Probability-driven K-space Based Multi-cycle 4D-MRI Reconstruction
by

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James Bowsher

Thesis submitted in partial fulfillment of
the requirements for the degree of Master of Science, in the Department of
Medical Physics in the Graduate School
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ABSTRACT

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Abstract

Purpose: Current 4D-MRI techniques are prone to motion artifacts caused by irregular breathing. This study aims to develop and evaluate a novel, motion-robust multi-cycle 4D-MRI technique to overcome this deficiency.

Materials/Methods: The breathing signal was first analyzed to determine the main breathing cycles, providing tumor motion probability information for 4D-MRI reconstruction. 4D-MRI was reconstructed for each main breathing cycle using an in-house developed result-driven k-space reordering method. The new method was tested on the 4D-XCAT phantom. For comparison, conventional phase sorting method is also applied to generate a single-cycle 4D-MRI. Tumor and liver SNRs, tumor volume consistency, and AIP accuracy were determined and compared between the two methods. The original XCAT images were used as reference for the evaluations.

Results: Three-cycle 4D-MRI images were generated using the new method, presenting less noise and higher tumor and liver SNRs (30.41 and 15.28, 30.07 and 15.17, 28.63 and 15.25 for cycle 1, 2, and 3 respectively) than those of 4D-MRI images generated using phase sorting (17.33 and 12.04). These images have reduced motion artifacts, reflected by the improved inter-phase tumor volume consistency: the coefficients of variation in tumor volume were lower in the new method (0.027, 0.033 and 0.042 for cycle 1, 2, 3 respectively) than that of the phase-sorting method (0.072). In addition, the
AIP generated from the new method was more similar to the reference AIP than that from the phase sorting method; both the image intensity difference (0.21) and standard deviation of the difference map (6.4296e-8) were lower than those from the phase sorting method (0.46 and 1.1562e-7, respectively).

**Conclusion:** These results demonstrated the feasibility of the motion-robust, multi-cycle 4D-MRI technique through probability-driven k-space reordering. This new technique holds great promises to improve the image quality of 4D-MRI and the accuracy of its clinical applications.
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1. Introduction

1.1 Respiratory Motion Management and Four-Dimensional Imaging

Primary liver cancer and liver metastases are the main causes of worldwide cancer morbidity and mortality. The difficulty of treating abdominal tumor sites is exacerbated by respiratory motion within the thorax and abdomen regions [1-3]. Respiratory motion due to pulmonary and cardiac movement compromises thorax and abdomen radiation therapy treatment outcomes in several ways, including producing errors in tumor volume delineation, radiation dose delivery and dose distribution [4-9]. The precision and accuracy of radiation treatment planning and dose delivery are the main goals in radiation therapy, since they directly impact the treatment outcome. In order to manage tumor motion and deformation due to respiration, a time dimension has been introduced into three-dimensional radiation therapy (3D-RT) to monitor patient’s anatomical changes occurring either within a single fraction (intra-fractional) or between successive fractions (inter-fractional) [10], leading to the new technology of four-dimensional radiation therapy (4D-RT). 4D-RT has been applied to remove anatomical variations induced dose errors and to guide adaptive radiation treatment planning. In addition, 4D-RT corrects for daily set-up errors, which are caused by the adaptation of the treatment plan or patient repositioning. It can also control and verify radiation dose
delivery based on internal or external fiducial markers or anatomy landmarks whose motion can be continuously tracked [6], [11-14].

1.1.1 Four-Dimensional Computed Tomography

4D imaging technique is a key component of 4DRT. Four-dimensional computed tomography (4D-CT) is the current clinical standard for imaging respiratory motion in radiation therapy. It improves radiation therapy accuracy and dose delivery precision by better determining safety margins and internal target volumes with respiratory motion presence [4], [5]. However, several limitations have restricted the application of 4D-CT imaging in abdominal cancers. These limitations, include low soft tissue contrast, involvement of high imaging radiation dose to patients, and different types of artifacts caused by data acquisition and postprocessing, such as blurring, duplication, overlapping, and incompletion [6-8], [15-17].

1.1.2 Four-Dimensional Magnetic Resonance Imaging

Four-dimensional magnetic resonance imaging (4D-MRI) techniques have been recently developed to overcome the aforementioned limitations of 4D-CT in abdominal imaging [7]. Owing to its superior soft tissue contrast and no ionizing radiation dose, 4D-MRI can provide improved image contrast without significantly increasing imaging time and expense, to benefit radiation therapy outcomes [18], [19]. A detailed review and summary of recent 4D-MRI studies is presented in the literature [20].
1.2 Image-Space Based 4D-MRI Reconstruction

1.2.1 Image-Space Conventional Single-Cycle 4D-MRI Reconstruction

The most commonly used approach in the development of 4D-MRI is the retrospective method [7]. In this method, fast 2D MR pulse sequence is used to successively acquire images at all respiratory phases and slice locations. The images are then retrospectively sorted based on their respiratory status [7]. There are two major image sorting methods used in retrospective 4D-MRI reconstruction: phase sorting and amplitude sorting [4]. The former sorts images based on their respiratory phases, which are defined by the equally spaced relative phase positions within certain respiratory cycle. One respiratory cycle is usually divided into 10 phases in current clinical implementation. The latter sorts images based on their relative amplitudes. Specific amplitude thresholds and intervals are set to determine the sampling data belonging to which amplitude bin. The limitations, however, of this amplitude sorting approach is loss of time information, which is crucial in the development of 4D-MRI. In addition, amplitude sorting can introduce significant errors in reconstructed images if respiratory curve is highly irregular.

Besides these image sorting methods, there are two main data acquisition modes in the development of 4D-MRI: cine mode [20], [21], and sequential mode [22], [19]. In cine mode, 2D MR image data is acquired repeatedly at each slice location for a
relatively long time. The minimum imaging time at each slice position should be longer than the patient’s respiratory period in order to capture all breathing phases of the breathing cycle [23]. This image data acquisition process should be performed at each slice location, until the data set for the whole volume of interest (VOI) is complete. On the contrary, some 4D-MRI techniques use sequential mode to acquire 2D image data [22], [24]. In sequential mode 4D-MRI, 2D MR images are acquired sequentially throughout the entire VOI [5]. In this mode, one slice of 2D MR image is acquired only once at each slice location, from the first slice location to the last slice location. This process is then repeated for a number of times to ensure that there is enough sampling data of all respiratory phases for all slice locations in the VOI for 4D image reconstruction [5].

