

# Brain Image Data Structure (BIDS): what, why, and how?

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# Stuff

## What is BIDS?

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- BIDS is a system for naming and organizing ‘raw’ neuroimaging files
- BIDS is not a new file format



# What is BIDS?

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- BIDS is a system for naming and organizing ‘raw’ neuroimaging files
- BIDS is not a new file format

Animals



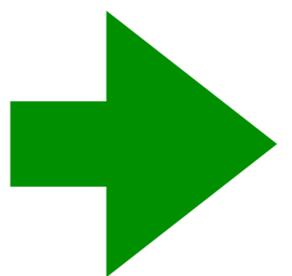
Household  
Items



Fruits  
and  
Vegetables



# In practice for MRI data



Name

- ▼ pilot
  - 📄 0002\_MPRAGE\_SAG\_iPAT2\_20190507101206\_2.json
  - .nii 0002\_MPRAGE\_SAG\_iPAT2\_20190507101206\_2.nii
  - 📄 0003\_ep\_bold\_mb3\_p2\_feedback\_20190507101206\_3.json
  - .nii 0003\_ep\_bold\_mb3\_p2\_feedback\_20190507101206\_3.nii
  - 📄 0004\_ep\_bold\_mb3\_p2\_feedback\_20190507101206\_4.json
  - .nii 0004\_ep\_bold\_mb3\_p2\_feedback\_20190507101206\_4.nii
  - 📄 0006\_ep\_bold\_mb3\_p2\_resting\_20190507101206\_6.json
  - .nii 0006\_ep\_bold\_mb3\_p2\_resting\_20190507101206\_6.nii
  - 📄 0007\_ep\_bold\_mb3\_p2\_resting\_20190507101206\_7.json
  - .nii 0007\_ep\_bold\_mb3\_p2\_resting\_20190507101206\_7.nii
  - 📄 0009\_ep2d\_diff\_mb2\_p2\_64dirs\_20190507101206\_9.bval
  - 📄 0009\_ep2d\_diff\_mb2\_p2\_64dirs\_20190507101206\_9.bvec
  - 📄 0009\_ep2d\_diff\_mb2\_p2\_64dirs\_20190507101206\_9.json
  - .nii 0009\_ep2d\_diff\_mb2\_p2\_64dirs\_20190507101206\_9.nii

Name

- 📄 CHANGES
- ▶ code
- 📄 dataset\_description.json
- 📄 participants.tsv
- 📄 README
- ▶ sourcedata
- ▼ sub-pilot
  - ▼ anat
    - 📄 sub-pilot\_acq-MPRAGE\_run-01\_T1w.json
    - 📄 sub-pilot\_acq-MPRAGE\_run-01\_T1w.nii.gz
  - ▼ dwi
    - 📄 sub-pilot\_run-01\_dwi.bval
    - 📄 sub-pilot\_run-01\_dwi.bvec
    - 📄 sub-pilot\_run-01\_dwi.json
    - 📄 sub-pilot\_run-01\_dwi.nii.gz
  - ▼ func
    - 📄 sub-pilot\_task-feedback\_run-01\_bold.json
    - 📄 sub-pilot\_task-feedback\_run-01\_bold.nii.gz
    - 📄 sub-pilot\_task-feedback\_run-01\_events.tsv
    - 📄 sub-pilot\_task-feedback\_run-01\_sbref.json
    - 📄 sub-pilot\_task-feedback\_run-01\_sbref.nii.gz
    - 📄 sub-pilot\_task-rest\_run-01\_bold.json
    - 📄 sub-pilot\_task-rest\_run-01\_bold.nii.gz
    - 📄 sub-pilot\_task-rest\_run-01\_events.tsv
    - 📄 sub-pilot\_task-rest\_run-01\_sbref.json
    - 📄 sub-pilot\_task-rest\_run-01\_sbref.nii.gz
  - 📄 sub-pilot\_scans.tsv
  - 📄 task-feedback\_bold.json
  - 📄 task-rest\_bold.json

# EEG-BIDS

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- Recommended to use European data format (.edf) or BrainVision data formats (.vhdr, .vmrk, .eeg)

```
/  
  README  
  CHANGES  
  dataset_description.json  
  participants.tsv  
  participants.json  
  task-TASKNAME_events.json  
  stimuli  
    stim1.png  
    :  
  sourcedata  
    sub-01  
      eeg  
        sub-01_task-TASKNAME_eeg.xdf  
      :  
    sub-01  
      anat  
        sub-01_T1w.nii.gz  
        sub-01_T1w.json  
      eeg  
        sub-01_task-TASKNAME_eeg.edf  
        sub-01_task-TASKNAME_eeg.json  
        sub-01_task-TASKNAME_events.tsv  
        sub-01_task-TASKNAME_channels.tsv  
        sub-01_task-TASKNAME_electrodes.tsv  
        sub-01_task-TASKNAME_coordsystem.json  
    :  
:
```

