Tomosynthesis reconstruction using an accelerated expectation maximisation algorithm with novel data structure based on sparse matrix ray-tracing method

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Abstract: Digital Breast Tomosynthesis (DBT) is a novel imaging technology to improve early breast cancer detection. It provides three-dimensional information of the breast to overcome the critical issues of overlapping anatomical structures of the breast. Among current available DBT reconstruction algorithms, Maximum Likelihood Expectation-Maximisation (MLEM) is a time-consuming iterative method to reconstruct three-dimensional image of the breast. In this paper, we proposed an accelerated MLEM algorithm with novel data structure based on sparse matrix ray-tracing method for DBT reconstruction. Compared with the standard MLEM, the proposed algorithm is effective to generate relative fast-speed tomosynthesis reconstruction and maintain the same image quality.

Keywords: mammography; tomosynthesis; MLEM; maximum likelihood expectation maximisation; ray-tracing; sparse matrix; impulse response.


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1 Introduction

Breast cancer is a major problem and the most common cancer among women (Bassett et al., 2005). Early detection of breast cancer is viewed as the best hope to decrease breast cancer mortality (Nass et al., 2001). It is universally accepted that mammography is the most efficient tool for the early detection of breast cancer (Nass et al., 2001). However, many limitations of mammography have been reported and about 30% of breast cancers are still missed in traditional mammography (Wu et al., 2004a). Due to tissue overlap and structural noise, it is difficult to detect some breast cancer cases, especially for dense breast cases. Improving breast imaging technologies may permit breast cancer to be detected at a smaller size and earlier stage, thereby reducing the number of women who die with such cancer. With the development of modern imaging technology, the fast read-out detector and digital radiography became available. Digital tomosynthesis refers to a new technique that provides three-dimensional images of the object with high detailed resolution based on the finite number of projection images (Dobbins and Godfrey, 2003). The radiation dose is relatively low for each projection image, while the total radiation dose to acquire all the projection images of a tomosynthesis sequence is equivalent to or slightly higher than that in the standard single-view mammography (Niklason et al., 1997). By adopting suitable image reconstruction algorithms, it is capable to reconstruct three-dimensional information of the breast. Digital Breast Tomosynthesis (DBT) can provide a series of reconstruction images of the entire breast, with each image displaying the in-focus plane at different locations passing through the breast.

There are a variety of available tomosynthesis reconstruction algorithms, including the image stretching method by Niklason et al. (1997), Tuned-Aperture Computed Tomography (TACT) developed by Webber and applied by Suryanarayanan et al. (2000), Filtered Back Projection (FBP) algorithms (Lauritsch and Haerer, 1998; Stevens et al., 2001; Mertelmeier et al., 2006), Maximum Likelihood Expectation Maximisation (MLEM) (Lange and Carson, 1984; Wu et al., 2003), Matrix Inversion Tomosynthesis (MITS) (Warp et al., 2000; Chen et al., 2004) and Algebraic Reconstruction Technique (ART) (Gordon et al., 1970; Andersen and Kak, 1984; Andersen, 1989; Zhang et al., 2006). Among available algorithms, MLEM is an effective image reconstruction algorithm (Wu et al., 2003, 2004a; Zhang et al., 2006). It shows effects of removing artifacts and enhancing image contrast. It facilitates observers to detect detailed structures. It has become one of the preferable DBT three-dimensional image reconstruction algorithms by a few research groups and manufacturers. However, due to its relatively complicated iteration expression, it is time-consuming to generate reconstructed images. Wu et al. have done much work to speed up this method (Wu et al., 2004b; Goddard et al., 2006). In one of their related works (Wu et al., 2004b), the entire reconstructed volume was separated into multiple segments along the chest-to-nipple direction and reconstructed every partial segment on a CPU node of the
cluster and merge the reconstructed volume. The reconstructed images can provide
equivalent diagnostic information as the standard serial MLEM algorithm.

In this paper, an accelerated MLEM reconstruction algorithm is presented. Feasible
speed-up schemes of MLEM algorithm are discussed. The implementation and analysis
of its performance with a typical computer of time complexity is provided to solve the
intensive computation problem of MLEM algorithm.

