

# Design of a Motion-Compensation OSEM List-mode Algorithm for Resolution-Recovery Reconstruction for the HRRT

Richard E. Carson, *Member, IEEE*, W. Craig Barker, Jeih-San Liow, and Calvin A. Johnson, *Member, IEEE*

**Abstract**--The HRRT PET system has the potential to produce human brain images with resolution better than 3 mm. To achieve the best possible accuracy and precision, we have designed MOLAR, a Motion-compensation OSEM List-mode Algorithm for resolution-recovery Reconstruction on a computer cluster with the following features: direct use of list mode data with dynamic motion information (Polaris); exact reprojection of each line-of-response (LOR); system matrix computed from voxel-to-LOR distances (radial and axial); spatially varying resolution model implemented for each event by selection from precomputed line spread functions based on factors including detector obliqueness, crystal layer, and block detector position; distribution of events to processors and to subsets based on order of arrival; removal of voxels and events outside a reduced field-of-view defined by the attenuation map; no pre-corrections to Poisson data, i.e., all physical effects are defined in the model; randoms estimation from singles; model-based scatter simulation incorporated into the iterations; and component-based normalization. Preliminary computation estimates suggest that reconstruction of a single frame in one hour is achievable. Careful evaluation of this system will define which factors play an important role in producing high resolution, low-noise images with quantitative accuracy.

## I. INTRODUCTION AND ALGORITHM OVERVIEW

The ECAT HRRT [1] is a state-of-the-art PET system with the potential for extremely high resolution ( $< 3$  mm) for human and large animal brain imaging. The use of phoswich detectors (10 mm LSO, 10 mm LYSO) provides the capability to achieve excellent uniformity in resolution across the field-of-view. The small aperture (46.9 cm diameter), long axial field-of-view (25.2 cm), and 20-mm crystal depth will provide high

sensitivity, allowing sufficient counts so that images with high resolution can have reasonable statistical quality.

In the current generation of PET scanners, iterative maximum likelihood reconstruction has provided only small advantages for brain reconstructions. This has been the case because 1) the typical number of counts per line-of-response (LOR) is sufficient so that use of a Poisson model is not critical, and 2) the attenuation and normalization corrections are rather uniform so there is only a small statistical penalty caused by the use of precorrected data. These considerations change, however, for the HRRT. First, given the very large number of LORs ( $4.5 \times 10^9$ ), even a high-count frame ( $2.0 \times 10^8$  counts) has very low occupancy of an uncompressed sinogram. Thus, the expected counts per LOR  $\ll 1$ , suggesting that inclusion of the Poisson characteristics of these data is likely to produce an improvement in reconstructed images. Secondly, the variation in efficiency between LORs due to the phoswich design and due to the gaps in the sinograms introduced by the octagonal detector panel arrangement, suggests that higher statistical precision can be achieved with an algorithm that does not pre-correct the projection data.

In addition to the statistical considerations, because of the high resolution, motion of the patient's head will seriously degrade image quality. Repositioning of events to account for subject motion can best be accomplished by online measurement of motion incorporated into the list mode acquisition

Based on these motivations, we designed a Motion-compensation OSEM List-mode Algorithm for Resolution-recovery Reconstruction (MOLAR) for application to the HRRT. Events are acquired in list mode in conjunction with hardware measurement of object position using the Polaris system [2]. Individual events are repositioned in space. Reconstruction is performed directly from the list mode data with no pre-corrections, using an OSEM-type algorithm (see, e.g., [3]). The expected value for the number of counts along each LOR is determined from the forward projection through the voxel grid accounting for attenuation, normalization, randoms, and scatter. Resolution recovery is achieved by the use of a full line spread function model. The contributions of

---

Manuscript received October 25, 2003.

Richard E. Carson is with the PET Department, Warren Grant Magnuson Clinical Center, National Institutes of Health, Bethesda, MD 20892 (email [richard-e-carson@nih.gov](mailto:richard-e-carson@nih.gov))

W. Craig Barker is with the PET Department, Warren Grant Magnuson Clinical Center, National Institutes of Health, Bethesda, MD 20892 (email [cbarker@cc.nih.gov](mailto:cbarker@cc.nih.gov))

Jeih-San Liow is with the Molecular Imaging Branch, NIMH, National Institutes of Health, Bethesda, MD 20892 (email [LiowJ@intra.nimh.nih.gov](mailto:LiowJ@intra.nimh.nih.gov))

Calvin A. Johnson is with the Division of Computational Bioscience, Center for Information Technology, National Institutes of Health, Bethesda, MD 20892 (email [johnson@mail.nih.gov](mailto:johnson@mail.nih.gov))

each voxel to each LOR (system matrix) are determined by computing the radial and axial voxel-to-LOR distances, which are used as indices to the appropriate pre-computed line spread function applicable to that event. The algorithm is implemented on a parallel computer cluster [4, 5]. Events are distributed to processors and subsequently into subsets based on the order of arrival in the list mode stream. The software is designed for portability with the potential for application to other scanners in addition to the HRRT.

