

Supplementary Materials

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user@host ~ $ SAMRI bru2bids --help
usage: SAMRI bru2bids [-h] [-b BIDS_EXTRA] [--dataset-authors DATASET_AUTHORS] [--dataset-license DATASET_LICENSE] [--dataset-name]
                    [--debug] [-d DIFFUSION_MATCH] [-e EXCLUDE] [-f FUNCTIONAL_MATCH] [-i] [--keep-crashdump] [--keep-work]
                    [-m [MEASUREMENTS [MEASUREMENTS ...]]] [-n N_PROCS] [-o OUT_BASE] [-s STRUCTURAL_MATCH] [-w WORKFLOW_NAME]
                    measurements-base

Convert and reorganize Bruker "raw" directories (2dseq and ParaVision-formatted metadata files) into a BIDS-organized file hierarchy containing
NIfTI files and associated metadata. If any exist, this workflow also repositos COSplay event files (already written according to BIDS) in the
correct place in the output hierarchy.

Parameters
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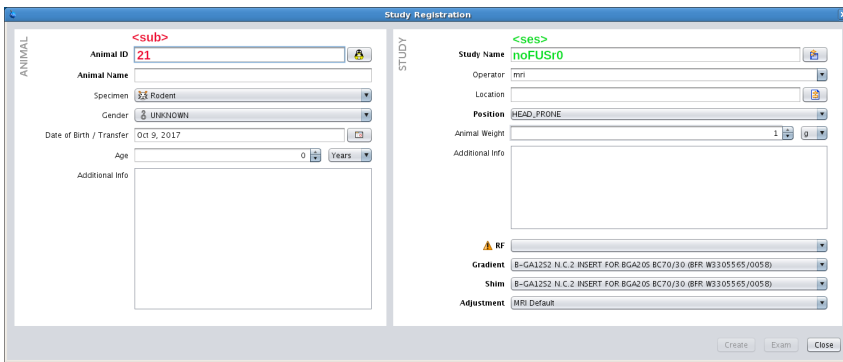
measurements_base : str
    Path of the top level directory containing all the Bruker ParaVision scan directories to be converted and reformatted.
bids_extra : list, optional
    List of strings denoting optional BIDS fields to include in the resulting file names. Accepted items are 'acq' and 'run'.
dataset_authors : list of string, optional
    A list of dataset author names, which will be written into the BIDS metadata file. Generally not needed, unless this is important for you.
dataset_license : string, optional
    A dataset license name that will be written into the BIDS metadata file. Generally not needed, unless this is important for you.
dataset_name : string, optional
    A dataset name that will be written into the BIDS metadata file. Generally not needed, as by default we use the dataset path to satisfy this
    BIDS requirement.
debug : bool, optional
    Whether to enable debug support. This prints the data selection before passing it to the nipype workflow management system, and turns on debug
    support in nipype (leading to more verbose logging).
diffusion_match : dict, optional
    A dictionary with any combination of "session", "subject", "task", and "acquisition" as keys and corresponding lists of identifiers as values.
    Only diffusion scans matching all identifiers will be included - i.e. this is a whitelist.
exclude : dict, optional
    A dictionary with any combination of "session", "subject", "task", and "acquisition" as keys and corresponding identifiers as values. Only scans
    not matching any of the listed criteria will be included in the workflow - i.e. this is a blacklist (for functional and structural scans).
functional_match : dict, optional
    A dictionary with any combination of "session", "subject", "task", and "acquisition" as keys and corresponding lists of identifiers as values.
    Only functional scans matching all identifiers will be included - i.e. this is a whitelist.
inflated_size : bool, optional
    Whether to inflate the voxel size reported by the scanner when converting the data to NIfTI. Setting this to `True` multiplies the voxel edge
    lengths by 10 (i.e. the volume by 1000); this is occasionally done in some small animal pipelines, which use routines designed exclusively for
    human data. Unless you are looking to reproduce such a workflow, this should be set to `True`.
keep_crashdump : bool, optional
    Whether to keep the crashdump directory (containing all the crash reports for intermediary workflow steps, as managed by nipyppe). This is
    useful for debugging and quality control.
keep_work : bool, optional
    Whether to keep the work directory (containing all the intermediary workflow steps, as managed by nipyppe). This is useful for debugging and
    quality control.
measurements : list, optional
    Whitelist of Bruker ParaVision scan directories to consider.
n_procs : int, optional
    Maximum number of processes which to simultaneously spawn for the workflow. If not explicitly defined, this is automatically calculated from the
    number of available cores and under the assumption that the workflow will be the main process running for the duration that it is running.
out_base : str, optional
    Base directory in which to place the BIDS repositated data. If not present the BIDS records will be created in the `measurements_base` directory.
structural_match : dict, optional
    A dictionary with any combination of "session", "subject", "task", and "acquisition" as keys and corresponding lists of identifiers as values.
    Only structural scans matching all identifiers will be included - i.e. this is a whitelist.
workflow_name : str, optional
    Top level name for the output directory.

positional arguments:
  measurements-base  -

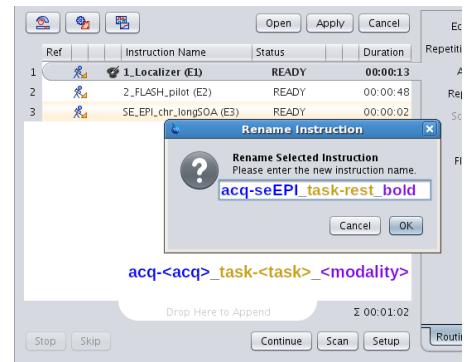
optional arguments:
  -h, --help            show this help message and exit
  -b BIDS_EXTRA, --bids-extra BIDS_EXTRA
                        ['acq', 'run']
  --dataset-authors DATASET_AUTHORS
                        []
  --dataset-license DATASET_LICENSE
                        ''
  --dataset-name       False
  --debug              False
  -d DIFFUSION_MATCH, --diffusion-match DIFFUSION_MATCH
  -e EXCLUDE, --exclude EXCLUDE
  -f FUNCTIONAL_MATCH, --functional-match FUNCTIONAL_MATCH
  -i, --inflated-size  False
  --keep-crashdump     False
  --keep-work          False
  -m [MEASUREMENTS [MEASUREMENTS ...]], --measurements [MEASUREMENTS [MEASUREMENTS ...]]
                        []
  -n N_PROCS, --n-procs N_PROCS
                        2
  -o OUT_BASE, --out-base OUT_BASE
                        -
  -s STRUCTURAL_MATCH, --structural-match STRUCTURAL_MATCH
  -w WORKFLOW_NAME, --workflow-name WORKFLOW_NAME
                        'bids'

```

Figure S1: Example of the SAMRI `bru2bids` repositing workflow parameter list as reported in the Bash command line in the 0.4.1 SAMRI release. This output is autogenerated for Bash from the Python docstring.



(a) Subject and session are entered into the “Study Registration” window, which is presented to the user before the onset of acquisition.



(b) Other operator input fields are entered into the “Instruction Name” column.

Figure S2: ParaVision graphical user interface examples, showing how metadata automatically interpretable by the repositing workflow can be specified when acquiring new data.