2 Methods

2.1 MLEM image reconstruction algorithm

MLEM algorithm is one kind of statistical iterative methods for breast tomosynthesis
reconstruction. It assumes that the relationship between incident and transmitted X-ray
follows Poisson distribution, and each projection is independent. Therefore, every pixel
value on the projection image read out from the detector is independent and random variable (Wu et al., 2003).

Given an object, when X-ray passes through the object, the X-ray intensity will be
attenuated. According to the attenuation model,

\[ T = I e^{-\mu l} \]  

where \( T \) denotes the intensity of transmitted X-ray, \( I \) denotes the intensity of incident
X-ray, \( \mu \) represents attenuation coefficient, and \( l \) denotes the length of the path where the
X-ray passes through the voxel.

In MLEM, given an object and the attenuation coefficients \( \mu \) of its voxels, we
formulate 

\[ L = P(T | \mu) \]  

(2)

to express the likelihood to acquire the projection image \( T \).

For all projection images, we hope \( L \) to be maximised. In other words, the probability
of getting the projection \( T \) in the incident X-ray intensity \( I \) and attenuation coefficient
\( \mu \) can be maximised.

According to related literatures (Wu et al., 2003, 2004a; Zhang et al., 2006),
the iterative procedure to acquire the attenuation coefficient \( \mu \) is shown as below:

\[ \mu_j^{(n+1)} = \mu_j^{(n)} + \Delta \mu_j^{(n)} = \mu_j^{(n)} + \frac{\mu_j^{(n)}}{\hat{a}} \left(l_{ij}(I e^{-\mu l_j} - T_i)\right) \] 

\[ <l, \mu > = \hat{a} l_{ij} \mu_j \]  

(3)

where \( T_i \) is the output X-ray intensity or pixel value on the detector, \( j \) is the individual
voxel in the three-dimensional attenuation model. \( <l, \mu > \) means the total attenuation
of the X-ray source to the pixel \( i \). \( I_i \) is the incident X-ray intensity to pixel \( i \) before
attenuation, usually, we can replace it with the flat image. \( l_{ij} \) is the path length of the
intersection between the voxel \( j \) and the X-ray projection line (hereafter X-ray \( i \) ) starting
from the X-ray source to the pixel \( i \) on the detector.
2.1.1 Standard implementation framework

To solve equation (3), a standard framework can be designed as below in Figure 1:

**Figure 1** Standard implementation framework of MLEM algorithm

```plaintext
1 for every iteration n
2     for every voxel j
3         for every pixel i
4             calculate the path length where x-ray i passes through voxels
5             for every x-ray i
6                 calculate total attenuation when passing through voxels
7                 end
8             calculate Δμ_j
9         end
10 end
11 update μ
12 end
```

It is not difficult to estimate that the most inner statement (Line 6) will run over n*j*i times. The time complexity is O(n*j*i^2). It will take much time to fulfill the computation. Accordingly, to lower loop complexity will contribute to the improvement of computation efficiency.

2.1.2 Acceleration techniques

2.1.2.1 A novel data structure based on sparse matrix ray-tracing method

Providing that the statement in Line 6 in Figure 1 will be executed for many times, how to solve the path length l_{i,j} and create the indices between each X-ray projection line and corresponding voxels it penetrates is very important to enhance the efficiency of the procedure. Here we introduce a simplified and equivalent implementation with a novel data structure by ray-tracing method.

Ray-tracing is a frequently used method to solve the length of the path where each X-ray projection line passes through each voxels (Chen, 2007). In fact, on every reconstruction plane, for each individual X-ray projection line i, only a few voxels are passed through. This results in the sparse matrix condition. The sparse condition is involved on the strategy to manage the relationship between the X-ray projection line i, the voxel j, and the path length l_{i,j}. Here we adopted the combination of the array and linked list. All voxels penetrated by X-ray i were simply organised into a linked list. The linked list was then mounted to the X-ray array.

Figure 2 illustrates the data structure. It utilises the feature of the sparse matrix to save allocated memory for path l_{i,j} calculation. It is convenient to visit the voxels which are penetrated by the X-ray projection line i. This linked list based on sparse matrix serves as the foundation to adjust loop order in Section 2.1.2.2.
Figure 2 Combined data structure to manage the relationship between X-ray projection lines and voxels

2.1.2.2 Loop order adjustment

Since the length of the path $l_{ij}$ is fixed during the total iteration, it can be extracted and calculated before the iteration. As illustrated before, Line 6 in Figure 1 runs many times. Line 6 can be put into the initial procedure.

