

Brain Imaging Data Structure

ISN Methods Meet

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‘With the Brain Imaging Data Structure (BIDS), we describe a simple and easy to adopt way of organizing neuroimaging and behavioral data.’ <https://bids.neuroimaging.io/>

Some advantages of using a standardized Protocol:

- **Minimized curation:** easier access to the data by others
- **Error reduction:** reducing misunderstanding of meaning of a given datum
- **Optimized usage of data analysis software:** automated workflows are enabled

Gorgolewski, Auer, [...] Poldrack (2016)
<https://www.nature.com/articles/sdata201644>



‘With the Brain Imaging Data Structure (BIDS), we describe a simple and easy to adopt way of organizing neuroimaging and behavioral data.’ <https://bids.neuroimaging.io/>

BIDS is based upon proven parts from:

- Clinical Experiment Data Exchange Schema (XCEDE)
- OpenfMRI database
- The World Wide Web Consortium (W3c)
- Common laboratory practices in the community

Gorgolewski, Auer, [...] Poldrack (2016)
<https://www.nature.com/articles/sdata201644>

BIDS offers a format for describing and standardizing data using

- a specific structure for directories
- specific pattern of names for directories and files
- nifti, JSON- and TSV-files for documenting metadata
- formats readable for humans AND machines



File-formats used in BIDS

- **Neuroimaging Informatics Technology Initiative (NIFTI) files:** format used for imaging files
- **JavaScript Object Notation (JSON) files:** used for storage of additional metadata (e.g., acquisition details)
 - Easier to write and comprehend than XML
 - Widely supported by major programming languages
 - Linkable to formal ontologies (e.g., Cognitive Atlas via JSON-LD)
- **Tab Separated Value files (.tsv):** used for other data (e.g., list of participants)

Data dictionaries are provided

<https://bids-specification.readthedocs.io/en/stable/>

- Strict naming conventions for structural, diffusion, fMRI and accompanying behavioral and physiological data
- Clear definitions of terms used in .tsv and .json files
- Additional files and subfolders should follow a set of general naming guidelines and common sense
- Data types will be added in future versions (e.g., eye-tracking data)

Mandatory:

- rawdata/ with the minimum of
 - A dataset_description.json file
 - 1 participant folder

```
my_dataset/  
    rawdata/  
        dataset_description.json  
        sub-01/
```

This file describes your dataset, using certain sets of key/value pairs

Example of dataset_description.json from OpenNeuro.org

Raw

```
{
  "Name": "multibandACQtests",
  "BIDSVersion": "1.1.0",
  "License": "CC0",
  "Authors": [
    "Joset A. Etzel",
    "Debbie Yee",
    "Bidhan Lamichhane",
    "Mitchell Jeffers",
    "Elisa Di Rosa",
    "Jenny Crawford",
    "Hongyu An",
    "Todd S. Braver"
  ],
  "Acknowledgements": "We thank Abraham Snyder, Aaron Tanenbaum, and Alexander Kizhner for assistance.",
  "Funding": [
    "This research was supported by NIH R37MH066078 and NIH R21AG058206 to Todd Braver.",
    "This research was supported by NIH NINDS 1P30NS098577 to Hongyu An.",
    "Image acquisition is partially supported by Mallinckrodt Institute of Radiology, Washington University in St. Louis."
  ],
  "ReferencesAndLinks": [
    "http://ccpweb.wustl.edu/",
    "https://www.mir.wustl.edu/research/research-support-facilities/center-for-clinical-imaging-research-ccir"
  ],
  "DatasetDOI": "doi:10.18112/openneuro.ds001399.v1.0.2"
}
```

Key name	Requirement level	Data type
DatasetDOI	OPTIONAL	string

Example:

```
1 {
2   "Name": "The mother of all experiments",
3   "BIDSVersion": "1.4.0",
4   "DatasetType": "raw",
5   "License": "CC0",
6   "Authors": [
7     "Paul Broca",
8     "Carl Wernicke"
9   ],
10  "Acknowledgements": "Special thanks to Korbinian Brodmann for help in formatting th
    Huxley for helpful comments and discussions about the experiment and manuscript
    Claudius Galenus for providing data for the medial-to-lateral index analysis.",
11  "HowToAcknowledge": "Please cite this paper: https://www.ncbi.nlm.nih.gov/pubmed/00
12  "Funding": [
13    "National Institute of Neuroscience Grant F378236MFH1",
14    "National Institute of Neuroscience Grant 5RMZ0023106"
15  ],
16  "EthicsApprovals": [
17    "Army Human Research Protections Office (Protocol ARL-20098-10051, ARL 12-040, an
18  ],
19  "ReferencesAndLinks": [
20    "https://www.ncbi.nlm.nih.gov/pubmed/001012092119281",
21    "Alzheimer A., & Kraepelin, E. (2015). Neural correlates of presenile dementia in
    :1920.8/jndata.2015.7"
22  ],
23  "DatasetDOI": "doi:10.0.2.3/dfjj.10",
24  "HEDVersion": "7.1.1"
25 }
```

contain information on the dataset. A reference may be textual or a URI.

General on JSON file format

JavaScript Object Notation (JSON) files **MUST** be used for storing **key/value pairs**.

JSON files **MUST** be in **UTF-8 encoding**.

Extensive documentation of the format can be found at <https://www.json.org/>

Several editors have built-in support for JSON syntax highlighting that aids manual creation of such files.

An **online editor** for JSON with built-in validation is available at <https://jsoneditoronline.org>.

It is **RECOMMENDED** that **keys** in a JSON file are written in **CamelCase** with the first letter in upper case

- SamplingFrequency and not samplingFrequency

Note however, when a JSON file is used as an **accompanying sidecar file for a TSV file**, the keys linking a TSV column with their description in the JSON file need to follow the exact formatting as in the TSV file.

The inheritance principle: key-value pairs from higher levels are inherited to lower levels but not vice-verse!

- JSON-files on lower levels are only necessary when specific to that lower level
- Avoid excessive amounts of overrides (then rather keep upper-level empty)

Mandatory:

- rawdata/ with the minimum of
 - A dataset_description.json file
 - 1 participant folder

Data files are contained in a directory named for the data type.

