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Accuracy of partial volume effect correction in clinical molecular imaging of dopamine transporter using SPECT

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Objectives: Partial volume effect (PVE) is a major source of bias in brain SPECT molecular imaging of dopamine transporter: radioactivity concentration measured within striatal volumes can be underestimated by more than 50% because of PVE only. Various PVE corrections appropriate for SPECT and making use of anatomical data have been developed. These methods yield encouraging results in studies involving simulations and/or phantom acquisitions. However, their accuracy in clinical data is difficult to demonstrate, first because the accurate value (gold standard –GS) of the parameters to be estimated is usually unknown, and second because PVE correction is greatly affected by the accuracy of segmentation of anatomical data and of co-registration of SPECT with anatomical images. The objective of this study was to assess the accuracy of a PVE correction on clinical dopamine transporter SPECT studies.

Method: 23 patients underwent MRI and dopaminergic neurotransmission 123I-FP-CIT SPECT. MRI studies consisted in 3D T1-weighted sequences with 2 mm thick slices. SPECT acquisitions were performed 4 hours after the injection of 185 MBq of 123I–FP-CIT. A 3 headed Prism 3000 XP camera equipped with low energy ultra high resolution fan beam collimators and with a transmission source device was used. SPECT projections were corrected for scatter and reconstructed using OSEM (12 subsets, 12 iterations) including attenuation compensation. Striata were manually segmented on the MR images. The binding potential values (BP) were measured in the striatal volumes of interest after coregistration of MRI data to SPECT data by mutual information maximization. BP were defined as [S-NS]/NS, where S was the striatal activity and NS represented non-specific activity measured in a posterior volume of interest. These values were calculated without and with an original PVE correction previously described (Soret et al, Eur J Nucl Med Mol Imaging 2006). In addition, for each patient, a Monte Carlo simulation of the patient SPECT scan was performed using the SimSET code. The anatomical data needed for each simulation were derived from the segmented MRI of the patient, and 123I activity concentrations were set equal to those found from the patient SPECT data after all corrections. The simulated projections were processed exactly as the real data. For the Monte Carlo simulations where true simulated BP values were known, percent biases in BP estimates were calculated. For the real data, an evaluation method that did not require the GS to be known was used. This method, derived from the one by Hoppin et al (IEEE Trans Med Imaging 2002), simultaneously estimates the GS and a quadratic relationship between the observed and the GS values, assuming the GS follows a beta law. It yields a surrogate mean square error (sMSE) between the estimated values and the estimated GS value.

Results: The averaged percent difference between BP measured for real patients and BP measured on the corresponding simulated patients was 0.7±9.7% without PVE correction and was -8.5±14.5% with PVE correction, suggesting that the simulated data reproduced the real data well enough. For the simulated patients, BP was underestimated by 66.6±9.3% on average without PVE correction and overestimated by 11.3±9.5% with PVE correction,

demonstrating the greatest accuracy of BP estimates when PVE correction was used. For the simulated data, sMSE obtained by assuming the GS was unknown were 27.3 without PVE correction and 0.90 with PVE correction, confirming that our sMSE index properly captured the greatest accuracy of BP estimates with PVE correction when the GS was not supposed to be known. When considering the real patient data for which no direct bias calculation was possible as the GS was unknown, sMSE in BP estimates was 50.8 without PVE correction and 3.5 with PVE correction. These results were very consistent with those obtained on the simulated data, suggesting that for clinical data, and despite probable segmentation and registration errors, BP were more accurately estimated with PVE correction than without.

Conclusion: By simulating real patient data and using an evaluation method appropriate for assessing the accuracy of estimation methods when the GS is unknown, we gathered evidences that the PVE correction considered in this study was very efficient in real patient to greatly reduce the error in BP estimates in clinical molecular imaging of dopamine transporter using SPECT.

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