Reducing short-scan artifacts in 3D axial cone-beam CT with extra views

Jang Hwan Cho, Debashish Pal, Jean-Baptiste Thibault and Jeffrey A. Fessler

***Abstract*—For 3D axial cone-beam CT, the short-scan approach has advantages, such as improved temporal resolution and lower dose, compared to the full-scan approach, due to significantly reduced data acquisition time. However, decreased angular span of the projections leads to insufficient sampling at certain voxel locations in third-generation CT geometries. Such sampling leads to artifacts in the reconstructed image, especially on slices away from the iso-plane. Using more projection views in the reconstruction can reduce such artifacts, but has the trade-off of decreased temporal resolution. This paper investigates a model-based iterative reconstruction (MBIR) method that reduces short-scan artifacts in the under-sampled slices while preserving the temporal resolution in the well-sampled slices. Clinical cardiac scans typically include extra views for the purpose of viewing different phases, motion-compensation algorithms, etc.. Here we use such extra views to reduce short-scan artifacts in the undersampled region. Using XCAT phantom simulations, we investigated an approach to modifying the statistical weights associated with the extra views. This approach reduced short-scan artifacts, particularly in slices near the ends of the axial field-of view (FOV).**

I. Introduction

When 3D axial cone-beam CT scanners are used for cardiac imaging, the short-scan approach, which has angular span of $\pi+2\gamma$ where γ is the fan angle of the projection, is the standard protocol due to its reduced data acquisition time compared to the full-scan approach. Short-scan approach allows improved temporal resolution and lower dose at the expense of increased image noise level. However, decreasing angular span of the measurement from 2π to $\pi + 2\gamma$ leads to a problem of insufficient sampling[1] at certain voxel locations in the third-generation CT geometry (see Fig. 1 for a diagram of sampling at each slice). More voxels in each slice become insufficiently sampled as one moves away from the iso-plane, and this situation becomes more severe as the cone angle becomes larger. Using more projection views for reconstruction can reduce such artifacts, but at the expense of decreased temporal resolution. Fig. 2 (b) shows that, for a short-scan, as we move toward end slices, we see noticeable artifacts (indicated by red arrows) in the reconstructed images resulting from insufficient sampling. On the other hand, reconstructed images from full-scan measurements (Fig. 2 (a)) do not show such artifacts, but suffer from severe motion artifacts (indicated by green arrows).

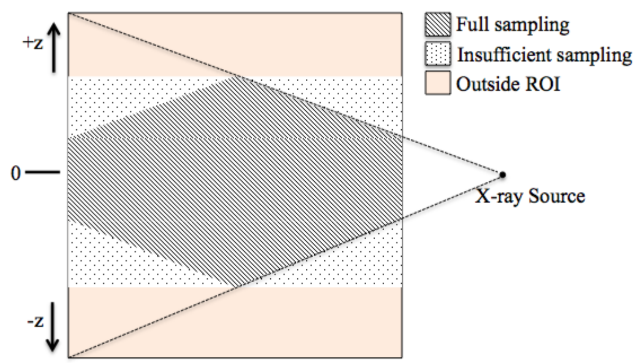

Fig. 1. Diagram of sampling at each slice for axial CT geometry.

Current iterative image reconstruction methods do not provide satisfactory images from short-scans for slices far away from the iso-plane. We want to develop a method that reduces short-scan artifacts on those slices. In clinical settings, it is common to acquire extra projection views for purposes such as viewing different phases, use of motion-compensation algorithms, etc.. Extra projection views may be prospectively acquired at much lower dose using tube current modulation, which would allow improved sampling condition without increasing the concern of patient dose. In this study, we investigate a method for model-based iterative reconstruction (MBIR) that uses such extra acquisition data to reduce short-scan artifacts in the undersampled region. The goal is to use the part of extra measurements to remove short-scan artifacts without compromising the temporal resolution in the sufficiently sampled region, or so called "football" region. We propose a statistical weighting modification approach, which was evaluated with the XCAT phantom simulation.