For the cine acquisition, which is used in 4D-CT and some 4D-MRI techniques, it is impossible to capture the breathing variation information across different respiratory phases at all slice locations due to its inherent data acquisition pattern. Since the time interval between consecutive data acquisitions at each slice location is so short that during which there is negligible breathing variation. As a result, in cine acquisition each slice experiences either less respiratory variation or no respiratory variation [23]. Under these circumstances, cine mode cannot be rendered to reveal the comprehensive respiration information, especially in terms of respiratory variation. On the other hand,
sequential acquisition that is used in some 4D-MRI techniques is capable of disseminating breathing variation information across all imaging slices attributing to the randomness of image acquisition in relation to the breathing signal [23].

1.2.2 Image-Space Probability-Driven Multi-Cycle 4D-MRI Reconstruction

Under comparison with cine mode, sequential mode is preferred for 4D-MRI imaging not only because it provides more accurate respiratory motion information, which was revealed in previous work [5], but also contains respiratory irregularity information. These properties make it possible for sequential mode to be utilized in probability-based multi-cycle 4D-MRI reconstruction [23]. Therefore, a novel probability-driven sorting method in image space that can generate multi-cycle 4D-MR images has been developed and presented in previous work [23]. The effectiveness of this novel method has been shown on significant motion artifacts reduction for 2D acquisition scenario in previous study [23]. This method originated from the probability density function (PDF) of tumor motion trajectory. The two major properties of which: stability and reproducibility over time had been studied and found by Cai et al. The irregular tumor motion trajectory due to patients’ irregular breathing compromises tumor motion management. Even for the same patient, the tumor motion trajectory varies from day to day. There is, however, an invariant parameter that can be extracted from the irregular tumor motion trajectory: the probability density function of tumor
motion. It has been shown that the tumor motion PDF becomes stable with the increment of time and the similar tumor motion PDF can be reproduced from day to day for the same patient. Based on these two key features, tumor motion PDF can be effectively utilized in tumor motion management. The generation of tumor motion PDF, however, using complete sampling data from tumor motion trajectory curve is time-consuming and impractical in clinical application. Even though the tumor motion trajectory is irregular, the main motion patterns still exist and can be extracted for generating the tumor motion PDF. It has been shown by Cai et al. in previous work that the tumor motion PDF obtained from the main cycles of tumor motion trajectory is basically the same as the real tumor motion PDF generated from the complete sampling data on the tumor motion trajectory. Therefore, the multiple main cycles of the tumor motion trajectory instead of single mean cycle can be rendered for the guidance of 4D-MR image reconstruction. The probability-driven multi-cycle sorting method in 2D acquisition scenario had then been developed. This method can be carried out in the following steps: The respiratory signal is first decomposed into individual breathing cycles which will be analyzed to determine the main breathing cycles of the patient. The average main cycles are determined by the average cycles of groups containing more than 10% of all the respiratory cycles. The raw 2D images are then selected and sorted
based on the main breathing cycles using a result-driven sorting method, resulting in multi-cycle 4D-MRI images [23].

Previous research has shown that the probability-based multi-cycle sorting method produces 4D-MRI images with better image quality with reduced motion artifacts as compared to the phase sorting method [23].

1.3 K-Space Based 4D-MRI Reconstruction

1.3.1 K-Space Conventional Single-Cycle 4D-MRI Reconstruction

In image-space based retrospective 4D-MRI, fast 2D MR pulse sequences and phase sorting method are utilized jointly. In this 2D acquisition scenario, k-space data is excited slice by slice, and each slice of k-space data is used for 2D image reconstruction. The 2D images are then sorted to generate 4D-MRI. However, there are various limitations for this approach: 1) the relatively low imaging rate (~3 frames/s) is insufficient to resolve complete breathing information and limits the temporal resolution of 4D-MRI; 2) irregular breathing often induces significant motion artifacts in 4D-MRI images, shown as tissue discontinuity at the tumor or organ boundary; and 3) the choices of fast 2D MR pulse sequences are limited. In order to overcome the aforementioned limitations of the 2D MRI based 4D image reconstruction, we introduced and developed in this work a new approach to generate 4D-MRI based on 3D k-space data acquisition and image reconstruction. In this new approach, we
intelligently integrated 3D k-space sorting and probability-based multi-cycle sorting methods to develop a novel, motion robust 4D-MRI technique. In the new 4D-MRI technique, the entire k-space volume is first excited, the k-space raw data instead of the reconstructed images then will be used for sorting. The sorted k-space volume data will be finally utilized to generate 4D-MRI. The temporal resolution of 4D-MRI can be potentially significantly improved since k-space data can be manipulated in a much finer manner than the image data.

1.3.2 K-Space Probability-Based Multi-Cycle 4D-MRI Reconstruction

Using a similar approach as described in the previous work of image-space probability-based multi-cycle 4D MRI [23], we first decompose the breathing signal to determine the main breathing cycles and for each main breathing cycle we reconstruct a set of 4D-MRI images by sorting the k-space data using the result-driven method [6].

Both 3D k-space phase sorting and 3D k-space probability-based multi-cycle sorting methods can potentially improve image quality as compared to current image-space based 4D-MRI technique. Furthermore, the new 4D-MRI technique can be implemented theoretically on any MR sequence, eliminating the requirement for high speed as in the image-space based 4D-MRI techniques. As a result, some of the slow but high quality MR sequences such as T2-w fast spine echo (FES) MR sequence which is
featured with high tumor contrast can be used for 4D-MRI development, potentially enhancing the final image quality of 4D-MRI.

