as $t_{k_{best,i}}$.
7. Choose the best respiratory cycle from the NS by selecting the highest geometric mean (geomean) using the following expression:

$$k_{best} = \arg \max [\prod_{i=1}^n (C_{k,i})]^{1/n}. \quad (2)$$

This best geomean value will ensure that the corresponding respiratory patterns found in the DSs have the closest similarity with the respiratory patterns found in the NS. As a result, the respiratory cycle in the reconstructed 4-D MR image is also very close to the respiratory cycle in the NS.

8. Finally, the 4-D MRI can be reconstructed by combining the DS $f_{data}(x, y_i, z, t_{data})$, where t_{data} ranges from $t_{k_{best,i}}$ to $t_{k_{best,i}} + w_{k_{best,i}}$.

An intuitive explanation why geomean is used in Eq. (2) instead of using the arithmetic mean is as follows. The geomean calculates the product of the given NCC values and then takes the n 'th root. The product of the NCC values should provide a more robust representation of the similarity measure compared to the arithmetic mean, which uses the sum. For example, if an arithmetic mean is used, the NCC values of 0.9 and 0.1 will

produce the same arithmetic mean as NCC values of 0.5 and 0.5, as well as NCC values of 0.7 and 0.3. The arithmetic mean (similarity measure) of those examples is 0.5, which is bias and not representing the quality of the reconstructed 4-D MRI. The use of geomean will avoid such bias. From the aforementioned examples, the geomean are 0.3, 0.5, and 0.46 for the first, second, and third case, respectively. The NCC value of 0.9 and 0.1 yields the lowest geomean (similarity measure) compared to the other two because one of the NCC values is very low (0.1). Therefore, using geomean to reconstruct 4-D MRI will eliminate the low NCC value to be included in the reconstructed 4-D MRI. It also ensures the quality of reconstructed 4-D MRI consists of similar quality of DSs.

2.3 Modification to Prospective Method

The intersection profile method to reconstruct 4-D MR images as explained in Sec. 2.2 is categorized as a retrospective method. A drawback of this method is that all data must be obtained first before the reconstruction process. We modify the method into a prospective method to reduce the time needed for DS acquisition. To find the best matching between respiratory patterns of the NS and ST pattern of DS, structural similarity (SSIM) is used instead of NCC. The SSIM index is measured by considering three important components of the image: luminance (mean), contrast (variance), and structure (cross-correlation).¹⁵ To measure the SSIM of two images, f and g , the following SSIM function is used:

$$\begin{aligned} \text{SSIM}(f, g) &= m(f, g)^\alpha \times v(f, g)^\beta \times c(f, g)^\gamma \\ &= \left(\frac{2\mu_f\mu_g + C_1}{\mu_f^2 + \mu_g^2 + C_2} \right)^\alpha \times \left(\frac{2\delta_f\delta_g + C_1}{\delta_f^2 + \delta_g^2 + C_2} \right)^\beta \\ &\quad \times \left(\frac{\delta_{fg} + C_3}{\delta_f\delta_g + C_3} \right)^\gamma, \end{aligned} \quad (3)$$

where μ_f and μ_g are mean value of image f and g ; δ_f and δ_g denote the standard deviation of image f and g ; and δ_{fg} denotes correlation coefficient. Three parameters α , β , and γ are parameters to adjust component's contribution (set to 1 in this study) and constants C_1 , C_2 , and C_3 are small positive constants (set to 0.001 in this study). The resultant SSIM is a decimal value between -1 and 1 . The more similar the two images, the larger the SSIM. It becomes unity in the case that two images are identical.

The use of SSIM is proven to be consistent with perceptual image distortion and works better than traditional similarity measures, such as root-mean square, normalized least-square error, and correlation in term of maintaining an image's structure.¹⁵⁻¹⁷

Figure 3 shows a schematic illustration of the modified version of the intersection profile method. Here steps 6, 7, and 8 of the previous method are changed as shown following:

6. Instead of using all respiratory patterns, choose one of the most frequent respiratory patterns from the NS and use it as a reference to compare with the corresponding

Fig. 3 Modification to the prospective method. The acquisition is stopped and proceeds to the next DS once the structural similarity (SSIM) value becomes higher than the threshold value.

