

### **M14-396: Dynamic Load Balancing on Distributed Listmode Time-of-Flight Image Reconstruction**

Z. Hu, W. Wang, E. E. Gualtieri, M. J. Parma, E. S. Walsh, D. Sebok, Y.-L. Hsieh, C.-H. Tung, J. J. Griesmer, J. A. Kolthammer, D. Gagnon

*Nuclear Medicine, Philips Medical Systems, Highland Heights, Ohio, USA*

A major obstacle in performing listmode reconstruction is the increased computation time compared to a conventional reconstruction. To overcome this computational challenge in a clinical setting, it is desirable to distribute the reconstruction task to multiple computation nodes. A previous work investigated the impact of high performance communication networks and focused mainly on static distribution. In practice, optimal static load balancing is difficult, therefore we have developed a dynamic load balancing approach, which is flexible and can easily be adapted to a varying number of nodes; and the performance is not constrained by variation of the load levels of nodes needed for other tasks or by asymmetric network. In this approach, one of the nodes is designated as the distributor, whose task is to partition the events into small chunks and then distribute those chunks to other nodes for processing. Other nodes, which do the actual data processing, are called workers. Each worker requests a new chunk of data to process upon completion of an old one. In case of the OSEM algorithm, when all chunks have been processed in a subset, the workers are synchronized and the image is updated. This image forms the basis for the next subset. This system was evaluated and deployed in a clinical PET product – Philips Gemini TF. For a whole-body patient scan of 150M events, the event processing time with 8 Xeon 3.6GHz dual-processor computers amounts to ~9 minutes for 3 iterations.

### **M14-399: Adaptive Spatially Variant Optimization of a Temporal Spline Basis for Dynamic PET Reconstruction**

J. Verhaeghe, R. Phlypo, S. Vandenberghe, S. Staelens, Y. D'Asseler, I. Lemahieu

*ELIS-MEDISIP, Ghent University, Ghent, Belgium*

We evaluated several strategies for the optimization of the number of basis functions in dynamic PET reconstructions. The goal of these methods is to avoid over-fitting in the reconstructed images or the introduction of too much bias. Two information theoretic (Akaike Information Criterion, AIC and Minimum Description Length, MDL) and one statistical (Cross-Validation) approach are considered. The optimal basis functions are spatially variant and are determined for different physiological regions in the image. The required segmentation of the regions is evaluated using different approaches. K-means clustering is compared to two factor analysis based segmentation approaches (Non-negative Matrix Factorization, NMF and Independent Component Analysis, ICA). We show that the information theoretic optimization of the spline basis and the factor analysis based segmentation are useful for dynamic PET reconstruction.

### **M14-402: Optimal and Robust Filter for PET Data Based on the System Response Matrix**

J. L. Herraiz<sup>1</sup>, S. España<sup>1</sup>, E. Vicente<sup>2</sup>, J. J. Vaquero<sup>2</sup>, M. Descó<sup>2</sup>, J. M. Udías<sup>1</sup>

<sup>1</sup>*Dpto. Física Atomica, Molecular y Nuclear, Universidad Complutense de Madrid, Madrid, Spain*

<sup>2</sup>*Unidad de Medicina y Cirugía Experimental, Hospital GU GREGORIO MARAÑÓN, Madrid, Spain*

This paper presents an optimal and robust technique for filtering positron emission tomography (PET) data based on parameters determined from the System Response Matrix (SRM), the kernel of iterative reconstruction methods. Sinograms for PET data are usually noisy and blurred, and different ways of filtering them prior to image reconstruction have been proposed. Most filtering methods, like Wiener filtering, require accurate knowledge both of the frequencies of the object to be acquired by the scanner and of the System Modulation Transfer Function (MTF). The MTF in small animal PET scanners depends mainly on the size and shape of the Tubes of Response (TOR, the volume of space from which an emitted positron can produce a coincidence count in a pair of crystals), which are also important ingredients of the SRM. We describe a method of exploiting this SRM information to deduce optimal filters for PET data. From our tests with actual scanner data, the improvement in quality of the reconstructed images obtained from the filtered data is very significant. The resolution can be increased from 1.4 mm (conventional FBP) to 1.0 mm (with the proposed method or Unfolded-FBP) without compromising accuracy and furthermore reducing the noise level. These results reveal that this technique, based upon knowledge of the SRM, closely connects iterative and analytical methods and could become a promising tool in the reconstruction arena in the near future.