BIDS defines eight data types:

func (task based and resting state functional MRI)

dwi (diffusion weighted imaging)

fmap (field inhomogeneity mapping data such as field maps)

anat (structural imaging such as T1, T2, PD, and so on)

meg (magnetoencephalography)

eeg (electroencephalography)

ieeg (intracranial electroencephalography)

beh (behavioral)

The names of these data-type folders are mandatory!

In raw datasets, the data type directory is nested inside subject and (optionally) session directories.

```
my_dataset/  
  rawdata/  
    dataset_description.json  
    sub-01/  
      sess-01/  
        anat/  
        dmap/  
        dwi/  
        func/  
      sess-02/  
        anat/  
        ...
```

Mandatory:

- rawdata/ with the minimum of
 - A dataset_description.json file
 - 1 participant folder

Optional:

- 1 participants.tsv

```
my_dataset/  
    rawdata/  
        dataset_description.json  
        participants.tsv  
        sub-01/
```

- The purpose of this RECOMMENDED file is to describe properties of participants such as age, sex, handedness.
- If this file exists, it MUST contain the column participant_id, which MUST consist of sub-<label> values identifying one row for each participant, followed by a list of optional columns describing participants.
- Each participant MUST be described by one and only one row.

participants.tsv example:

```
1 participant_id age sex handedness group  
2 sub-01 34 M right read  
3 sub-02 25 F left no-read
```

General on TSV file format

Tabular data **MUST** be saved as tab delimited values (.tsv) files, that is, CSV files where commas are replaced by tabs. Tabs **MUST** be true tab characters and **MUST NOT** be a series of space characters.

Each TSV file **MUST** start with a header line listing the names of all columns (with the exception of physiological and other continuous recordings).

Names **MUST** be separated with tabs.

It is **RECOMMENDED** that the column names in the header of the TSV file are written in snake_case with the first letter in lower case (for example, variable_name, not Variable_name).

String values containing tabs **MUST** be escaped using double quotes.

Missing and non-applicable values **MUST** be coded as n/a.

Numerical values **MUST** employ the dot (.) as decimal separator and **MAY** be specified in scientific notation, using e or E to separate the significand from the exponent.

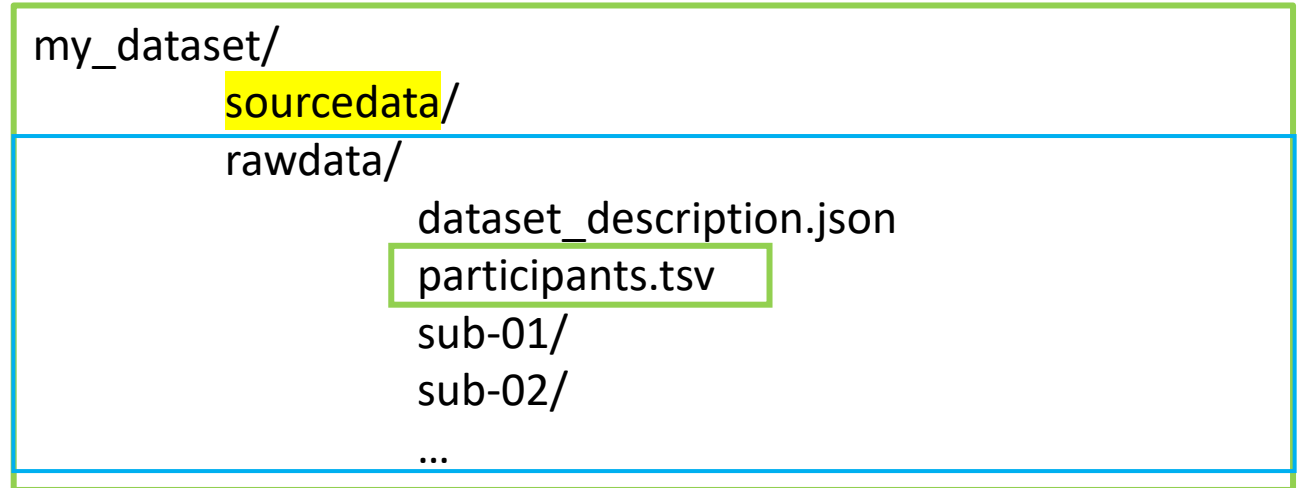
TSV files **MUST** be in UTF-8 encoding.

Mandatory:

- rawdata/ with the minimum of
 - 1 participant folder
 - A dataset_description.json file

Optional:

- 1 participants.tsv
- sourcedata/



Sourcedata is defined as data before harmonization, reconstruction, and/or file format conversion (for example, event logs or DICOM files). Storing actual source files with the data is preferred over links to external source repositories.

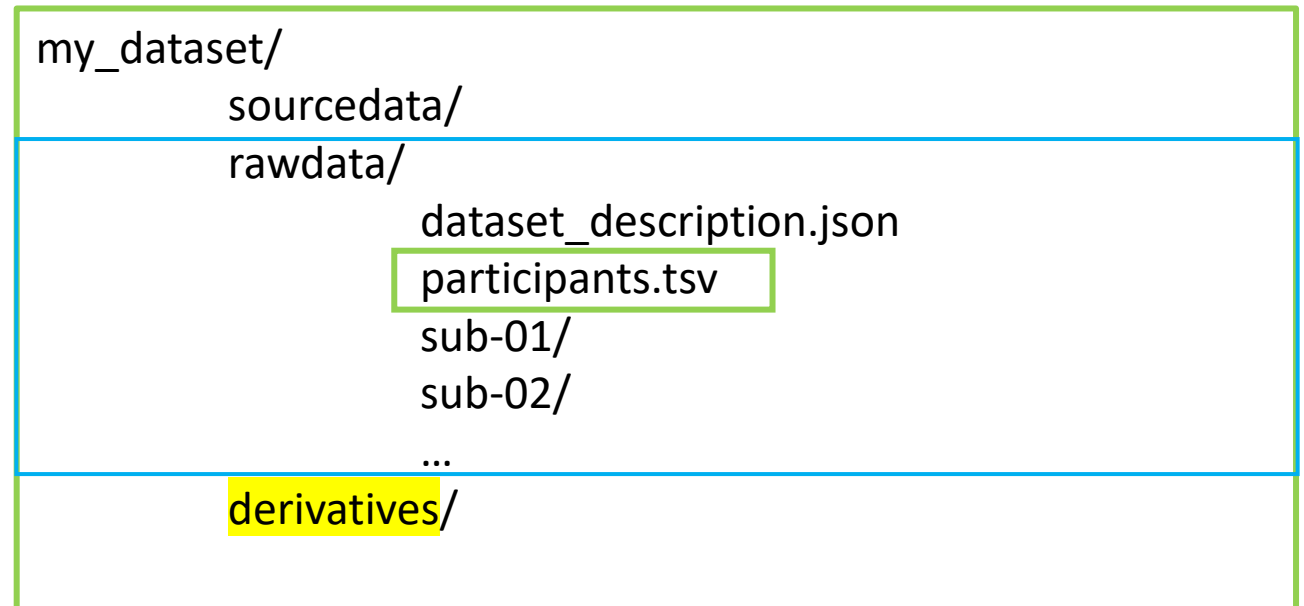
MUST be kept separate from the raw data.

