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cermep-bids-retro V.1

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We use this protocol and it's working

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Abstract

cermep-bids-retro enables the formatting of retrospective PET and MRI data to BIDS standards from DICOM databases. When dealing with pre-clinical imaging modalities, numerous metadata are overlooked during acquisitions making it difficult to automatically format following BIDS guidelines. This python-based project is a flexible method for BIDS formatting with input csv files to compensate for lacking DICOM tags. And advanced data quality assessment.

cermep-bids-retro installation

1 Clone repository

In GitBash:

```
git clone https://gitlab.in2p3.fr/cermep/cermep-bids-retro.git
```

2 Create conda environment

```
cd cermep-bids-retro
conda env create -f environment.yml
conda activate bids-retro
```

Fill-in input files

- 3 This step is key to a functional method. It requires a good knowledge of the available tags and fields in the DICOM data and one can always refer to the BIDS [specifications](#) to define all required tags for their modality. Substeps below provide description and example for each column of the 3 input files.

3.1 Table 2. Sequence overview configuration file description and examples.

sequences	src	filename	folder	trc	bids-tag1 PulseSequence	bids-tag2 EchoTime	bids-tagX InjectedMass
Sequence name in BIDS standards	Variable name of location of folder for database in DICOM format	Sequence name in DICOM database	Storing folder in BIDS standards	Tracer name for PET data	Example of BIDS required metadata for each sequence. These tags will be integrated in the JSON file upon formatting following instructions: 0- non-required tag; 1- required tag available in DICOM file; 2- required tag available with additional formatting steps; str- replacement value for missing tag; file- subject specific value available in PET configuration file.		
T2w trc-PK11195	raw_mri raw_pet	SE_32TE PK11195	anat pet	0 PK11195	Spin Echo 0	2 0	0 file

1st row: header; 2nd row: column description; 3rd row: examples for MRI and PET acquisitions.

Description and examples to fill in seq_overview.csv

3.2 This table must be filled in simultaneously with seq_overview.csv

**Table 4.** DICOM to BIDS tags conversion configuration file description and examples.

bids-tag	dicom-tag
BIDS tag naming convention	DICOM tag equivalent
Manufacturer	Manufacturer
TimeZero	AcquisitionTime
PulseSequence	None*

1st row: header; 2nd row: column description; 3rd row: example of tags

*tag not in DICOM metadata: refer to sequence overview configuration file

Description and examples to fill in dcm2bids_tags.csv.

3.3 This table is necessary for formatting of PET data, otherwise optional

Table 3. PET doses configuration file description and examples.

subject	session	trc	Specific Radioactivity	Injected Radioactivity	InjectedMass
Subject name in DICOM database	Session name in DICOM database	Tracer name as set in sequence overview configuration file	Measured specific radioactivity in units specified in BIDS tag SpecificRadioactivityUnits	Measured injected radioactivity in units specified in BIDS tag InjectedRadioactivityUnits	Calculated injected mass in units specified in BIDS tag InjectedMassUnits
SUBJECT-XA	Baseline	H2O15	na	259	na
SUBJECT-XB	Baseline	PK11195	49.8	138	2.77
SUBJECT-XB	Post-op	PK11195	48.9	126	2.58

1st row: header; 2nd row: column description; 3rd row: examples for PET tracers and sessions.

Description and examples to fill in pet_doses.csv

Run formatting task

4 Replace argument values and run task from command line:

```
python bids_retro\\main.py \
--src_mri "path\\to\\modality" \
--src_pet "E:\\PhD\\temp\\data_fabien\\raw_dcm" \
--sequences_overview "inputs\\seq_overview.csv" \
--pet_doses "inputs\\pet_doses.csv" \
--dcm2bids_tags "inputs\\dcm2bids_tags.csv" \
--species "name of species" \
--src_structure "A" \
--in_sub_dcm_list "subjectA,subjectB" \
--in_ses_dcm_list "session" \
--dest "path\\to\\bids\\formatted\\destination" \
--quality_testing 1 \
--results "path\\to\\save\\quality_analysis\\results" \
--include_dicom 0 --verbose 1
```

