An in vitro evaluation of cone-beam breast CT methods

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Abstract. Tomosynthesis was developed for mammography, especially breast cancer detection. However, its limited-angular range scan and resultant data incompleteness causes strong image artifacts and distortions. To address this problem, a hybrid imaging method was proposed in our previous work, which combines tomosynthesis and low-resolution CT into a single system to produce fewer artifacts and distortions at a similar dose level. The purpose of this paper is to evaluate the images reconstructed using the proposed method as compared with that using the conventional tomosynthesis method (ML-convex). For that purpose, the projection datasets are acquired in both numerical simulation and phantom experiments on our breast imaging platform. Three kinds of phantoms are used in our work, including a numerical phantom, a physical phantom and 8 in vitro phantoms made of breast specimens. In addition to visual comparison of the reconstructed images, we employ spatial resolution, image contrast, reconstruction error, and convergence rate to evaluate the results quantitatively. It is observed that the results from our method can achieve significantly higher spatial resolution, higher contrast, smaller reconstruction error and faster convergence rate. Besides, a reader study using 8 in vitro phantoms of breast specimens demonstrates the clinical potential of our method, which significantly outperforms the conventional tomosynthesis.

Keywords: Cone-beam CT, tomosynthesis, mammography, breast imaging, image quality

1. Introduction

Breast malignancy is ranked as the second leading cause of cancer death in women in the United States. It has been recognized that mass screening and early treatment are extremely important to improve the cancer prognosis and minimize the healthcare burden, which can reduce the breast cancer mortality about 48 percent. Due to its specificity and sensitivity, x-ray mammography has been the method of choice for screening and diagnosis [17,20]. However, x-ray mammography is far from being perfect because up to 17% of breast cancers are not identified with mammography, it also produces a large number of artifacts.
false positive findings [19]. A major limitation of mammography is its 2D projective nature, while the real anatomy and pathology is truly 3D. To address this problem, X-ray tomosynthesis was introduced to improve mammography with more 3D information.

Tomosynthesis is a 3D imaging technique to reconstruct a series of images from a limited number of projections [8]. Since its introduction in 1972, the area of tomosynthesis has been significantly advanced largely due to the development of the area detectors [4]. A primary application of tomosynthesis is for breast imaging [21–23]. The tomosynthetic algorithms are either analytic or iterative. The analytic algorithms are straightforward and efficient, such as self-masking [3], selective plane removal [5], and matrix inversion tomosynthesis [6]. The iterative algorithms are robust with noisy data and flexible to incorporate a priori knowledge, such as algebraic reconstruction techniques (ART) [1,7], expectation-maximization (EM) [25]. However, none of these algorithms can avoid the inherent drawback of tomosynthesis, namely, data incompleteness. Therefore, additional information is desirable to improve the image quality fundamentally. In our previous work [12], a hybrid imaging scheme was proposed, which combines a low-resolution CT scan with a tomosynthesis scan. The results showed a promising improvement as compared with the conventional tomosynthesis method.

The purpose of this paper is to evaluate our low-dose CT-based tomosynthesis method against the traditional tomosynthesis methods using three kinds of phantoms including a numerical phantom, a physical phantom and eight in vitro phantoms made of breast specimens. In the following section, our method and the traditional tomosynthesis method will be briefly reviewed. Also, the experimental platform, phantoms and evaluation criteria are explained in detail. In the third section, the reconstruction and evaluation results are presented and analyzed. In the last section, we discuss relevant issues and conclude the paper.

2. Materials and methods

2.1. Conventional tomosynthesis method

In our evaluation, the transmission EM algorithm [16] was chosen for tomosynthesis [24]. This EM algorithm is based on the Poisson model of the photon count. For each projection indexed by \( i \), let \( W_i \) be the total number of photons from the source to the detector, and \( Y_i \) the actual number of photons detected. The initial photons reach the detector with a probability \( e^{-\sum_{j\in I_i} l_{ij} \mu_j} \), where \( j \) is the voxel index, \( I_j \) represents the set of voxels contributing to the \( i \)th x-ray path, and \( l_{ij} \) gives the equivalent length of the line along the projection line \( i \) that intersects voxel \( j \). Therefore, the log-likelihood over all projections is given by:

\[
\ln g(Y, \mu) = \sum_i \left\{ -d_i e^{-\sum_{j\in I_i} l_{ij} \mu_j} - Y_i \sum_{j\in I_i} l_{ij} \mu_j + Y_i \ln d_i - \ln Y_i! \right\}.
\]