respiratory patterns in the DS. The most frequent respiratory pattern is defined by a pattern that has the smallest mean distance from other respiratory patterns. We then determine the location of most frequent respiratory pattern as follows:

$$k'_{\text{best}} = \arg \min_{\substack{j=1 \\ j \neq k}}^m \{ \sum_{z,t} [A_{j,i_{\text{max}}}(z,t) - A_{k,i_{\text{max}}}(z,t)]^2 \}, \quad (4)$$

where m is the number of respiratory pattern found in the NS. The most frequent respiratory pattern is then defined as $A_{k'_{\text{best}},i}(z,t)$, where t ranges from $t_{k'_{\text{best}},i}$ to $t_{k'_{\text{best}},i} + w_{k'_{\text{best}},i}$.

In Eq. (4), $A_{j,i_{\text{max}}}$ represents the j 'th respiratory pattern in intersection location i_{max} , where j ranges from $1, 2, 3, \dots, m$. We can see $A_{j,i_{\text{max}}}$ in Fig. 3 as a box with certain width and height. Terms z and t in Eq. (4) represent the height and width of the box (respiratory pattern). Therefore, the range of t is limited by the width of the box. Note that the location to pick most frequent respiratory pattern is the intersection location that has the largest diaphragm movement. To obtain the intersection location that has the largest diaphragm motion, we measured the displacement of the diaphragm for each intersection location from end inhalation to end exhalation automatically and determine the intersection location that has the largest displacement. This location is denoted as i_{max} .

Once the position of the most frequent pattern (k'_{best}) at i_{max} was obtained, the same position is used for other intersection locations ($y_1, y_2, y_3, \dots, y_n$). Thus, the position of k'_{best} is always the same for each intersection location. Another reason why k'_{best} is picked at only one intersection location rather than picked at each intersection location is that different k'_{best} that is picked at each intersection location might produce an out-of-phase or asynchronous reconstruction, since the respiratory patterns ($1, 2, 3, \dots, m$) were not obtained in the same time frame.

7. For y_i , $i = 1, 2, 3, \dots, n$, evaluate the SSIM value between $A_{k'_{\text{best}},i}$ and B_i as image acquisition of DS proceeds. When the SSIM value becomes greater than a predetermined value, stop the data acquisition in the current position and proceed to the next intersection position.
8. Reconstruct the 4-D MRI by combining DS $f_{\text{data}}(x, y_i, z, t_{\text{data}})$, where t_{data} ranges from $t_{k'_{\text{best}},i}$ to $t_{k'_{\text{best}},i} + w_{k'_{\text{best}},i}$.

A fixed threshold is used to implement 4-D MRI reconstruction using the prospective method. It sets a certain threshold that will be used to stop the acquisition process if the SSIM value exceeds it. The SSIM value has an influence on the image quality of 4-D MRI. In this paper, three threshold values 0.5, 0.4, and 0.3 are investigated.

3 Experiment

3.1 Image Data Used in Experiment

The MR images were acquired using a 1.5T INTERA ACHIVA nova-dual (Philips Medical Systems) whole-body scanner with a 16ch SENSE TORSO XL coil. A 2-D balanced FFE sequence was used. The imaging parameters were as follows: SENSE factor, 2.2; flip angle, 45 deg; repetition time, 2.2 ms; echo time, 0.9 ms; FOV, 384 mm; in-plane resolution, 256×256 pixels and 1.5×1.5 mm²; slice thickness, 7.5 mm; slice gap, 6.0 mm; scan time, 150 ms/frame. All subjects were instructed to breathe normally during the acquisition process. The image acquisition experiment was conducted under the approval of the ethical review board of Chiba University. The software used to implement our method was MATLAB® 7.10, and we ran it on a PC with Intel®Core™2 Quad, 2.66 GHz, 16 GB RAM. Total processing time for one subject to complete the 4-D MRI reconstruction after obtaining a set of raw data was <1 min.

Fourteen subjects (seven healthy subjects and seven patients with known pulmonary diseases) participated in this study. The number of DSs varied from 10 to 25 slices, where each slice contained 400 frames. The number of NS frames also varied from 400 to 1200. Statistical data for the subjects are summarized in Table 1.