Mandatory:

- rawdata/ with the minimum of
 - 1 participant folder
 - A dataset_description.json file

Optional:

- 1 participants.tsv
- sourcedata/
- derivatives/



Derivatives of the raw data (other than products of DICOM to NIfTI conversion): e.g., preprocessing and analysis of data.

MUST be kept separate from the raw data. This way one can protect the raw data from accidental changes by file permissions. In addition, it is easy to distinguish partial results from the raw data and share the latter.

Mandatory:

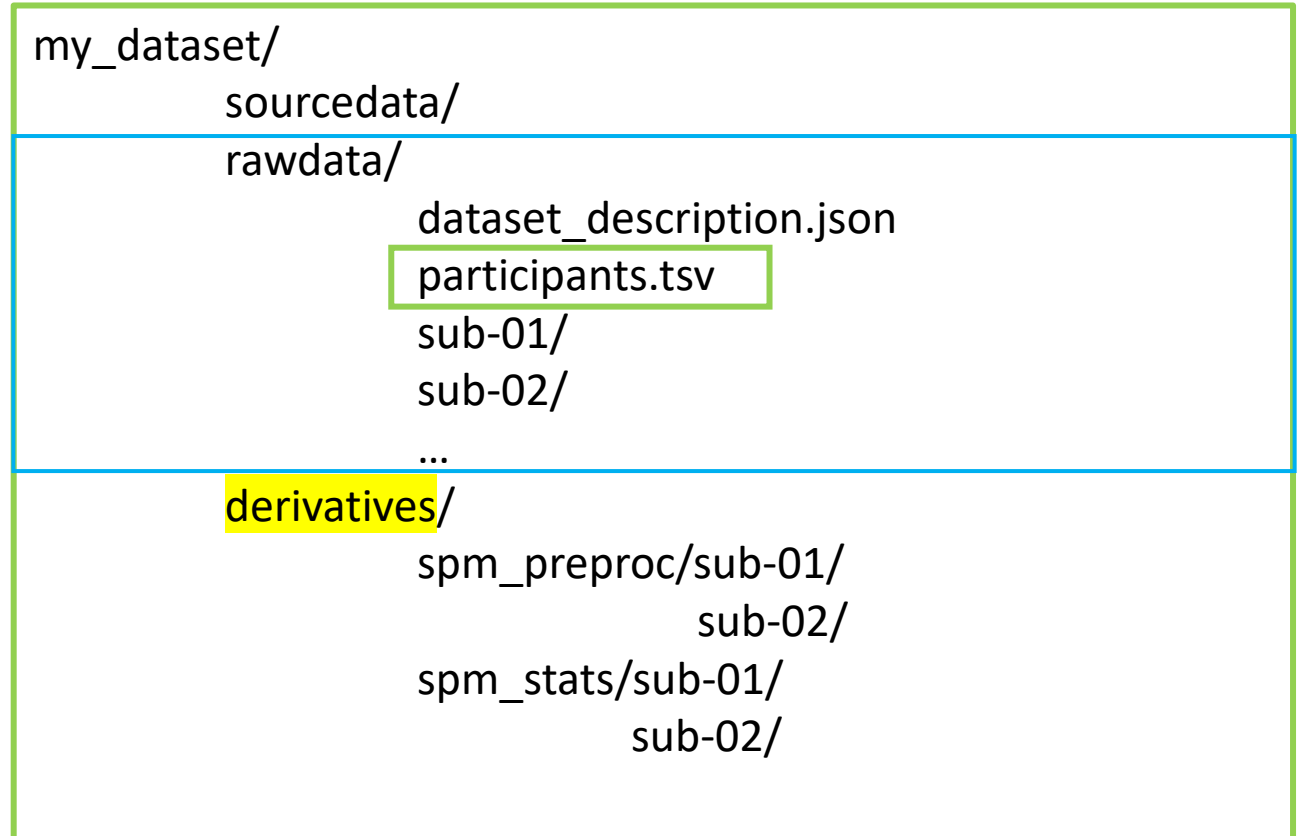
- rawdata/ with the minimum of
 - 1 participant folder
 - A dataset_description.json file

Optional:

- 1 participants.tsv
- sourcedata/
- derivatives/

Derivatives can be stored in two ways:

- as a subdir of my_dataset



Mandatory:

- rawdata/ with the minimum of
 - 1 participant folder
 - A dataset_description.json file

Optional:

- 1 participants.tsv
- sourcedata/
- derivatives/

Derivatives can be stored in two ways:

- as an independent directory

```
my_dataset/  
  sourcedata/  
  rawdata/  
    dataset_description.json  
    participants.tsv  
    sub-01/  
    sub-02/  
    ...  
my_processed_data/  
  code/  
    processing_pipeline-1.0.0.img  
    hpc_submitter.sh  
    ...  
  sourcedata/  
    dataset_description.json  
    participants.tsv  
    sub-01/  
    sub-02/  
    ...
```

Mandatory:

- rawdata/ with the minimum of
 - 1 participant folder
 - A dataset_description.json file

Optional:

- 1 participants.tsv
- sourcedata/
- Derivatives/

NOTE: The NAMES of **these folders** are not prescribed!

```
AwesomeStuff/  
    sourceAwesomeStuff/  
    rawAwesomeStuff/  
        dataset_description.json  
        participants.tsv  
        sub-01/  
        sub-02/  
        ...  
    bestAnalysisEver/
```

The **naming of files** are prescribed:

Filenames are formed with a series of key-values and end with a file type, where **keys and file types are predefined**, and **values are chosen by the user**.

```
sub-01_sess-01_task-epiMyTask_run-01_bold.nii  
sub-01_sess-01_task-epiMyTask_run-01_bold.json
```

NOTE: ,run' versus ,sess'
Both optional!