where \( Y \) and \( \mu \) are vectors whose components are \( Y_i \) and \( \mu_j \) respectively, \( d_i \) is the x-ray dose per ray which is equal to \( \Delta t_i \alpha_i = I_0 \Delta t_i \), the time interval over which the \( i \)th projection is collected, and \( \alpha_i \) the source intensity (tube flux). The projection data can be computed as \( p_i = \ln(d_i/Y_i) = \ln(I_0/Y_i) \). As it was formulated in [15], the updating scheme can be written as:

\[
\mu_j^{(n+1)} = \mu_j^{(n)} + \Delta \mu_j^{(n)}.
\]
\[
\Delta \mu_j^{(n)} = \frac{\sum_l l_{ij} (D_{ij} e^{-\langle l, \mu_j^{(n)} \rangle_i} - Y_i)}{\sum_l (l_{ij} \langle l, \mu_j^{(n)} \rangle_i D_{ij} e^{-\langle l, \mu_j^{(n)} \rangle_i})},
\]

(2)

Where \( D_i \) is the photon count for that detector pixel when no object presents.

2.2. Proposed hybrid cone-beam method

As described in [13], our work incorporates two imaging methods. A priori knowledge can be incorporated into the EM framework by adding regularization terms, choosing a proper initial guess, etc. As the optimization with regularization terms is not very effective and increases the computational time significantly, we proposed to use a low-dose/low-resolution CT image as the initial guess \( f_{CT} \). Due to the data incompleteness, the final tomosynthetic result of the EM algorithm is not unique. As such, setting the initial value to \( f_{CT} \) gives the tomosynthesis process an unbiased starting point. That is, we can use the following formulas:

\[
\begin{align*}
\mu_j^{(0)} &= f_{CT,j}, \\
\mu_j^{(n+1)} &= \mu_j^{(n)} + \Delta \mu_j^{(n)}, \\
\Delta \mu_j^{(n)} &= \frac{\sum_l l_{ij} (D_{ij} e^{-\langle l, \mu_j^{(n)} \rangle_i} - Y_i)}{\sum_l (l_{ij} \langle l, \mu_j^{(n)} \rangle_i D_{ij} e^{-\langle l, \mu_j^{(n)} \rangle_i})},
\end{align*}
\]

(3)

Our method does not require higher dose than conventional method. As the radiation dose from one view is inversely proportion to the detector size, if with same SNR and same geometry [12]. Therefore, the dose from conventional tomosynthesis is redistributed to a low-resolution CT scan and a tomosynthetic scan so that the overall dose is the same as before.

Generally speaking, our algorithm consists of the following steps (Fig. 1):

1. Acquire a low-resolution CT (for example, 4 fold degradation in image resolution relative to what is actually used for the tomosynthesis);
2. Acquire a high-resolution tomosynthetic scan (for example, 30 projections over a 60 degree angular range);
3. Reconstruct an image volume from a low resolution CT dataset using the CT algorithm. As the radiation dose is very low, some de-noising method can be used;
4. Perform tomosynthesis from high resolution projections based on the low-resolution CT result using the transmission EM algorithm. Its update formulas are given in (3) with the initial value being the low resolution CT reconstruction.

2.3. System setup and phantom design

The experimental system was setup as shown in Fig. 2. The experimental platform was based on a commercial digital mammography system (Selenia system, Hologic Company, Fig. 2c). A translation-rotation stage was built in our laboratory to simulate scans around the phantom for both low-resolution CT and tomosynthesis. The geometric parameters are shown in Tables 1–2, which are used for all the experiments. And CT scan is also used as a reference method for the evaluation, the geometry of CT
scan is the same as low-resolution CT scan Table 1, except the detector resolution is 4 times higher which is the same to that from tomosynthesis scan (Table 2).

The numerical and physical breast phantoms were made with similar clinically relevant structures, such as masses, fibers and calcifications, as shown in Fig. 3. Its detailed geometric parameters can be found in [11,13]. The breast specimens were provided from the surgical pathology lab in University of Iowa. To make in vitro phantoms of breast specimens, each set of the tissues was packed in a plastic container with stuffing foams, as shown in Fig. 4.

2.4. Evaluation criteria

2.4.1. Visual image artifacts

The general image quality is compared by displaying reconstruction results from competitive methods side by side in the same display window. Since strong artifacts in the reconstruction images are a
Fig. 2. System pictures. (a) is our stage and phantom, (b) is the inner structures of the phantom, and (c) is the Hologic’s Selenia Mammo system and our stage.

major problem with tomosynthesis, we evaluate the artifacts in reference to benchmark images. Here either phantom images (numerical experiments) or CT images (physical phantom and phantoms of breast specimens) are used as the reference.

