

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

Inés Mérida^{1,2,3}, Alexander Hammers^{4,5}, Jérôme Redouté³, Colm McGinnity⁵, Clara Fonteneau^{6,7}, Marie-Françoise Suaud-Chagny^{6,7}, Anthonin Reilhac³, Nicolas Costes³

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neurodis

KING'S
College
LONDON

¹Université de Lyon 1, INSERM, CNRS, Lyon Neuroscience Research Center, France, ²Siemens Healthcare France SAS, Saint-Denis, France, ³CERMEP-Imagerie du vivant, Lyon, France, ⁴Neurodis Foundation, Lyon, France, ⁵King's College London & Guy's and St Thomas' PET Centre, Division of Imaging Sciences and Biomedical Engineering, Kings' College London, UK, ⁶Centre de Recherche en Neurosciences de Lyon, Equipe PSYR2 (INSERM U1028, CNRS UMR5292, UCBL, Université de Lyon), Lyon, France ⁷Centre Hospitalier Le Vinatier, Lyon, France

Introduction

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, using realistic simulated PET data. We compare our multi-atlas technique (*MaxProb*) [1] and the standard UTE [2] to ground-truth CT. We focus on the detectability of endogenous dopamine release with PET-MR.

Materials and Methods

Brain PET data was simulated for 21 subjects with PET-SORTEO [3] to reproduce a 100-minute bolus-infusion [¹¹C]raclopride protocol. The emission phantoms were defined with 15 regions of interest on the MRI (including striatum and cerebellum, Fig. 1), and the input time-activity-curves were derived from real PET/CT data (Fig. 2).