1.4 Study Purpose

The existence of motion artifacts in 4D images can cause errors in target volume delineation which subsequently can adversely impact radiation treatment outcome. There are mainly two forms of irregular breathing induced motion artifacts in 4D-MR techniques, tissue discontinuity and noise. The former usually can be found in images reconstructed by conventional phase sorting method in image-space based 4D-MRI, while the latter mostly exists in k-space based 4D-MRI. In terms of clinical application, tissue discontinuity motion artifacts affect more on target volume delineation than noise. Current 4D-MRI development techniques, both single cycle phase sorting method and multi-cycle probability-driven sorting method under 2D acquisition scenario poorly handle breathing variations. In addition, they are prone to motion artifacts caused by irregular breathing. The general thesis work content is shown in Table 1. The three checked combinations (2D acquisition with single cycle phase sorting method; 3D acquisition with single cycle phase sorting method; 2D acquisition with multi-cycle probability-driven sorting method) had been presented by previous work [4-7], [20], [23].
Table 1: Thesis work structure and content

<table>
<thead>
<tr>
<th>Image acquisition approaches</th>
<th>2D acquisition</th>
<th>3D acquisition</th>
</tr>
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</tr>
<tr>
<td>Multi-cycle probability-driven sorting</td>
<td>✓</td>
<td>My work</td>
</tr>
</tbody>
</table>

Referring back to Table 1, the overall objective of this work is to develop and evaluate a novel, motion-robust multi-cycle 4D-MRI technique to overcome this deficiency. We will investigate the image quality improvement for 4D-MRI using 3D k-space phase sorting method and probability-driven k-space reordering method. The comparison between 2D and 3D acquisitions with single cycle phase sorting method in terms of image quality improvement was demonstrated. In addition, the comparison between 3D acquisition with single cycle sorting method and multi-cycle probability-driven sorting method was studied (the red arrows indicated in Table 1). The overall goal is achieved through two specific aims:

- Aim 1: Investigate the 3D k-space phase sorting method for single cycle 4D-MRI;
- Aim 2: Investigate and evaluate 3D k-space probability-driven sorting method for multi-cycle 4D-MRI.

This thesis paper is structured as follows: in the Method section, the principles and realizations of 3D k-space phase sorting and 3D k-space probability-based multi-
cycle reordering methods are introduced and explained in details; the calculations of the evaluation metrics: signal to noise ratio (SNR), tumor volume consistency and AIP are also presented in this section. In the Results section, the quantitative results and corresponding evaluations are shown. Finally, the discussion on the results, further study direction and conclusion are included in the Discussion and Conclusion sections.
2. Materials and Methods

2.1 **Aim 1: Investigate the 3D k-space phase sorting method for single cycle 4D-MRI**

This entails studying and comparing the motion artifacts in 4D-MR images reconstructed from both 2D phase sorting and 3D k-space phase sorting methods, evaluating the level of the artifacts and the efficacy of 3D k-space phase sorting method in image quality improvement.

2.1.1 **Aim 1.1: Study and compare the motion artifacts in 4D-MR images reconstructed by using 2D image-based phase sorting and 3D k-space phase sorting methods.**

The 4D-XCAT phantom [25] and on site MATLAB© are used in this simulation study. 4D-XCAT phantom is a digital human phantom that can generate realistic imaging data when it is combined with accurate imaging process models [25]. Generally, there are three k-space data sampling schemes: 1). Cartesian coordinate data sampling; 2). Axial data sampling; and 3). Helical data sampling. In addition, there are two main image sorting methods: 1). Phase sorting; and 2). Amplitude sorting. In the simulation study for **Aim 1.1**, Cartesian coordinate data sampling and phase sorting method are used on 4D-XCAT phantom for 4D-MRI reconstruction. In the Cartesian coordinate system simulation, there are two major data acquisition scenarios: 2D acquisition and 3D acquisition. The general 4D-MRI simulation workflows for 4D-XCAT phantom in 2D and 3D acquisition scenarios are shown in Figure 1.
In the simulation of 4D-MRI on 4D-XCAT for the 2D phase sorting method, the k-space data acquisition is performed on $uv$ plane and stepped in $w$ direction (axial direction) to fully cover the volume of interest. The respiratory curve is input as a breathing signal to drive the 4D-XCAT phantom program for generating multiple 2D MR images at different slice locations. These 2D MR images are then sorted based on their respiratory phases using phase sorting method \cite{4, 23}. The phase of each image slice location is determined as follows \cite{23}:

$$\varphi = \frac{t - t_{peak,i}}{t_{peak,i+1} - t_{peak,i}} \times 100\%$$  \hspace{1cm} (2.1)
where $t$ is the time point that image slice data is being acquired. It locates between the $i$th and the $(i+1)$th peaks. The set of sorted 2D MR images are grouped together to form a 3D MR image volume, and these 2D MR images within that 3D image volume are then sequentially arranged to form the 4D MR images. The data sampling interval of the respiratory curve is 0.03s; the image size is 512×512×50; the image resolution is 1mm at $x$ and $y$ directions, and 5mm at $z$ direction; tumor size is 30mm in diameter. The data acquisition completeness is set to be 95% [7]. Based on previous study [7], the data is considered to be enough for image reconstruction when the respiratory phase bin filling is 95% completed. The sampling period range is determined by the scan rate of conventional MR scanner, 1 frame/s to 5frames/s. Therefore, the data sampling period for image reconstruction ranges from 0.21s (5frames/s) to 0.99s (1 frame/s) with the step size of 0.03s. The optimal sampling period within the above range (0.21s - 0.99s) was used to do image data acquisition. The criterion of selecting the optimal sampling period is that by achieving the designated data acquisition completeness (95%) with the minimum time. The 0.03s step size of sampling period is set to be consistent with the respiratory curve sampling interval (0.03s). The benefit of this step size is that no need of interpolation for sampling. The above parameters apply to the whole thesis work.

In the simulation of 4D-MRI on 4D-XCAT for the 3D phase sorting method, similar to the processes in the 2D phase sorting scenario, the k-space data acquisition is performed in the $uvw$ volume. The k-space volume of interest is first excited, followed
by data acquisition on $uv$ plane along $w$ direction. In our simulation study, the three directions, $u$, $v$, and $w$ are not equivalent. Therefore, the data acquisitions on $uv$ plane along $w$ direction and on $vw$ plane along $u$ direction are different, because the direction of tumor motion was set only along $z$ direction. The respiratory curve is used as breathing signal. The 4D-XCAT phantom program is then driven to generate 3D volume MR images, instead of 2D slice images. In this study, the physical phantom and MR scanner are replaced by 4D-XCAT phantom and on site MATLAB®. Therefore, in order to simulate the k-space data acquisition process, the sampling data was converted into Fourier k-space by applying three dimensional fast Fourier Transform (3D-FFT). The three-dimensional forward Fourier Transform of a real-space function $f(x, y, z)$ can be mathematically expressed as:

$$F(\xi_x, \xi_y, \xi_z) = \iiint f(x, y, z)e^{-2\pi i(\xi_x x + \xi_y y + \xi_z z)} \, dx \, dy \, dz$$  \hspace{1cm} (2.2)$$

where the variables $\xi_x$, $\xi_y$, $\xi_z$ are real numbers, $f(x, y, z)$ is the real-space function, $F(\xi_x, \xi_y, \xi_z)$ is the expression of $f(x, y, z)$ in k-space (Fourier space). The triple integrals are taken over the entire three-dimensional real-space.