## II. THEORETICAL FRAMEWORK

The activity  $\lambda$  (Bq/mL) in voxel  $j$  is defined in an object space which is considered to be stationary. The detector LORs are indexed by  $k = 1, \dots, K$ , with the geometric relationship of detector LORs to the voxel space varying with time according to the subject motion. Divide the time frame  $T$  into  $n_T$  time bins of duration  $\Delta t$ , defined by the Polaris sampling rate. Let  $i(k, t)$  be the mapping from the detector LOR  $k$  at time  $t$  into the appropriate image chord  $i$  using the motion information. Let  $Y_{k,t}$  equal the number of counts acquired in detector LOR  $k$  in time bin  $t$ , with expected value based on the image at iteration  $n$ :

$$E(Y_{k,t}^{(n)}) = \Delta t \left( \sum_j c_{i(k,t),j} A_{i(k,t)} N_k \lambda_j^{(n)} + R_k + S_{i(k,t)} \right) \quad (1)$$

In (1), detector LOR-based factors (indexed by  $k$ ) are normalization ( $N_k$ , actually a sensitivity factor with units of (counts/sec)/(Bq/mL·mm)) and randoms ( $R_k$ , estimated from the measured singles rates, counts/sec). The image chord-based factors (indexed by  $i$ ) are attenuation ( $A_i$ , dimensionless) and Scatter ( $S_i$ , counts/sec). The system matrix  $c_{i(k,t),j}$  (mm) is the contribution of voxel  $j$  to chord  $i$  defined by detector LOR  $k$  in time bin  $t$ . The geometry of this LOR is defined by the motion mapping function  $i(k, t)$ . In specifying the resolution of each chord, we assume that resolution components can be decomposed into separable transverse and axial line spread functions,  $f^r(\Delta r)$  and  $f^z(\Delta z)$ , respectively. These functions are indexed by the perpendicular distances ( $\Delta r$  and  $\Delta z$ ) from voxel  $j$  to chord  $i$ :

$$c_{i(k,t),j} = f_k^r(\Delta r_{i(k,t),j}) f_k^z(\Delta z_{i(k,t),j}) \quad (2)$$

The choice of line spread function for each event is based on the detector LOR geometry (see III.B).

For list mode acquisition, the data stream is indexed by  $i = 1, \dots, I$ . For ease of notation, we use  $i$  to index the image chord associated with event  $i$  (for  $c_{i,j}$ ,  $A_i$ , and  $S_i$ ) and for the detector LOR associated with event  $i$  (for  $N_i$  and  $R_i$ ). The EM equation [6, 7] at iteration  $n$  is, thus:

$$\lambda_j^{(n+1)} = \frac{\lambda_j^n}{TQ_j} \sum_{i=1}^I \frac{c_{i,j} A_i N_i}{\sum_j c_{i,j} A_i N_i \lambda_j^n + R_i + S_i} \quad (3)$$

$Q_j$  in the denominator of the leading term of (3) is the global sensitivity image, which is quite complex in the case of motion:

$$Q_j = \frac{1}{T} \int_0^T \sum_{k=1}^K c_{i(k,t),j} A_{i(k,t)} N_k dt \quad (4)$$

An ideal calculation of  $Q_j$  would account for the position of all detector LORs at all times in the scan frame. As written, (4) is computationally impractical (see III.G).