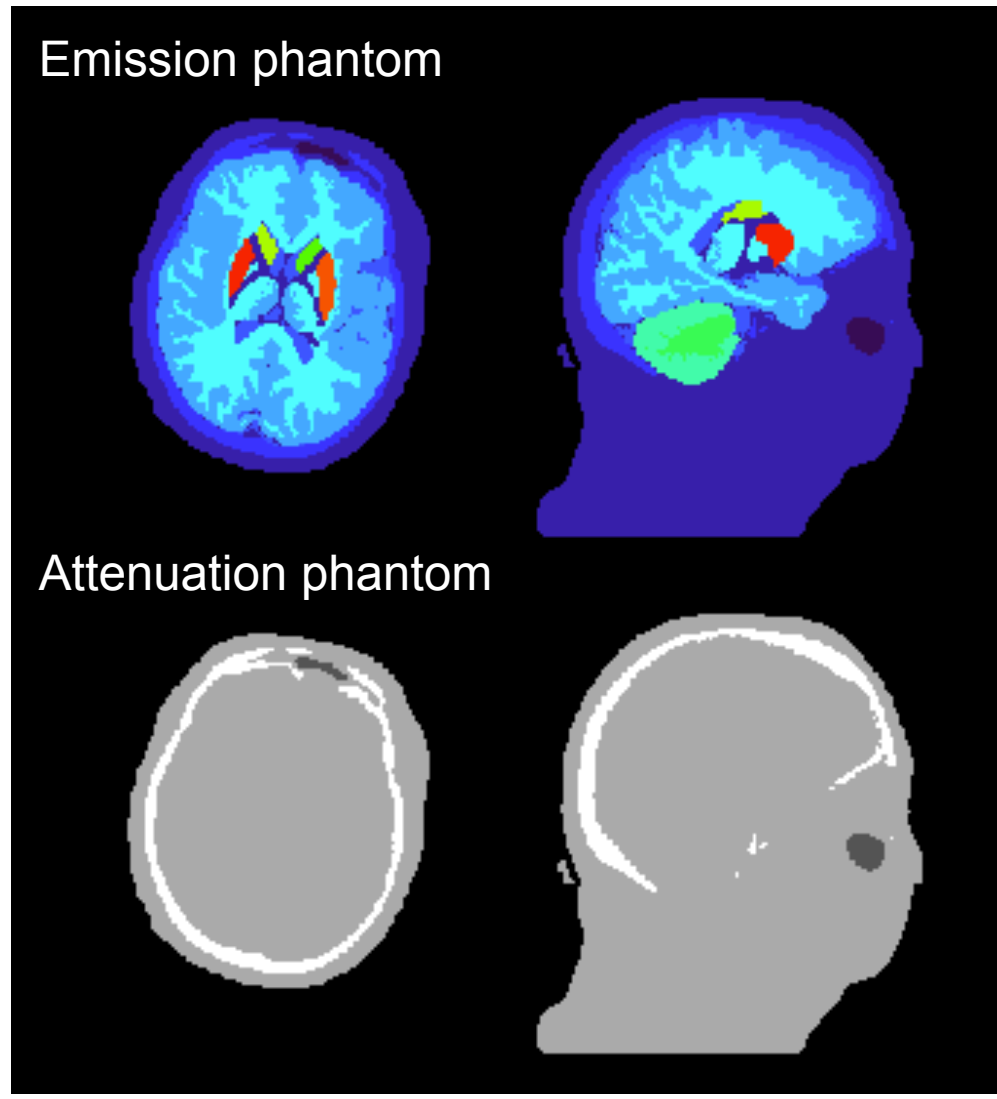


Fig 1: Emission and attenuation phantoms.