The formula (2.2) is in continuous form, which cannot be utilized in a computer program for discretized data. Instead, a discrete Fourier Transform is being used in digitized image and signal processing, which can be expressed in vector form as follows:

$$X_k = \sum_{n=0}^{N-1} e^{-2\pi i k \frac{n}{N}} x_n$$  \hspace{1cm} (2.3)$$
where \( x_n \) is three-dimensional array, \( X_k \) is the discrete Fourier Transform of \( x_n \),

\[ n = (n_1, n_2, n_3) \] and \( k = (k_1, k_2, k_3) \) are defined as three-dimensional vectors of indices from 0 to \( N-1 \), which is defined as \( N-1 = (N_1-1, N_2-1, N_3-1) \), and \( n/N = (n_1/N_1, n_2/N_2, n_3/N_3) \).

After the k-space data was obtained from 3D Fourier Transform, the k-space data was sorted based on specific respiratory phases. The three-dimensional inverse fast Fourier Transform (3D-IFFT) was then applied to convert the sorted k-space image data back into image space. The image space data was finally driven and sequentially arranged based on the time sequence information (respiratory phases) to generate the 4D-MR images.

3D k-space phase sorting is the inheritance and the extension of 2D image-space phase sorting method. For studying the efficacy of this 3D phase sorting method, tumor volume consistency was chosen as the image quality evaluation metric. Images driven by the same patient respiration curve were generated by both 2D phase sorting and 3D phase sorting methods, and tumor volume consistencies were calculated accordingly. To evaluate the tumor volume consistency, the tumor volumes at 10 respiratory phases were calculated for 2D image-space phase sorting method and 3D k-space phase sorting method, respectively. The determination of tumor volume consistency was executed as follows: In 4D-XCAT phantom, different organs and tumors are assigned with different metabolism values. Since tumors usually have relatively higher metabolisms than healthy organs in real clinical situation. In this 4D-XCAT phantom, the tumor
metabolism is assigned with the highest value (tumor metabolism = 150). Therefore, certain metabolism threshold (metabolism = 121) was set, and the voxel metabolism that was equal to or above the threshold was counted as tumor voxel. The number of tumor voxels was then determined and it was used to represent the tumor volume. A total of ten tumor volumes were normalized to the maximum tumor volume among those at ten respiratory phases. The standard deviation of the ten phases of tumor volumes was calculated for both 2D image space phase sorting method and 3D k-space phase sorting method. Please refer to the Results section.

2.1.2 Aim 1.2: Further determine the causes of the motion artifacts in 4D-MR images reconstructed from 3D k-space phase sorting method.

The improvement of image quality in terms of tumor volume preservation was observed in images reconstructed from 3D k-space phase sorting method. However, the motion artifacts still exist in the form of noise in images reconstructed from 3D k-space phase sorting method. The conventional phase sorting method, either in image-space or k-space, is performed based on single respiratory cycle, which is the mean cycle of the respiratory curve composed of multiple respiratory cycles. This single cycle phase sorting method, however, can be easily affected by respiration irregularity. Therefore, we assumed the motion artifacts (noise) in images reconstructed from the 3D k-space phase sorting method were caused by breathing irregularity. To test our assumption, the irregular respiratory curve was replaced by a regular cosine curve to generate 4D-MR images for comparison with the irregular respiratory curve scenario. The diagram of
irregular curve and regular curve is shown in Figure 2. The irregular curve is composed of multiple breathing cycles with different periods, usually 3 – 5 seconds. The regular curve is a cosine wave, which is the simple multiplication of one cycle. The period of the regular curve is set as 3.1 seconds.

![Figure 2: Irregular breathing curve (a) and regular cosine wave (b)](image)

The images reconstructed by 3D k-space phase sorting method based on irregular respiratory curve and regular cosine curve are illustrated in the Result 3.1.2. Significant motion artifacts (noise) reduction was observed in images reconstructed based on regular cosine curve compared with those by irregular breathing curve (patient respiratory curve). This is consistent with our assumption that breathing curve irregularity is one of the causes of noise in reconstructed images. The motion artifacts as a form of noise, however, still exist even in the regular cosine curve scenario. There must be another cause that accounts for the motion artifacts. One possible cause we proposed was intra-phase motion. To test our hypothesis, the phase bins of the regular cosine curve were shrunk into narrower ones. The general steps are illustrated in Figure 3.
Figure 3: The general steps of shrinking the original phase bins into narrower ones

As can be seen from Figure 3, the average displacement within one phase bin is determined by:

\[ d_{\text{Avg}} = \frac{d_{\text{Max}} + d_{\text{Min}}}{2} \]  

(2.4)

where the \( d_{\text{Max}} \) and \( d_{\text{Min}} \) are the maximum displacement and minimum displacement of the sampling data in one phase bin, the \( d_{\text{Avg}} \) is the mean displacement within that phase bin. Then the corresponding new displacements were calculated by:

\[ d_{\text{New}} = d_{\text{Avg}} + F \times (d_{\text{Orig}} - d_{\text{Avg}}) \]  