The number of frames of NS varies only for the volunteers (healthy subjects). During the acquisition, when the breathing patterns of the subjects are considered as a regular breathing, the acquisition does not have to be 3 min long. One or two min should be enough to get the variation of the breathing

Table 1 Subjects' data statistic. For each subject, the number of data slice (DS), number of frames of navigator slice (NS), and diagnosis are given.

	Subject	#DS	#NS' frame	Diagnosis
Volunteer	V1	20	400	—
	V2	24	800	—
	V3	24	800	—
	V4	14	1200	—
	V5	14	1200	—
	V6	13	1200	—
	V7	13	1200	—
Patients	P1	14	1200	Pulmonary tumor
	P2	25	1200	COPD
	P3	23	1200	Right-giant bulla
	P4	10	1200	COPD
	P5	25	1200	COPD
	P6	12	1200	COPD
	P7	12	1200	COPD

Note: COPD, chronic obstructive pulmonary disease.

patterns from the subjects. In most cases, healthy volunteers have regular respiratory patterns. When the operator does not spot any irregular breathing within 1 min, he or she stops the acquisition in 1 min. However, if there seems to be irregular breathing within 1 min, the acquisition will be continued for another 1 min. For the patients having irregular breathing patterns, the acquisition time must be 3 min long to capture the breathing patterns' variation.

3.2 Time Reduction Using a Predetermined Threshold Value

As described previously, by applying the retrospective method, DS acquisition time by minutes is equivalent to the number of slices. Time reduction is possible using the prospective method that employs a predetermined threshold value. During the DS acquisition, when the SSIM value in the y_i position is larger than the threshold value, the acquisition process will be stopped and the process will proceed to the next slice position.

By applying a smaller threshold value, better time reduction can be achieved. Complete comparison of time reduction is shown in Table 2. Here “w/o T” stands for “without threshold,” which means that the modified method is applied without thresholding. The total acquisition time for volunteer data can be reduced by 23.1, 53.1, and 75.6% on average for 0.5, 0.4, and 0.3 threshold values, respectively. For patient data, the averages of the time reductions are 32.5, 59.3, and 84.0% for 0.5, 0.4, and 0.3 threshold values.

Fig. 4 Average of SSIM and DS time reduction of (a) patients and (b) volunteers. Solid line indicates the average of SSIM (left scale) and dashed line indicates time reduction (right scale).

Table 2 Comparison of total DS acquisition time and time reduction of without threshold (w/o T), 0.5, 0.4, and 0.3 threshold values.

		w/o T	0.5		0.4		0.3	
Subject		Total DS acquisition time	Total DS acquisition time	Time reduction (%)	Total DS acquisition time	Time reduction (%)	Total DS acquisition time	Time reduction (%)
Volunteers	V1	20:00	17:57	10.3	14:14	28.8	3:01	84.9
	V2	24:00	5:14	78.2	2:05	91.3	1:36	93.3
	V3	24:00	15:08	36.9	7:06	70.4	4:11	82.6
	V4	14:00	10:20	26.2	5:33	60.4	4:05	70.8
	V5	14:00	12:39	9.6	8:07	42.0	6:17	55.1
	V6	13:00	10:14	21.3	6:45	48.1	4:35	61.8
	V7	13:00	10:07	22.2	6:10	52.6	2:27	81.2
Mean		16:49	10:58	23.1	6:18	53.1	3:26	75.6
Patients	P1	14:00	8:46	37.4	4:53	65.1	1:55	86.3
	P2	25:00	19:51	20.6	11:14	55.1	4:06	83.6
	P3	23:00	6:40	71.0	2:15	90.2	1:42	92.6
	P4	10:00	6:12	38.0	2:41	73.2	1:43	82.8
	P5	25:00	17:02	31.9	10:26	58.3	6:30	74.0
	P6	12:00	8:28	29.4	5:50	51.4	2:14	81.4
	P7	12:00	9:38	19.7	7:38	36.4	1:24	88.3
Geomean		16:10	9:59	32.5	5:30	59.3	2:24	84.0

The quality of the 4-D MRI reconstructions was also assessed by the geomean of all the best SSIM values between the reference ST image of the NS and ST image of the DSs at all intersection locations. Figure 4 shows the plot of geomean of SSIM and time reduction. Overall results indicated that the best geomean of the SSIM was achieved by the w/o T method.