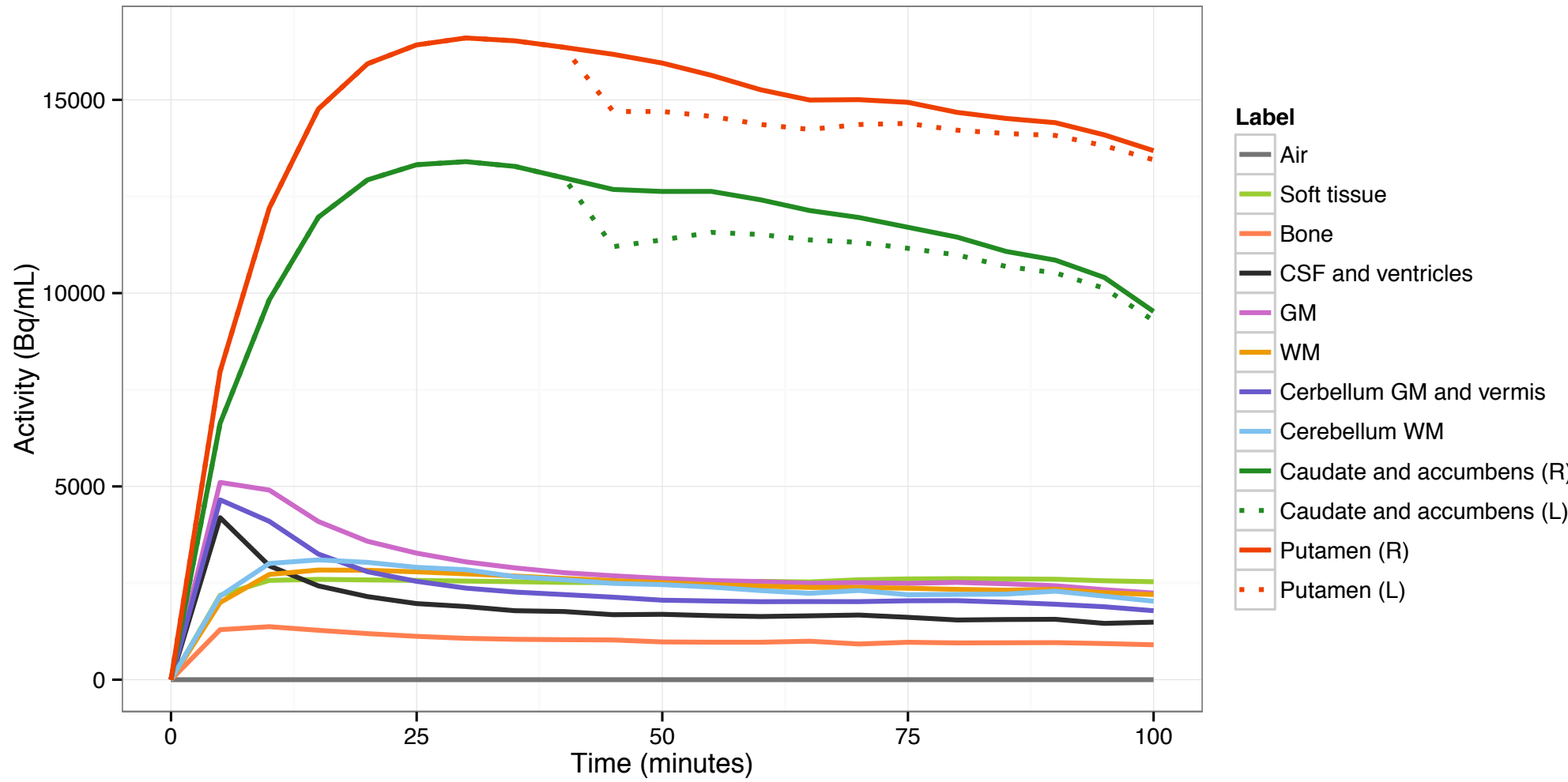


Fig 2: Regional TACs used as input for PET-SORTEO simulations. Dotted lines indicate TACs with PET displacement ($\Omega = 10\%$).

For 10 subjects, endogenous dopamine release was modelled at 40 min with an exponential function (Eq. 1). Dopamine curves were subtracted from initial PET TACs, in the left striatal ROIs, to generate PET TACs with displacement (Fig. 2).

$$DA(t) = C_{\max} \Omega e^{-(t-t_s)/\tau} u(t-t_s) \quad (\text{Eq. 1}) \quad \text{where } t_s = 40 \text{ min}, \tau = 30 \text{ min and } \Omega = \{5\%; 10\%; 25\%\}$$