## III. IMPLEMENTATION

### A. Chords

A primary consideration is the cost of computing the system matrix,  $c_{i,j}$ . We have devised and tested an approximation method that computes the perpendicular distances in transverse and axial directions from the center of each voxel to its corresponding nearest point in the central axis of the chord, and then imposes a separable resolution model (2) using these distances as indices. The line spread functions are precomputed with much finer sampling than the voxel grid for accurate interpolation. This approximation method results in a 63-fold reduction in the cost of computing  $c_{i,j}$  compared with resolution-based ray tracing. For each event, the trajectory through the image voxels is determined and saved. For forward and backprojection, the transverse and axial “widths” of the chord are defined by the line spread function chosen for each event, i.e., lower resolution chords include more voxels in the projection calculation. Furthermore, since the “sign” of the chord-to-voxel distance is known, e.g., positive for distance to the left, asymmetric line spread functions are permitted.

Preliminary timing estimates have been performed to determine the computation time for forward and backprojections. For a high-count frame of 200 million events on a 24-node dual processor system (AMD 1800+ processors with 2 GB memory per node), the expected computation time for a forward and backprojection is less than 10 min. This suggests that a complete reconstruction of a single frame can be achieved in one hour using a subset-based algorithm.

### B. Line Spread Functions

Initially, line spread functions are defined as Gaussian functions with varying FWHM as a function of the 2 detectors associated with each event. Ultimately, the resolution kernels will be based on measured line spread functions. Adjustments to the resolution for average effects of the obliqueness of the LOR with respect to primary axes of the crystals, the detector layer (front/back), the crystal position within the block, and the block position within the panel are applied. Additional secondary effects can easily be incorporated in these functions. These include blur due to uncertainty in the motion correction data (e.g., based on the standard deviation of the Polaris measurements within a short time window of each event), definition of a voxel shape (i.e., blobs), and positron range and noncollinearity effects. On the first pass through the list mode file, transverse and axial line spread functions are selected from the pre-computed sets for each event.

### C. Normalization

Normalization based on each LOR is the most obvious and accurate approach. However, as currently implemented, these data are only available for compressed sinograms (span 3 or 9). Furthermore, a very long scan is required to collect sufficient statistics for the large number of LORs. Component based normalization [8] expresses the normalization factor as the product of individual detector efficiencies, transverse geometrical effects, and axial geometrical effects. The geometric effects are stored as tables based on the incident angle of the LOR to the surface of the detector, the position of the detector within the block, and the detector layer (front/back). In addition, in this model (1), normalization includes calibration, i.e., the normalization terms  $N_i$  has absolute sensitivity units to relate voxel activities in Bq/mL to LOR counts per second.

### D. Attenuation

The attenuation factor  $A_i$  is computed per list mode event by forward projecting through an attenuation image volume, produced by a preliminary reconstruction of a transmission scan. Preliminary masking of the attenuation volume defines the voxels to be reconstructed, thus in performing this forward projection, the intersection of each chord with the relevant portion of voxel grid is defined. All events that do not intersect the attenuation object are eliminated from the primary list of events to reduce computation time for forward and backprojection. These out-of-object events are retained for possible scaling of the scatter estimate.

### E. Scatter

Scatter estimation is performed using the single-scatter simulation method [9]. The chord scatter rate is proportional to the sum of the contributions from scatter points randomly distributed in the attenuation volume. Scatter estimates are first determined along a set of chords connecting an idealized group of detectors arranged on a cylinder of approximate dimensions of the actual detectors. For computational speed and because scatter is slowly varying in space, the sampling in this space is coarse and the estimate for each chord ( $S_i$ ) is interpolated from this low resolution space.

An exact computation of scatter would require precise tracking of absolute detector positions with respect to the moving scatter points, to properly normalize the scatter estimate for distance effects and to account for altered photon angles of incidence relative to the detectors, particularly for the non-cylindrical HRRT. This is too computationally expensive, so motion effects on scatter are approximated by using the average position of the detector panels during each scan frame, computed on first pass through the list mode data.

For iterative reconstruction, the initial activity distribution used for scatter computation is uniform with its boundary defined by the attenuation volume. This activity distribution is subsequently replaced by that iteratively determined by the

reconstruction algorithm and the scatter estimate is updated as needed. Computational efficiency is improved by using a very coarse spatial sampling for both the scatter points and scatter chords during early iterations when spatial resolution is low, with progressively increased spatial sampling with iterations. Also, the computations are distributed across the computer cluster where each node processes a subset of the scatter points and the final scatter estimate is determined by a global sum across the cluster. These factors combine to limit the total computational cost for the final scatter estimate to be on the order of that of a single forward/backprojection.