Hands-on HowTo according to the 2016 paper <https://www.nature.com/articles/sdata201644>

Step 1: Convert Dicom to Nifti

Step 2: Create folder structure according to the BIDS rules <https://bids-specification.readthedocs.io/en/stable/>

Step 3: Add remaining data (behavioral etc.)

Step 4: Add metadata (especially create .asv and .json files!)

Step 5: Validate the dataset (tools for validation are provided) <https://github.com/bids-standard/bids-validator>

Or you simply use someone else's existing code to do the job for you ...

You can find many converters here: <https://bids.neuroimaging.io/benefits.html>

Using different languages (matlab, , R, C++, python, python, python, python, python)



BIDS has its own youtube channel https://www.youtube.com/channel/UCxZUcYfd_nvIVWAbzRB1tlw

Presentation by Remi Gau

Other BIDS-stuff e.g.,

bids-matlab

https://de.mathworks.com/matlabcentral/fileexchange/93740-bids-matlab?s_tid=srchtitle_bids-matlab_1

Pybids

<https://github.com/bids-standard/pybids>

BIDS-Apps (pipelines for dataanalysis on data in BIDS-format)

<https://journals.plos.org/ploscompbiol/article?id=10.1371/journal.pcbi.1005209>

openNeuro (one of several places to share BIDS-conform datasets)

<https://openneuro.org/>

Publications on other than MRI DATA in BIDS:

MEG-Data in BIDS <https://www.nature.com/articles/sdata2018110>

EEG-Data in BIDS <https://www.nature.com/articles/s41597-019-0104-8>

iEEG-Data in BIDS <https://www.nature.com/articles/s41597-019-0105-7>



HowTo using **dicm2nii** (this happens to be the first one I came across)

This is a dicom to nifti converter which on-top offers to convert according to BIDS rules

It is written by Xiangrui Li, one of the coauthors from the 2016 publication on BIDS and It refers to a publication on issues with conversion from dicom to nifty (for citation if you use dicm2nii):

Xiangrui Li et al., (2016) The first step for neuroimaging data analysis: DICOM to NIfTI conversion *J.Neurosci.Methods*
<https://www.sciencedirect.com/science/article/abs/pii/S0165027016300073>

NOTE: This is not from the <https://www.fil.ion.ucl.ac.uk/spm/ext/> where you can find **dicom2nii** (a SPM utility)

You can download it from <https://github.com/xiangruili/dicm2nii.git>

It is linked from the BIDS website (this is where I found it)

It is also linked from mathworks.com: https://de.mathworks.com/matlabcentral/fileexchange/42997-xiangruili-dicm2nii?s_tid=srchtitle_xiangruili%252Fdicm2nii_1

dicm2nii

- is well commented (starts with 150 lines of comments)
- takes 3 input arguments:
 - **src** source file (directory or file-names, wild-cards can be used)
 - **niiFolder** folder where to save the converted files
 - **fmt** output file format -> multiple options are listed. To obtain BIDS structure (incl. json and .tsv-files)
 - ,bids' (output-files are 4D and gzipped)
 - 'BIDSNII' (output-files are 4D and not gzipped. This specific option is not listed)

If no (first or second) argin is given, a GUI will pop up (*I have not tried this*): then several preferences can be set from the GUI.

'A Matlab data file, **dcmHeaders.mat**, is always saved into the data folder. This file contains some dicom header information from the first file for created series ...'

➤ **Caution with sensitive patient information!**

My personal issues with dicm2nii

Input argument **src** = source file (directory or file-names, wild-cards can be used)

I get the path to my dicoms using **the dicq command**

```
27 %%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
28 % subfunction: call dicq with the current exam
29 function out = dicom_query_main_folder(exam,scanner)
30 out = struct([]);
31 for cexam = 1:size(exam,2)
32     if strcmp(scanner, 'TRIO')
33         [status t] = unix(sprintf('/common/apps/bin/dicq -5 -f --noseries --force TRIO_%05.0f',exam
34     elseif strcmp(scanner, 'PRISMA')
35         [status t] = unix(sprintf('/common/apps/bin/dicq -5 -f --noseries --force PRISMA_%05.0f',ex
36     end
37     if status ~= 0 % check whether call was successful
38         error('error while calling UNIX(/common/apps/bin/dicq)');
39     end
40     patternDir = '/common/mrt\d*/prisma[\w\.\.\+]*';
41     pathExam = regexp(t,patternDir,'match');
42     out(cecam).t = t;
43     out(cecam).pathExam = pathExam;
44 end
45
```

Xiangrui Li's dicm2nii.m 20210724 (feedback to xiangrui.li@gmail.com)

Validating 3435 files ... Starting parallel pool (parpool) using the 'local' profile ...

Connected to the parallel pool (number of workers: 12).

(3418 valid)

Inconsistent 'ImageOrientationPatient' for Subject V17290, localizer (pdev, bromberg) (Series 1). Series skipped.

Inconsistent 'ImageOrientationPatient' for Subject V17290, AAHead_Scout_64ch-head-coil_MPR_sag (Series 3). Series skipped.

Inconsistent 'ImageOrientationPatient' for Subject V17290, AAHead_Scout_64ch-head-coil_MPR_cor (Series 4). Series skipped.

Inconsistent 'ImageOrientationPatient' for Subject V17290, AAHead_Scout_64ch-head-coil_MPR_tra (Series 5). Series skipped.