Now we are able to prepare all parameters for the update of $\mu$. In equation (3), the update of $\mu$ can be divided into two parts correspondingly, and the whole procedure can be adjusted as below:

Because of the combination of array and linked list discussed in 2.1.2.1, the statements of Line 5 and Line 10 in Figure 3 will be speeded up significantly.

Figure 3 Accelerated MLEM implementation framework

1 calculate $l_{ij}$ by ray-tracing method
2 for every iteration $n$
3 for every X-ray $i$
4 for every voxel which is affiliated to $i$ in Figure 2
5 calculate the total attenuation when passing through voxels
6 end
7 end
8 for every X-ray $i$
9 for every voxel which is affiliated to $i$ in Figure 2
10 calculate the nomination and denominator of $\Delta \mu_j$
11 end
12 end
13 for every voxel $j$
14 update $\mu_j$
15 end
16 end
2.1.2.3 Eliminating the update of voxels that are not passed through by any X-ray

As shown in Figure 4, the reconstruction plane is located at H distance above the detector. For this reconstruction plane only, voxels on the grey area will never be passed through by any individual X-ray projection line. Therefore, during the reconstruction of this single plane, the related attenuation updates for grey area can be eliminated.

**Figure 4** Illustration of voxels which are not passed through by any X-ray projection line

Instead, we calculated the borders of the voxel matrix. During the iteration procedure, if the voxel is located inside the grey area, we will not update its attenuation coefficient in corresponding steps. This improves the computation speed accordingly.

2.1.3 Time complexity

Two main factors should be taken into account to evaluate the time complexity of our accelerated implementation of MLEM algorithm:

- to compute the path length $l_{ij}$ when X-ray projection line passes through voxels
- to iterate and update the attenuation coefficient of each voxel.

Here we assume that the variable $p$ represents the total number of reconstructed planes. As mentioned before, X-ray $i$ denotes the X-ray projection line and $j$ denotes the voxel on reconstruction object. For path length $l_{ij}$ calculation, the required time complexity is $O(p)$. For reconstruction iteration, the required time complexity is estimated as $O(n^*p\eta)$ ($n$ is the iteration number), where $\eta$ is not greater than the maximum number of the voxels associated with X-ray $i$. According to Section 2.1.1.1, the relationship is sparse and $\eta < j$, therefore the time complexity decreases from $O(n^*j^2)$ for standard MLEM algorithm to be $O(n^*p\eta)$ for our accelerated MLEM algorithm.
2.2 Computer simulation study

2.2.1 Breast tomosynthesis system

The imaging geometry of a parallel-imaging system (Lalush et al., 2006) was simulated to evaluate the proposed accelerated MLEM algorithm. Figure 5 shows the geometry of the simulated DBT imaging system. Image size of 1024 × 1024 pixels was used for simulation, with a pixel size of 50 µm. The X-ray sources were aligned along the $x$-axis that is parallel to the detector. A tomosynthesis data set of nine projection images was simulated. The distance from X-ray sources to the detector (SID) is 193.0 mm.

Figure 5  Simulated imaging geometry of the tomosynthesis system

2.2.2 Impulse response and spherical object response analysis

In order to compare our accelerated algorithm with the standard algorithm, impulse response and spherical object response analysis were performed. The non-linear characteristics of MLEM may require more sophisticated task-based methods of evaluation. However, the impulse response and spherical object response analysis still provide us relative fair comparison to evaluate the performance of standard MLEM and presented accelerated one.