# MEG-BIDS

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- Unprocessed MEG data MUST be stored in the native file format of the MEG instrument used to collect the data



The contents of a BIDS directory

# General format for BIDS filenames

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- MRI anatomy  
sub-<label>\_sess-<label>\_acq-<label>\_run-<index>\_T1w.nii.gz
- fMRI  
sub-<label>\_sess-<label>\_task-<label>\_run-<index>\_bold.nii.gz
- EEG  
sub-<label>\_sess-<label>\_task-<label>\_run-<index>\_eeg.edf
- MEG  
sub-<label>\_sess-<label>\_task-<label>\_run-<index>\_meg.ds

# Why should I adopt the BIDS standard?

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- BIDS directory contains all necessary information about a study and its data in one place
- Make use of a growing number of BIDS apps, such as fmriprep, HCP pipelines, C-PAC, etc.
- Required format for many data repositories
- Warm, fuzzy feeling from actively supporting the open neuroscience/reproducibility movement

# How do I get my data into BIDS format?

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- Growing number of tools available to convert MRI, EEG, and MEG data into BIDS format
  - [AFNI BIDS-tools](#)
  - [BIDS2ISATab](#)
  - [BIDSto3col](#)
  - [BIDS2NDA](#)
  - [bidskit](#)
  - [Data2Bids](#)
  - [Dcm2Bids](#)
  - [DCM2NIIx](#)
  - [DICM2NII](#)
  - [HeuDiConv](#)
  - [OpenfMRI2BIDS](#)
  - [ReproIN \(HeuDiConv-based turnkey solution\)](#)
  - [bids2xar \(for XNAT import\)](#)
  - [XNAT2BIDS](#)
  - [Horos \(Osirix\) export plugin](#)
  - [BIDS2NIDM](#)
  - [BIDScoin](#)
  - [MNE-BIDS \(MEG/EEG/iEEG\)](#)
  - [EEGLAB with plugin \(MEG/EEG analysis package\)](#)
- Most popular for MRI/fMRI is HeuDiConv
- MNE-BIDS is a free option for converting both EEG and MEG data

HeuDiConv

# General strategy

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- ‘Look-up table’ matching DICOM sequences to BIDS filenames
- ‘Look-up table’ is user-specified
- Only DICOM sequence-BIDS filename pairs in the ‘look-up table’ will be converted

dicominfo

example_dcm_file	series_id	dcm_dir_name	unspecified2	unspecified3	dim1	dim2	dim3	dim4	TR	TE	protocol_name
example_dcm_file	series_id	dcm_dir_name	unspecified2	unspecified3	dim1	dim2	dim3	dim4	TR	TE	protocol_name
2019_05_07_PILOT.MR.BODELL^PEERSTUDY.00	1-localizer	1	-	-	384	384	15	1	0.0086	4.0	localizer
2019_05_07_PILOT.MR.BODELL^PEERSTUDY.00	2-MPRAGE SAG iPAT2	2	-	-	256	256	192	1	2.3	2.98	MPRAGE SAG iPAT2
2019_05_07_PILOT.MR.BODELL^PEERSTUDY.00	3-ep_bold_mb3_p2_feedback	3	-	-	84	84	48	1	1.0	30.0	ep_bold_mb3_p2_feedback
2019_05_07_PILOT.MR.BODELL^PEERSTUDY.00	4-ep_bold_mb3_p2_feedback	4	-	-	84	84	48	766	1.0	30.0	ep_bold_mb3_p2_feedback
2019_05_07_PILOT.MR.BODELL^PEERSTUDY.00	6-ep_bold_mb3_p2_resting	6	-	-	84	84	48	1	1.0	30.0	ep_bold_mb3_p2_resting
2019_05_07_PILOT.MR.BODELL^PEERSTUDY.00	7-ep_bold_mb3_p2_resting	7	-	-	84	84	48	360	1.0	30.0	ep_bold_mb3_p2_resting
2019_05_07_PILOT.MR.BODELL^PEERSTUDY.00	9-ep2d_diff_mb2_p2_64dirs	9	-	-	98	98	78	68	3.5	55.0	ep2d_diff_mb2_p2_64dirs
2019_05_07_PILOT.MR.BODELL^PEERSTUDY.00	10-ep2d_diff_mb2_p2_64dirs	10	-	-	98	98	156	1	3.5	55.0	ep2d_diff_mb2_p2_64dirs
2019_05_07_PILOT.MR.BODELL^PEERSTUDY.00	12-ep2d_diff_mb2_p2_64dirs_PA	12	-	-	98	98	78	1	3.5	55.0	ep2d_diff_mb2_p2_64dirs_PA