2.4.2. Spatial resolution (Full width at half maximum)

Spatial resolution is important to indicate how well the image reveals high frequency information. It is defined as a response to an infinite small pulse, which is not practical to measure. Hence, in practical applications it is usually calculated from the response of an edge signal, i.e., the width from 5% height to 95% height [10] or full width at half maximum of the derivative of the edge response. In this context,
2.4.3. Reconstruction error

Reconstruction error is to evaluate the overall reconstruction difference between the reconstructed and ideal images. Here two kinds of errors are used, root of mean square error (RMSE) and max error (ME), which are defined in Eqs (4) and (5). Again, the results from CT method are the reference.

\[
RMSE = \sqrt{\frac{1}{N} \sum_{i=0}^{N-1} (F_{\text{Phantom}}(x_i) - F_{\text{Re con}}(x_i))^2}
\]  

(4)

\[
ME = \max |F_{\text{Phantom}}(x_i) - F_{\text{Re con}}(x_i)|
\]  

(5)

2.4.4. Convergence rate

As both the proposed method and conventional method (ML-convex) are iterative, the convergence rate is an important factor to be considered. Here the convergence behaviors are compared in terms of RMSE and ME. After every iteration, the RMSE and ME are calculated from the updated reconstruction, and then the curves of RMSE or ME from both the methods are plotted together to show which one converges faster.

2.4.5. Image contrast

Image contrast is also a key factor to reflect the reconstructed difference between various structures, which can be calculated from Eq. (6):

\[
\text{Contrast} = \frac{I_{\text{foreground}} - I_{\text{background}}}{I_{\text{foreground}} + I_{\text{background}}}
\]  

(6)

where \( I_{\text{foreground}} \) and \( I_{\text{background}} \) are calculated by averaging all the pixel in the selected homogenous regions respectively. Similarly, the results from the CT method are the reference.
Fig. 3. Uncompressed Breast Phantom. It contains mass, calcifications and fibrous structures with different sizes and densities.

2.4.6. Reader study

Finally, to test the clinical potential of our proposed method, 3 board certified practicing radiologists were recruited for a reader study using 8 in vitro phantoms of breast specimens. All the results from the proposed and conventional methods were scored by each of the readers, in a randomized order to avoid biased score. The score was based on the subjective impression on image quality, from 1 to 5 as defined in Table 3 [2]. Then, the averaged scores from these doctors were used for statistical analysis. Specifically, t-test was used to analyze the relative performance of the two methods [14]. Let the null hypothesis be that our method is not better than the conventional method ($Score_{our} - Score_{conventional} \leq 0$), and the alternative hypothesis is that our method is better than conventional method ($Score_{our} - Score_{conventional} > 0$).

Then, the evaluation criteria are summarized in Table 4 for each of the three kinds of phantoms.
Fig. 4. System setup for breast specimens experiments.

Table 3
Description of subjective image quality scores

<table>
<thead>
<tr>
<th>Score</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>Poor visualization</td>
</tr>
<tr>
<td>2</td>
<td>Barely visible, but not diagnostically useful</td>
</tr>
<tr>
<td>3</td>
<td>Visible and diagnostically useful</td>
</tr>
<tr>
<td>4</td>
<td>Diagnostically useful, but less than CT quality</td>
</tr>
<tr>
<td>5</td>
<td>Same as CT</td>
</tr>
</tbody>
</table>

Table 4
Image quality evaluation criteria used for the three kinds of phantoms

<table>
<thead>
<tr>
<th></th>
<th>Visual image artifacts</th>
<th>Spatial resolution along X, Y, Z</th>
<th>Reconstruction errors</th>
<th>Convergence rate</th>
<th>Image contrast</th>
<th>Reader study</th>
</tr>
</thead>
<tbody>
<tr>
<td>Numerical phantom</td>
<td>X</td>
<td>X</td>
<td>X</td>
<td>X</td>
<td>X</td>
<td>X</td>
</tr>
<tr>
<td>Physical phantom</td>
<td>X</td>
<td>X</td>
<td>X</td>
<td>X</td>
<td>X</td>
<td>X</td>
</tr>
<tr>
<td>In vitro phantom</td>
<td>X</td>
<td>X</td>
<td>X</td>
<td>X</td>
<td>X</td>
<td>X</td>
</tr>
</tbody>
</table>

3. Evaluation results

3.1. Numerical phantom experiments

Figure 5 presents the results of our numerical simulation. Clearly, the proposed method produced excellent images quite similar to the phantom slices. All the internal structures were reliably reconstructed without distortions. Particularly, our method also revealed more low contrast structures. On the other hand, tomosynthesis induced serious geometrical distortions and coupling artifacts, which compromised contrast and resolution significantly.