Simulated PET data was reconstructed in frames of 5 minutes, with the OP-OSEM3D algorithm, using *MaxProb*, *UTE* and ground-truth CT for AC. Simple tissue-to-reference ratios were used to estimate the binding ratio (BR) in caudate, accumbens, and putamen, at equilibrium, with cerebellar grey matter as the reference region.

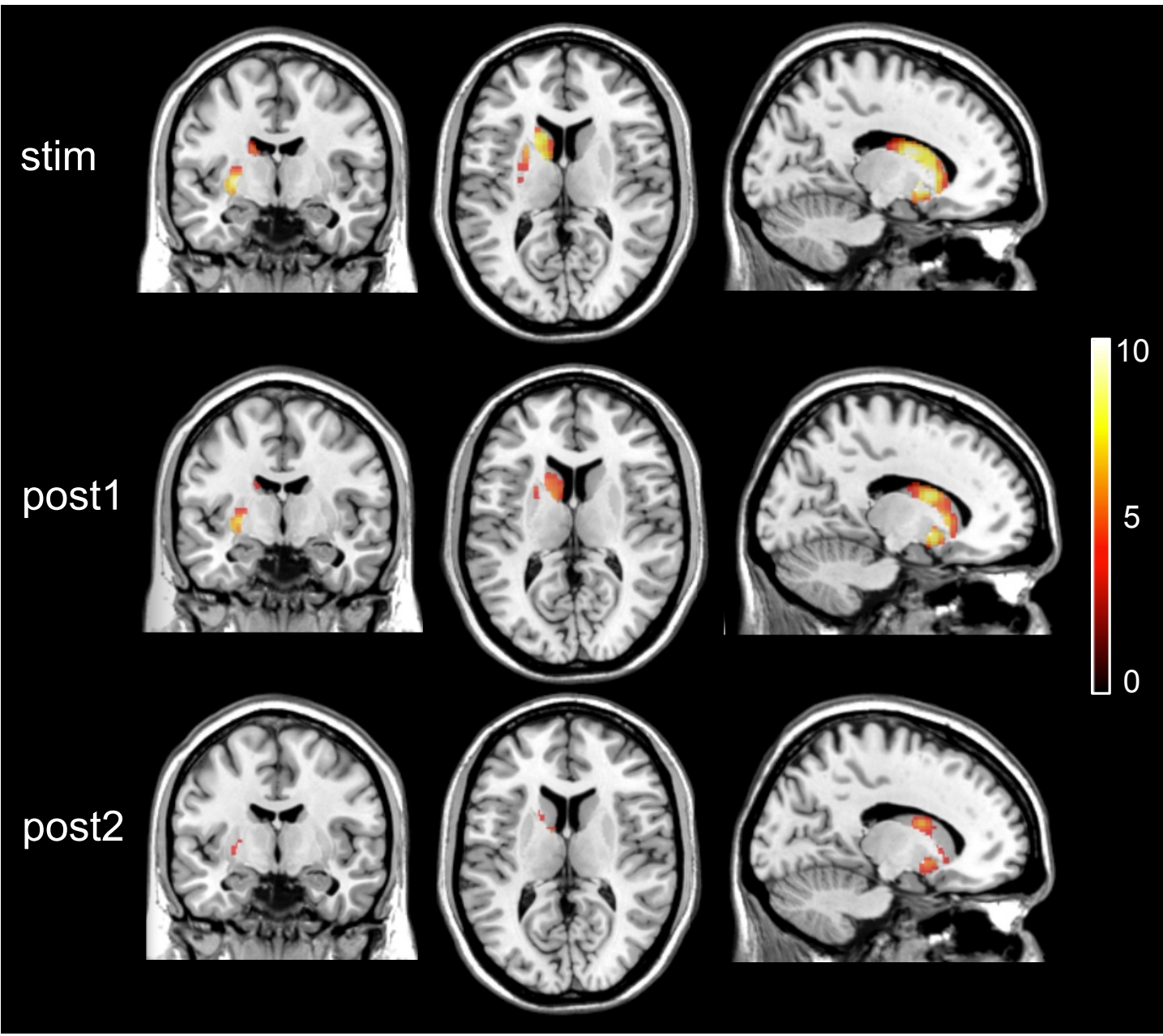
Differences between placebo and active groups were assessed in terms of BR variation (Δ) at different time-intervals:

- baseline: 30 – 40 min (grey)
 - stim: 40 – 55 min (red)
 - post1: 55 – 70 min (green)
 - post2: 70 – 85 min (yellow)
- $$\Delta(\%) = \frac{BR\{\text{stim or post1 or post2}\} - BR\{\text{baseline}\}}{BR\{\text{baseline}\}} 100 \quad (\text{Eq. 2})$$

Results

Effect of dopamine release

Fig 3: Comparison of parametric images of binding ratio (BR), between active and placebo groups for stim25 (i.e. $\Omega=25\%$ for DA release curve simulated in the left striatum), obtained with CT AC. Color scale: t statistic.



Quantification error

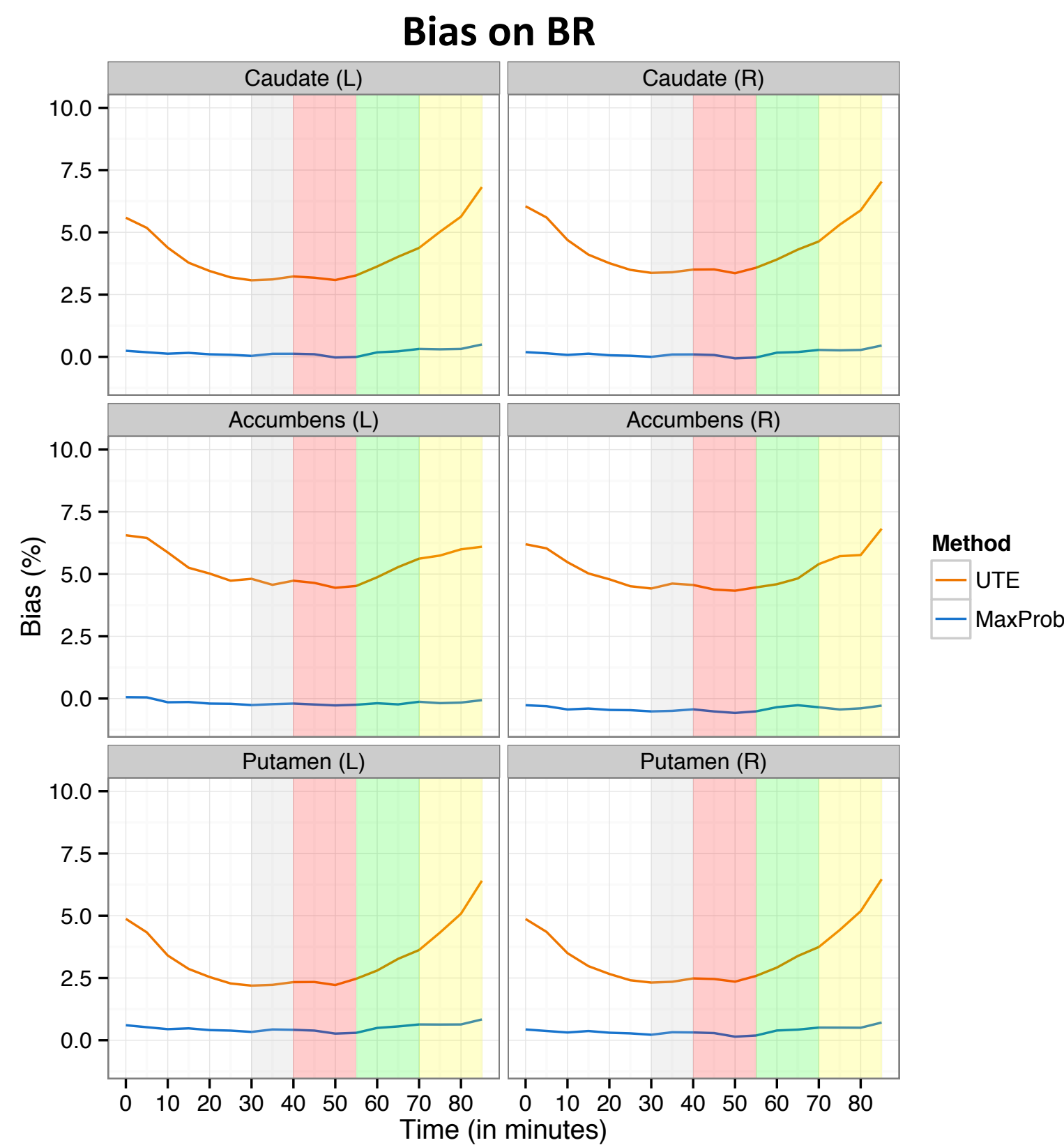
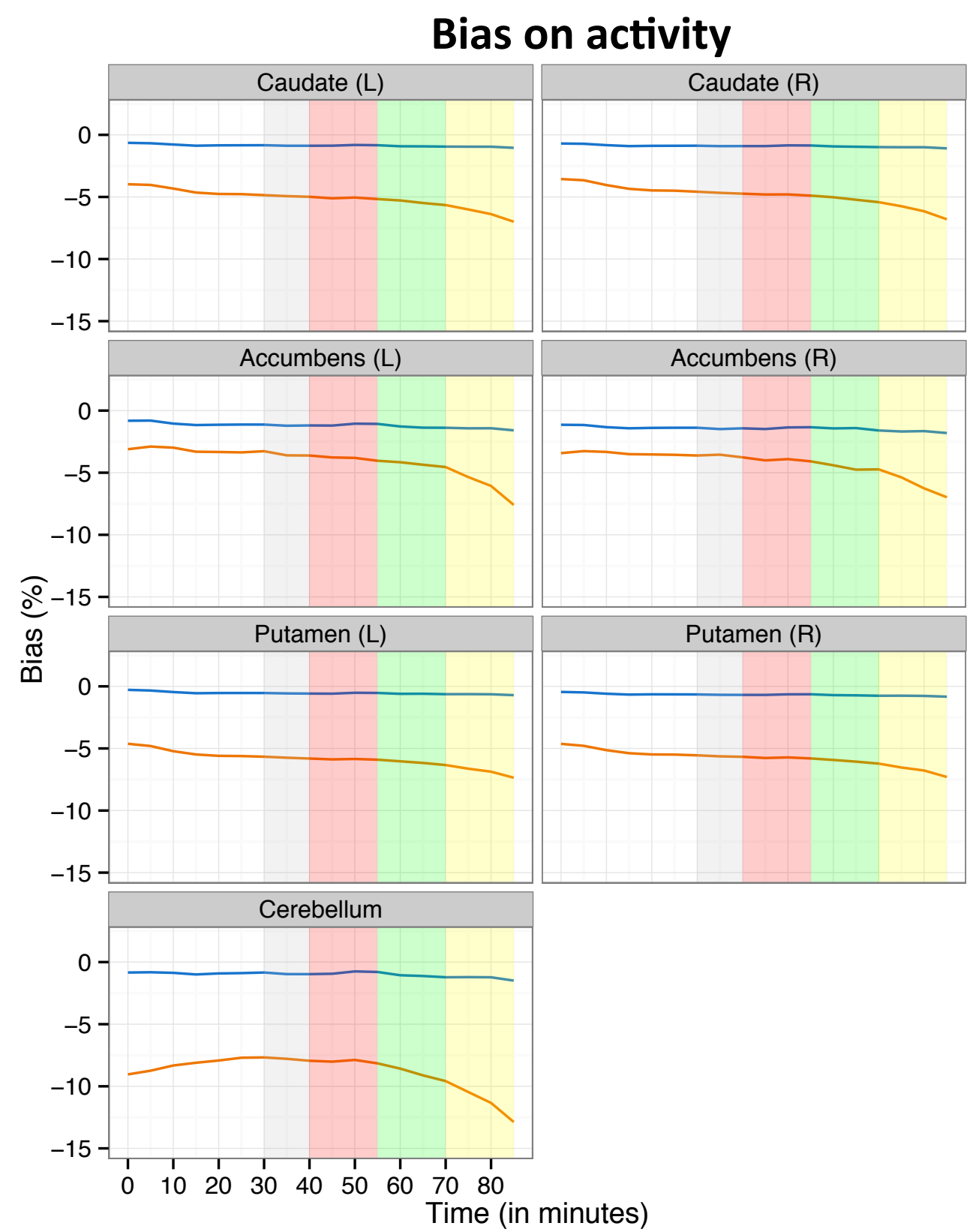