dicominfo-1

patient_id	study_description	referring_physician_name	series_description	sequence_name	image_type
patient_id	study_description	referring_physician_name	series_description	sequence_name	image_type
2019_05_07_pilot	Bodell^PeerStudy		localizer	*fl2d1	('ORIGINAL', 'PRIMARY', 'M', 'ND', 'NORM')
2019_05_07_pilot	Bodell^PeerStudy		MPRAGE SAG iPAT2	*tf13d1_16ns	('ORIGINAL', 'PRIMARY', 'M', 'ND', 'NORM')
2019_05_07_pilot	Bodell^PeerStudy		ep_bold_mb3_p2_feedback_SBRef	epfid2d1_84	('ORIGINAL', 'PRIMARY', 'M', 'ND', 'NORM', 'MOSAIC')
2019_05_07_pilot	Bodell^PeerStudy		ep_bold_mb3_p2_feedback	epfid2d1_84	('ORIGINAL', 'PRIMARY', 'M', 'MB', 'ND', 'NORM', 'MOSAIC')
2019_05_07_pilot	Bodell^PeerStudy		ep_bold_mb3_p2_resting_SBRef	epfid2d1_84	('ORIGINAL', 'PRIMARY', 'M', 'ND', 'NORM', 'MOSAIC')
2019_05_07_pilot	Bodell^PeerStudy		ep_bold_mb3_p2_resting	epfid2d1_84	('ORIGINAL', 'PRIMARY', 'M', 'MB', 'ND', 'NORM', 'MOSAIC')
2019_05_07_pilot	Bodell^PeerStudy		ep2d_diff_mb2_p2_64dirs	ep_b995#55	('ORIGINAL', 'PRIMARY', 'DIFFUSION', 'NONE', 'MB', 'ND', 'NORM', 'MOSAIC')
2019_05_07_pilot	Bodell^PeerStudy		ep2d_diff_mb2_p2_64dirs_TRACEW	ep_b1000t	('DERIVED', 'PRIMARY', 'DIFFUSION', 'TRACEW', 'MB', 'ND', 'NORM')
2019_05_07_pilot	Bodell^PeerStudy		ep2d_diff_mb2_p2_64dirs_PA	ep_b0	('ORIGINAL', 'PRIMARY', 'DIFFUSION', 'NONE', 'MB', 'ND', 'NORM')

```
import os
import numpy
from cfmm_base import infotodict as cfmminfodict
from cfmm_base import create_key

def infotodict(seqinfo):
    """Heuristic evaluator for determining which runs belong where
    allowed template fields - follow python string module:
    item: index within category
    subject: participant id
    seqitem: run number during scanning
    subindex: sub index within group
    """

    # call cfmm for general labelling and get dictionary
    info = cfmminfodict(seqinfo)

    rest = create_key('{bids_subject_session_dir}/func/{'
                      'bids_subject_session_prefix}_task-rest_run-{item:02d}_bold')
    rest_sbref = create_key('{bids_subject_session_dir}/func/{'
                           'bids_subject_session_prefix}_task-rest_run-{item:02d}_sbref')

    feedback = create_key('{bids_subject_session_dir}/func/{'
                          'bids_subject_session_prefix}_task-feedback_run-{item:02d}_bold')
    feedback_sbref = create_key('{bids_subject_session_dir}/func/{'
                               'bids_subject_session_prefix}_task-feedback_run-{item:02d}_sbref')

    info[rest] = []
    info[rest_sbref] = []
    info[feedback] = []
    info[feedback_sbref] = []

    for idx, s in enumerate(seqinfo):

        if ('resting' in (s.series_description).strip()):
            if (s.dim4==1 and 'SBRef' in (s.series_description).strip()):
                info[rest_sbref].append({'item': s.series_id})
            elif (s.dim4==360):
                info[rest].append({'item': s.series_id})

        elif ('feedback' in (s.series_description).strip()):
            if (s.dim4==1 and 'SBRef' in (s.series_description).strip()):
                info[feedback_sbref].append({'item': s.series_id})
            elif (s.dim4>700):
                info[feedback].append({'item': s.series_id})

    return info
```

Want to learn more on how to script your own heuristics?