In this paper, a single delta function was simulated as the input impulse to evaluate the sharpness of the in-plane structures. The impulse was located at 10 mm away from the detector ($H = 10$ mm in Figure 5). Parameters of the DBT device described in Figure 5 were used as imaging geometry of the simulation. For the impulse response analysis, nine projection images of a tomosynthesis sequence were simulated. During the ray-tracing simulation procedure, if the simulated impulse was projected onto a non-integer location on the detector, four-neighbour pixel linear interpolation was performed. Reconstructed impulse responses on the reconstruction plane ($H = 10$ mm) were normalised and compared, to evaluate the in-plane performance of accelerated algorithm and the standard one.
Spherical object response was also studied to further compare the performance of our accelerated MLEM algorithm with standard MLEM method. A three-dimensional spherical object (simulating mass) that is 4 mm in diameter with the central point located at \( H = 10 \) mm distance away from the detector surface plane was computer-simulated as the object. A tomosynthesis dataset of nine projection images was simulated by ray-tracing method. The accelerated MLEM algorithm and standard MLEM algorithm were then applied to reconstruct the spherical object. Reconstruction performance of a slice passing through the central point (\( H = 10 \) mm) was compared and analysed. Based on the impulse response and spherical object response analysis, performance of accelerated MLEM and standard MLEM algorithms was compared.

3 Results

Figure 6(a) and (b) show the in-focus impulse responses of standard MLEM and our accelerated MLEM algorithm, respectively. Figure 6(c) shows the subtraction of impulse responses of Figure 6(a) and (b). One can see that both standard MLEM algorithm and our accelerated one can reconstruct the impulse by showing sharp response on in-plane reconstruction. There is no obvious difference between the impulse responses when compared Figure 6(a) and (b) by subtraction as shown in Figure 6(c).

Figure 6 Comparison of impulse response of standard MLEM and accelerated MLEM algorithm: (a) impulse response of MLEM (\( H = 10 \) mm); (b) impulse response of accelerated MLEM and (c) subtraction results

Figure 7(a) and (b) show the in-focus reconstruction responses of simulated spherical object. Figure 7(c) shows the subtraction of responses of Figure 7(a) and (b). Both standard MLEM algorithm and accelerated one can reconstruct the three-dimensional spherical object by showing response correctly on in-plane reconstructions. There is no obvious difference between the performance of standard MLEM and accelerated MLEM when compared Figure 7(a) and (b) by subtraction as shown in Figure 7(c).
Tomosynthesis reconstruction

Figure 7  Comparison of sphere-based simulation on MLEM and accelerated MLEM algorithms: (a) impulse response of MLEM ($Z = 10$ mm); (b) impulse response of accelerated MLEM and (c) subtraction results

Table 1 shows the computation time needed to reconstruct a single reconstruction plane. Image sizes of $256 \times 256$ pixels, $512 \times 512$ pixels and $1024 \times 1024$ pixels (full size) were investigated. Iteration numbers of 3, 8 and 20 were tested. A 2.4G HZ desktop computer with 3 GB memory was used to implement our algorithms coded in Visual C++. One can find that the typical computation time with eight iterations was only 97 s with accelerated MLEM algorithm to reconstruct a single slice of $1024 \times 1024$ pixels in size. The accelerated MLEM algorithm is capable to fulfil the clinical application requirements of relatively fast computation.

<table>
<thead>
<tr>
<th>Iteration</th>
<th>$256 \times 256$ pixels</th>
<th>$512 \times 512$ pixels</th>
<th>$1024 \times 1024$ pixels</th>
</tr>
</thead>
<tbody>
<tr>
<td>3</td>
<td>2</td>
<td>10</td>
<td>52</td>
</tr>
<tr>
<td>8</td>
<td>3</td>
<td>15</td>
<td>97</td>
</tr>
<tr>
<td>20</td>
<td>6</td>
<td>33</td>
<td>210</td>
</tr>
</tbody>
</table>

4 Conclusion

A fast MLEM algorithm for 3D image reconstruction in DBT was developed. In this algorithm, we designed novel data structure and adjusted loop order to decrease the time complexity. The accelerated MLEM algorithm with our novel data structure based on sparse matrix ray-tracing method demonstrated fast-speed computation. It can reconstruct a single $1024 \times 1024$ pixel slice in less than two minutes. Impulse response and spherical object simulation were also investigated to compare the performance of the standard MLEM and accelerated MLEM. Results showed that the accelerated MLEM is capable to maintain good image quality with fast-speed reconstruction.

Future work will be done to apply this acceleration technique to other breast tomosynthesis iterative reconstruction algorithms (Andersen, 1989; Zhang et al., 2006).
References