### F. Randoms

The random rate ( $R_i$ ) is estimated from the timing window and the block singles rates, stored in the list mode file. The conversion from block to crystal singles rates uses the crystal efficiency data from the normalization. Delayed coincidences in the list mode stream are not used in the reconstruction, except to validate the randoms estimates

### G. Global Sensitivity Image

A particularly difficult aspect of performing iterative reconstructions on the full HRRT projection space is the computation of the global sensitivity image, denoted  $Q$  (4). Exact calculation of  $Q$  requires an integration over the duration of the scan of the back-projections of all LORs, including motion correction. This calculation accounts for the possibility that the gaps in the projection data are “filled in” by subject motion. Since the exact formula is computationally unworkable,  $Q$  is estimated by a random sampling of detector LORs accounting for subject motion. This involves building a preliminary “randomized” event list with  $n_Q$  random detector LORs ( $k'$ ) chosen for each time bin  $\Delta t$ , motion corrected based on the Polaris data associated with that bin. Then,  $Q$  is estimated as follows:

$$Q_j = \frac{K}{n_Q n_T} \sum_{t=1}^{n_T} \sum_{k'=1}^{n_Q} c_{i(k',t),j} A_{i(k',t)} N_{k'} \quad (5)$$

The leading scale factor in (5) corrects for the undersampling.  $Q$  is computed once and used by all subsets. Care must be taken with respect to the randomization strategy. In particular, the seed to the random number generator is keyed to the data, so that identical inputs will produce identical results.

### H. Software Design

The controlling element of the reconstruction process is called the “dealer” which executes on the master node of the cluster. The dealer retrieves events one by one from an HRRT-specific module (the “house”) which reads and pre-processes the list mode file, including motion correction, normalization, and randoms. The dealer then distributes events to the processing nodes. Each processor stores in memory a set of event lists, one list per subset. As events “arrive” at each node, they are concatenated to the appropriate subset-list. Linked lists are used to facilitate easy removal of out-of-object events. The

list stores all information required by the reconstruction algorithm to represent every event, a maximum of 100 bytes each. Thus, a 24-node cluster with 1 GB of memory per node can maintain a total list of 240 million events.

The algorithm requires relatively little interprocessor communication. The majority of processing time is spent in forward and backprojection of the events stored in that processor's event lists. Interprocessor computation (global array summing) is performed in the calculations of  $Q$  (5), the correction matrix for  $\lambda$  (3), and the scatter estimation.

One aspect of algorithm evaluation involves the reconstruction of simulated list mode data that include subject motion. Using a "true" image and motion information derived from a template list mode file, the modules that comprise the forward projection engine of the reconstruction algorithm are used to calculate the expected number of events per LOR (1), from which random realizations of list mode files are produced.

As a major software development effort with multiple contributors, application programming interfaces (APIs) are defined for the major components of the code. The interface serves as an agreement between the developers regarding the functionality of the affected modules. Another benefit of defining these APIs is that it provides an interface for members of the HRRT research community to make contributions. The APIs define C++ classes, constants, class variables, instance variables, and functions.

The HRRT reconstruction software is designed for portability. The reconstruction codes are written in C++ and MPI is used for message passing. Thus, the reconstruction codes will be able to run on symmetric multiprocessor (SMP) systems, as well as clusters.

#### IV. SUMMARY AND FUTURE WORK

This design provides the framework to achieve the highest possible resolution for the HRRT. Every aspect of the implementation has tradeoffs in terms of ultimate image accuracy and precision versus computational cost. With an ultimate goal of reconstruction of a single frame in one hour or less, ideal accuracy in the implementation of each factor cannot be achieved. Thus, careful evaluation of this system will define which of these factors play an important role in producing quantitative, high resolution, low-noise images in a reasonable computation time.

The initial evaluation will concentrate on simulated list-mode data of a variety of phantom-like objects. These studies will be used to validate the algorithms, optimize parameters such as number of iterations and subsets, determine the achievable resolution and noise characteristics of the images, and assess the sensitivity of these characteristics to randoms, scatter, and motion. As actual data from the scanner become available, a careful physics characterization will be undertaken, focusing on the line spread function models, normalization, randoms, and scatter correction. With the advent of combined

list mode and Polaris data, the motion correction aspects of the algorithm will be validated using phantom measurements with and without motion. These data will also be used to investigate the utility of incorporating time-dependent uncertainty of the motion data into the line spread functions.

