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Tailored ML-EM Algorithm for Reconstruction of Truncated Projection Data using Few View-Angles

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Abstract

Dedicated cardiac Single Photon Emission Computed Tomography (SPECT) systems have the advantage of high speed and sensitivity at no loss, or even a gain, in resolution. The potential drawbacks of these dedicated systems are data truncation by the small field of view (FOV) and the lack of view-angles. Serious artifacts, including streaks outside the FOV and distortion in the FOV, are introduced to the reconstruction when using the traditional emission data Maximum-Likelihood Expectation-Maximization (ML-EM) algorithm to reconstruct images from the truncated data at small number of views. In this paper, we propose a tailored ML-EM algorithm to suppress the artifacts caused by data truncation and insufficient angular sampling by reducing the image updating step sizes for the pixels outside the FOV. As a consequence, the convergence speed for the pixels outside the FOV is decelerated. We applied the proposed algorithm to truncated analytical data, Monte Carlo simulation data and real emission data at different numbers of views. The computer simulation results show that the tailored ML-EM algorithm outperforms the conventional ML-EM algorithm in terms of streak artifacts and distortion suppression for reconstruction from truncated projection data with a small number of views.

1. Introduction

Single Photon Emission Computed Tomography (SPECT) myocardial perfusion imaging is a non-invasive and effective method for diagnosing coronary artery disease. The conventional SPECT system usually has two large detectors mounted with parallel-hole collimators. The detectors rotating around the patient provide a sufficient number of untruncated projections. In spite of the advantages offered, the conventional SPECT system is inefficient because only a small portion of the detector area is used to image the heart. In addition, the rotation of the detector during the acquisition produces temporally inconsistent projections and degrades the quality of the image.

In an effort to overcome the limitations of the conventional SPECT system, many groups have proposed dedicated cardiac SPECT systems, *e.g.*, UC San Francisco and Western Cardiology Associate's stationary multi-pinhole system [1, 2], Discovery NM 530c (GE Healthcare, Haifa, Israel) [3, 4]. A dedicated cardiac SPECT system has the advantage of acquiring consistent projections and ease of performing dynamic studies. In a dedicated cardiac SPECT system, the main drawbacks are data truncation by the small field of view (FOV) and insufficient view-angles.

Image reconstruction from truncated projections fall into two classes: the FOV is 1) partially, or is 2) completely contained by the object, the latter is also known as the interior problem. In 1986, Natterer systematically described this problem and pointed out that the interior problem is not uniquely solvable [5]. Not all tomographic problems with truncated

data are interior problems and some may be solvable. For example, in 2004, Noo *et al* introduced the concept of differentiated backprojection (DBP) so that some truncation problems became solvable for some special truncation geometries [6]. Based on this concept, more recent studies indicate that the solution to the interior problem is unique if the value of a tiny sub-region in the ROI is known [7–10]. Others have investigated this problem from the singular value decomposition (SVD) aspect [11, 12].

To our knowledge, most studies on truncated data tomography presuppose sufficient angular sampling; little has been done for insufficient angular sampling cases [13], as in stationary cardiac SPECT imaging [3, 4, 14]. It has been shown that with sufficient projection views, truncation has a slight bias effect on the reconstruction [15]. However, for many stationary or fast cardiac SPECT systems, view-angles are not sufficient, making the truncation problem more ill-conditioned.

The Maximum-Likelihood Expectation-Maximization (ML-EM) algorithm [16, 17] is the most popular image reconstruction algorithm for nuclear medicine, due to the advantage of providing accurate modeling of the imaging geometries, physics effects, and Poisson noise. Although the algorithm is robust against noise and systematic inconsistencies when the projection data are not truncated, it may converge to a highly distorted reconstruction if the data are truncated and the view-angles are not sufficient at the same time. To remedy this, we propose a tailored ML-EM algorithm for suppressing the severe streak artifacts and distortion caused by data truncation and insufficient angular sampling. We first tested the reconstruction algorithm on an analytical heart phantom and a pixelated Nurbs-based cardiac-torso (NCAT) phantom [18]. Subsequently, we tested the algorithm on a real Jaszczak torso phantom and its projections were acquired with a SPECT camera using different numbers of view-angles. All of these results indicate that the tailored ML-EM algorithm significantly improve the reconstruction from truncated data using few view-angles, compared to the conventional ML-EM algorithm.

