HBM 2004 Poster # TH360

A new method for voxel-based partial volume effect correction

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Introduction: Many methods using MRI data to correct NM studies for partial volume effect (PVE) have been proposed. Two approaches were followed: ROI-based and voxel-based approach. The ROI approach doesn't produce corrected images, but only regional information. Voxel-based methods normally gain the noise at edges.
The proposed method tries to hold the accuracy of ROI-based methods furnishing low noise images.

Method: If C is the activity distribution in the brain, the PET count distribution is:

$$PET(p) = \int_{Volume} C(\rho) \cdot g(p-\rho) \cdot d\rho + noise$$

where g (PSF of scanner) represents the probability function that a point of C contributes to PET counts in its neighborhood. The deconvolution of the PET distribution could exactly correct for PVE, but the noise gain prevents the use of deconvolution methods. The proposed method, knowing from segmented MRI the GM distribution T(p), defines a new probability function g' defined as:

$$g'(p,\rho) = T(\rho) \cdot g(p-\rho) \Big/ \int_{Volume} T(\psi) \cdot g(p-\psi) \cdot d\psi$$

if the denominator is not zero and 0 otherwise. It represents the probability that PET counts in the point p come from the point ρ. Each voxel of PVE corrected GM (R_{GMPET}) is calculated as:

$$R_{GMPET}(p) = \int_{Volume} GMPET(\xi) \cdot g'(p,\xi)\, d\xi$$

where GMPET is PET activity due to the GM alone, obtained as follows.
As proposed by other authors[3], the WM activity can be assumed constant and an estimation of its value can be obtained in a region large enough to be free from PVE. Since a WM region totally free from PVE may not exist, we propose to estimate WM activity concentration as the intercept of the linear fitting of PET counts vs. GMc/(GMc+WMc), where GMc and WMc are the convolution of, respectively, segmented GM and segmented WM by the PSF of the PET scanner.

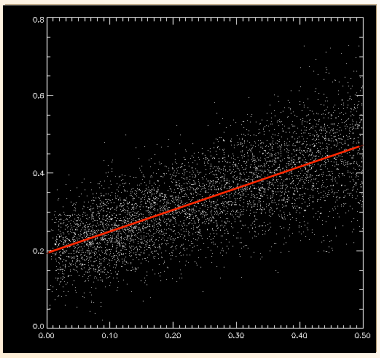

Fig. 1 Linear fitting of PET counts vs. GMc/(GMc+WMc)

The fitting is limited to values of GMc/(GMc+WMc) < 10% to assume the linear model, as exemplified in figure 1 (note that in this case no pure WM voxels exist).

Preliminary results: Figure 2 shows two virtual phantoms obtained from a segmented MRI. In both cases original distribution, simulated PET, recovered distribution and corresponding error map are reported. In the first one the GM activity concentration is four times the WM; in the second one also three lesions with different characteristics are simulated. Maps of errors (doubled to allow visualization) show that, in presence of constant concentrations, recovery of original distribution is affected only by low frequency noise, while in presence of lesions the recovery is better when smoother activity variations are present. In figure 3 a representative slice from a PVE-corrected FDG-PET study is represented.

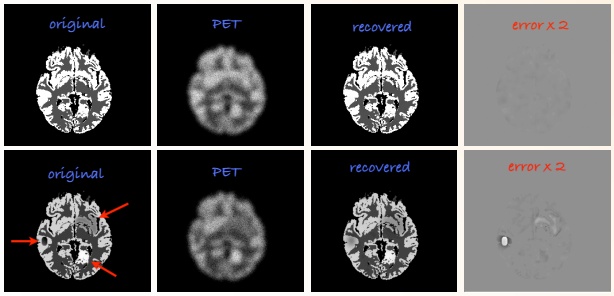

Fig. 2 Computer simulations used for validation with homogeneous distribution (upper row) and with three focal lesions (lower row). Original distribution, simulated PET, recovered distribution and corresponding error map are reported left to right.

Conclusions: The proposed method accurately recovers PVE from different tissues, while reproduces smoothly the variation of concentration inside the same tissue providing PVE-corrected images potentially useful for voxel-based analysis.

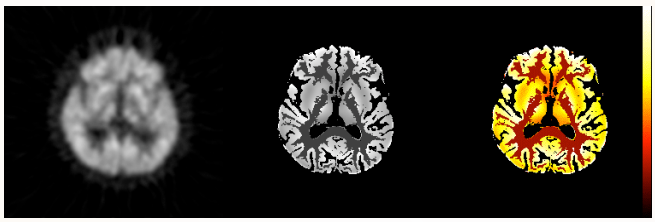

Fig. 3 FDG-PET study from a normal subject (left) with corresponding PVE-corrected image (grayscale in the center and color-scale on the right).

References:

1 Rousset et al. J Nucl Med 1998;39:904-911
2 Meltzer et al. J Comput Assist Tomogr 1990;14:561-570
3 Muller-Gartner et al. J Cereb Blood Flow Metab 1992;12:571-583

Acknowledgment:
EU fifth framework program QLG3-CT2000-00594 has funded the project.

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