detectors may result in a noticeable degradation of the image resolution. For this reason, in such systems an exact characterization of misalignments is critical for a good reconstruction quality. While this subject is widely studied for computed tomography (CT) and single photon emission computed tomography (SPECT) systems based on cone beam geometry, it seems that this is not the case for PET scanners based on rotating planar detectors. The purpose of this work is to analyze misalignment effects in these systems and to define a protocol for geometric characterization. Materials and methods: The effects of misalignments have been simulated and the results have been validated with data from a real scanner (rPET, SUINSA), using both phantom and rodent studies. Results and conclusions: The effects of detector misalignments are presented. A testing protocol for detecting and measuring misalignments in the three axes in PET scanners based on rotating planar detectors is proposed. This protocol uses simple phantoms and is robust and easy to perform. Implementation details are given for the high-resolution animal rPET scanner. The results show the importance of detector alignment: for instance, a misalignment of 0.8 mm in one detector resulted in an increase of 14% in tangential FWHM of a point source in the center of field-of-view (FOV). The correction performed with the proposed protocol provided a significant improvement in resolution.

No. 121

ISSUES IN THE QUANTITATIVE RECONSTRUCTION OF POSITRON EMISSION TOMOGRAPHY STUDIES

M. Abella, J. Vaquero, E. Vicente, J. Sãnchez, S. Redondo, M. Desco; Hospital GU Gregorio Maranon, Madrid, SPAIN.

Introduction: In order to make quantitative analysis of positron emission tomography (PET) studies it is necessary to obtain an "exact" reconstructed image. This is not trivial to obtain as each step in the process from list mode data can be a source of bias or artifacts. Sinogram statistical distribution may be altered due to the acquisition process: scatter, decay, dead time, geometrical effects and crystal sensitivity. Subsequent sinogram rebinning may also change this statistical distribution. Finally, FBP may introduce DC component bias and aliasing, depending on the particular implementation used. This work analyzes the whole process to ensure that all these undesirable effects are properly compensated at every point of the reconstruction chain to guarantee a true quantitative reconstruction. Materials and methods: The study of quantitative reconstruction was applied to a real scanner (rPET, SUINSA). Different theoretical and experimental methods were tested for sinogram correction. Several methods for SSRB statistics recovery and for count recovery and aliasing elimination after FBP were tested. Results were validated on real data using a NEMA-like contrast phantom, considering attenuation and scatter. The linear behavior of detected trues versus activity in the field-of-view was verified. Results and Conclusions: A complete reconstruction algorithm for the rPET system is presented. An experimental correction of the sinogram based on an acquisition of a field flood provided best results. Counts recovering in the SSRB step and adequate slice uniformity have been achieved. Regarding FBP implementation, the Crawford method was selected for compensating DC bias and aliasing after filtering in Fourier domain.

No. 122

STATISTICAL PARAMETRIC MAPPING IN SMALL ANIMAL BRAIN ACTIVATION STUDIES

P. D. Acton[1], C. Cardi[1], H. S. Bal[1], P. T. Meyer[2];
[1]Thomas Jefferson University, Philadelphia, PA, [2]University Hospital Aachen, Aachen, GERMANY.

Ultra-high resolution positron emission tomography (PET) has enabled the visualization of biochemical processes in the brain in small animals, and changes due to disease or stimuli. Conventional analysis methods using manually-drawn regions-of-interest (ROIs) to extract counts are highly subjective, and it is difficult to identify subregions of the brain. Pixel-based analysis, such as statistical parametric mapping, perform automated analysis of brain images to detect differences within or between groups. This work describes the application of pixel-based analysis to an 2-deoxy-2-[F-18]fluoro-D-glucose (FDG) brain activation study in rats. A total of seven rats were scanned 45 minutes after injection of FDG. Each animal received two randomized scans, one with vibrissae stimulation for 15 minutes during the uptake phase of FDG, the other with no stimulation as a control. The brains were extracted from the PET images using a region-growing method, and coregistered to each other using a mutual information algorithm. Stimulated and unstimulated images were compared using pixel-by-pixel paired t-tests to determine statistically significant differences ($p<0.01$). Clusters of significant pixels were further assessed to compensate for correlated multiple comparisons (corrected $p<0.05$). Statistically significant regions were compared against conventional ROI analysis. Different methods of normalization, using either whole brain or cerebellum counts, were tested. Contralateral somatosensory cortices were activated by the vibrissae stimulation, with increased FDG uptake. Both pixel-based and ROI analyses agreed in the regions affected by the activation. Only cerebellar normalization gave the expected hypermetabolic regional differences, while whole brain normalization produced hypometabolism in regions that should be unaffected.

No. 123

SIMPLIFIED QUANTIFICATION OF SMALL ANIMAL 2-DEOXY-2-[F-18]FLUORO-D-GLUCOSE- POSITRON EMISSION TOMOGRAPHY STUDIES USING A STANDARD ARTERIAL INPUT FUNCTION

P. D. Acton[3], P. T. Meyer[1], V. Circiumaru[2], C. Cardi[3], D. H. Thomas[2], H. Bal[3];
[1]Department of Neurology, University Hospital Aachen, Aachen, GERMANY, [2]Department of Radiology, University of Pennsylvania, Philadelphia, PA, [3]Department of Radiology, Thomas Jefferson University, Philadelphia, PA.

Arterial input function (AIF) measurement for quantification of small animal positron emission tomography (PET) studies is technically challenging and limited by the small blood volume of small laboratory animals. The present study investigates the use of a standard arterial input function (SAIF) to simplify the experimental procedure. Methods: Twelve 2-deoxy-2-[F-18]fluoro-D-glucose (FDG)-PET studies accompanied by serial arterial blood sampling were acquired in seven male Sprague-Dawley rats under isoflurane anesthesia without (every rat) and with additional (five rats) vibrissae stimulation. A leave-one-out procedure was employed to validate the use of a SAIF with individual scaling by one (1S) or two (2S) arterial blood samples. Results: Automatic slow bolus infusion of FDG resulted in highly similar AIF in all rats. The average difference of the area under curve of the measured AIF and the individually scaled SAIF was $0.11 \pm 4.26\%$ and $0.04 \pm 2.61\%$ for the 1S (six-minutes sample) and 2S (four-minutes/43-minutes samples) approach, respectively. The average difference between the cerebral metabolic rates of glucose (CMR_{glc}) calculated using the measured AIF and the scaled SAIF were $1.31 \pm 5.45\%$ and $1.30 \pm 3.84\%$ for the 1S and 2S approach, respectively. Conclusions: The use of a SAIF scaled by one or (preferably) two arterial blood samples can serve as a valid substitute for individual AIF measurements to quantify FDG-PET studies in rats. The SAIF approach minimizes the loss of blood and should be ideally suited for longitudinal quantitative small animal FDG-PET studies.

No. 124

BIOLUMINESCENCE IMAGING CONFIRMS THAT WEEKLY COMPUTED TOMOGRAPHY STUDIES DO NOT CHANGE TUMOR GROWTH IN AN ANIMAL MODEL OF BREAST CANCER METASTASIS

A. J. Adams, S. L. Cowey, J. C. Kappes, R. W. Hardy, K. R. Zinn; University of Alabama at Birmingham, Birmingham, AL.

The use of X-ray computed tomography (CT) to monitor tumor growth in animal models is becoming widespread. The purpose of this study was to determine whether X-ray exposure would change metastatic tumor development in an animal model. Methods. Female BALB/c nude mice