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PICNIC: an open-source Python library for preprocessing of dynamic Positron Emission Tomography (PET) brain imaging data

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Software

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Summary

PICNIC (Pipeline Initializing Container for Neuro-Imaging Computations) is an open-source Python-based coding library that includes modular wrappers for most standard preprocessing steps for quantification of Positron Emission Tomography (PET) brain imaging data. PICNIC uniquely allows full, transparent modular control over the selection of strategy/software package and associated parameters for each preprocessing step throughout the pipeline. Therefore, the user is provided with the flexibility to select different methods depending on the target of interest and/or radiotracer properties, study population, or other preferences. These settings can be saved as a text-based "input deck" file to support consistent preprocessing across scans, participants, and projects. Furthermore, PICNIC supports freezing software versions within Docker containers, ensuring robust reproducibility.

PICNIC does not require Brain Imaging Data Structure (BIDS) source-level data, but instead takes reconstructed PET static or dynamic data in industry standard imaging filetypes (e.g., DICOM, Nifti, ANALYZE), and converts them to be BIDS-compliant (Knudsen et al., 2020). PICNIC employs the most commonly used brain imaging software packages, including Advanced Normalization Tools (Avants et al., 2008), Analysis of Function NeuroImages (Cox, 1996), FSL (Jenkinson et al., 2012), FreeSurfer (Fischl, 2012), dcm2niix (Li et al., 2016), and SPM (Laboratory, 2020). PICNIC was designed with PET in mind, but includes steps involving data from multiple imaging modalities, most prominently structural magnetic resonance imaging (sMRI). PICNIC preprocessing capabilities include image reorientation (to force all images into a standard orientation regardless of scanner defaults), brain extraction (to perform skull-stripping of associated sMRI images), tissue segmentation (to classify sMRI voxels within the brain boundary as grey matter vs. white matter vs. cerebrospinal fluid), automatic anatomical parcellation (to identify regions of interest using any available atlas/parcellation), post-reconstruction rigid-body motion-correction (to correct inter-frame participant motion over the duration of the scan), PET-sMRI co-registration (with 20 different PET-sMRI rigid-body transformations that are automatically ranked based on mutual information), and extraction of time-activity-curves (curves that represent the PET signal over the duration of the scan in delineated regions of interest or in each brain voxel).

PICNIC can be run from the command line or through the provided graphical user interface. An html summary output with interactive quality control features allows the user to inspect, comment, and approve/disapprove each module for each participant upon completion. Pre-loaded templates have been provided for commonly used workflows. The user can add, remove or edit pre-processing steps to fully customize their pipeline with regards to their dataset.

PICNIC currently supports over 100,000 module/parameter combinations.

PICNIC is designed for in vivo brain investigations by expert PET researchers, and has already been applied to preprocess data for recent scientific publications from our Lab (Bartlett, Patil, et al., 2023, 2024; Bartlett, Zanderigo, Stanley, et al., 2023; Bartlett, Zanderigo, Ogden, et al., 2023; Bartlett, Herzog, et al., 2024; Bartlett, Sublette, et al., 2024; Graves et al., 2024; Herzog et al., 2024, 2025; Mann et al., 2022; Matheson et al., 2024; Miller et al., 2022) (https://www.columbiapsychiatry.org/research-labs/brain-imaging-lab). PICNIC's modular nature enables extensive customization of preprocessing for a variety of brain PET studies, and its design may allow future extension to preprocessing of data from imaging modalities other than PET. The source code for PICNIC is available at the following link: https://github.com/bil-mind-nyspi/PICNIC.

Statement of need

PET is a valuable tool used in research and clinical settings to noninvasively image the human brain in vivo. PET can quantify up to nanomolar levels of specific components of brain metabolic and neurochemical processes, thus providing information on the distribution of specific biological targets, such as receptors and enzymes, or on the uptake of specific compounds into the brain, like glucose and polyunsaturated fatty acids. Rigorous preprocessing of the raw data captured by the PET scanner (Norgaard et al., 2019) is key to obtaining the most accurate estimates of the distribution of a biological target or uptake of a substance using PET. Although a few software packages already exist (Funck et al., 2018; Karjalainen et al., 2020; Routier et al., 2021) that perform most of the required preprocessing steps, a fully open-source library that can modularly and flexibly combine appropriate preprocessing strategies depending on the study design at hand is still missing.

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