Converting 13 series (SIEMENS) into 4-D .nii: subject 'V17290'

70-11-2021 has been skipped

,ProtocolName' from dicom-header

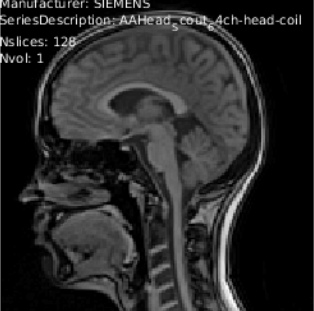
dicm2nii - BIDS Converter -1-

help

Subject	Session	AcquisitionDate	Comment
sub03		2022-01-13	N/A

Name	Type	Modality
AAHead_Scout_64ch_head_coil	skip	skip
ninNoise_v14_thermode	skip	skip
ninNoise_v14_thermode	skip	skip
ninFLASH_v14A_df_mprage_defa_SAT	skip	skip
ninFLASH_v14A_df_mprage_defa_SAT_DEFA	anat	T1w
ep2d_bold_1_5mm3_mb3_run_1	func	task-ep2dbold15mm3mb3_run-01_bold
ep2d_bold_1_5mm3_mb3_run_2	func	task-ep2dbold15mm3mb3_run-02_bold
ep2d_bold_1_5mm3_mb3_run_3	func	task-ep2dbold15mm3mb3_run-03_bold
ep2d_diff_1_5mm3_mb3_PE_std	dwi	dwi
ep2d_diff_1_5mm3_mb3_PE_inv	dwi	dwi
gre_field_map_3mm_filter_M_e1	fmap	magnitude1
gre_field_map_3mm_filter_M_e2	fmap	magnitude2
gre_field_map_3mm_filter_M_phase	fmap	fieldmap

EchoTime: 1.37
RepetitionTime: 3.15
FlipAngle: 8
MRAcquisitionType: 3D
Manufacturer: SIEMENS
SeriesDescription: AAHead_scout_64ch-head-coil
Nslices: 128
Nvol: 1



OK

Names to be used for converted files are taken from dicom-headers

Naming issues:

- Change PatientName ,V12345'

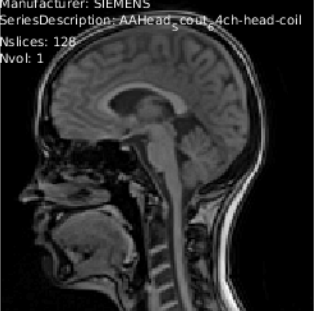
dicm2nii - BIDS Converter -1-

help

Subject	Session	AcquisitionDate	Comment
sub03		2022-01-13	N/A

Name	Type	Modality
AAHead_Scout_64ch_head_coil	skip	skip
ninNoise_v14_thermode	skip	skip
ninNoise_v14_thermode	skip	skip
ninFLASH_v14A_df_mprage_defa_SAT	skip	skip
ninFLASH_v14A_df_mprage_defa_SAT_DEFA	anat	T1w
ep2d_bold_1_5mm3_mb3_run_1	func	task-ep2dbold15mm3mb3_run-01_bold
ep2d_bold_1_5mm3_mb3_run_2	func	task-ep2dbold15mm3mb3_run-02_bold
ep2d_bold_1_5mm3_mb3_run_3	func	task-ep2dbold15mm3mb3_run-03_bold
ep2d_diff_1_5mm3_mb3_PE_std	dwi	dwi
ep2d_diff_1_5mm3_mb3_PE_inv	dwi	dwi
gre_field_map_3mm_filter_M_e1	fmap	magnitude1
gre_field_map_3mm_filter_M_e2	fmap	magnitude2
gre_field_map_3mm_filter_M_phase	fmap	fieldmap

EchoTime: 1.37
RepetitionTime: 3.15
FlipAngle: 8
MRAcquisitionType: 3D
Manufacturer: SIEMENS
SeriesDescription: AAHead_scout_64ch-head-coil
Nslces: 128
Nvol: 1



OK

My personal issues with dicm2nii

It takes the value from the dicom header field ,PatientName' as the subject name:

sub-V12345_task-epiMyTask_run-01_bold.nii

My solution: added inarg ,subName' and one line of code:

```
if exist(subName,'var'), subjs{i} = subName; else, subjs{i} = PatientName(s); end
```

sub-01_task-epiMyTask_run-01_bold.nii

Names to be used for converted files are taken from dicom-headers

Naming issues:

- Change PatientName ,V12345'
- If measurements have identical names on the scanner-console (ProtocolName) it will convert only one (epi-runs)

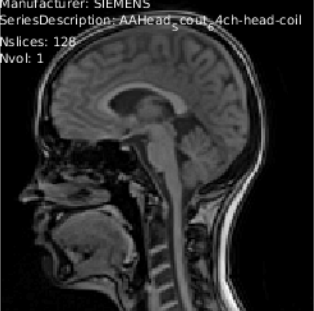
dicm2nii - BIDS Converter -1-

help

Subject	Session	AcquisitionDate	Comment
sub03		2022-01-13	N/A

Name	Type	Modality
AAHead_Scout_64ch_head_coil	skip	skip
ninNoise_v14_thermode	skip	skip
ninNoise_v14_thermode	skip	skip
ninFLASH_v14A_df_mprage_defa_SAT	skip	skip
ninFLASH_v14A_df_mprage_defa_SAT_DEFA	anat	T1w
ep2d_bold_1_5mm3_mb3_run_1	func	task-ep2dbold15mm3mb3_run-01_bold
ep2d_bold_1_5mm3_mb3_run_2	func	task-ep2dbold15mm3mb3_run-02_bold
ep2d_bold_1_5mm3_mb3_run_3	func	task-ep2dbold15mm3mb3_run-03_bold
ep2d_diff_1_5mm3_mb3_PE_std	dwi	dwi
ep2d_diff_1_5mm3_mb3_PE_inv	dwi	dwi
gre_field_map_3mm_filter_M_e1	fmap	magnitude1
gre_field_map_3mm_filter_M_e2	fmap	magnitude2
gre_field_map_3mm_filter_M_phase	fmap	fieldmap

EchoTime: 1.37
RepetitionTime: 3.15
FlipAngle: 8
MRAcquisitionType: 3D
Manufacturer: SIEMENS
SeriesDescription: AAHead_Scout_64ch-head-coil
Nslces: 128
Nvol: 1



OK

Names to be used for converted files are taken from dicom-headers

Naming issues:

- Change PatientName ,V12345'
- If measurements have identical names on the scanner-console (ProtocolName) it will convert only one (epi-runs)
- Modality might not differentiate between measurements and it will convert only one (in my case: of two)