Certain threshold values used in reconstruction reduced the DS acquisition time in the exchange of the lower SSIM geomean (or in other words, lower quality of the 4-D MRI reconstruction). Both volunteer and patient data results demonstrated that a 0.4 to 0.5 threshold value may reduce data acquisition time up to 50%. Reconstructing 4-D MRI using higher threshold value, for example 0.6, is also possible. However,

Fig. 5 Examples of two different phases after volume rendering of V1 using Osirix: (a) reconstructed using the retrospective method, total time of data acquisition was 24 min; (b) reconstructed using the prospective method without threshold (w/o T), total time of data acquisition was 24 min; (c) reconstructed using the prospective method with 0.3 threshold value, the total time of data acquisition was 3 min 1 s (84.9% time reduction).

(a)

(b)

(c)

Fig. 6 Three maximum intensity projection images of reconstructed four-dimensional (4-D) magnetic resonance imaging (MRI) of V1: (a) reconstructed using the retrospective method, (b) reconstructed using the prospective method w/o T, and (c) reconstructed using the prospective method with 0.3 threshold value.

the time reduction in this scenario would be very small since most data slices have SSIM values < 0.6 .

The trade-off of time reduction is the quality of 4-D MRI reconstruction. Image quality of 4-D MRI is discussed in the next section. Visual evaluation is first discussed, followed by a quantitative evaluation.

4 Image Quality Evaluations

4.1 Visual Evaluation

4.1.1 Volume rendering image and maximum intensity projection image of reconstructed 4-D MRI

Reconstructed 4-D MR images were visualized by a volume rendering technique implemented in Osirix. Three images of 4-D MRI reconstruction from the same subject (V1) are shown in Fig. 5. Figures 5(a)–5(c) show the reconstruction using the retrospective method, the prospective method w/o T, and the prospective method with 0.3 threshold value, respectively. End inhalation phase is shown on the left-hand side and end exhalation is shown on the right-hand side of Fig. 5. In order to show the difference between left-hand and right-hand images, we drew a white dashed line at the top level of the diaphragm of the left-hand image. The total time required to obtain a complete data set of 4-D MRI using the retrospective method and the prospective method w/o T were 21 min (1 min to obtain NS and 20 min to obtain DSs). By using the prospective method with a 0.3 threshold value, the total DS acquisition time can be reduced to 3 min, 1 s. From the visual inspection, we confirmed that these volume rendering images look very similar.

Another visual evaluation of reconstructed 4-D MRI of V1 was also performed using maximum intensity projection (MIP).¹⁸ We compared the MIP images of 4-D MRI between the retrospective and the prospective method. Figures 6(a)–6(c) show the MIP images of the reconstruction using the retrospective method, the prospective method w/o T, and the prospective method with 0.3 threshold value, respectively. As shown in the figure, these MIP images also look similar.

4.1.2 Sagittal slice evaluation

The shape of diaphragm extracted from 4-D MRI in sagittal plane can also be used as an indicator of reconstruction quality. We extracted a sagittal cut at NS location X_s and other sagittal cuts at two locations different from NS as shown in Fig. 7. The

Fig. 7 Extraction of sagittal cuts from reconstructed 4-D MRI. The distances of the extracted sagittal cuts are 30 mm on the left side and 30 mm on the right side of original NS position.

distances between the sagittal cuts and original location of NS were 30 mm on the left-hand side ($X_s - 30$ mm) and 30 mm on the right-hand side ($X_s + 30$ mm).

The visual comparisons of extracted sagittal cuts at the same location as NS and two locations different from NS are shown in Fig. 8. We picked one volunteer and two patients who have 20 slices or more as examples and 4-D MRI reconstruction using the retrospective method, the prospective method w/o T, and the prospective method with 0.3 threshold value. Figure 8 shows sagittal cuts extracted from V1, P2, and P3.

