Motion correction and multi-atlas attenuation correction applied to a simultaneous bolus/infusion PET-MR brain study

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Abstract—With the aim to improve PET quantification acquired during a simultaneous PET-MR brain imaging, we compared attenuation and motion correction techniques in a bolus/infusion PET protocol studying variations of endogenous dopamine concentration across time. The target parameter was the [^{11}C]raclopride striatum/cerebellum binding ratio. Acquired data were corrected for both motion, with the list-mode rebinner *Eber*, and for photon attenuation, with standard UTE solution and the multi-atlas-based *MaxProb* approach. Combination of *Eber* and *MaxProb* improved the signal quality significantly by reducing the variance of binding ratio calculated on each region of interest, and at each time-point.

Keywords—PET-MR; attenuation correction; motion correction; kinetic modelling; neuroimaging; dopaminergic neurotransmission.

I. Introduction

In simultaneous PET-MR systems, accurate attenuation maps need to be derived from the MR (or PET) data to ensure correct PET quantification. Inaccurate attenuation correction (AC) affects PET quantification [1]. We have recently shown [2], [3] that dynamic PET data and physiological parameters derived from kinetic modelling, such as Binding Ratios (BR), can also be affected by inaccurate AC, especially in the late frames of the acquisition. In addition, when dealing with real data, subject motion during long acquisitions can also increase the quantification error, in particular in small brain structures. In this work we apply a novel approach for motion correction (*Eber*, Reilhac et al., abstract submitted to PSMR 2017) combined with our multi-atlas AC method [2] on PET data acquired with a simultaneous PET-MR system and investigate the influence of those techniques on data quality.

II. Materials and Methods

A. Protocol and data

PET-MR imaging was used to explore dopaminergic neurotransmission in healthy subjects in subcortical areas, such as the striata. Eighteen subjects (8 male, 10 female) [mean age ± SD, 25.6 ± 2.9 y; range, 22-34 y] had a simultaneous PET-MR exam with a 110 minute [^{11}C]raclopride bolus-infusion protocol to measure variations of D2 receptor occupancy [4]. T1 and UTE MRI sequences were acquired (as well as other functional sequences - BOLD, ASL and DTI - not analysed in this preliminary work).

B. PET motion and attenuation corrections

PET data were corrected for head motion with the *Eber* algorithm, which corrects the listmode data directly by rebinning the detected events according to the estimated inter-frame motion. For motion estimation, dynamic PET data were first reconstructed without AC in 63 frames of 100s each. Then the 63 motion correction matrices were applied to the listmode data, rebinned in sinograms of 21 regular 5-minute frames. Images were reconstructed from the corrected sinograms with AC, and the OP-OSEM3D algorithm incorporating PSF, using 12 iterations and 21 subsets. For AC, *MaxProb* [2] which is a recently proposed multi-atlas method and the standard UTE [5] method were used.

C. Data analysis

Time-activity curves (TACs) were extracted from the striatal regions (caudate and putamen) and from the

cerebellum, considered here as the reference region. Tissue-to-reference BR were deduced from these TACs for both striatal regions. Parametric BR images were generated from the 21-frame dynamic series, for the following time-points after the injection of the tracer: T1 (30-40 min), T2 (45-70 min), T3 (75-90 min) and T4 (90-105 min)). Means and standard deviations of BRs were extracted from the ratio images. Results were compared with or without applying *Eber* motion correction, incorporating *UTE* or *MaxProb* AC. An analysis of variance was performed with a Tukey honest significant difference (HSD) test for each time-point.

III. Results

A. Example

Figure 1 shows the BR curves across time for one subject that showed important motion artefacts. In the absence of motion correction (top), regional BR decreased after 30 minutes, whereas the BR was recovered after applying *Eber* motion correction (bottom).

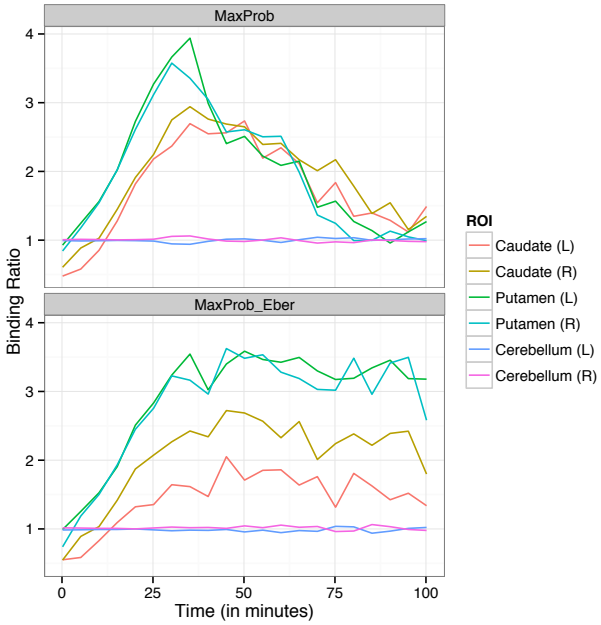

Fig. 1. Example of BR TACs per ROI for one subject with important motion before motion correction (top) and after *Eber* motion correction (bottom). *MaxProb* AC was applied in the two cases.

B. Quantitative results

Overall, both *MaxProb* AC and *Eber* motion correction contributed individually to decrease the intra-regional variance of regional BR.

At T1, the mean standard deviation over subjects and striatal regions decreased from 1.23 to 1.09 for *UTE* and from 1.16 to 1.03 for *MaxProb* when applying *Eber* motion correction. Significant improvement produced by motion correction was seen for T1 and T2. At T1, no significant differences were found between *UTE* and *MaxProb*, with or without *Eber* motion correction. At T2, T3, T4, the BR standard deviation was significantly reduced with *MaxProb*, compared to *UTE* AC. For example, at T4, the BR standard deviation was 1.65 for *UTE_Eber*, and 1.52 for *MaxProb_Eber*.

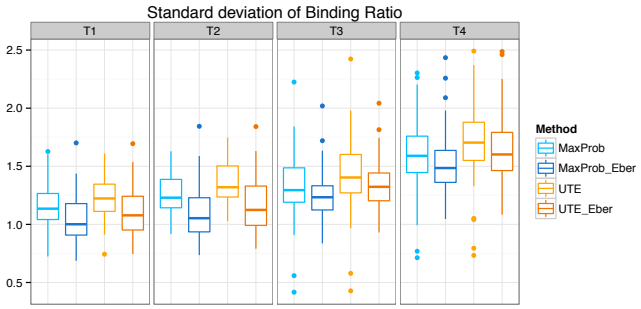

Fig. 2. Boxplot of standard deviation of intra-regional BR, measured on the striata, per time-point, and per AC method applied. *: $p < 0.05$ with the Tukey HDS test. Significant statistical tests for motion correction comparisons are indicated by brackets on the top of the graph, and significant statistical tests for AC comparisons at the bottom of the graph.

IV. Conclusion

Used singly and together, *Eber* motion correction and multi-atlas *MaxProb* AC contributed to reduce the intra-regional variance of BR. Further work will investigate the sensitivity gain generated by the proposed methods in stimulation conditions aiming to evoked extracellular dopamine concentration variation by contrasting groups receiving an active or placebo stimulation.

References

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