In our simulation, the spatial resolutions were measured on the edge profiles along X, Y and Z directions, as shown in Fig. 6. The measured spatial resolutions are shown in Table 5, in comparison to...
Table 5

<table>
<thead>
<tr>
<th>Spatial resolution measures based on the edge profiles</th>
</tr>
</thead>
<tbody>
<tr>
<td>FWHM</td>
</tr>
<tr>
<td>------</td>
</tr>
<tr>
<td>Proposed method (voxel)</td>
</tr>
<tr>
<td>Conventional method (voxel)</td>
</tr>
<tr>
<td>CT method (voxel)</td>
</tr>
</tbody>
</table>

Fig. 5. Breast Phantom and reconstructed images (gray level window [0.23,0.27] cm\(^{-1}\). The images in first, second and third columns are from phantom, our method and conventional method, respectively.

Fig. 6. Locations to measure the edge responses along different directions.

the results obtained using the CT method.

In terms of the reconstruction error, the results are shown in Table 6. All the reconstruction errors were calculated after the 8\(^{th}\) iterations for both the methods. The results showed that our method achieved smaller reconstruction errors than the conventional method, being close to that from the CT method.
Table 6
Reconstruction error in terms of RMSE and ME

<table>
<thead>
<tr>
<th>Method</th>
<th>RMSE</th>
<th>ME</th>
</tr>
</thead>
<tbody>
<tr>
<td>Proposed method</td>
<td>0.016</td>
<td>2.73</td>
</tr>
<tr>
<td>Conventional method</td>
<td>0.053</td>
<td>2.81</td>
</tr>
<tr>
<td>CT method</td>
<td>0.012</td>
<td>2.69</td>
</tr>
</tbody>
</table>

And for the convergent properties, the curves of RMSE and ME are plotted in Fig. 7. It is observed that our proposed method has nicer convergent properties.

The contrast measures were calculated according to Eq. (6). Here the region shown in Fig. 8a was used to calculate $I_{\text{foreground}}$, and the region in Fig. 8b used to calculate $I_{\text{background}}$. The calculated contrast values are shown in Table 7. It was observed that our method achieved higher contrast than the conventional method. The contrast from our method was much closer to that from the CT method.
Table 7
Calculated contrast values obtained using the proposed and conventional methods

<table>
<thead>
<tr>
<th>Method</th>
<th>Contrast</th>
</tr>
</thead>
<tbody>
<tr>
<td>Proposed method</td>
<td>3.7e-2</td>
</tr>
<tr>
<td>Conventional method</td>
<td>1.7e-2</td>
</tr>
<tr>
<td>CT method</td>
<td>4.0e-2</td>
</tr>
</tbody>
</table>

3.2. Physical phantom experiments

Representative results obtained using several methods are shown in Fig. 9, where we can observe that our method produced much better image quality than that from low-resolution CT and tomosynthesis separately. Our method can achieve higher resolution and reveal more detailed structures than low-resolution CT, since higher resolution data from the tomosynthetic scan are incorporated. Also, our
method has less geometrical distortion and artifacts than traditional tomosynthesis results, since our method is regulated by low-resolution CT. For example, the contrast resolution with our method is improved as compared with the normal tomosynthesis. Currently, the image quality has not been optimized yet, as our system is still in the prototype stage. There exists some x-ray hardening effect in the reconstructed image.

Here the spatial resolutions are measured through edge profiles along X, Y and Z directions at the locations shown in Fig. 10. And the measured spatial resolutions are shown in Table 8. CT method is used as a reference standard to show how much improvement can be achieved through our method.