II. Methods

Consider a PWLS objective function of the form

$$\Psi(\boldsymbol{x}) = \mathsf{L}(\boldsymbol{x}) + \mathsf{R}(\boldsymbol{x}), \quad \mathsf{L}(\boldsymbol{x}) = \frac{1}{2}\|\boldsymbol{y} - \boldsymbol{A}\boldsymbol{x}\|^2_{\boldsymbol{W}}, \qquad (1)$$

where $\boldsymbol{y}$ is a measurement vector, $\boldsymbol{A} = \{a_{ij}\}$ is the system matrix, $\boldsymbol{x}$ is the discretized version of the object being imaged, $\boldsymbol{W} = \text{diag}\{w_i\}$ is a statistical weighting matrix, and $\mathsf{R}(\boldsymbol{x})$ is a regularizer. The basic idea behind our proposed statistical weighting modification is to selectively use additional

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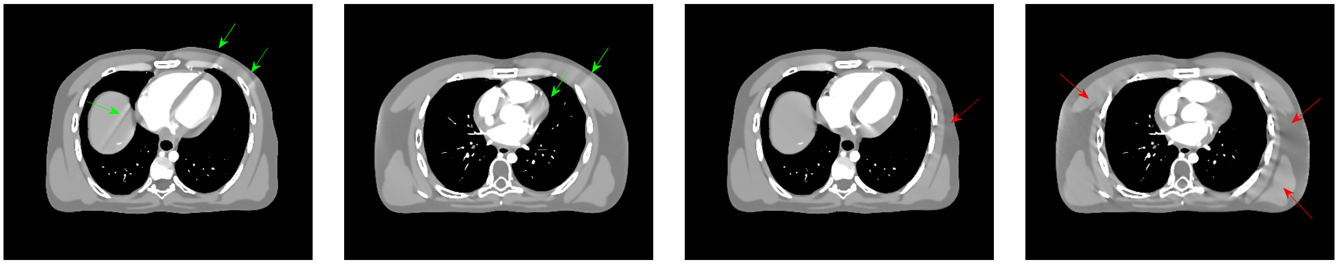
[1]In this document, "full" or "sufficient" sampling does not mean that they satisfy the complete sampling conditions [1], [2], but rather mean that the voxel is seen in every projection view. Thus, insufficient sampling indicates the voxel is seen in only part of the projection views.



(a) Full-scan, end slices (b) Short-scan, end slices

Fig. 2. Reconstructed images of the XCAT phantom using full-scan measurements and short-scan measurements at end slices. Measurements were obtained from a 64-slice CT scanner with 40 mm collimation. Green and red arrows indicate motion artifacts and short-scan artifacts, respectively. Display window is [850 1150] (HU).

measured views for each voxel depending on the sampling properties of the short-scan views. Undersampled voxels can benefit from using the additional measurements. However, some of these additional measurements affect not only the undersampled voxels but also other sufficiently sampled voxels, thus potentially degrading their temporal resolution. At one extreme, using all the additional measured views would lead all voxels to have the deteriorated temporal resolution of the full-scan reconstruction. Therefore, our goal is to optimize the use of additional measurements so that the temporal resolution of the well-sampled reconstructed slices are minimally affected and at the same time the short-scan artifacts are reduced. Since there is a trade-off between the temporal resolution and the short-scan artifact reduction, we need to determine which characteristic is more important for each voxel. For our analysis below, we strongly encourage the voxels inside the football region to have the same temporal resolution as the short-scan reconstruction. For all other voxels, we maximize the use of additional measurements.

First, we introduce the following new metric to quantify the effect of the ith detector measurement for a targeted region

$$e_i = \frac{\sum_{j=1}^{n_\mathrm{p}} a_{ij} m_j^{(t)}}{\sum_{j=1}^{n_\mathrm{p}} a_{ij} m_j^{(c)}}, \tag{2}$$

where a_{ij} is the elements of the system matrix, n_p is the number of voxels, $m_j^{(t)}$ is the jth element of the mask for a targeted region, and $m_j^{(c)}$ is the jth element of the cylindrical mask. The value of this metric varies from 0 to 1 where 0 means that the ray corresponding to the detector cell does not pass through the targeted region. As mentioned above, we use football region as our targeted region, but one may define the mask differently depending on the purpose.