2. Theory

2.1. Tailored ML-EM Algorithm

The ML-EM algorithm [16, 17], which incorporates physical models of photon emission and detection, is commonly used in emission tomography. Generally, the ML-EM algorithm converges to the maximum likelihood solution after a large number of iterations. In the dedicated cardiac SPECT system, the FOV is usually small and barely covers the heart. As a result, the background and other organs are severely truncated. Another potential drawback of the few-view SPECT system is the lack of a sufficient number of views. Both drawbacks cause part of the object outside the FOV not to be fully scanned by the detector. Therefore, incorrect values (usually extremely large values) appear in pixels outside the FOV, resulting in a highly distorted reconstruction within the FOV. Equation 1 displays the conventional ML-EM algorithm [17]

$$x_j^{k+1} = \frac{x_j^k}{\sum_i a_{ij}} \sum_i a_{ij} \frac{p_i}{\sum_m a_{im} x_m^k} \quad (1)$$

where p_i is the measured projection, x_j^k is the j th element of the reconstructed image after the k th iteration, and a_{ij} denotes the probability that the photon in pixel j is detected by detector bin i . The summations over i and m present the backprojector and projector, respectively.

In order to suppress the distortion in the reconstruction, we first expand the projection array to match the size of a virtual detector that can measure truncation-free projections. The array

expansion does not change the values of measured projection data, but the unmeasured values are set to the forward-projection of the current estimate of the image. Figure 1 illustrates the changes of the coefficient matrix A before and after array expansion. It can be seen that some pixels outside the FOV are not fully covered by all views before expansion. However, the matrix A , whose elements are a_{ij} , is extended and the entire object is fully covered from every view after array expansion.

For a more clear explanation, we write the conventional ML-EM algorithm in an additive form:

$$x_j^{k+1} = \frac{x_j^k}{\sum_i a_{ij}} \sum_i a_{ij} \frac{p_i}{\sum_m a_{im} x_m^k} = \frac{x_j^k}{\sum_i a_{ij}} \sum_i a_{ij} \left(\frac{p_i - \sum_m a_{im} x_m^k}{\sum_m a_{im} x_m^k} + 1 \right) = x_j^k + \frac{x_j^k}{\sum_i a_{ij}} \sum_i a_{ij} \frac{1}{\sum_m a_{im} x_m^k} \left(p_i - \sum_m a_{im} x_m^k \right). \quad (2)$$

We can see that the adjustment to the ratios $\frac{p_i}{\sum_m a_{im} x_m^k}$ does not change the value of

$$\sum_i a_{ij} \frac{1}{\sum_m a_{im} x_m^k} \left(p_i - \sum_m a_{im} x_m^k \right), \text{ because } \left(p_i - \sum_m a_{im} x_m^k \right) \text{ is always zero for unmeasured data,}$$

before and after array expansion. The array extension only makes the step size $\frac{x_j^k}{\sum_i a_{ij}}$ smaller, which decelerates the convergence speed for the pixels outside the FOV. In the conventional

ML-EM algorithm, the normal step size $\frac{x_j^k}{\sum_i a_{ij}} \approx \frac{x_j^k}{nang}$ when there is no truncation, where

$nang$ is the number of views. When there is truncation, the step size is approximately $\frac{x_j^k}{nang_t}$, where $nang_t$ is the number of views at which the detector can “see” the pixel x_j . In general, $nang_t < nang$. Our modified algorithm aims to replace $nang_t$ by $nang$, so that the step size of non-FOV pixels is reduced, and as a result, the reconstruction is better stabilized.

3. Experiments

The last section elaborated the reason for using the tailored ML-EM algorithm and provides implementation details. In this section, we design several simulation experiments to verify the advantages of the tailored ML-EM algorithm in the reconstruction of truncated data. The comparisons between the tailored ML-EM algorithm and the conventional ML-EM algorithm are studied using analytical simulation data, Monte Carlo simulation data and real SPECT data.