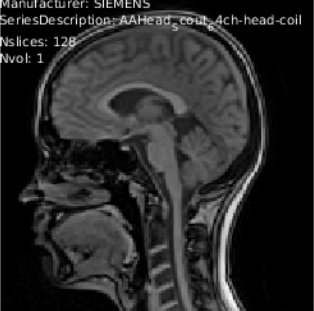
dicm2nii - BIDS Converter -1-

help

Subject	Session	AcquisitionDate	Comment
sub03		2022-01-13	N/A

Name	Type	Modality
AAHead_Scout_64ch_head_coil	skip	skip
ninNoise_v14_thermode	skip	skip
ninNoise_v14_thermode	skip	skip
ninFLASH_v14A_df_mprage_defa_SAT	skip	skip
ninFLASH_v14A_df_mprage_defa_SAT_DEFA	anat	T1w
ep2d_bold_1_5mm3_mb3_run_1	func	task-ep2dbold15mm3mb3_run-01_bold
ep2d_bold_1_5mm3_mb3_run_2	func	task-ep2dbold15mm3mb3_run-02_bold
ep2d_bold_1_5mm3_mb3_run_3	func	task-ep2dbold15mm3mb3_run-03_bold
ep2d_diff_1_5mm3_mb3_PE_std	dwi	dwi
ep2d_diff_1_5mm3_mb3_PE_inv	dwi	dwi
gre_field_map_3mm_filter_M_e1	fmap	magnitude1
gre_field_map_3mm_filter_M_e2	fmap	magnitude2
gre_field_map_3mm_filter_M_phase	fmap	fieldmap

EchoTime: 1.37
RepetitionTime: 3.15
FlipAngle: 8
MRAcquisitionType: 3D
Manufacturer: SIEMENS
SeriesDescription: AAHead_scout_64ch-head-coil
Nslices: 128
Nvol: 1



OK

My personal issues with dicm2nii

It uses the matlab-function

`setpref(group,pref,value)`

sets the specified preference in the specified group to the specified value. If the preference or group does not exist, MATLAB creates it. **Preferences are persistent and maintain their values** between MATLAB sessions. Whatever values were defined for ,group' and ,pref' stay until `setpref()` is set again.

One solution:

- I create a .mat file containing all names needed and load it into workspace before the `setpref`-command
- Then those specific names pop up in the GUI and are being used for the conversion
- You need not set anything in the GUI – just use the GUI to check that Type and Modalty is correct

```
8
9
10 M.Type(1)='skip';
11 M.Modality(1)='skip';
12 M.Type(2)='skip';
13 M.Modality(2)='skip';
14 M.Type(3)='skip';
15 M.Modality(3)='skip';
16 M.Type(4)='skip';
17 M.Modality(4)='skip';
18 M.Type(5)='anat';
19 M.Modality(5)='T1w';
20 M.Type(6)='func';
21 M.Modality(6)='task-pdev_bold';
22 M.Type(7)='func';
23 M.Modality(7)='task-pdev_bold';
24 M.Type(8)='func';
25 M.Modality(8)='task-pdev_bold';
26 M.Type(9)='dwi';
27 M.Modality(9)='dwi_std';
28 M.Type(10)='dwi';
29 M.Modality(10)='dwi_inv';
30 M.Type(11)='fmap';
31 M.Modality(11)='magnitude1';
32 M.Type(12)='fmap';
33 M.Modality(12)='magnitude2';
34 M.Type(13)='fmap';
35 M.Modality(13)='fieldmap';
36 MType = categorical(M.Type);
37 MModality = categorical(M.Modality);
38
39 save('/vicepa/imagen2/bromberg/cases/pdev/TypeModalityNames.mat','MType','MModality')
```

My personal issues with dicm2nii

It uses the matlab-function

`setpref(group,pref,value)`

sets the specified preference in the specified group to the specified value. If the preference MATLAB creates it. **Preferences are persistent and maintain their values** between MATLAB were defined for ,group' and ,pref' stay until `setpref()` is set again.

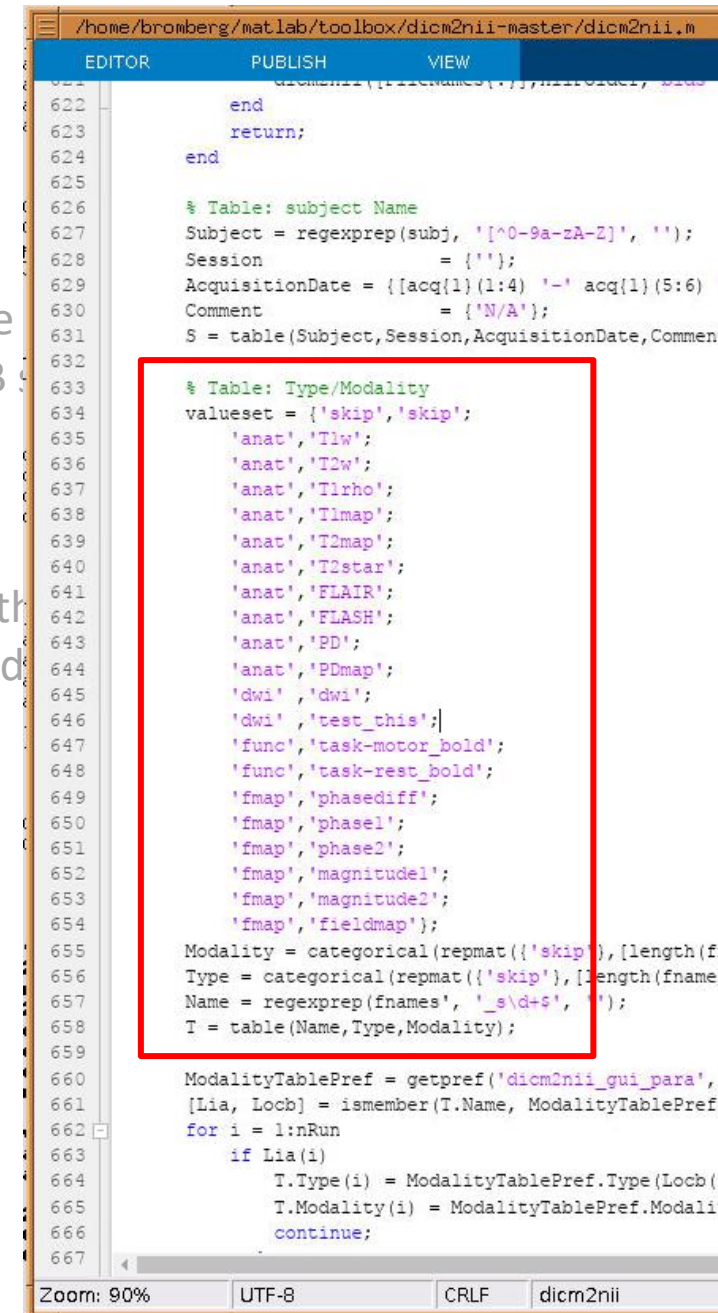
One solution:

- I create a .mat file containing all names needed and load it into workspace before the
- You need not set anything in the GUI – just use the GUI to check that Type and Mod

It also creates a `value_set = {...}` which contains the choice-options for the GUI

Another solution:

- Insert needed name in `value_list` and choose from the GUI when it pops up



```
622     end
623     return;
624 end
625
626 % Table: subject Name
627 Subject = regexprep(subj, '^[^0-9a-zA-Z]', '');
628 Session = {' '};
629 AcquisitionDate = {[acq{1}(1:4) '-' acq{1}(5:6)}];
630 Comment = {'N/A'};
631 S = table(Subject, Session, AcquisitionDate, Comment);
632
633 % Table: Type/Modality
634 valueset = {'skip', 'skip';
635     'anat', 'T1w';
636     'anat', 'T2w';
637     'anat', 'T1rho';
638     'anat', 'T1map';
639     'anat', 'T2map';
640     'anat', 'T2star';
641     'anat', 'FLAIR';
642     'anat', 'FLASH';
643     'anat', 'PD';
644     'anat', 'PDmap';
645     'dwi', 'dwi';
646     'dwi', 'test_this';
647     'func', 'task-motor_bold';
648     'func', 'task-rest_bold';
649     'fmap', 'phasediff';
650     'fmap', 'phase1';
651     'fmap', 'phase2';
652     'fmap', 'magnitude1';
653     'fmap', 'magnitude2';
654     'fmap', 'fieldmap'};
655 Modality = categorical(repmat({'skip'}, [length(fnames), 1]));
656 Type = categorical(repmat({'skip'}, [length(fnames), 1]));
657 Name = regexprep(fnames, '_s\d+$', '');
658 T = table(Name, Type, Modality);
659
660 ModalityTablePref = getpref('dicm2nii_gui_para', 'dicm2nii');
661 [Lia, Locb] = ismember(T.Name, ModalityTablePref);
662 for i = 1:nRun
663     if Lia(i)
664         T.Type(i) = ModalityTablePref.Type(Locb(i));
665         T.Modality(i) = ModalityTablePref.Modality(Locb(i));
666         continue;
667     end
```


dicm2nii - BIDS Converter -1-

help

Subject	Session	AcquisitionDate	Comment
V17290		2022-01-13	N/A

Name	Type	Modality
AAHead_Scout_64ch_head_coil	skip	skip
ninNoise_v14_thermode	skip	skip
ninNoise_v14_thermode	skip	skip
ninFLASH_v14A_df_mprage_defa_SAT	skip	skip
ninFLASH_v14A_df_mprage_defa_SAT_DE...	anat	T1w
ep2d_bold_1_5mm3_mb3_run_1	func	task-pdev_bold
ep2d_bold_1_5mm3_mb3_run_2	func	task-pdev_bold
ep2d_bold_1_5mm3_mb3_run_3	func	task-pdev_bold
ep2d_diff_1_5mm3_mb3_PE_std	dwi	dwi_std
ep2d_diff_1_5mm3_mb3_PE_inv	dwi	dwi_inv
gre_field_map_3mm_filter_M_e1	fmap	PD
gre_field_map_3mm_filter_M_e2	fmap	PDmap
gre_field_map_3mm_filter_M_phase	fmap	dwi
		test_this
		task-motor_bold
		task-rest_bold
		phasediff
		phase1
		phase2
		magnitude1
		magnitude2
		fieldmap
		task-pdev_bold
		dwi_std

EchoTime: 65
RepetitionTime: 3000
FlipAngle: 90
MRAcquisitionType: 2D
Manufacturer: SIEMENS
SeriesDescription: ep2d_diff_1.5mm3_mb3_PE_inv
Nsllices: 66
Nvol: 1



OK

,test_this'

/home/bromberg/matlab/toolbox/dicm2nii-master/dicm2nii.m -1-

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```
621     dicm2nii([fnames{:}];ninfo{1}, 'bids',
622         end
623         return;
624     end
625
626     % Table: subject Name
627     Subject = regexp(subj, '^[^0-9a-zA-Z]', '');
628     Session = {' '};
629     AcquisitionDate = {[acq{1}(1:4) '-' acq{1}(5:6) '-' acq
630     Comment = {'N/A'};
631     S = table(Subject,Session,AcquisitionDate,Comment);
632
633     % Table: Type/Modality
634     valueset = {'skip','skip';
635         'anat','T1w';
636         'anat','T2w';
637         'anat','T1rho';
638         'anat','T1map';
639         'anat','T2map';
640         'anat','T2star';
641         'anat','FLAIR';
642         'anat','FLASH';
643         'anat','PD';
644         'anat','PDmap';
645         'anat','dwi';
646         'dwi','test_this';
647         'func','task-rest_bold';
648         'func','task-rest_bold';
649         'fmap','phasediff';
650         'fmap','phase1';
651         'fmap','phase2';
652         'fmap','magnitude1';
653         'fmap','magnitude2';
654         'fmap','fieldmap'};
655     Modality = categorical(repmat({'skip'},[length(fnames),
656     Type = categorical(repmat({'skip'},[length(fnames),1]),
657     Name = regexp(fnames, '_s\d+s', '');
658     T = table(Name,Type,Modality);
659
660     ModalityTablePref = getpref('dicm2nii_gui_para', 'Modal
661     [Lia, Locb] = ismember(T.Name, ModalityTablePref.Name);
662     for i = 1:nRun
663         if Lia(i)
664             T.Type(i) = ModalityTablePref.Type(Locb(i));
665             T.Modality(i) = ModalityTablePref.Modality(Locb
666             continue;
667
```

Zoom: 90% UTF-8 CRLF dicm2nii

bromberg@aither:/vicepa/imagen2/bromberg/cases/pdev -3-

```
bromberg@aither:/vicepa/imagen2/bromberg/cases/pdev $ tree pdev_raw
pdev_raw
├── sub-01
│   ├── anat
│   ├── beh
│   │   ├── run-01
│   │   ├── run-02
│   │   └── run-03
│   ├── dwi
│   ├── fmap
│   └── func
└── sub-02
    ├── anat
    ├── beh
    │   ├── run-01
    │   ├── run-02
    │   └── run-03
```

18 directories

