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

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Software

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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 brain imaging repositories (e.g., OpenNeuro (Markiewicz et al., 2021), PublicnEUro (*Public nEUro*, 2023)), data management tools (e.g., COINS (Landis et al., 2016), XNAT (Marcus et al., 2007)) and computational platforms (e.g. BrainLife (Hayashi S, 2023)). BIDS allows data to be shared much more efficiently, enables the development of automated data analysis pipelines, and improves reproducibility.

The BIDS extension for Positron Emission Tomography (PET-BIDS) (Norgaard et al., 2022) provides nomenclature for structured data and metadata, including all the necessary information to share and report on PET blood and metabolite (Knudsen et al., 2020). Here we present a code library, developed in both Matlab and Python, allowing the conversion of DICOM (*DICOM PS3.3 2020b - Information Object Definitions*, 2020) and ECAT (CTI/Siemens proprietary data format) PET imaging data and metadata (e.g., timing information such as 'time zero' or blood measurements) into files that follow the BIDS specification (nifti, json, tsv).

Statement of need

Conversion tools from native format to BIDS are essential to help researchers to use BIDS. While tools for MRI and MEEG exist, PET2BIDS is the first tool to convert both DICOM and ECAT PET data and PET metadata to BIDS files. Because PET2BIDS is a code library, conversion is done using the command line. PET2BIDS can, however, also be integrated into software (with a graphical user interface) that aims at more general BIDS conversion, and current efforts are underway integrating PET2BIDS with ezBIDS (Levitas et al., 2024) and BIDSCoin (Zwiers et al., 2022). While our library allows to convert and name files, these more generic tools also allow data to be structured following the BIDS specification.

File conversion: The conversion for PET data stored in DICOM format to NIfTI is performed using the `dcm2niix4pet` functions, which are wrappers around dcm2niix (Xiangrui Li et al., 2016; Rorden, 2023). Those functions can extend the image sidecar JSON file generated by dcm2niix with user-provided metadata, making them BIDS-compliant. The conversion of PET data stored in ECAT format is performed using the dedicated ecat2nii functions. The Matlab code relies on the `readECAT7.m` (Christian & Muzic, 1998) function written by B.T. Christian (1998) and revised by R.F. Muzic (2002) to read the data while writing Nifti files relies on `nii_tool` (X. Li, 2016). The Python code mirrors the Matlab code, except writing of Nifti files, which are delegated to Nibabel (Brett et al., 2023). For both Matlab and Python, the data conversion and writing are thoroughly tested (see ecat validation). Mirroring the DICOM conversion, the ecat2nii functions generate JSON sidecar files from image data, and users must provide additional metadata to make files BIDS-compliant. Note that the Python tools are command line tools, i.e. they can be called directly from a terminal.

PET Metadata: Some radiotracer and pharmaceutical information are always missing in the JSON sidecar files created from reading PET scanner data which is why `dcm2niix4pet` and `ecat2nii` take additional metadata. It is also possible to update existing JSON sidecar files with new metadata directly using `updatejsonpetfile.m` or `update_json_pet_file.py`.

Spreadsheet conversion: Tabular data formats are ubiquitous in the PET community, mainly to keep track of radiotracer information injected per participant and record time and radiotracer concentration from the blood sampling. Functions were created to read preformatted tabular data to create or update existing sidecar JSON files. In addition, dedicated functions were created to convert either a preformatted tabular file or PMOD files (PMOD being a popular commercial pharmacokinetic modeling software (Burger & Buck, 1997)) to a BIDS blood.tsv file with it's sidecar JSON. Supported formats are .xls, .xlsx, .csv, .tsv and .bld.

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