The contrast is calculated according to the equation 6 Here the region shown in Fig. 11 is used to calculate $I_{\text{foreground}}$ and $I_{\text{background}}$. The calculated contrast values are shown in Table 9. It is observed that our method achieves higher contrast for same tissue. The contrast measures from our method were much closer to that from the CT method.
Table 9
Calculated contrast values obtained using the proposed and conventional methods

<table>
<thead>
<tr>
<th></th>
<th>Contrast</th>
</tr>
</thead>
<tbody>
<tr>
<td>Proposed method</td>
<td>0.29</td>
</tr>
<tr>
<td>Conventional method</td>
<td>0.14</td>
</tr>
<tr>
<td>CT method</td>
<td>0.31</td>
</tr>
</tbody>
</table>

3.3. Breast specimen studies

Several representative images were reconstructed using our proposed method, conventional method and cone-beam CT to compare key image quality indexes. As shown in Fig. 12, structures can be better resolved using our hybrid method than the conventional method. In the conventional tomosynthetic images, the tissue and structures were significantly blurred, which can be easily determined in reference
Table 10

<table>
<thead>
<tr>
<th></th>
<th>Contrast</th>
</tr>
</thead>
<tbody>
<tr>
<td>Proposed method</td>
<td>0.162</td>
</tr>
<tr>
<td>Conventional method</td>
<td>0.074</td>
</tr>
<tr>
<td>CT method</td>
<td>0.17</td>
</tr>
</tbody>
</table>

The contrast was calculated according to Eq. (6). For that purpose, the region shown in Fig. 13 was used to calculate $I_{\text{foreground}}$, and the region in Fig. 13 used to calculate $I_{\text{background}}$. The calculated contrast values are shown in Table 10. It was observed that our method produced higher contrast measures than the conventional method.

For the reader study, the scores were given for each method, as shown in Table 11.

Then, the t-test was conducted on the above-described datasets to evaluate the difference between the conventional and proposed methods. Specifically, we analyzed the overall image quality difference (including mass, fibrosis and calcifications), the difference in low contrast resolution (fibrosis and mass) and the difference in high contrast resolution (calcifications). All the data were processed by the SAS software. The results are shown in Table 12. Based on these results, the p-value of the overall image quality difference is much smaller than 0.05. Therefore, the statistical results strongly favor the alternative hypothesis, i.e., our method performs significantly better than the conventional method. For low contrast tissues, such as mass and fibrosis tissues, the average score difference is more than 2, while for calcifications (high contrast tissues), the average score difference is less than 1. Therefore, based on the results, our method achieves more improvements in visualizing low contrast tissues.

4. Discussions and conclusions

In this comparative study, two phantoms and eight specimens have been used to evaluate the image quality between the proposed hybrid imaging method and conventional tomosynthesis method. Based
Table 11
Scores given by 3 radiologists for images from each of the 8 specimens

<table>
<thead>
<tr>
<th>Specimen</th>
<th>Lesion description</th>
<th>Conventional method</th>
<th>Proposed method</th>
<th>Averaged score for the conventional method</th>
<th>Averaged scores for the proposed method</th>
</tr>
</thead>
<tbody>
<tr>
<td>Specimen 1</td>
<td>Mass</td>
<td>2</td>
<td>2</td>
<td>2</td>
<td>4</td>
</tr>
<tr>
<td></td>
<td>Calcifications 1</td>
<td>1</td>
<td>1</td>
<td>1</td>
<td>3</td>
</tr>
<tr>
<td></td>
<td>Calcifications 2</td>
<td>1</td>
<td>2</td>
<td>1</td>
<td>3</td>
</tr>
<tr>
<td>Specimen 2</td>
<td>Mass</td>
<td>1</td>
<td>1</td>
<td>1</td>
<td>1</td>
</tr>
<tr>
<td></td>
<td>Calcifications 1</td>
<td>1</td>
<td>3</td>
<td>1</td>
<td>3</td>
</tr>
<tr>
<td></td>
<td>Calcifications 2</td>
<td>1</td>
<td>2</td>
<td>1</td>
<td>2</td>
</tr>
<tr>
<td>Specimen 3</td>
<td>Mass</td>
<td>1</td>
<td>1</td>
<td>1</td>
<td>1</td>
</tr>
<tr>
<td></td>
<td>Calcifications</td>
<td>3</td>
<td>5</td>
<td>3</td>
<td>4</td>
</tr>
<tr>
<td>Specimen 4</td>
<td>Mass</td>
<td>1</td>
<td>1</td>
<td>1</td>
<td>1</td>
</tr>
<tr>
<td></td>
<td>Fibrosis</td>
<td>2</td>
<td>1</td>
<td>1</td>
<td>1</td>
</tr>
<tr>
<td>Specimen 5</td>
<td>Mass</td>
<td>1</td>
<td>1</td>
<td>1</td>
<td>1</td>
</tr>
<tr>
<td></td>
<td>Fibrosis</td>
<td>4</td>
<td>3</td>
<td>4</td>
<td>4</td>
</tr>
<tr>
<td>Specimen 6</td>
<td>Mass</td>
<td>2.5</td>
<td>1</td>
<td>1</td>
<td>1.5</td>
</tr>
<tr>
<td></td>
<td>Calcifications</td>
<td>4</td>
<td>4</td>
<td>4</td>
<td>4</td>
</tr>
<tr>
<td>Specimen 7</td>
<td>Mass</td>
<td>2.5</td>
<td>1</td>
<td>1</td>
<td>1.5</td>
</tr>
<tr>
<td></td>
<td>Calcifications</td>
<td>3</td>
<td>3</td>
<td>4</td>
<td>4</td>
</tr>
<tr>
<td>Specimen 8</td>
<td>Calcifications</td>
<td>1</td>
<td>1</td>
<td>1</td>
<td>1</td>
</tr>
<tr>
<td></td>
<td>Fibrosis</td>
<td>1</td>
<td>2</td>
<td>2</td>
<td>4</td>
</tr>
</tbody>
</table>