Only at the location of the original NS (X_s), we can compare the appearance of the original NS image and sagittal cuts extracted from the reconstructed 4-D MRI. Since the number of DSs is limited and the spatial resolution of the sagittal cuts is low, the sharpness of the sagittal cuts is clearly lower than the original NS images. However, the general structure was natural and similar to that of the original NS image. The

diaphragm boundary of sagittal cuts from the retrospective method and the prospective method w/o T were found to be smoother compared to 0.3 threshold. The diaphragm shape of the 0.3 threshold had more crease over the boundary (indicated by white arrow). The quantitative evaluation of such comparison will be discussed in Sec. 4.2.

4.2 Quantitative Validation

Focusing on the sagittal cut of 4-D MRI corresponding to the NS, we performed two validation experiments to assess the accuracy of the prospective 4-D MRI reconstruction using 0.5, 0.4, and 0.3 threshold values. We defined the sagittal slice from NS as a ground truth and evaluated the sagittal cuts in the NS location from the 4-D MRI.

In the first validation, the measurement was performed by calculating the difference of the Z axis displacement at the

Fig. 8 Visual comparison of original NS and sagittal cuts extracted from location of NS (X_s) and two locations different from NS ($X_s - 30$ mm and $X_s + 30$ mm). The sagittal cuts were extracted from the retrospective method, the prospective method w/o T, and the prospective method with 0.3 threshold value. White arrow indicates crease over the diaphragm boundary.

Fig. 9 Displacement error of diaphragm measured based on the difference diaphragm boundary position between the sagittal slice from NS as ground truth and sagittal cuts from reconstructed 4-D MRI.

intersection location ($y_i, i = 1, 2, 3, \dots, n$). The schematic diagram of how to measure the Z displacement error is shown in Fig. 9. Each column of the sagittal cut in the intersection location ($y_i, i = 1, 2, 3, \dots, n$) was extracted. In general, the pattern of the extracted column consists of two major intensities, dark and gray. The extracted column of sagittal cut is then

matched using cross-correlation along the Z axis with the corresponding column of the original NS. The Z displacement error is determined from the position of the best cross-correlation value. Ideally, the extracted column of sagittal cut has the same pattern as the extracted column of original NS along the intersection location. In such a case, the Z displacement errors along the intersection location are equal to 0 and the diaphragm shape of sagittal cut is also the same as the NS. However, since our method tries to find the best matching of the respiratory pattern between NS and DS, such an ideal condition is difficult to obtain. Therefore, in the first validation, we calculate the average of the Z differences over intersection locations ($y_i, i = 1, 2, 3, \dots, n$) and respiratory phases (frames).

In the second validation, we compare the similarity of the sagittal cuts extracted from the reconstructed 4-D MRI with the original NS. The similarity measure is done using a cross-correlation function. We used NCC since contrast variation between the NS and DS may have been present. Higher NCC indicates that the diaphragm structure extracted from 4-D MRI is moving synchronously with the original NS.

Table 3 shows the results of two validation experiments: one is Z displacement error (in mm) and the other is geomean of NCC. The geomean of NCC is also shown in Fig. 10.

Table 3 Comparison of Z displacement error of diaphragm and geomean of normalized cross-correlation (NCC) of w/o T, 0.5, 0.4, and 0.3 threshold values.