(2.5)

where \( d_{\text{New}} \) and \( d_{\text{Orig}} \) are the new displacement and original displacement, and the scale factor \( F \), introduced in equation (2.5), was chosen as 100% (original displacement), 40%, 10% and 1%. The comparison among these images with different scale factors is shown in the Result 3.1.2. Reducing the intra-phase motion caused artifact by shrinking the
phase bin range is impractical in clinical application. Because smaller phase bin implies that more data acquisition times are needed to obtain the optimal acquisition data point within the phase bin, which usually is selected if it locates at the center of phase bin. In that case, the data acquisition time is inevitably prolonged. Shrinking the phase bin to reduce intra-phase motion caused artifact is only for verification, that the intra-phase motion is another cause of motion artifacts. A practical approach of improving time efficiency of data acquisition meanwhile reduce the effect of intra-phase motion is k-space sparse data acquisition. It can be realized by acquiring less k-space boundary data whereas performing dense acquisition at the center of the k-space data. The feasibility of this sparse acquisition is based on the fact that the most important image data information is aggregated in the central low frequency region of the k-space, the boundary high frequency data usually appears as noise and can be ignored or weakened by assigning lower weighting. Since the acquisition data is not evenly distributed in k-space (sparse at the boundary, dense in the center), the sparse data region needs to be filled for subsequent image reconstruction. There are three approaches of doing data filling in k-space: (a). Zero boundary filling; (b). Data sharing; (c). Compressed sensing. Approaches (a) and (b) have been attempted in our study. For approach (a). Zero boundary filling, it is realized by simply padding 80% of the k-space boundary region with 0, and retaining the specific 20% central k-space data for each phase. The general idea of approach (b). Data sharing, is shown in Figure 4.
In k-space, the low frequency portion which locates at the central region of the data set contains dominant information. Based on Figure 4, the central portion (20%) of the data set is retained for each phase; for the remaining 80% of data of each phase, the combination of 8% data from each phase (10 phases combine to form the 80% high frequency data for each phase) was used to fill in the non-central region for each phase. In this case, all ten phases share the same 80% high frequency data, while their specific central portion data is retained. The images generated based on approaches (a) and (b) are shown in the Results 3.1.2 section.
2.2 Aim 2: Investigate and evaluate 3D k-space probability-driven sorting method for multi-cycle 4D-MRI

2.2.1 Aim 2.1: Develop and determine the feasibility of probability-driven k-space reordering method for multi-cycle 4D-MRI.

The fact that respiratory curve irregularity is one of the causes of motion artifacts has been revealed in the previous section, and significant motion artifact reduction has been observed via eliminating curve irregularity by replacing the irregular respiratory curve with a regular cosine curve. A previous study has presented the feasibility of the image-space probability-based multi-cycle sorting method for 4D-MRI in motion artifacts reduction [23]. A detailed review of this probability-based multi-cycle sorting method for 4D-MRI can be found in the literature [23]. The general workflow of performing this probability-driven k-space reordering method for multi-cycle 4D-MRI is shown in Figure 5 [23].
Figure 5: The workflow of probability-driven k-space reordering method for multi-cycle 4D-MRI

The transition from 2D image-space probability-based multi-cycle sorting method to 3D k-space probability-based multi-cycle sorting method is realized as follows: The breathing signal was first analyzed to determine the main breathing cycles, providing tumor motion probability information for 4D-MRI reconstruction. 4D-MRI was reconstructed for each main breathing cycle using an in-house-developed result-
driven k-space reordering method. The new method was tested on the 4D-XCAT phantom.

2.2.2 Aim 2.2: Evaluate the potential clinical efficacy of this probability-driven k-space reordering method (comparing with k-space single-cycle phase sorting method) for multi-cycle 4D-MRI.

For comparison purposes, a conventional phase sorting method is also applied to generate a single-cycle 4D-MRI. The signal-to-noise ratios (SNRs) for tumor and liver, tumor volume consistency, and average intensity projection (AIP) accuracy were determined and compared between the two methods. The original 4D-XCAT images were used as reference for the evaluations.

The equation of calculating SNR can be expressed as follows:

$$\text{SNR} = \frac{\mu}{\sigma}$$  \hspace{1cm} (2.6)

in which $\mu$ is the mean value of signal, and $\sigma$ is the standard deviation of the background noise. The determination of tumor volume consistency was described in section 2.1.1. The comparisons between these two methods in terms of SNR and tumor volume consistency are shown in the Results section.

Since the AIP reflects the weighted average static image over the entire respiratory phases at certain location, it can be used to evaluate the 4D-MR image quality for both 3D k-space phase sorting method and Probability-driven k-space multi-cycle sorting method. To evaluate the AIP accuracy, one volume of images is generated at each respiratory phase (10 phases in total), for 3D phase sorting method, probability-
driven k-space reordering method and original XCAT, respectively. The AIP images for the original 4D-XCAT phantom and images reconstructed from 3D k-space phase sorting method are the simple average volume image of the total volume images at 10 phases. However, for images reconstructed from probability-driven k-space reordering method, the AIP image is determined in a more complex way. Since there are three average main cycles in this method, not a single cycle as in the phase sorting method, the weightings of the three average main cycles and their specific periods should be incorporated in AIP image generation. Based on previous work [23], the frequencies of appearance and the periods of three average main cycles are 48%, 3.13 s; 32%, 3.25 s; and 20%, 3.70 s, respectively [23]. Following which, the calculation of AIP for 3D k-space probability-based multi-cycle sorting method is expressed as follows [23]:

\[
AIP_{\text{probability-based}} = \frac{\sum I_{j,k} w_{j,k} T_{\text{main cycle},j}^{w_{\text{main cycle},j}}}{\sum T_{\text{main cycle},j}^{w_{\text{main cycle},j}}}
\]  

(2.7)

in which, \(T_{\text{main cycle},j}\) and \(w_{\text{main cycle},j}\) are the period and the weighting (frequency of occurrence) of the \(j\)th main cycle; \(I_{j,k}\) is the 3D image volume at the \(k\)th amplitude bin of the \(j\)th main cycle; and \(\mu_{j,k}\) is the ratio of the time interval at the \(k\)th amplitude bin in the \(j\)th main cycle to the \(j\)th main cycle period, \(T_{\text{main cycle},j}\) [23]. Furthermore, the difference maps of AIPs between AIP reference and 3D k-space phase sorting AIP; and between AIP reference and probability-driven k-space reordering method AIP were calculated by [23]:

25
\[ dAIP_v = \frac{1}{n_v} \sum_{(i,j,k) \in V} |AIP(i,j,k) - AIP_{ref}(i,j,k)| \] (2.8)

where \( dAIP_v \) is the AIP difference in image volume, \( n_v \) is the number of voxels in that image volume, \( AIP(i,j,k) \) and \( AIP_{ref}(i,j,k) \) are the intensities of AIP at coordinate \((i,j,k)\) in reconstructed images and reference images, respectively. The summation was taken in the entire image volume. In this simulation study, patient breathing curve and artificial respiratory curve composing of two main cycles were used for verification and comparison between 3D k-space phase sorting method and probability-driven k-space reordering method. The frequencies of appearance, amplitudes and periods of these two main cycles of the artificial curve are 50\%, 14.5mm and 2.77s; 50\%, 30.0mm and 2.25s, respectively [23]. The evaluation between the difference maps of AIPs is shown in the Results section.
3. Results

3.1 Quantitative evaluation of 3D k-space phase sorting method in 4D-MRI reconstruction

3.1.1 The comparison of motion artifacts between 4D-MR images reconstructed by 2D image-space phase sorting method and 3D k-space phase sorting method.