What: Khan Lab Tutorial - Data Retrieval and Conversion

When: Friday, September 27, 9:30-noon

Where: Fisher Conference Room, Robarts

Special case: autobids

# What is autobids?

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- autobids is a tool developed by the Khan Lab to automatically download DICOM files from the CFMM server and convert them to nifti format using BIDS standard filenames

# Who can make use of autobids?

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- Any researcher collecting MRI data using either the CFMM 3T or 7T scanner

# How it works

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1. You register your study for autobids conversion
2. I (Suzanne Witt) create the necessary configuration and heuristic files to ensure your scans are correctly converted into BIDS format
3. You receive an email from me with a link to download your data from Compute Canada via an online ‘ftp’ service called Globus

# What you need to do

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1. Register your study using the google form (link can be found on BrainsCAN Neuroimaging Wiki)
2. Create a Globus account ([globus.org](https://globus.org))
3. Add ‘bidsDump’ is an authorized user for your PI’s scans on the CFMM DICOM server, if not already
4. Decide on a single scheme for naming your subjects and scans on the CFMM DICOM server

# Your responsibilities as an autobids user

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1. Adopt a single, consistent naming scheme for subject IDs, session IDs, task names, etc.
2. Use the following pattern for patient IDs in the DICOM server: <date>\_<otherInfo>\_<subjectID>\_<sessionID>

20190923\_Study3T\_s101\_001

3. Include task information in fMRI series descriptions:

ep\_bold\_mb3\_p2\_FingerTapping

4. Let me know about any changes to the protocol

# Where can I get more information on autobids?

- Check out the ‘BIDS & autobids’ page on the BrainsCAN neuroimaging wiki
- [https://brainscan.uwo.ca/research/cores/computational\\_core/index.html](https://brainscan.uwo.ca/research/cores/computational_core/index.html)
- Click on the ‘Neuroimaging Wiki’ link on the left hand side of the page under ‘Computational Core’

Home > Research > Research Cores > Computational Core

## Research

### Research Cores

Computational Core

Colloquium Series

Methods Lunch

Training Series

Neuroimaging Wiki

Human Cognition &

Sensorimotor Core

Imaging Core

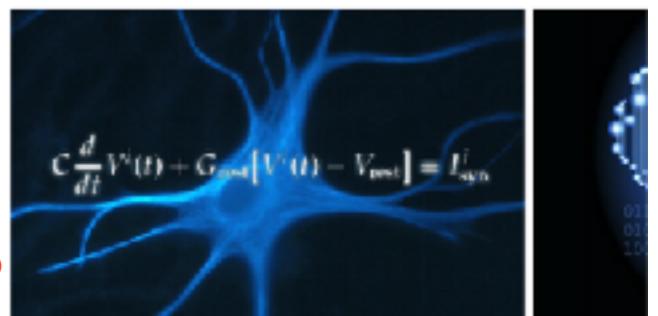
NHP Core

Rodent Cognition Core

Project Summaries

Research Summaries

## Computational Core



The brain is a biological structure that has evolved over millions of years. The Computational Core focuses on cross-disciplinary research to understand how the brain works at all levels, from molecules to behavior. We do so by developing mathematical, quantitative language. This is especially important as measurements are becoming increasingly complex. The Computational Core attracts a diverse set of backgrounds, including Neuroscientists, Engineers, and Mathematicians.

## BIDS & autobids

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### What is BIDS and why should I use it?

BIDS is a simple and intuitive way to organize and describe your neuroimaging and behavioral data.

By using this standard you will benefit in the following ways:

- It will be easy for another researcher to work on your data. By using BIDS you will save time trying to understand an analysis done by a graduate student or postdoc that has already left the lab.
- There is a growing number of data analysis software packages that can understand data organized according to BIDS.
- Databases such as [OpenNeuro.org](http://OpenNeuro.org) and others will accept and export datasets organized according to BIDS. If you enter your data in BIDS, you can easily share it with the scientific community.

# Further information

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- BIDS documentation: <https://bids.neuroimaging.io/>
- Heudiconv tutorial: <http://reproducibility.stanford.edu/bids-tutorial-series-part-2a/>
- Online BIDS validator: <https://bids-standard.github.io/bids-validator/>
- MNE BIDS tool: <https://mne.tools/mne-bids/index.html>
- BrainsCAN Neuroimaging wiki autobids page: [https://osf.io/k89fh/wiki/autobids/?view\\_only=8281493cc75d429285735c98c1267261](https://osf.io/k89fh/wiki/autobids/?view_only=8281493cc75d429285735c98c1267261)
- BIDS-MEG: <https://www.nature.com/articles/sdata2018110>
- BIDS-EEG: <https://www.nature.com/articles/s41597-019-0104-8>
- BIDS: <https://www.nature.com/articles/sdata201644>