Subject		w/o T			0.5			0.4			0.3		
		Z disp. error (mm)		Geomean of NCC	Z disp. error (mm)		Geomean of NCC	Z disp. error (mm)		Geomean of NCC	Z disp. error (mm)		Geomean of NCC
		Mean	SD		Mean	SD		Mean	SD		Mean	SD	
Volunteers	V1	2.51	0.24	0.85	2.56	0.26	0.85	2.63	0.37	0.84	2.60	0.33	0.83
	V2	2.32	0.53	0.86	2.39	0.55	0.84	2.71	0.72	0.82	2.94	0.89	0.81
	V3	2.46	0.47	0.80	2.83	0.68	0.79	3.14	0.75	0.78	3.62	0.82	0.75
	V4	3.06	1.12	0.85	3.13	1.17	0.84	3.27	1.23	0.84	3.36	1.29	0.83
	V5	2.56	0.72	0.73	2.61	0.81	0.73	2.83	0.83	0.73	3.05	0.89	0.72
	V6	2.98	1.00	0.67	3.27	1.14	0.67	3.39	1.27	0.66	3.03	1.38	0.66
	V7	2.52	1.17	0.80	2.48	1.17	0.80	2.62	1.22	0.80	2.43	1.33	0.79
Mean		2.63	0.75	0.79	2.75	0.83	0.79	2.94	0.91	0.78	3.00	0.99	0.77
Patients	P1	3.01	0.71	0.79	3.04	1.06	0.78	3.01	1.28	0.78	2.90	1.26	0.76
	P2	2.34	0.43	0.63	2.33	0.47	0.63	2.29	0.61	0.62	2.30	0.70	0.61
	P3	3.65	0.89	0.89	4.45	0.94	0.87	4.51	1.07	0.85	4.26	0.83	0.83
	P4	4.44	0.67	0.92	4.28	0.62	0.92	4.28	0.96	0.92	4.16	1.05	0.89
	P5	2.67	0.35	0.84	2.73	0.37	0.83	2.70	0.42	0.83	2.58	0.40	0.83
	P6	2.75	1.31	0.81	2.78	1.30	0.80	2.81	1.36	0.80	3.22	1.28	0.80
	P7	2.55	0.78	0.87	2.58	0.82	0.86	2.73	0.90	0.86	3.02	1.20	0.86
Mean		3.06	0.73	0.82	3.17	0.80	0.81	3.19	0.94	0.81	3.21	0.96	0.80

Fig. 10 Range and distribution of geomean of normalized cross-correlation (NCC) of (a) volunteers, (b) patients, and (c) all. The differences of geomean of the NCC among w/o T, 0.5, 0.4, and 0.3 threshold values were small for both volunteers and patients.

The averages of the geomean of NCC for volunteers were 0.80, 0.79, 0.78, and 0.77 for w/o T, 0.5, 0.4, and 0.3 threshold values, respectively. For the patients, the averages were 0.82, 0.81, 0.81, and 0.80 for w/o T, 0.5, 0.4, and 0.3 threshold values, respectively. The differences were very small, which indicates that the reconstructions using w/o T, 0.5, 0.4, and 0.3 threshold values were similar.

Figure 11 shows the range and distribution of Z displacement error when pooling all displacement differences of all phases of all subjects. The maximum errors for volunteers were 8.0, 8.0, 9.0, and 9.0 mm for w/o T, 0.5, 0.4, and 0.3 threshold values, respectively. For patients, the maximum errors were 8.0, 8.0, 8.0, and 9.0 mm for w/o T, 0.5, 0.4, and 0.3 threshold values, respectively.

The interval and range of the 95% confidence level are listed in Table 4.

5 Discussion

In this study, we implemented a fixed threshold using SSIM for our prospective method to reconstruct a 4-D MRI consisting of one breathing cycle. The main purpose of implementing the prospective method is to reduce the acquisition time of the DSs. In the cases when all SSIM values were lower than the threshold value, maximum acquisition time will be required. Also, when most SSIM values were lower than the threshold value, the time reduction was very small.

Reconstruction using a 0.5 threshold value for V5, for example, showed that the total DS acquisition time was 12 min, 39 s, while the original time acquisition was 14 min. The acquisition was only reduced by 1 min and 21 s, or 9.6%. Using the same

Fig. 11 Range and distribution of Z displacement error of diaphragm of (a) volunteers and (b) patients after pooling displacement differences of all phases of all subjects.

0.5 threshold value, V2 was reduced to 5 min and 14 s, while the original time acquisition was 24 min (reduced by 78.2%). Only a 9.6% time reduction was observed in V5 because most of the SSIM values in the intersection location were found to be lower than the threshold. As a result, the full acquisition time, 1 min, was required in most DSs.

We validated the 4-D MRI reconstruction visually and quantitatively. The visual validation includes MIP volume rendering and comparison of sagittal cuts between original NS and sagittal cuts extracted from 4-D MRI. Since the 4-D MRI is composed of a stack of coronal images captured, the thickness of the coronal image determines the resolution of the sagittal cut. Currently, the slice thickness is 7.5 mm. There may be a room to reduce the slice thickness 1 or 2 mm, but it is difficult to improve this resolution markedly, for example, twice. When the thickness is lowered, for example, to 3.0 or 4.0 mm, the signal-to-noise ratio becomes worse. Consequently, the image quality will also be degraded. Even if possible, the acquisition of many more DSs is needed. It does not meet the aim of time reduction. In spite of lower resolution of the sagittal cuts, the diaphragm shape of the sagittal cuts in Fig. 8, extracted from $X_s - 30$ mm, X_s , and $X_s + 30$ mm of the NS location, are clearly separable with other organs and the shapes look natural.