```
bromberg@aither:/vicepa/imagen2/bromberg/cases/pdev $ ls -l pdev_raw/sub-01/func/
total 7254480
```

```
-rw-r--r-- 1 bromberg imagen2      1460 2022-01-09 17:56 sub-01_task-pdev_run-01_bold.json
-rw-r--r-- 1 bromberg imagen2 2476189920 2022-01-09 17:56 sub-01_task-pdev_run-01_bold.nii
-rw-r--r-- 1 bromberg imagen2      1466 2022-01-09 17:56 sub-01_task-pdev_run-02_bold.json
-rw-r--r-- 1 bromberg imagen2 2476189920 2022-01-09 17:56 sub-01_task-pdev_run-02_bold.nii
-rw-r--r-- 1 bromberg imagen2      1472 2022-01-09 17:57 sub-01_task-pdev_run-03_bold.json
-rw-r--r-- 1 bromberg imagen2 2476189920 2022-01-09 17:57 sub-01_task-pdev_run-03_bold.nii
bromberg@aither:/vicepa/imagen2/bromberg/cases/pdev $
```

JSON-file generated by dicm2nii

```
{
  → "ConversionSoftware": "dicm2nii.m-20210724",
  → "SeriesNumber": 10,
  → "SeriesDescription": "ep2d_bold, 1.5mm3, mb3, run 1",
  → "ImageType": ["ORIGINAL", "PRIMARY", "M", "ND", "NORM", "MOSAIC"],
  → "Modality": "MR",
  → "AcquisitionDateTime": "20220104124515.387500",
  → "TaskName": "ep2dbold15mm3mb3",
  → "TotalReadoutTime": 0.048510049,
  → "SliceTiming": [
    → 1.4875,
    → 1.4175,
    → 1.345,
    → 1.275,
    → 1.205,
    → 1.1325,
    → 1.0625,
    → 0.9925,
    .....
    → 0.14,
    → 0.07,
    → 0],
  → "RepetitionTime": 1.58,
  → "PhaseEncodingDirection": "j-",
  → "EffectiveEchoSpacing": 0.00033000033,
  → "EchoTime": 0.026,
  → "SliceThickness": 1.5,
  → "FlipAngle": 60,
  → "Manufacturer": "SIEMENS",
  → "SoftwareVersion": "syngo MR E11",
  → "MRAcquisitionType": "2D",
  → "InstitutionName": "Systems Neuroscience / UKE",
  → "InstitutionAddress": "Martinistrasse 52, Hamburg, Nord, DE, 20246",
  → "DeviceSerialNumber": "167015",
  → "ScanningSequence": "EP",
  → "SequenceVariant": "SK",
  → "ScanOptions": "PFP\\FS",
  → "SequenceName": "*epfid2d1_148"
}
```

Scripts contained in the folder **dicm2nii_master** (used in dicm2nii):

- # dicm2nii: Convert DICOM into NIfTI. It can also convert PAR/XML/REC, HEAD/BRIK, MGZ and BrainVoyager files into NIfTI.
- # nii_tool: Create, load, save NIfTI file. Support both version 1 and 2 NIfTI, and variety of data type.
- # nii_viewer: Visualize NIfTI. Can also visualize any file convertible to NIfTI by dicm2nii.
- # nii_moco: Perform motion correction on a NIfTI.
- # nii_stc: Perform slice timing correction on a NIfTI.
- # nii_xform: Transform a NIfTI into different resolution, or into a template space.
- # RT_moco: Real time motion/image monitor and more for Siemens scanner.

- # dicm_hdr, dicm_img, dicm_dict, dicm_save: Read/write DICOM header and image, independent of Matlab Image Processing Toolbox.
- # rename_dicm, sort_dicm, anonymize_dicm: DICOM tools performing the tasks as indicated by the name.

Thank you for your attention!

The comments in dicm2nii

‘**Slice timing information**, if available, is stored in nii header, such as slice_code and slice_duration. But the simple way may be to **use the field SliceTiming in dcmHeaders.mat**. That timing is actually those numbers for FSL when using custom slice timing. This is the universal method to specify any kind of slice order, and for now, is the only way which works for **multiband**. Slice order is one of the most confusing parameters, and it is recommended to use this method to avoid mistake. Following shows how to convert this timing into slice timing in ms and slice order for SPM:

```
% load('dcmHeaders.mat'); % or drag and drop the MAT file into Command Window
% s = h.myFuncSeries; % field name is the same as nii file name
% spm_ms = (0.5 - s.SliceTiming) * s.RepetitionTime;
% [~, spm_order] = sort(-s.SliceTiming);'
```

I found that **spm_ms** is equal to the information given in the field name: ‘**MosaicRefAcqTimes**’ in **dcmHeaders.mat**

The comments in dicm2nii

‘Some information, such as TE, phase encoding direction and effective dwell time, are stored in fieldname **Description** of nii header. These are useful for fieldmap B0 unwarp correction. Acquisition start time and date are also stored, and this may be useful if one wants to align the functional data to some physiological recording, like pulse, respiration or ECG.’

‘If there is **DTI series**, bval and bvec files will be generated for FSL etc. bval and bvec are also saved in the dcmHeaders.mat file.’

Starting from 20150514, the converter stores some useful information in NIfTI text extension (ecode=6). nii_tool can decode these information easily: `ext = nii_tool('ext', 'myNiftiFile.nii');` % read NIfTI extension `ext.edata_decoded` contains all above mentioned information, and more. The included nii_viewer can show the extension by Window->Show NIfTI ext.

Several preference can be set from dicm2nii GUI. The preference change stays in effect until it is changed next time.

One of preference is to save a .json file for each converted NIfTI. For more information about the purpose of json file, check <http://bids.neuroimaging.io/>

The comments in dicm2nii

By default, the converter will use parallel pool for dicom header reading if there are 2000+ files. User can turn this off from GUI.

By default, the PatientName is stored in NIfTI hdr and ext. This can be turned off from GUI.

Please note that some information, such as the slice order information, phase encoding direction and DTI bvec are in image reference, rather than NIfTI coordinate system. This is because most analysis packages require information in image space. For this reason, in case the image in a NIfTI file is flipped or re-oriented, these information may not be correct anymore.