Table 12
Statistical analysis on image quality

<table>
<thead>
<tr>
<th>Sample number</th>
<th>Average score difference</th>
<th>t-value</th>
<th>p-value</th>
</tr>
</thead>
<tbody>
<tr>
<td>Overall quality difference</td>
<td>20</td>
<td>1.71</td>
<td>6.53</td>
</tr>
<tr>
<td>Mass tissue image quality difference</td>
<td>7</td>
<td>2.5</td>
<td>4</td>
</tr>
<tr>
<td>Fibrosis tissue image quality difference</td>
<td>4</td>
<td>2.2</td>
<td>4.72</td>
</tr>
<tr>
<td>Calcification image quality difference</td>
<td>9</td>
<td>0.9</td>
<td>3.07</td>
</tr>
</tbody>
</table>

on the results from the numeric and physical phantom experiments, the proposed hybrid imaging method has achieved similar spatial resolutions along X and Z directions, and better spatial resolution along Y direction than the conventional tomosynthesis method. While the conventional method performs poorly in localizing structures in that the Y direction, our method can produce excellent image quality with spatial resolution of 8 pixels along the Y direction. In term of contrast resolution, our method performs consistently better than the conventional method, being very similar to the CT method. This advantage is very helpful to visualize low contrast structures, such as mass and fibrosis tissues.

Moreover, our iterative reconstruction scheme is computationally more efficient than other iterative algorithms. Typically, tomosynthetic EM algorithms need 8 or more iterations [24]. However, since we use an exact CT reconstruction as the initial image, the MSE with our method changes very slowly after a few iterations, which means that the image reconstruction converges to the real image much faster than the case with a poor initial image. As a result, we can greatly reduce the computational cost using our hybrid imaging method.

The clinical potential of our proposed method has been tested in a reader study. The null hypothesis was defined as that the conventional method performs better than our method. The statistical results have
favored the alternative hypothesis that our method performs better than the conventional method.

Our hybrid imaging method has more requirements on the imaging hardware, such as a gantry needed to rotate over a much larger angular range to acquire projection data. However, it can be implemented in the current C-arm digital mammography framework with little modification. Also, the two scans (low-resolution/high-noise CT scan and high-resolution tomosynthetic scan) can be physically realized in a single scan with the mA modulation technique, i.e., low mA for a global CT dataset and normal mA for tomosynthesis. Nevertheless, the advantages in image quality with our proposed method have been shown to be so clear that can justify the additional hardware cost.

An enlarged scanning range will increase the data acquisition time a little bit than a conventional tomosynthetic scan. Thus, the patient motion could be more involved. Nevertheless, temporal resolution can be improved using a faster C-arm rotational speed. More importantly, in our scheme the low-dose CT scan is not sensitive to small motion because of its low resolution. The tomosynthetic scan is still performed within a very short scan, which will reveal detailed structures at uncompromised temporal resolution. Therefore, the overall temporal resolution is still quite comparable to that with the conventional tomosynthetic scan.

In conclusion, we have evaluated our hybrid imaging scheme in comparison with the conventional tomosynthesis method. It has been observed that the results from our method performs significantly better than the conventional method in terms of spatial resolution, contrast resolution, reconstruction error, convergence rate, and scores in the reader study. These data, especially scores from the-reader study, have demonstrated the clinical potential of our method. In future, more systematic clinical experiments will be used to explore the its clinical impact and our scheme may be further improved by recent cone-beam reconstruction results in ref [9,18].

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References

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