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MicroPET reconstruction with random coincidence correction via a joint Poisson model

Tai-Been Chen[a], Jyh-Cheng Chen[c,e], Henry Horng-Shing Lu[b,*], Ren-Shyan Liu[d]

[a] *Department of Medical Imaging and Radiological Sciences, I-Shou University, Taiwan, ROC*
[b] *Institute of Statistics, National Chiao Tung University, 1001 Ta Hsueh Road, Hsinchu 30050, Taiwan, ROC*
[c] *Department of Biomedical Imaging and Radiological Sciences, National Yang-Ming University, Taiwan, ROC*
[d] *School of Medicine, National Yang-Ming University, Taiwan, ROC*
[e] *Department of Education and Research, Taipei City Hospital, Taiwan, ROC*

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Abstract

Positron emission tomography (PET) can provide *in vivo*, quantitative and functional information for diagnosis; however, PET image quality depends highly on a reconstruction algorithm. Iterative algorithms, such as the maximum likelihood expectation maximization (MLEM) algorithm, are rapidly becoming the standards for image reconstruction in emission-computed tomography. The conventional MLEM algorithm utilized the Poisson model in its system matrix, which is no longer valid for delay-subtraction of randomly corrected data. The aim of this study is to overcome this problem. The maximum likelihood estimation using the expectation maximum algorithm (MLE-EM) is adopted and modified to reconstruct microPET images using random correction from joint prompt and delay sinograms; this reconstruction method is called PDEM. The proposed joint Poisson model preserves Poisson properties without increasing the variance (noise) associated with random correction. The work here is an initial application/demonstration without applied normalization, scattering, attenuation, and arc correction. The coefficients of variation (CV) and full width at half-maximum (FWHM) values were utilized to compare the quality of reconstructed microPET images of physical phantoms acquired by filtered backprojection (FBP), ordered subsets-expected maximum (OSEM) and PDEM approaches. Experimental and simulated results demonstrate that the proposed PDEM produces better image quality than the FBP and OSEM approaches.

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Keywords: MLE-EM; FBP; OSEM; PDEM; FORE; CV; FWHM

1. Introduction

The high spatial resolution and sensitivity of microPET make it an ideal modality for *in vivo* gene imaging. Those images can be employed to monitor the effects of gene therapy inside animal bodies. High-quality image reconstruction is important when establishing a solid basis for quantitative study of microPET images [1,2].

The maximum likelihood estimation with expectation-maximization (MLE-EM) algorithms has been utilized to reconstruct emission-computed tomography [3,4]. Statistical analysis that supports positron emission tomography (PET) has been discussed elsewhere [5]. The MLE-EM technique can model randomness in emission tomography with the asymptotic efficiency of MLE by applying the row operation and monotonic convergence using the EM algorithm. Furthermore, the EM algorithm can be parallelizable for 3D PET image reconstruction [6].

The generation of quantitative PET images requires that the effects of random coincidences and coincidence efficiency are corrected [7,8]. One random correction approach applies single count rates to a prompt sinogram [9]. This approach is generally based on geometrical and physical characteristics. However, this approach makes many assumptions for approximations that can decrease the accuracy of random

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* Corresponding author. Tel.: +886 3 5731870; fax: +886 3 5728745.
E-mail address: hslu@stat.nctu.edu.tw (H.H.-S. Lu).

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correction below that obtained using methods that utilize both prompt and delay sinograms. An alternative approach applies random pre-correction to sinograms by subtracting the delay sinogram from a prompt sinogram before processing of images reconstruction. The random pre-correction using various approximations has been applied to correct accidental (or random) coincidental events [10,11]. Novel methods have been developed to approximate random pre-correction [12–14]. However, random pre-correction increases variance (noise) [13,15]. Since the distribution of random pre-correction is no longer Poisson-distributed, the shifted Poisson methods and saddle-point (SD) approximation have been generated to enhance approximation in [16]. This study proposes a joint Poisson model with MLE-EM reconstruction and random correction to prompt and delay sinograms without using approximations or increasing variance.

Simulations, physical phantoms and real mouse studies of the proposed reconstruction method using the microPET R4 system were performed. This study considered analyzed and assessed reconstruction of 2D data obtained from 3D sinograms after applying the Fourier rebinning (FORE) method [17] to verify the proposed approach. The proposed technique can also be utilized by future studies reconstructing 3D images.