3.1. Simulated Projections of the Analytical Heart Phantom

A simple 3D heart phantom (Figure 2) of size $256 \times 256 \times 256$ was used in the first experiment, where the bright hollow sphere represents the left ventricle and the darker sphere and ellipsoid represent other organs/background. Using an analytical projector to generate projections helps to avoid an “inverse crime”, which occurs when the same (or very nearly the same) numerical methods are employed in the forward solver and the inversion scheme. In our case, an inverse crime is committed if the reconstruction algorithm uses the same projector that is used to generate the projection data. With the increase in the iteration number, the reconstructed image becomes noisier. For the sake of focusing on the effects of angular sampling and truncation, other effects such as noise, attenuation, collimator blurring and scattering are not included in this part of the computer simulations. Therefore, the

conventional and tailored ML-EM algorithms can iterate to a large number until the reconstructed image converges. In this simulation, the detector size was 64×64, which barely contained the heart. Both the conventional ML-EM algorithm and the tailored ML-EM algorithm were stopped at the 500th iteration where the reconstructed image almost converged.

3.2. Simulated Projections of the NCAT Phantom

In the second set of computer simulations, a 3D numerical myocardial phantom (NCAT phantom) [18] and the GATE (Geant4 Application for Tomographic Emission) Monte Carlo simulation tool [19, 20] were used to generate more realistic projections, which include the effects of noise, attenuation, collimator-detector response and scatter. The Monte Carlo code simulated a dual-head SPECT system, which has a FOV of 53.3×38.7 cm and a low-energy high-sensitivity (LEHS) collimator (hole length 24.05 mm and diameter 1.11 mm), and acquired 60 or 14 projections over a range of 180°. The projection data were acquired in 64×64 arrays with a pixel size of 6.25 mm. The distance between the detector and the axis of rotation was 29 cm. For isotope ^{99m}Tc, a photopeak window of 140 keV ± 10% was used in the simulation. Small FOV (12×12 cm) projections were obtained from full FOV projections by removing the pixels outside the small FOV. Due to noise, only 10 iterations were used in the reconstruction algorithms.

3.3. Real Emission Data using Jaszczak Torso Phantom

A realistic emission data set was acquired using a Siemens E-CAM Signature Series[®] SPECT scanner with low energy high resolution collimators (hole length 24.05 mm, hole diameter 2.54 mm) (Figure 3b). The thorax phantom used in this experiment was the large Jaszczak torso phantom consisting of the lungs, liver, bones and cardiac insert, as shown in Figure 3a. A circular orbit with a radius of 26.7 cm was used. In order to reduce the acquisition time, the activities in all organs as well as in the background were increased 6 times, during data acquisition we used 1/6 of the normal acquisition time. A total activity of 1480 MBq (40,000 μCi) ^{99m}Tc was injected into various parts of the phantom, with 740 MBq (20,000 μCi; ~16μCi/cc) in the liver, 148 MBq (4,000 μCi; ~37μCi/cc) in the cardiac wall, and 592 MBq (16,000 μCi; ~1.8μCi/cc) in the major chamber. Therefore, the acquisition time was reduced to about 1/6 that of the ASNC protocol [21] for a low count rest study. Projection sets with view-angles of 60, 20 and 10 were acquired, respectively. The acquisition time varied with the projection number to keep the total counts approximately the same. The size of the projection array was 256×256. A small data set (58×58) was cut out from the full FOV to generate the truncated data.

3.4. Assessment of Image Quality

Different methods were used to evaluate the quality of the conventional ML-EM and the tailored ML-EM reconstruction. For the noise-free images in the analytical heart phantom study, we measured the average activity in the myocardium as l and the average activity in a surrounding region within the FOV as b . The contrast was then defined by

$$Contrast = \frac{|l - b|}{l + b}. \quad (3)$$

The ratio of reconstruction contrast and phantom contrast was defined as relative contrast. The mean squared error (MSE) with N voxels in the FOV was calculated as follows:

$$MSE = \frac{1}{N} \sum_{i=1}^N (x_i - x_i^{true})^2. \quad (4)$$

For further quantitative assessment, image profiles through central slice of the reconstructed images are shown and compared in all three experiments.

4. Results

In this section, we compared the reconstruction results of the conventional ML-EM algorithm and the tailored ML-EM. For display purpose only, all images were scaled to [0 255] and were displayed using the same linear gray scale.

4.1. Simulated Projections of the Analytical Heart Phantom

The simulation results obtained from the reconstruction of the analytical heart phantom, together with corresponding vertical profiles through the center of the heart, are shown in Figures 4 and 5 for the conventional ML-EM algorithm and the tailored ML-EM algorithm, respectively.