Subsequently, biologically relevant radioactivity distributions will be evaluated, first by simulation. These studies will be used to determine optimal reconstruction parameters and characterize the quantitative accuracy of small brain regions with focal activity. The inclusion of Bayesian priors in the algorithm will be evaluated, particularly for data sets with insufficient counts to support unconstrained resolution recovery. Reconstructions of actual PET data will be performed to assess the effects of improved resolution on quantification of small structures and physiological model parameters determined from kinetic analysis.

The ultimate direction of this development is 4D reconstruction, i.e., direct reconstruction of parametric images of kinetic model parameters [10-12]. Based on the initial timing estimates, ~1 day of computation are required for reconstruction of a 2-hour multi-frame dynamic study. Since the purpose of the multi-frame reconstruction is to perform voxel-by-voxel kinetic analysis, the direct calculation of such images has the potential to provide a large reduction in computation time, possibly with increased statistical accuracy.

#### V. ACKNOWLEDGMENT

The authors greatly appreciate the active participation of Shanthalaxmi Thada, Anthony Iano-Fletcher, Yongsheng Zhao, and Stephen Adler in this project. The helpful discussions with Mark Lenox and Christian Michel of CPS are also extremely valuable.

#### VI. REFERENCES

- [1] K. Wienhard, M. Schmand, M. E. Casey, K. Baker, J. Bao, L. Eriksson, W. F. Jones, C. Knoess, M. Lenox, M. Lercher, P. Luk, C. Michel, J. H. Reed, N. Richerzhagen, J. Treffert, S. Vollmar, J. W. Young, W. D. Heiss, and R. Nutt, "The ECAT HRRT: Performance and first clinical application of the new high resolution research tomograph," *IEEE Trans Nucl Sci*, vol. 49, pp. 104-110, 2002.
- [2] P. M. Bloomfield, T. J. Spinks, J. Reed, L. Schnorr, A. M. Westrip, L. Livieratos, R. Fulton, and T. Jones, "The design and implementation of a motion correction scheme for neurological PET," *Phys Med Biol*, vol. 48, pp. 959-78, 2003.
- [3] R. Levkovitz, D. Falikman, M. Zibulevsky, A. Ben-Tal, and A. Nemirovski, "The design and implementation of COSEM, an iterative algorithm for fully 3-D listmode data," *IEEE Trans Med Imaging*, vol. 20, pp. 633-42, 2001.
- [4] C. A. Johnson, Y. C. Yan, R. E. Carson, R. L. Martino, and M. E. Daube-Witherspoon, "A system for the 3D reconstruction of retracted-septa PET data using the EM algorithm," *IEEE Trans Nucl Sci*, vol. 42, pp. 1223-1227, 1995.
- [5] C. A. Johnson, J. Seidel, R. E. Carson, W. R. Gandler, A. Sofer, M. V. Green, and M. E. Daube-Witherspoon, "Evaluation of 3D reconstruction algorithms for a small animal PET," *IEEE Trans Nucl Sci*, vol. 44, pp. 1303-1308, 1997.
- [6] L. A. Shepp and Y. Vardi, "Maximum likelihood reconstruction for emission tomography," *IEEE Trans Med Imag*, vol. MI-1, pp. 113-122, 1982.

- [7] K. Lange and R. Carson, "EM reconstruction algorithms for emission and transmission tomography," *Journal of Computer Assisted Tomography*, vol. 8, pp. 306-316, 1984.
- [8] B. Bai, Q. Li, C. H. Holdsworth, E. Asma, Y. C. Tai, A. Chatziioannou, and R. M. Leahy, "Model-based normalization for iterative 3D PET image reconstruction," *Phys Med Biol*, vol. 47, pp. 2773-84, 2002.
- [9] C. C. Watson, "New, faster image-based scatter correction for 3D PET," *IEEE Trans Nucl Sci*, vol. 47, pp. 1587-1594, 2000.
- [10] D. L. Snyder, "Parameter-estimation for dynamic studies in emission-tomography systems having list-mode data," *IEEE T Nucl Sci*, vol. 31, pp. 925-931, 1984.
- [11] R. E. Carson and K. Lange, "The EM Parametric Image Reconstruction Algorithm," *J Amer Stat Assoc*, vol. 80, pp. 20-22, 1985.
- [12] T. E. Nichols, J. Qi, E. Asma, and R. M. Leahy, "Spatiotemporal reconstruction of list-mode PET data," *IEEE Trans Med Imaging*, vol. 21, pp. 396-404, 2002.