Second, we modify the statistical weighting based on this metric. We investigated the following modified statistical weighting:

$$\hat{\boldsymbol{W}} \triangleq \boldsymbol{W}\boldsymbol{D}[p_i]\boldsymbol{D}[u_i] = \boldsymbol{D}[w_i p_i u_i], \tag{3}$$

where $\boldsymbol{W} = \{w_i\}$ is the conventional choice for the statistical weighting, p_i indicates the Parker weighting used to match the temporal resolution of the FBP reconstruction, and

$$u_i = \left\{ \begin{array}{cc} 1, & \text{if } i \text{ is within short-scan view range} \\ 1 - e_i & \text{otherwise} \end{array} \right\}. \tag{4}$$

To add more freedom to our design, we investigated the following design

$$\bar{u}_i = f(u_i) = (u_i)^p, \tag{5}$$

where p is a tuning parameter that we explored empirically.

In addition to visual comparison, we need a metric to quantitatively evaluate the reconstructed image obtained by the proposed method. The most intuitive measure would be counting the number of views or detector elements affecting each voxel when our modified weighting is used. However, calculating such measure may not be trivial or computationally efficient. Instead, we propose the following metric called "view mask" for a given statistical weighting w_i:

$$m_j \triangleq \sum_v \frac{\sum_{s,t} a_{(s,t,v)j} w_{(s,t,v)}}{\sum_{s,t} a_{(s,t,v)j} o_{(s,t,v)}}, \tag{6}$$

where $o_i = o_{(s,t,v)} = 1$, $\forall i$, and s, t, and v indicate channel, row, and view indexes in the projection domain, respectively. The ratio between the view masks of two different weightings, or "view ratio", can be used to quantify the "closeness" of the proposed method to either full-scan MBIR or short-scan MBIR at certain location. For example, the view ratio between the proposed method and short-scan MBIR is given by

$$r_j \triangleq \frac{m_j^{\text{proposed}}}{m_j^{\text{short-scan}}} = \sum_v \frac{\sum_{s,t} a_{(s,t,v)j} \hat{w}_{(s,t,v)}}{\sum_{s,t} a_{(s,t,v)j} \bar{w}_{(s,t,v)}}, \tag{7}$$

where $\hat{w}_i = w_i p_i \bar{u}_i$, and $\bar{w}_i = w_i p_i$. For this case, if the jth voxel has $r_j = 1$, then, the temporal resolution of the proposed method is (approximately) equivalent to that of short-scan MBIR at that location. For our analysis, we want the voxels inside the football region to have the view ratio r_j close to 1.

III. Results

The proposed method was investigated on a 3D cone-beam CT imaging problem with 40 mm collimation. The simulated system has 888 channels, 64 detector rows, and 984 evenly spaced view angles over 360°. The XCAT phantom with cardiac motion of 75 bpm was used as an object. To focus on the sampling induced artifacts, we generated noiseless measurements. ICD with spatially non-homogeneous updates [3] was used to reconstruct images. For illustration purposes, we assumed that the acquisition time is long enough so that