The patient breathing curve that drives 4D-MR image generation is shown in Figure 6. The comparison of 4D-MR images reconstructed accordingly from 2D phase sorting method and 3D k-space phase sorting method based on patient breathing curve is shown in Figure 7.

Figure 6: The patient breathing curve that drives 4D-MR images reconstruction
From Figure 7, the discontinuity artifact can be observed in the 2D image (indicated by yellow arrows), whereas the continuity is better preserved in the 3D image; the noise (motion artifact), however, is introduced. The tumor continuities (tumor volume consistencies) of 2D phase sorting images and 3D k-space phase sorting images are shown in Table 2.
Table 2: Tumor volume consistencies for 2D phase sorting method and 3D phase sorting method based on patient breathing curve

<table>
<thead>
<tr>
<th>TVC</th>
<th>3D K-Space Phase Sorting Single Cycle</th>
<th>2D Cine Phase Sorting Single Cycle</th>
</tr>
</thead>
<tbody>
<tr>
<td>Phase 1</td>
<td>98.58%</td>
<td>88.01%</td>
</tr>
<tr>
<td>Phase 2</td>
<td>100.00%</td>
<td>99.04%</td>
</tr>
<tr>
<td>Phase 3</td>
<td>90.96%</td>
<td>92.00%</td>
</tr>
<tr>
<td>Phase 4</td>
<td>84.73%</td>
<td>88.70%</td>
</tr>
<tr>
<td>Phase 5</td>
<td>82.56%</td>
<td>86.57%</td>
</tr>
<tr>
<td>Phase 6</td>
<td>81.27%</td>
<td>81.56%</td>
</tr>
<tr>
<td>Phase 7</td>
<td>82.27%</td>
<td>59.24%</td>
</tr>
<tr>
<td>Phase 8</td>
<td>82.78%</td>
<td>84.97%</td>
</tr>
<tr>
<td>Phase 9</td>
<td>95.84%</td>
<td>100.00%</td>
</tr>
<tr>
<td>Phase 10</td>
<td>89.29%</td>
<td>93.45%</td>
</tr>
<tr>
<td>Std. of 10 Phases</td>
<td>0.0720</td>
<td>0.1149</td>
</tr>
</tbody>
</table>

As can be seen from Table 2, images reconstructed by 3D phase sorting method show less tumor volume fluctuation among 10 respiratory phases with a lower standard deviation compared with that in 2D phase sorting method. In comparison, the 3D phase sorting method provides better tumor volume consistency, which can subsequently benefit target volume delineation in treatment planning.

3.1.2 Determination of the causes of the motion artifacts in 4D-MR images reconstructed from 3D k-space phase sorting method.

The images reconstructed through 3D k-space phase sorting method with patient respiratory curve and regular cosine wave are illustrated in the Figure 8.
Figure 8: The comparison between images reconstructed from irregular respiratory curve and regular cosine curve using 3D k-space phase sorting method

From Figure 8, motion artifacts (noise) were significantly reduced in images reconstructed with regular cosine curve (the second row in Figure 8) compared with those by patient breathing curve (the first row in Figure 8). This fact is consistent with our hypothesis that breathing curve irregularity is one cause of the motion artifacts in images reconstructed by 3D k-space phase sorting method.

The images generated by 3D k-space phase sorting method with shrunk phase bin range, mentioned in Materials and Methods 2.1.2, are shown in Figure 9.
Figure 9: Images reconstructed by 3D k-space phase sorting method based on regular cosine wave with scale factors 100% (the top row), 40% (the second row), 10% (the third row) and 1% (the last row), respectively.

Figure 9 demonstrates the motion artifacts (in the form of noise) were reduced by shrinking the phase bin range. This is consistent with our previous hypothesis that the intra-phase motion is another cause of the motion artifacts in images reconstructed by 3D k-space phase sorting method.

The images generated by the k-space data sharing method are shown in Figure 10.
Figure 10: Comparison among coronal view images (slice 256) without data sharing (right upper corner), 10 phases boundary data sharing (right lower corner) and zero boundary data filling (left upper corner)

As can be seen from Figure 10, the image with zero boundary data filling is smoother than the original image without data sharing. Referring to the image with 10-phase boundary data sharing, there are some ghost artifacts. The further evaluation on this result is presented in the Discussion section.
3.2 Quantitative evaluation of probability-driven k-space reordering method for multi-cycle 4D-MRI

3.2.1 The development and the feasibility determination of probability-driven k-space reordering method for multi-cycle 4D-MRI.

The coronal view images reconstructed from both 3D phase sorting and probability-driven multi-cycle sorting methods based on artificial curve and patient breathing curve are demonstrated in Figure 11 and Figure 12, respectively.

Figure 11: 10 phases of images reconstructed by 3D phase sorting (single cycle) method and probability-driven multi-cycle sorting method (two cycles). The yellow circles indicate the tumor locations.
Figure 12: 10 phases of images reconstructed by 3D phase sorting (single cycle) method and probability-driven sorting method (three cycles). The yellow circles indicate the tumor locations.

As can be observed from Figure 11 and Figure 12, the images guided by multi-cycle respiratory motion can be reconstructed through probability-driven k-space reordering method. This shows the feasibility of the application of this method for multi-cycle 4D-MRI. The quantitative evaluation of the images reconstructed by 3D phase sorting and probability-driven k-space reordering methods is presented in the following section.

3.2.2 The potential clinical efficacy evaluation of probability-driven k-space reordering method (compared with k-space single-cycle phase sorting method) for multi-cycle 4D-MRI.

Figure 11 and Figure 12 show the noise level reductions in cycle 1 and cycle 2 images in the artificial-curve scenario, and cycle 1, cycle 2 and cycle 3 images in the patient-curve scenario compared with the single cycle images. The quantitative
evaluations of SNRs in tumor and liver regions at 10 respiratory phases for both methods using artificial curve and patient curve are shown in Table 3 and Table 4, respectively.