2. Methodology

Two independent Poisson models associated with prompt and delay sinograms are labeled (1) and (2).

$$n_{\rm p}^*(d) \sim \text{Poisson}(\lambda^*(d)), \tag{1}$$

$$n_{\rm d}^*(d) \sim \text{Poisson}(\lambda_{\rm r}^*(d)), \tag{2}$$

where $\lambda^*(d) = \lambda_{\rm t}^*(d) + \lambda_{\rm r}^*(d) = \sum_{\rm b} P(b, d)\lambda_{\rm t}(b) + \lambda_{\rm r}^*(d)$, $b = 1, 2, \ldots, B$, and $d = 1, 2, \ldots, D$.

The term $n_{\rm p}^*(d)$ is the number of coincidental events in the prompt sinogram at the dth projection line of response (LOR), which is formed by two detectors with the Poisson parameter or mean, $\lambda^*(d)$; $n_{\rm d}^*(d)$ is the number of random coincidental events in the delay sinogram with the Poisson parameter $\lambda_{\rm r}^*(d)$; $P(b,d)$ is the system probability matrix from the bth pixel to the dth detection tube. Parameters $\lambda_{\rm t}(b)$ and $\lambda_{\rm r}^*(d)$ are unknown and must be estimated. Parameter $\lambda_{\rm t}(b)$ represents the intensities of true coincidental events. Appendix (A.3) lists the log-likelihood of observed data in the prompt and delay sinograms. Since the MLE is difficult to determine by maximizing Eqs. (1) and (2) numerically, the EM algorithm is utilized (see Appendix A). Eqs. (3) and (4) are the ith iteration steps of the PDEM.

$$\lambda_{\rm t}^i(b) = \frac{\lambda_{\rm t}^{i-1}(b)}{\sum_{d=1}^{D} P(b, d)} \sum_{d=1}^{D} \frac{n_{\rm p}^*(d)p(b, d)}{\sum_{b'=1}^{B} p(b', d)\lambda_{\rm t}^{i-1}(b') + \lambda_{\rm r}^{*i-1}(d)}, \tag{3}$$

$$\lambda_{\rm r}^{*i}(d)=\frac{1}{2}\left[\frac{n_{\rm p}^*(d)\lambda_{\rm r}^{*i-1}(d)}{\sum_{b'=1}^{B} p(b', d)\lambda_{\rm t}^{i-1}(b') + \lambda_{\rm r}^{*i-1}(d)} + n_{\rm d}^*(d)\right], \tag{4}$$

where $i = 1,2, \ldots I$ is the number of iterations.

The MLE-EM algorithm of joint the prompt and delay sinograms is described as follows and such a scheme is called PDEM reconstruction.

2.1. Algorithm for PDEM reconstruction

1. Set initial parameters using filtered backprojection (FBP), the method of moments (MME) or alternative approach.
2. Update the parameters by applying Eqs. (3) and (4).
3. If $|l_{\rm in}(\lambda_{\rm t}^{i-1}(b), \lambda_{\rm r}^{*i-1}(d)) - l_{\rm in}(\lambda_{\rm t}^{i}(b), \lambda_{\rm r}^{*i}(d))| <$ tolerance, then the iteration is terminated; otherwise, go to step 2 and replace the old parameter values with new values.

This method preserves Poisson properties and corrects bias iteratively. In this study, $P(b,d)$ was computed from LORs and the locations of pixels based on the geometric characteristics of the microPET R4, including number of detectors, image size, field of view (FOV), ring diameter, and number of angular views. The matrix size of one slice is 96 × 84. There are 96 angular views and 84 LORs for each angular view during image scanning. Furthermore, each $P(b,d)$ can be identified from its detector pairs of LOR and image pixel location. Therefore, the PDEM reconstructs the sinogram after being rebinned by FORE approach in the microPET system.

3. System configurations of microPET R4 and data handling

The phantoms and small animals were injected with F-18 FDG and were scanned by the microPET R4. The microPET R4 system consists of 32 rings with 192 detectors per ring; the images were reconstructed using 128 × 128 pixels. Transaxial projection bin size was 1.213 mm, and axial slice thickness was 1.2115 mm. Coincidence timing window was set at 6×10^{-9} s. The lower and upper level energy thresholds were 350 and 750 keV, respectively. Span of the data set was 3, and maximum ring difference (MRD) of the data set was 31.

The data handling is described as follows: first, list mode data were histogramed into the 3D data with a span of 3 and MRD of 31, which are sized 2 × 703 × 96 × 84 (i.e., 2 sinograms (prompt and delay) × 703 slices × 96 angular views × 84 projection lines (LORs)) and stored as floating type data. The second data were obtained using random pre-correction and were sized 1 × 703 × 96 × 84. These 3D data were rebinned into 2D sinograms using the FORE method with dead time and decay corrections. The attenuation, normalization, scattering, and arc corrections were not