The first quantitative validation was performed by measuring the displacement error of diaphragm. Mean of Z displacement error using w/o T, 0.5, 0.4, and 0.3 threshold values was <5 mm. The standard deviation was also found to be small, which indicates that the displacement error in each respiratory phase is close to the mean.

The second quantitative validation was carried out by comparing the similarity of sagittal cuts from a reconstructed 4-D MRI with the NS as the ground truth. As shown in Fig. 11, the differences of geomean of the NCC among w/o T, 0.5, 0.4, and 0.3 threshold values were small for both volunteers and patients. Thus, the quality of reconstruction using the threshold method was very similar with the ground truth and, at the same time, the total data acquisition can be reduced up to 75%.

Table 4 Interval and range of 95% confidence level after pooling all displacement differences of all phases of all subjects.

Subject	w/o T		0.5		0.4		0.3	
	Interval (mm)	Range (mm)	Interval (mm)	Range (mm)	Interval (mm)	Range (mm)	Interval (mm)	Range (mm)
Volunteers	± 0.26	2.32 to 2.84	± 0.27	2.45 to 2.98	± 0.28	2.64 to 3.20	± 0.28	2.75 to 3.32
Patients	± 0.25	2.72 to 3.21	± 0.28	2.86 to 3.42	± 0.28	2.86 to 3.42	± 0.28	2.83 to 3.40

Fig. 12 Comparison of (a) sagittal cuts extracted from reconstructed 4-D MRI and (b) original NS of patient P2. The fat on the left bottom of the original NS reduces the NCC value.

The geomean of NCC for P2 was found to be smallest among the others. Figure 12 shows the sagittal cuts extracted from reconstructed 4-D MRI and the original NS of P2. In the bottom-left of the original NS, white region supposed to be fat was clearly observed. On the other hand, the bottom-left of the sagittal cut showed an unclear white region. Although the exact reason of this difference is unclear to us, the difference of spatial resolution could be a possible reason. This difference mainly seems to reduce the NCC value. However, the diaphragm surface from the sagittal cuts was also similar as the original NS. In fact, the displacement error was <3 mm from Table 3.

Finally, we introduce one application of 4-D MRI briefly. In Ref. 3, we demonstrated how to extract the diaphragm motion from 4-D MRI. The advantage of using 4-D MRI to extract diaphragm motion is that both the surface and its motion of wide region of the diaphragm can be captured. We then analyzed and compared displacement map that is derived from the diaphragm motion of healthy volunteers and COPD patients. Using the displacement map, we found that COPD patients tended to have smaller displacements in certain area compared to healthy volunteers. We were also able to locate paradoxical motion of the diaphragm, which is one of the COPD characteristics. Such information obtained from 4-D MRI will be beneficial for the physician and leads to a better treatment for COPD. In such an application, the aforementioned stable extraction of a diaphragm was very useful.

6 Conclusion

We have improved the intersection profile method proposed previously to reconstruct 4-D MR images. We carried out a prospective 4-D MRI reconstruction to shorten acquisition time.

Although the prospective synchronization method was tested only in simulations using previously acquired full data sets, we found that the prospective methods with 0.3 threshold value successfully reduced acquisition time of DSs by 75.6 and 84.0%, for volunteer and patient data, respectively.

The quality of the 4-D MRI reconstruction was visually evaluated in three aspects: volume rendering, MIP images, and sagittal cut images. In most cases, the image quality of prospective reconstruction of 4-D MRI was satisfactory. The quality of the 4-D MRI reconstruction was also validated by calculating the displacement of diaphragm and calculating the geomean NCC value between the reconstructed 4-D MRI and the original NS. Both validations showed that the prospective method is implementable for clinical applications.

One limitation in full-scale implementation of this method is the need of modification in terms of the manufacturing of an MR scanner system. However, upon implementation of this method, it is reasonable to expect that similar results will be achieved.

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