<table>
<thead>
<tr>
<th>SNR (Artificial curve)</th>
<th>3D K-Space Phase Sorting</th>
<th>Probability-driven (Cycle 1)</th>
<th>Probability-driven (Cycle 2)</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Tumor (SNR)</td>
<td>Liver (SNR)</td>
<td>Tumor (SNR)</td>
</tr>
<tr>
<td>Phase 1</td>
<td>37.3692</td>
<td>21.9359</td>
<td>52.0291</td>
</tr>
<tr>
<td>Phase 2</td>
<td>14.7073</td>
<td>14.4562</td>
<td>25.0920</td>
</tr>
<tr>
<td>Phase 3</td>
<td>11.5669</td>
<td>9.8530</td>
<td>35.7739</td>
</tr>
<tr>
<td>Phase 8</td>
<td>22.6895</td>
<td>16.2455</td>
<td>53.1538</td>
</tr>
<tr>
<td>Phase 9</td>
<td>38.3730</td>
<td>15.7697</td>
<td>39.2259</td>
</tr>
<tr>
<td>Phase 10</td>
<td>41.9463</td>
<td>18.6611</td>
<td>70.1919</td>
</tr>
<tr>
<td>Average SNR</td>
<td>20.7753</td>
<td>13.1140</td>
<td><strong>40.9009</strong></td>
</tr>
</tbody>
</table>
Table 4: The SNRs of tumor and liver regions in the patient-curve scenario, at all phases, for 3D k-space phase sorting and probability-driven k-space reordering methods

<table>
<thead>
<tr>
<th>SNR (Patient curve)</th>
<th>3D K-Space Phase Sorting</th>
<th>Probability-driven (cycle 1)</th>
<th>Probability-driven (cycle 2)</th>
<th>Probability-driven (cycle 3)</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Tumor (SNR)</td>
<td>Liver (SNR)</td>
<td>Tumor (SNR)</td>
<td>Liver (SNR)</td>
</tr>
<tr>
<td>Phase 1</td>
<td>20.2812</td>
<td>13.5426</td>
<td>32.4675</td>
<td>16.0142</td>
</tr>
<tr>
<td>Phase 6</td>
<td>13.3773</td>
<td>12.4678</td>
<td>34.8270</td>
<td>15.1115</td>
</tr>
<tr>
<td>Phase 7</td>
<td>10.0402</td>
<td>11.8377</td>
<td>20.2977</td>
<td>14.0437</td>
</tr>
<tr>
<td>Average SNR</td>
<td>17.3273</td>
<td>12.0419</td>
<td><strong>30.4141</strong></td>
<td><strong>15.2844</strong></td>
</tr>
</tbody>
</table>

From Table 3 and Table 4, significant SNR improvement, especially in the tumor region, can be observed in images reconstructed by the probability-driven k-space reordering method in both the artificial-curve and patient-breathing-curve cases. Which meets our expection.

The quantitative results of tumor volume consistencies for both 3D k-space phase sorting and probability-driven k-space reordering methods for both artificial and patient curves are shown in Table 5 and Table 6, respectively.
Table 5: Tumor volume consistencies (artificial curve) for 3D k-space phase sorting vs probability-driven k-space reordering

<table>
<thead>
<tr>
<th>TVC (Artificial curve)</th>
<th>Probability-driven k-space reordering</th>
<th>3D K-Space Phase Sorting</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Cycle 1</td>
<td>Cycle 2</td>
</tr>
<tr>
<td>Phase 1</td>
<td>98.95%</td>
<td>95.45%</td>
</tr>
<tr>
<td>Phase 2</td>
<td>100.00%</td>
<td>92.26%</td>
</tr>
<tr>
<td>Phase 3</td>
<td>93.63%</td>
<td>92.46%</td>
</tr>
<tr>
<td>Phase 4</td>
<td>90.50%</td>
<td>82.56%</td>
</tr>
<tr>
<td>Phase 5</td>
<td>88.67%</td>
<td>79.62%</td>
</tr>
<tr>
<td>Phase 6</td>
<td>90.47%</td>
<td>79.71%</td>
</tr>
<tr>
<td>Phase 7</td>
<td>92.00%</td>
<td>82.75%</td>
</tr>
<tr>
<td>Phase 8</td>
<td>97.41%</td>
<td>90.81%</td>
</tr>
<tr>
<td>Phase 9</td>
<td>94.48%</td>
<td>91.46%</td>
</tr>
<tr>
<td>Phase 10</td>
<td>93.94%</td>
<td>93.65%</td>
</tr>
<tr>
<td>Std. of 10 Phases</td>
<td>0.0379</td>
<td>0.0616</td>
</tr>
</tbody>
</table>

Table 6: Tumor volume consistencies (patient breathing curve) for 3D k-space phase sorting vs probability-driven k-space reordering

<table>
<thead>
<tr>
<th>TVC (Patient curve)</th>
<th>Probability-driven k-space reordering</th>
<th>3D k-space phase sorting</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Cycle 1</td>
<td>Cycle 2</td>
</tr>
<tr>
<td>Phase 1</td>
<td>94.49%</td>
<td>93.98%</td>
</tr>
<tr>
<td>Phase 2</td>
<td>96.31%</td>
<td>94.20%</td>
</tr>
<tr>
<td>Phase 3</td>
<td>93.18%</td>
<td>88.41%</td>
</tr>
<tr>
<td>Phase 4</td>
<td>89.97%</td>
<td>88.60%</td>
</tr>
<tr>
<td>Phase 5</td>
<td>88.86%</td>
<td>87.07%</td>
</tr>
<tr>
<td>Phase 6</td>
<td>88.60%</td>
<td>88.41%</td>
</tr>
<tr>
<td>Phase 7</td>
<td>91.02%</td>
<td>88.78%</td>
</tr>
<tr>
<td>Phase 8</td>
<td>92.98%</td>
<td>90.39%</td>
</tr>
<tr>
<td>Phase 9</td>
<td>93.98%</td>
<td>95.82%</td>
</tr>
<tr>
<td>Phase 10</td>
<td>95.25%</td>
<td>94.88%</td>
</tr>
<tr>
<td>Std. of 10 Phases</td>
<td>0.0271</td>
<td>0.0329</td>
</tr>
</tbody>
</table>
Tables 5 and 6 show that at 10 respiratory phases, tumor volumes are better preserved and the tumor volume fluctuation is less (with lower standard deviation of tumor volumes at 10 phases) in probability-driven k-space reordering method compared with 3D k-space phase sorting method in both artificial-curve and patient-curve scenarios.