Figure 4 shows the 120th and 128th slices from the 3D reconstruction results as representatives. At 60 view-angles, the results from the conventional ML-EM algorithm are similar to those from the tailored ML-EM algorithm, except for the presence of a dark line in the center of the ventricular wall, which degrades the uniformity of the myocardium. Streak artifacts are observed outside the truncation edge of the conventional ML-EM reconstructed image. The profiles in Figure 5a show a large bias between the profile of the conventional ML-EM reconstructed image and that from the phantom. However, the profile curve of the tailored ML-EM reconstructed image follows that of the phantom reasonably well. At 20 and 10 views, the reconstruction results of the conventional ML-EM algorithm show greater distortion especially at 10 view angles. In other words, the distortion increases as the number of view angles decreases from 60 to 10. The profiles in Figures 5b and 5c show large biases between the conventional ML-EM results and the phantom. Competitively, the tailored ML-EM algorithm has fairly good image quality at 20 views as well as at 10 views.

The relationship between the MSE and the relative contrast for the conventional ML-EM and the tailored ML-EM reconstruction is shown in Figure 6. The tailored ML-EM has a much lower MSE than the conventional ML-EM at the same relative contrast level, indicating a more accurate reconstruction. The relative contrast of the conventional ML-EM reconstruction is larger than 1 at the number of views higher than 10, due to a large number of voxels in the background close to the edge of FOV are nearly equal to zero. This can also be seen in Figure 5. In this situation, the value of voxels in the background is incorrect. Therefore, a large MSE is observed for the conventional ML-EM reconstruction. With the reduction of the number of view-angles, the MSE increases and the relative contrast decreases. At 10 view-angles, the tailored ML-EM reconstruction has higher relative contrast and a lower MSE than the conventional ML-EM reconstruction.

We also compared the two algorithms at different iterations, as shown in Figure 7. The reconstructed image from truncated projections using the conventional ML-EM algorithm starts to deteriorate once the iteration number is larger than 5. Furthermore, it converges to a non-uniform shape after 10 iterations. High frequency artifacts occur outside the FOV; as a consequence, propagate into the FOV. The tailored ML-EM algorithm significantly suppresses the artifacts and improves the image quality in all cases.

4.2. Simulated Projections of the NCAT Phantom

We next used more realistic Monte Carlo data, including attenuation, scatter, noise and distance dependent collimator resolution, to compare the conventional ML-EM algorithm and the tailored ML-EM algorithm. Similar observations are made at 60 truncated projections and no distortion is evident. The conventional ML-EM results at 14 view angles

shows lower quality, where more severe streak artifacts outside the truncation edge and lower contrast are obtained as compared to those from the tailored ML-EM algorithm (see Figure 8).

The profiles in Figure 9 show only small differences between the conventional and tailored ML-EM reconstructions at 60 views. Nevertheless, the profiles of the conventional ML-EM reconstruction has much lower counts at 14 views.

These results reconfirm that the tailored ML-EM algorithm is superior to the conventional ML-EM algorithm for reconstruction of acquisitions with small numbers of views and truncated data. The Monte Carlo simulations provide a better impression of the advantages of the tailored ML-EM algorithm. No attenuation, scatter, and blurring corrections are performed during image reconstruction in this paper.

4.3. Real Emission Data using Jaszczak Torso Phantom

Given the highly encouraging results with the noise-free analytical heart phantom and the noisy NCAT phantom, we next proceeded to real emission SPECT data using a Jaszczak torso phantom. Each reconstruction was stopped at the 30th iteration. Overall the image quality is better for the results of the tailored ML-EM algorithm than those of the conventional ML-EM algorithm (Figure 10 and 11). Moreover, the tailored ML-EM algorithm decelerates the convergence speed and keeps the value of pixels outside the FOV under control. When the number of view-angles is small, superior myocardial edge definition in the images obtained by using the tailored ML-EM algorithm is again evident (see Figure 11).

Figure 10 clearly shows the advantages of the tailored ML-EM algorithm at the reconstruction of truncated projection data at small number of view-angles. The shape of the heart is well conserved even when the number of view-angles is less than 20.

