

The Quantitative Accuracy and Efficiency of the Dual Reconstruction Scheme Including a Practical Scatter/Random Approximation in Dynamic PET Imaging

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Abstract— We describe a time-efficient reconstruction scheme with a practical approximate scatter and random correction for dynamic PET imaging on scanners with large data sets such as the High Resolution Research Tomograph (HRRT). This dual (histogram/list-mode) reconstruction scheme makes use of the efficiency advantage of both histogram and list-mode reconstructions (i.e. histogram-mode reconstruction is applied to the dynamic frames with a large number of counts, and list-mode reconstruction is applied to the frames with a low number of counts). The practical scatter and random approximation technique is based on a time averaged scatter and random estimate followed by scaling according to the global numbers of true and random events for each temporal frame. The quantitative accuracy of this dual reconstruction scheme including the scatter and random approximation was examined by comparing the time activity curves (TAC) obtained from the images reconstructed using the conventional histogram-mode algorithm and those obtained from applying the dual reconstruction scheme with the practical approximation. A representative dynamic ^{11}C non-human primate study with 14 temporal frames is presented here, and an excellent agreement between the conventional and the proposed scheme was found, while an overall gain of about 35% in time (which depends on the number of dynamic frames; the more frames with a similar spatial activity distribution there are, the more time we gain) and an over 4 times less storage cost for the scatter and random data sets (sinograms) was achieved in this case.

I. INTRODUCTION

LIST-mode reconstruction for high-resolution PET imaging has been established to be particularly advantageous for studies with a low number of counts; data are reconstructed on an event basis thus rendering the reconstruction times proportional to the number of acquired events [1,2]. In

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contrast, histogram-mode reconstruction is time-wise more efficient for studies with a large number of counts. As a result, especially in dynamic imaging, it would be practically advantageous to have the ability to choose the time-wise optimal reconstruction mode for each frame on the basis of the number of events acquired during that temporal frame. A dual (histogram/list-mode) reconstruction scheme has currently been developed to reduce the time cost for dynamic PET imaging using the HRRT scanner which often has a high number of LORs/number of counts ratio [3].

In dynamic imaging, the expected scatter and random events are generally estimated on a frame-by-frame basis. The justification for this approach is that the tracer distribution changes as a function of time, and therefore the scatter and random distributions will change accordingly. As a consequence, the time and storage requirements for the scatter and random estimates are proportional to the number of dynamic frames. Furthermore, given the often highly variable number of events per frame typical of dynamic scanning, the numbers of counts in the frame-based approach might not always be sufficiently high to produce an accurate scatter estimate. As a result, a more practical scatter and random approximation technique was developed.

In this work, we present a dual reconstruction scheme which incorporates a modified Ordinary Poisson List-Mode Expectation Maximization algorithm (OP-LMEM) [3] and a modified histogram-mode 3D Ordinary Poisson Ordered Subset Expectation Maximization algorithm (3D-OP) [4] using a scatter correction based on the Single Scatter Simulation (SSS) [5] and a random correction based on the variance reduced delay coincidence technique [6]. The dual reconstruction scheme including the following approximation is discussed together with a comparison of images reconstructed with the conventional 3D-OP.

II. A PRACTICAL SCATTER AND RANDOM APPROXIMATION TECHNIQUE

This technique is based on two observations:

- The scatter and random distributions are not very sensitive to the changes in tracer distribution (i.e. the spatial scatter and random distributions are spatially much smoother compared to the distribution of the unscattered true events which correctly identifies the tracer distribution).

- The amount (magnitude) of scatter in each dynamic frame is proportional to the number of true counts in the frame, and likewise that of randoms is proportional to the global randoms counts in each frame.

In addition, the random estimate becomes less and less significant in the later frames of dynamic studies since the random fraction drops as the square of the activity thus increasing the ‘tolerance’ of the random estimate. As a result, we obtained a scatter and random estimate for each frame by first calculating a scatter and random estimation using the data from a set of summed frames and then scaling this estimate according to the frame trues and randoms. Compared to the traditional frame-by-frame calculation, this method is computationally much more efficient and potentially more accurate due to the higher statistical quality of the data used in the scatter and random estimation.