The axial view AIP images containing tumor for XCAT reference, 3D phase sorting method, probability-driven k-space reordering method are shown in Figure 13 for artificial curve; and Figure 14, for patient breathing curve. The corresponding AIP difference maps are illustrated in Figure 15 and Figure 16, respectively. The corresponding quantitative results on the images are demonstrated in Table 7 and 8.

![Figure 13](image)

**Figure 13:** Axial view AIP images containing tumor sites for the XCAT reference (first row), 3D k-space phase sorting method (second row), and probability-driven k-space reordering method (third row) in artificial curve scenario.
Figure 14: Axial view AIP images containing tumor sites for the XCAT reference (first row), 3D k-space phase sorting method (second row), and probability-driven k-space reordering method (third row) in patient breathing curve case.

Figure 15: Coronal view of AIP difference maps containing tumor sites for 3D phase sorting vs XCAT (the first row) and probability-driven k-space reordering vs XCAT (the second row) in artificial curve scenario.
Figure 16: Coronal view of AIP difference maps containing tumor sites for 3D phase sorting vs XCAT (the first row), and probability-driven k-space reordering vs XCAT (the second row) in patient breathing curve scenario.

<table>
<thead>
<tr>
<th>AIP evaluation (Artificial curve)</th>
<th>Standard deviation of the AIP difference map</th>
<th>Intensity difference per voxel averaged over the entire volume</th>
</tr>
</thead>
<tbody>
<tr>
<td>(3D k-space sorting) vs (origin XCAT ref AIP)</td>
<td>1.0310e-7</td>
<td>0.3914</td>
</tr>
<tr>
<td>(Probability-driven) vs (origin XCAT ref AIP)</td>
<td>5.0812e-8</td>
<td>0.1530</td>
</tr>
</tbody>
</table>
Table 8: 3D k-space phase sorting vs probability-driven k-space reordering in AIP evaluation (Patient Curve)

<table>
<thead>
<tr>
<th>AIP evaluation (Patient curve)</th>
<th>Standard deviation of the AIP difference map</th>
<th>Intensity difference per voxel averaged over the entire volume</th>
</tr>
</thead>
<tbody>
<tr>
<td>(3D k-space sorting) vs (origin XCAT ref AIP)</td>
<td>1.1562e-7</td>
<td>0.4602</td>
</tr>
<tr>
<td>(Probability-driven) vs (origin XCAT ref AIP)</td>
<td>6.4296e-8</td>
<td>0.2105</td>
</tr>
</tbody>
</table>

From Figure 13 to Figure 16, and Table 7 and Table 8, images reconstructed by the probability-driven k-space sorting method provide more accurate AIP compared with the 3D k-space phase sorting method, in both the artificial-curve and patient-breathing-curve scenarios. The probability-driven k-space reordering method yields lower standard deviation of the AIP difference map and less AIP intensity difference per voxel in the artificial-curve case (5.0812e-8, 0.1530), and patient-breathing case (6.4296e-8, 0.2105), compared with 3D phase sorting method in the artificial-curve case (1.0310e-7, 0.3914) and patient curve case (1.1562e-7, 0.4602).
4. Discussion

This study shows the image quality improvement in terms of reducing discontinuity artifacts by 3D phase sorting method compared with conventional 2D phase sorting method. The development of a probability-driven k-space reordering method has been developed, and its feasibility has been shown. For evaluation of this probability-driven k-space reordering method, and estimation of its clinical efficacy, SNR, tumor volume consistency, AIP accuracy, and AIP difference maps have been investigated. Compared with 3D k-space phase sorting method, the probability-driven k-space reordering method can improve image quality by providing higher SNRs in tumor and liver regions, and better tumor volume consistency and more accurate AIPs. The results are promising.

However, there are several limitations in our study. The method of k-space data sharing and sparse acquisition to solve the intra-phase motion issue is not finalized. Even though the images gotten from zero boundary data filling are smoother than the original image without data sharing, it is impossible to apply this method in clinical application because throwing away the boundary data is not practical. Zero boundary data filling is just for comparison purpose. Furthermore, there are some ghost artifacts in images reconstructed by 10-phase boundary data sharing method.

The possible reasons for ghost artifacts are:
(1) No correction was made for phase shift in k-space which originates from time shift in the spatial domain when doing the Fast Fourier Transform [26]:

\[ f_1(t) = f(t - t_0) \leftrightarrow F_1(\Omega) = F(\Omega)e^{-j\Omega t_0} \]  

(2.9)

(2) Boundary data acquisition has an obvious regular pattern, which is believed to be the main cause of the ghost artifacts;

(3) The k-space volume data is non-centrosymmetric. In theory, MR k-space image data is centrosymmetric, however, this aspect was not considered in our first trial.

The above possible reasons lead to corresponding possible solutions, which may be the further study directions:

(1). Apply phase shift correction for each phase of k-space data;

(2). Use random phase shift correction to eliminate the regular boundary data acquisition pattern;

(3). Rotate the upper half k-space volume data to pad the lower half to make corrections for the non-centrosymmetric issue.

Future study will focus on 3D k-space data sharing, sparse data acquisition in the k-space volume and corresponding image reconstruction algorithms. We believe the combination of a probability-driven k-space reordering method and a k-space data sharing and sparse acquisition method has potential to further improve image quality for 4D-MRI.
5. Conclusion

Our results showed that, as compared to current image-space based 4D-MRI techniques, both the 3D k-space phase sorting method and the probability-driven k-space reordering method can improve image quality, image consistency, precision and accuracy for 4D-MRI. The 3D k-space phase sorting method preserves tumor volume continuity even with irregular-breathing induced noise. The novel probability-driven k-space reordering method can further improve image quality by reducing the irregular-motion induced motion artifacts (noise). As the evaluation metric for image consistency, precision and accuracy, the AIP in probability-driven k-space reordering method performs better than the AIP in 3D k-space phase sorting method, when both are compared with the reference AIP of XCAT phantom. Overall, this research work has developed a novel, motion robust 4D-MRI technique based on probability-driven k-space reordering and has demonstrated the effectiveness of this method in improving image quality for 4D-MRI. The improvements are manifest in reduced irregular-breathing induced motion artifacts. The generality and robustness of this new 4D-MRI technique warrants further evaluation for real patients.
Bibliography