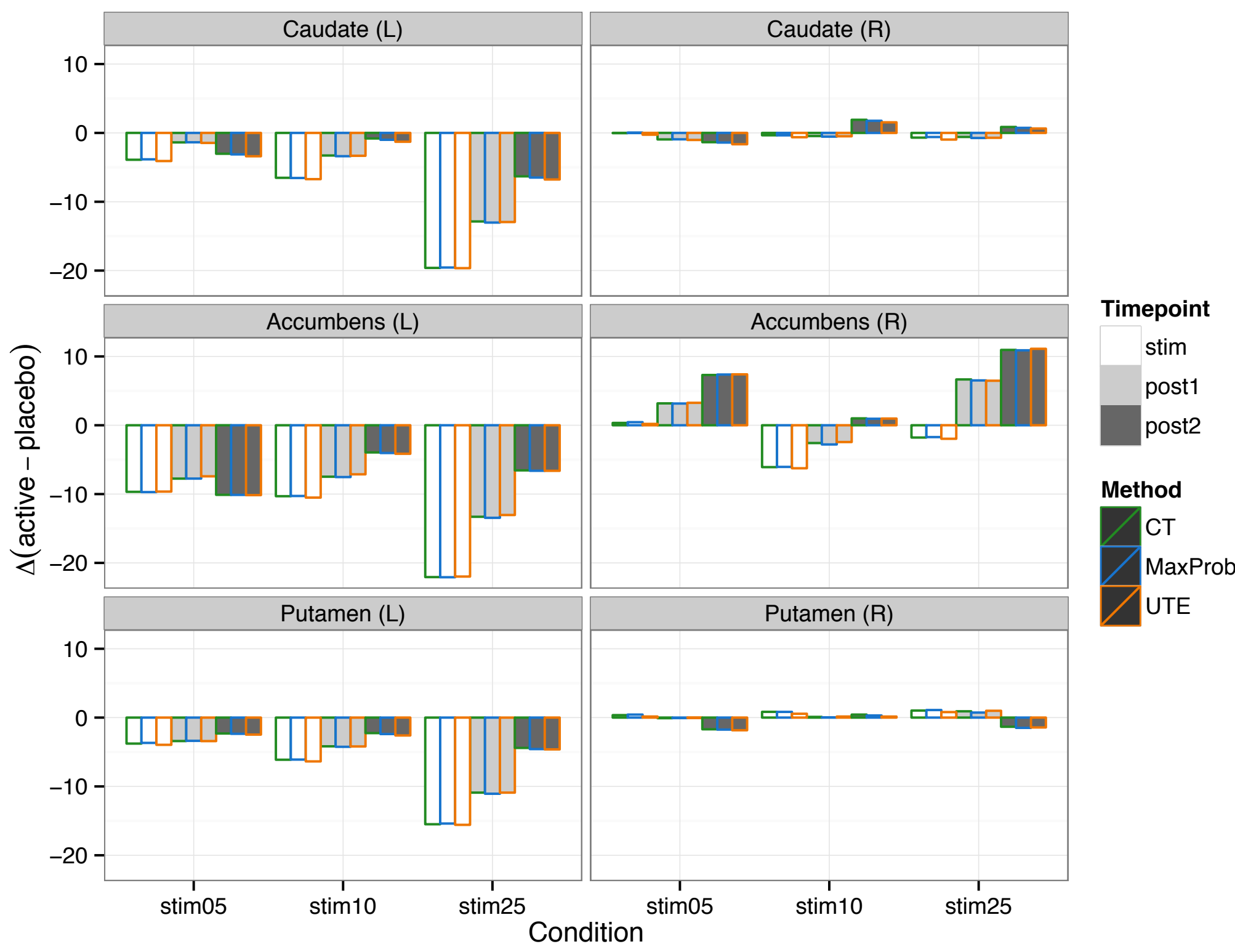
Fig 4: Mean bias across subjects for *UTE* and *MaxProb* MRAC methods as a function of time, i.e. during the 100-minute [¹¹C]Raclopride PET acquisition, and resulting BR bias.