After incorporating this approximation technique, the OP-LMEM algorithm [3] becomes:

$$\lambda_j^{m,l+1} = \frac{\lambda_j^{m,l}}{\sum_{i=1}^I w_{ii} g_{ij}} \sum_{k=1}^N g_{ikj} \frac{1}{\sum_{b=1}^J g_{ibb} \lambda_b^{m,l} + \left[\frac{c_{rf}}{c_{ri}} \bar{r}_{ik}^A + \frac{c_{sf}}{c_{si}} \bar{s}_{ik}^A \right] / w_{ii}} \quad (1)$$

where C_{rf} is the number of random events (counts) in each individual frame, C_{ri} is the total number of random counts in the summed frame, C_{sf} is the number of true counts in each individual frame, C_{si} is the total number of true counts in the summed frame, \bar{r}_{ik}^A is the random estimate for the summed frame (i.e. time-averaged estimate), and \bar{s}_{ik}^A is the scatter estimate for the summed frame. In a similar fashion, this approximation can be incorporated into the 3D-OP algorithm. This technique can be used reliably (as quantitatively demonstrated later) by using the plot of global trues count rate vs time, i.e. the dead time and decay corrected global Time Activity Curve (TAC), in order to guide the decision-making procedure as to which frames are to be grouped together for the scatter/random-estimation tasks. It has been indeed found empirically that whenever there is a large change (i.e. high slope) in the global TAC, there is generally a larger change in the spatial radioactivity distribution, and a separate scatter and random estimate needs to be performed for those frames. Fig. 1 shows a global TAC for a ^{11}C dynamic non-human primate study. The frames grouped by the ellipses are summed to perform the average scatter and random estimates.

This work demonstrates the quantitative accuracy and efficiency of the dual reconstruction scheme including the aforementioned practical scatter and random approximation on the real data of rapidly changing tracers with spatially variant distribution such as ^{11}C -dihydrotrabenazine in dynamic PET imaging using the HRRT scanner.

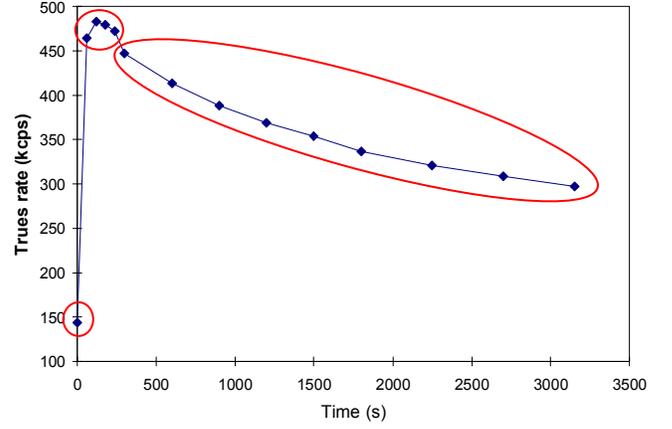


Fig. 1: A global TAC for a ^{11}C -dihydrotrabenazine dynamic non-human primate study. The solid line connects the measured data points and aids in determining larger changes in the trues count rate.

III. METHODS

Tomograph: Data were acquired on the second generation of the High Resolution Research Tomography (HRRT) [7]. This HRRT scanner has an octagonal detector ring design, with detector heads consisting of a double 10 mm layer of LSO/LYSO for a total of 119,808 detector crystals.

Non-human primate study: A non-human primate underwent a 60 min ^{11}C -dihydrotrabenazine (DTBZ – a vesicular monoamine transporter VMAT2 marker) scan on the HRRT (after a 6 min transmission scan and a 5mCi bolus injection). Data were acquired in list-mode and then framed into a 5x1 min, 5x5 min and 4x7.5 min framing sequence. The number of counts/frame in this study ranged from 140M to 13M and the count rate ranged between 600 and 50 kcps. According to the dual reconstruction scheme [3], 4 frames with the number of counts greater than 50M have been reconstructed using 3D-OP, and the other 10 frames have been reconstructed using OP-LMEM including the practical scatter and random approximation. In addition, all 14 frames were also reconstructed using the conventional 3D-OP as well as OP-LMEM with the frame-based scatter and random estimation. The following comparisons were performed:

1) *Time activity curve (TAC) comparisons:* The time activity curve, with the ROIs in the striatum (right/left caudate, putamen, and ventral striatum), cerebellum, cortices, and a number of selected cold regions, was plotted over 14 frames of the non-human primate scan for the emission (trues) images. The TACs were then compared between the images reconstructed using the conventional 3D-OP and the dual reconstruction scheme including the practical scatter and random approximation (i.e. approximated dual reconstruction scheme). The result for one of the ROIs was arbitrarily chosen to be shown here (Fig. 2).

