Attenuation correction with a multi-atlas method for brain PET-MR imaging: assessment with realistic simulated [^{11}C]raclopride bolus-infusion PET data

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Objectives
We have recently shown that inaccurate MR-based attenuation maps used in PET-MR systems can induce an error on dynamic PET data that depends on tracer distribution and varies over time [1]. Here we assess the impact of different MR-based attenuation correction (AC) methods on PET quantification and kinetic modelling. We compare our multi-atlas technique *(MaxProb)* [2] and the segmented-UTE [3] to ground-truth CT.

Methods
Brain PET data was simulated for twelve subjects with PET-SORTEO [4] to reproduce a bolus-infusion [^{11}C]raclopride protocol. For the simulations, emission phantoms were defined with 15 regions of interest on MRI [5], and the input 90-minute time-activity-curves were derived from real PET/CT data. Simulated PET data was reconstructed using *MaxProb*, segmented-UTE and ground-truth CT AC. Simple tissue-to-reference ratios were used to estimate the BP_{ND} in caudate, accumbens and putamen, at equilibrium, with cerebellum as the reference region.

Results
For the cerebellum, mean bias on time-activity-curves varied over time from -7.7 to -13.1% with segmented-UTE and from -2.5 to -5.2% with *MaxProb*. Mean bias in caudate, accumbens and putamen varied from -2.8 to -7.1% for segmented-UTE and from -2.2 to -4.6% for *MaxProb*. The bias tended to increase at later time-points. Mean error on tissue-to-reference ratios reached +5.4% for UTE but remained below +1% for *MaxProb*.

Conclusions
Compared with segmented-UTE, *MaxProb* produces less bias for time-activity-curves and hardly any bias for tissue-to-reference ratios. Multi-atlas AC may enhance sensitivity to detect physiological variations between groups of subjects or experimental conditions. Further work will focus on the sensitivity of the AC method to detect tracer displacement induced by endogenous dopamine.

References
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