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# PET2BIDS: a library for converting Positron Emission Tomography data to BIDS

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**Software**

- Review
- Repository
- Archive

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## Summary

The Brain Imaging Data Structure (Gorgolewski et al., 2016) is a standard for organizing and naming neuroimaging data which has quickly become successful and popular in the community with adoption by major brain imaging repositories (e.g. OpenNeuro (*OpenNeuro*, 2023), PublicnEUro (*Public nEUro*, 2023), CONP (*The Canadian Open Neuroscience Platform – a Partnership with Brain Canada*, 2023)) and data management tools (e.g. COINS (Landis et al., 2016), XNAT (Marcus et al., 2007), Loris (Das et al., 2012)). This not only allows data to be shared much more easily, but also enables the development of automated data analysis pipelines, and together improves reproducibility.

The BIDS extension for Positron Emission Tomography (PET-BIDS) (Norgaard et al., 2022) provides a structured data and metadata nomenclature, including all the necessary information to share and report on PET blood and metabolite (Knudsen et al., 2020). Here we present a new code library, developed in both Matlab and Python, allowing the conversion of PET imaging data (ECAT and DICOM format) and metadata (e.g., time or blood measurements) into the BIDS specification.

## Statement of need

`PET2BIDS` was designed as a library code, allowing conversion of PET data to BIDS using the command line. Thanks to its modular structure, it can be integrated into software (with a graphical user interface) that aim at more general BIDS conversion, and current efforts are underway integrating PET2BIDS with ezBIDS (*ezBIDS*, 2023) and BIDSCoins (Zwiers et al., 2022).

*File conversion*: The conversion for PET data stored in DICOM files is performed using a wrapper around dcm2niix (Li et al., 2016; Rorden, 2023) and then extending the JSON file with details that are not included in the source images but are required for BIDS. For ECAT files, dedicated functions were written to support this conversion. The Matlab code relies on the readECAT7.m function from BT Christian (1998) and revised by RF Muzic (2002) to read the data, while new ecat2nii (.m .py) functions were written to convert into NIfTI and produce a JSON sidecar file, and optionally a (non-BIDS compliant) SIF file (Scan Information File -

used by different pharmacokinetic modelling software for model weighting). The Python code was subsequently developed in line with the Matlab code, with further testing of data reading (i.e., which parts are read according to the PET data frames) and writing, relying here on Nibabel (Brett et al., 2023).

*PET Metadata*: JSON files created from reading PET scanner data are always missing some of the radiotracer and pharmaceutical information. To accommodate this, a dedicated PET JSON updater was created. The PET JSON updater function takes the original JSON file and new metadata to add as input, checks that the full BIDS specification is respected (correct metadata but also consistency of metadata values for the different metadata keys) and updates the JSON file.

*Spreadsheet conversion*: tabular data formats (xls, xlsx, csv, tsv, bld) are ubiquitous in the PET community in particular to (a) keep track of radiotracer information injected per participant and (b) recording of time and radiotracer concentration from the blood sampling. To facilitate conversion to BIDS, dedicated functions were created to (i) convert pre-formatted tabular data to JSON files, (ii) use pre-formatted tabular data to update JSON files, and (iii) convert a tabular PMOD file to a blood.tsv file (PMOD being a popular commercial pharmacokinetic modelling software (Burger & Buck, 1997)).

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