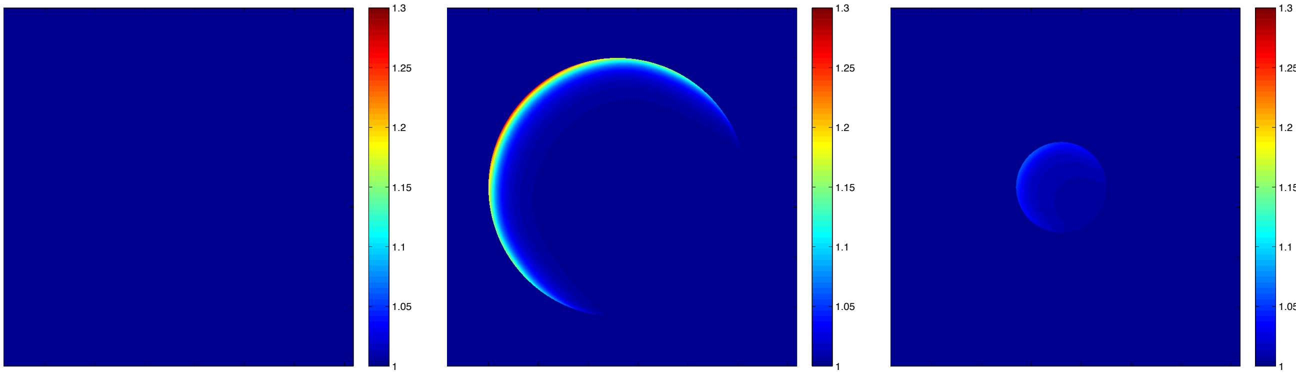


Fig. 3. View ratio (7) values between the proposed method and short-scan MBIR within the football region. From left to right, each column corresponds to center, 13th, and 5th slice of ROI (out of 64 slices), respectively. Display range is [1 1.3].

full-scan measurements is available. However, the proposed method can be applied with any amount of extra acquisition.

Fig. 3 shows the view ratio between the proposed method with $p = 5$ and short-scan MBIR within the football mask. The view ratio values at most of the voxels are very close to 1, which indicates that the proposed method provides reconstructed images having the desired temporal resolution in most spatial locations of the targeted region.

Fig. 4 compares reconstructed images obtained by the proposed method to those of other methods at different slice locations. The reconstructed image obtained by the proposed method removes short-scan artifacts while preserving the temporal resolution in the football region, and thus shows improved image quality compared to that of short-scan MBIR. Notice that the slices on the far end have much less artifacts. However, when compared to reconstructed images from full-scan MBIR, some residual artifacts are still noticeable on end slices. Tuning the design parameter p changes the image quality of the reconstructed image, but does not remove the entire short-scan artifacts while preserving the temporal resolution. This suboptimal results come from the inherent limitation of the statistical weighting modification. Since we only control the contribution of each ray, which affects multiple voxels at the same time, we have only limited control over sampling of each voxel. More sophisticated design for (5) may improve the results, but the trade-off between the temporal resolution and the short-scan artifact cannot be avoided with the proposed statistical weighting modification approach.