Mean bias on BR was substantially affected for UTE due to quantification errors in cerebellum, and tended to vary with time. With *MaxProb* the BR bias remained close to zero.

Group comparison with different AC approaches

Regional level

Fig 5: Mean Δ difference between active (stim05, i.e. $\Omega=5\%$, stim10 i.e. $\Omega=10\%$ and stim25 i.e. $\Omega=25\%$) and placebo groups, for CT, *UTE* and *MaxProb* AC methods.



At regional level, the three AC approaches showed similar performance for detecting dopamine release (Fig. 5).

At the voxel level, the SPM analysis showed that *MaxProb* had better sensitivity in detecting endogenous dopamine release than *UTE* (Tab. 1).

Voxel level

	stim25		stim10		stim05	
	<i>MaxProb</i>	<i>UTE</i>	<i>MaxProb</i>	<i>UTE</i>	<i>MaxProb</i>	<i>UTE</i>
stim	100	99	90	89	94	91
post1	100	98	100	77	82	62
post2	97	89	100	79	93	77

Tab. 1: Percentage of detected significant voxels in the striatum obtained with the SPM analysis, compared to CT AC.

Conclusion

Compared to a standard approach (UTE) *MaxProb* multi-atlas MR-based AC enhanced sensitivity to detect physiological variations in a dynamic PET study.

References

- [1] Merida et al., Multi-atlas attenuation correction supports full quantification of static and dynamic brain PET data in PET-MR, *Phys. Med. Biol.* 2017
[2] Catana et al., Toward Implementing an MRI-Based PET Attenuation-Correction Method for Neurologic Studies on the MR-PET Brain Prototype, *JNM*, 2010
[3] Reilhac et al., PET-SORTEO: A Monte Carlo-Based Simulator With High Count Rate Capabilities, *IEEE TNS*, 2004
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