







# Mapping a Parkinson's disease-specific metabolic network in short time frames of dynamic fPET data

Falk K. Thiemig<sup>1</sup>, Vanessa Heinecke<sup>1</sup>, Kenan Steidel<sup>1,2</sup>, Damiano Librizzi<sup>4</sup>, Maya Beckersjürgen<sup>1</sup>, Tino Schurrat<sup>4</sup>, Hans-Helge Müller<sup>5</sup>, Markus Luster<sup>4</sup>, Lars Timmermann<sup>1,2,3</sup>, Carsten Eggers<sup>1,2,6</sup>, Marina C. Ruppert-Junck<sup>1,2,3</sup>, David Pedrosa<sup>1,2,3</sup>

1 Department of Neurology, Philipps-Universität Marburg, Germany

2 Department of Neurology, Universitätsklinikum Giessen und Marburg, Germany

- 3 Center for Mind, Brain and Behavior CMBB, Universities Marburg and Gießen, Germany
- 4 Department of Nuclear Medicine, Philipps-Universität Marburg, Germany
- 5 Institute for Medical Bioinformatics and Biostatistics, Philipps-Universität Marburg, Germany
- 6 Knappschaftskrankenhaus Bottrop GmbH, Bottrop, Germany

#### **1. Objective**

To identify Parkinson's disease-related brain networks by applying an independent component analysis to 10-minute time windows of dynamic fPET time series

### 2. Background

- Unraveling specific network signatures as biomarkers for neurodegenerative diseases represents a significant objective in contemporary research.
- A seminal study utilizing continuous infusionbased functional PET (fPET) recently showed distinct disease-related patterns in Parkinson's disease (PD)[1].
- Identifying these networks within shorter time **4. Results**

## **3. Methods**

- A 90-minutes resting-state functional PET measurement was performed in 14 PD patients (OFF-state) and 13 age-matched controls.
- Data were acquired in list-mode, reconstructed offline, and preprocessed using standardized pipelines.
- The last 30 minutes were retained for analysis due to low intensity in initial frames.
- Each participant's time series was split into three 10-minute time windows and analyzed via ICA at the group-level for the whole sample (Figure 1).



Figure 1: Schematic description of the applied ICA procedure

windows than the initial 90-min period could facilitate shorter scanning durations.

- Here, we conducted Independent Component Analyses (ICA) on different segments of our fPET time series to unravel if the metabolic network we recently described can be detected with shorter time periods.
- The sliding window ICA yielded two consistent networks in all three time windows for PD patients (Figure 2).
- The first mainly covered occipital areas and particularly the left temporal and parietal regions with a similar cluster found in the control group only in the second time window (Figure 2 A).
- The second component was observed exclusively in PD and represented a sensorimotor network that included the cerebellum, bilateral thalami, bilateral putamina and the motor cortex similar to our former study (Figure 2 B) [1].



Figure 2: Resting-state networks detected via ICA of 10-min time windows (W1-W3) of the fPET time series A Occipital component B Sensorimotor component

#### **5. Conclusions**

Our findings show that even in short time windows of (f)PET scanning a PD-specific metabolic network can be accessed with similar spatial precision. Thus, our results support shorter scanning durations combined with initial bolus injection and constant infusion for a cost- and time-effective scanning protocol for the disease spectrum.

**References**: [1] Ruppert-Junck MC, Heinecke V, Librizzi D, Steidel K, Beckersjürgen M, Verburg FA, Schurrat T, Luster M, Müller HH, Timmermann L, Eggers C, Pedrosa D. Connectivity based on glucose dynamics reveals exaggerated sensorimotor network coupling on subject-level in Parkinson's disease. Eur J Nucl Med Mol Imaging. 2024 Oct;51(12):3630-3642. doi: 10.1007/s00259-024-06796-6. Epub 2024 Jun 17. PMID: 38884774; PMCID: PMC11445336.