5. Discussion and Conclusions

A tailored ML-EM algorithm has been proposed for the reconstruction of projection data with insufficient angular sampling and data truncation. Under these conditions, the analytical heart phantom, NCAT phantom and Jaszczak torso phantom simulation results verify that the tailored ML-EM algorithm provides a clear improvement in reconstructed image quality and accuracy, compared with the conventional ML-EM algorithm. The tailored algorithm chooses a smaller step size for pixels outside the FOV to stabilize the iterative algorithm, which in turn suppresses the streak artifacts outside the FOV and reduces distortion in the FOV.

For a sufficient number of views, such as 60 view angles, the effect of truncation on the reconstruction is negligible and no significant difference is observed between the reconstruction results of the tailored ML-EM algorithm and those of the conventional ML-EM algorithm.

Truncation mainly affects the reconstruction at small numbers of projections, where the conventional ML-EM algorithm performs poorly. Insufficient angular sampling makes the truncation artifacts more severe. As a result, severe artifacts appear outside the FOV. The errors outside the FOV propagate into the FOV as the iteration number increases, causing distortion in the reconstruction of the conventional ML-EM algorithm. In addition, the presence of bias in the background increases the MSE and reduces the relative contrast of images. Nonetheless, the streak artifacts and image distortion are significantly reduced after

using the tailored ML-EM algorithm. The shape and the value of the heart are well conserved at 10 view-angles, even when data truncation is present.

In conclusion, the tailored ML-EM algorithm can substantially suppress the artifacts and distortions associated with small FOV cardiac imaging. It also extends the conventional ML-EM algorithm to the reconstruction of truncated projections at small number of views. The data extension strategy in the tailored ML-EM algorithm can be directly extended into the OS-EM algorithm.

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Figure 1.

The change of $\sum_i a_{ij}$ before and after array expansion. The pixel x_j outside the FOV is affected by the array expansion.

(a) The 110th slice

(b) The 120th slice

(c) The 128th slice

Figure 2.

From left to right: the 110th, 120th and 128th axial slices of the 3D heart phantom. The FOV covered by the small detector is indicated by the dashed circle.

(a)

(b)

Figure 3.

(a) The Jaszczak torso phantom. (b) The Siemens E-CAM Signature Series[®] SPECT scanner used in the experiment.

Figure 4. Images of the analytical heart phantom reconstructed by the conventional ML-EM and the tailored ML-EM algorithms using different number of views. The projections were truncated and 500 iterations were applied.

Figure 5.

The vertical profiles through the center of slice 128 of the analytical heart phantom and the reconstructed images using the conventional ML-EM and the tailored ML-EM algorithms. The images were reconstructed from 60, 20, and 10 truncated projections. The solid line represents the true heart phantom, the solid line with plus sign represents the tailored ML-EM reconstruction and the dash line represents the conventional ML-EM reconstruction.

Figure 6. MSE as a function of relative contrast in the reconstructed analytical heart phantom using conventional ML-EM and tailored ML-EM algorithms. The points on the curves represent the numbers of views. For each curve, the view number increases from the left side to the right side.

Conventional
ML-EM

Tailored
ML-EM

5 iterations

10 iterations

50 iterations

Figure 7. Sample reconstructed central axial slices of the conventional and tailored ML-EM reconstructions at different iterations in the analytical heart phantom experiment. All images were reconstructed from 20 truncated projections.

Figure 8.

The reconstruction results of Monte Carlo simulation using the NCAT phantom. The first column shows the central slices of the reconstructions. Vertical long-axis (VLA), short-axis (SA), and horizontal long-axis (HLA) cuts are shown in the last three columns. 10 iterations were used.

Figure 9.

The vertical profile curves for slice 128 of reconstructed images with 60 (top row) and 14 views (bottom row). Solid lines on slice 128 of the NCAT phantom indicate the profile positions. The profiles on the right side correspond to the lines from left to right in the left-hand image.

Figure 10.

The vertical profiles for slice 128 of the reconstructed images using conventional ML-EM and tailored ML-EM algorithms. The images were reconstructed from 60, 20, and 10 truncated projections. Solid lines on slice 128 of the reconstructed images indicate the profile positions.

Figure 11.

The reconstruction results obtained from physical phantom study. From top to bottom: the reconstruction results of 60, 20 and 10 truncated projections, respectively. The first column shows the central slices of the reconstructions. Vertical long-axis (VLA), short-axis (SA), and horizontal long-axis (HLA) cuts are shown in the last three columns. 30 iterations were used.