2) *Ratio of TAC comparisons:* The ratios of the above TACs were also calculated to check the quantitative accuracy of the approximated dual reconstruction scheme. The results for 4 of the ROIs were arbitrarily chosen to be shown here (Fig. 3).

3) *Binding potential comparisons*: The binding potential for the non-human primate study was computed using the tissue input Logan graphical approach for the conventional 3D-OP and the approximated dual reconstruction scheme.

4) *Reconstruction time cost comparisons*: The frames were sorted by number of counts in a descending order, and the reconstruction time cost was plotted as a function of the sorted-frames for the 3D-OP and OP-LMEM reconstructions. In all cases, the same number of computer processors was used.

IV. RESULTS

As shown in Fig. 2, the TACs agree very well between the conventional 3D-OP and the approximated dual reconstruction. The variation in the TAC ratio (up to 5%) as shown in Fig. 3 is mainly contributed from the statistical difference between the histogram-mode angular subset and the list-mode temporal subset (2). Fig. 3 also demonstrates the accuracy of the practical scatter and random approximation: the TACs of the 4 frames (as circled in Fig. 3) reconstructed using the approximated 3D-OP agree with those using the conventional 3D-OP within 1%.

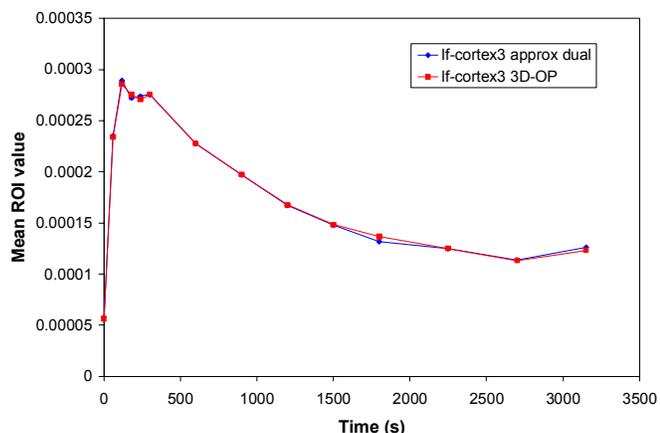


Fig. 2: The TAC comparison for a cortex ROI between conventional 3D-OP and the approximated dual reconstruction scheme

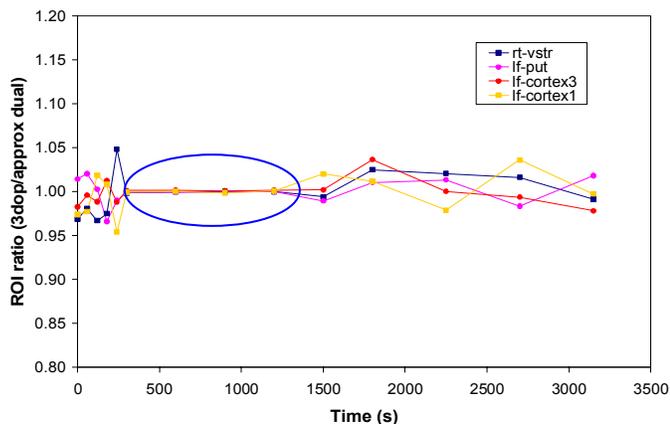


Fig. 3: The ratio of the TAC between the conventional 3D-OP and the approximated dual reconstruction scheme comparison

In addition, the binding potentials obtained from the conventional 3D-OP agree with those obtained from the approximated dual reconstruction scheme within 3% as shown in Fig. 4.