IV. Conclusions

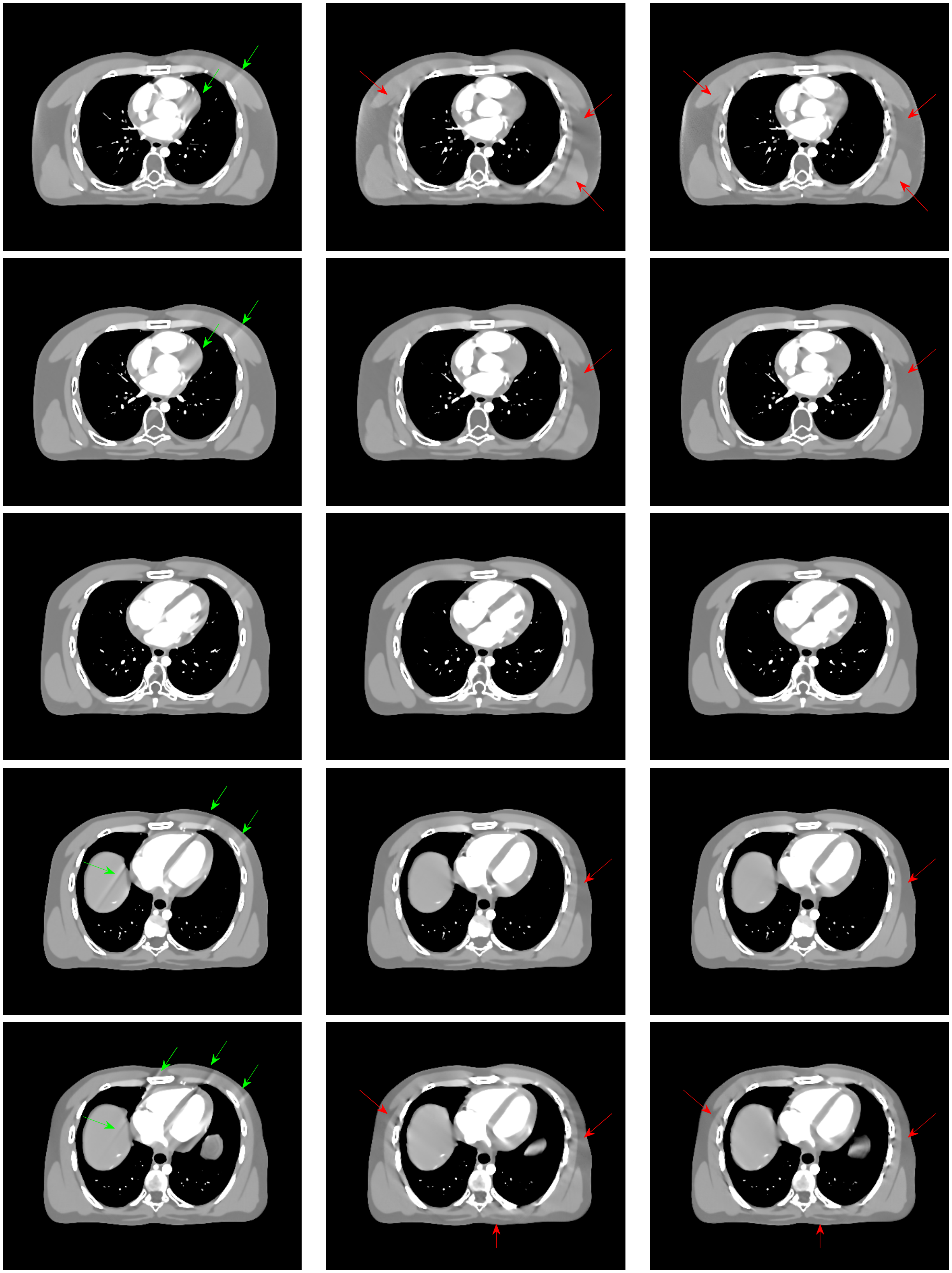
We presented a statistical weighting modification approach to reduce short-scan artifacts while maintaining temporal resolution in the target region. The proposed statistical weighting modification showed improvements compared to short-scan MBIR, especially on end slices. Future work will address other possible designs to further remove residual artifacts. By the time of the conference, we will apply the method to clinical data.

References

[1] S. S. Orlov, "Theory of three dimensional reconstruction. I. Conditions for a complete set of projections," *Sov. Phys. Crystallography*, vol. 20, pp. 312–14, 1976.

[2] H. K. Tuy, "An inversion formula for cone-beam reconstruction," *SIAM J. Appl. Math.*, vol. 43, no. 3, pp. 546–52, Jun. 1983.

[3] Z. Yu, J.-B. Thibault, C. A. Bouman, K. D. Sauer, and J. Hsieh, "Fast model-based X-ray CT reconstruction using spatially non-homogeneous ICD optimization," *IEEE Trans. Im. Proc.*, vol. 20, no. 1, pp. 161–75, Jan. 2011.



(a) Full-scan MBIR (b) Short-scan MBIR (c) Proposed method with $p = 5$

Fig. 4. Comparison of reconstructed images from different reconstruction methods. From left to right, each column corresponds to (a) full-scan MBIR, (b) short-scan MBIR, and (c) proposed method with $p = 5$. Each row corresponds to different axial locations (from top to bottom, 1st, 5th, 32nd, 60th, and 64th slice). Green and red arrows indicate motion artifacts and short-scan artifacts, respectively. Display window is [850 1150] (HU).