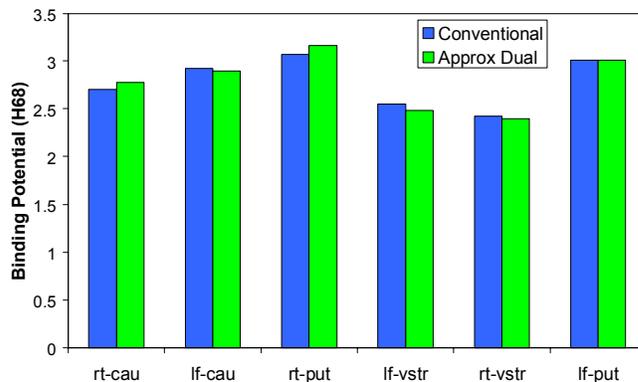


Fig. 4. The binding potential comparison

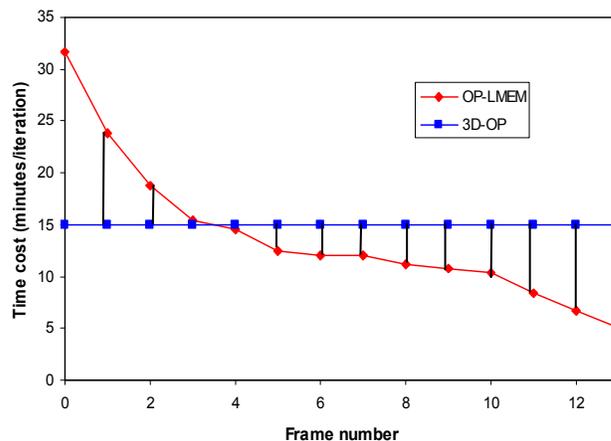


Fig. 5. ROI The reconstruction time cost comparison (the number of counts ranges from 140M to 13M, and the frames were sorted by number of counts in a descending order.)

Fig. 5 shows the reconstruction time cost for both histogram and list-mode OP algorithms. 3D-OP shows a constant time cost for each frame since the number of LORs stays constant, whereas OP-LMEM shows an decrease of time cost at frames with a lower number of counts since the time cost in list-mode is proportional to the number of counts in the frame. The time we gained by applying the dual reconstruction scheme is depicted by the shaded area; in the case of the non-human primate study, we gained about (i) 20% of time as compared to reconstructing every frame with 3D-OP and (ii) nearly 4 times faster performance on the scatter and random estimations (i.e. computing 3 estimates instead of 14) and (iii) 4 times less storage cost by applying the practical approximation. An overall gain of about 35% in time (which depends on the number of dynamic frames) was achieved in this case.

V. FUTURE WORK

The approximated dual reconstruction scheme will be applied to human studies with and without motion correction [8], but some additional issues will need to be addressed. For the non-human primate studies in which no motion was present and there is a sufficient number of counts within each frame to obtain a consistent scatter fraction with the

conventional method, a very good agreement in the TAC comparisons between the conventional and approximate method was obtained. On the other hand, for human studies the frame-based estimate might not be very accurate since it is sensitive to both motion and the potentially low number of events (i.e. the number of counts in each frame for the human studies ranges from 57M to 2.6M which is about 2-3 times lower than that for the non-human primate studies) in the frame thus possibly producing somewhat inaccurate results; this would invalidate the use of the frame-based estimate as the absolute reference. A fully motion-corrected data set would therefore need to be used to further demonstrate the validity of the approximate method in the human studies for tracers with rapidly varying spatial distribution. For tracers with relatively uniform spatial distribution and phantom studies, the approximate method is expected to be more accurate than the conventional method due to the higher statistical quality of the data used in the scatter and random estimates.

VI. CONCLUSION

Preliminary results obtained from non-human primate studies look very promising. In particular the excellent agreement in TACs and binding potentials are reached between 3D-OP and the approximated dual reconstruction. By applying the dual reconstruction scheme and the practical approximation for the non-human primate study presented here, we gain about 35% of time overall as compared to reconstructing all frames using conventional 3D-OP. All in all, we have developed an efficient reconstruction scheme with a practical scatter and random approximation thus contributing to making dynamic imaging on scanners with large data sets such as HRRT more promptly manageable.

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