bxh2bids: Goals, Structure, and Usage

John Graner 12/13/2019

github.com/jlgraner/bxh2bids

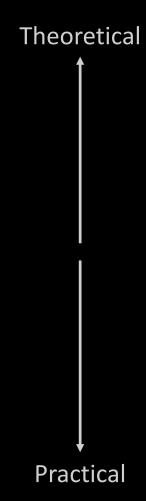
Outline

What is BIDS and why is it useful?

What does bxh2bids do?

How does bxh2bids work?

Short bxh2bids demo

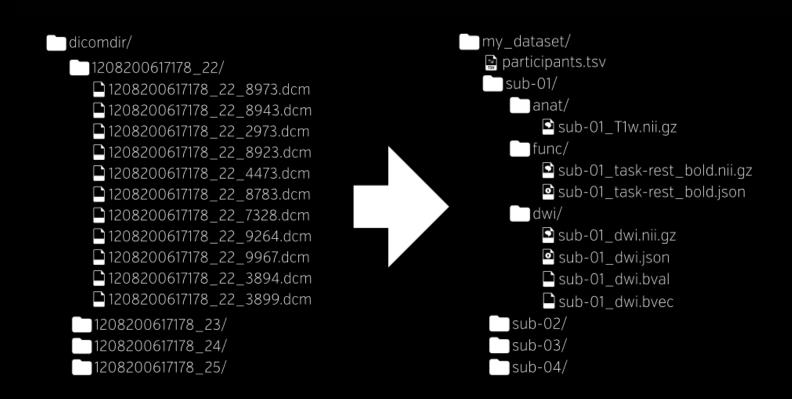


BRAIN IMAGING DATA STRUCTURE

A simple and intuitive way to organize and describe your neuroimaging and behavioral data.



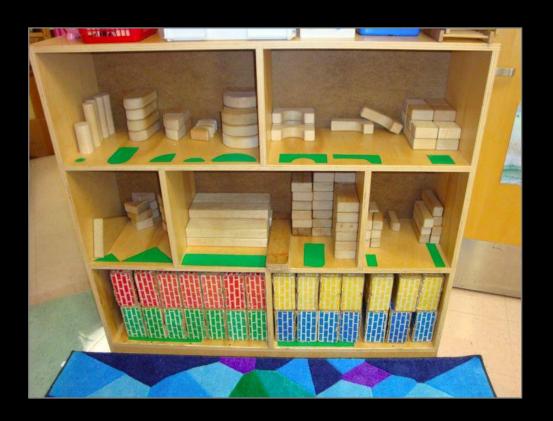
http://bids.neuroimaging.io/



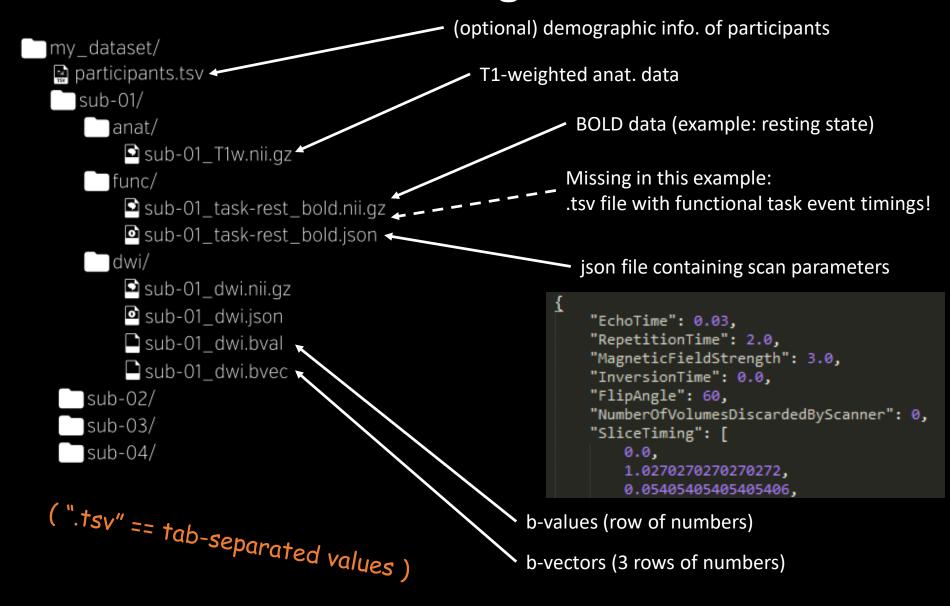
http://bids.neuroimaging.io/

Dissecting BIDS

```
my_dataset/
 participants.tsv
    sub-01/
       lanat/
         sub-01_T1w.nii.gz
       Ifunc/
         sub-01_task-rest_bold.nii.gz
         sub-01_task-rest_bold.json
     □ dwi/
         sub-01_dwi.nii.gz
         sub-01_dwi.json
         sub-01_dwi.bval
         sub-01_dwi.bvec
     |sub-02/
     |sub-03/
     |sub-04/
```



Dissecting BIDS



How does this support open science and reproducibility?

- my_dataset/
 - participants.tsv
 - sub-01/
 - anat/
 - sub-01_T1w.nii.gz
 - func/
 - sub-01_task-rest_bold.nii.gz
 - sub-01_task-rest_bold.json
 - dwi/
 - sub-01_dwi.nii.gz
 - sub-01_dwi.json
 - sub-01_dwi.bval
 - sub-01_dwi.bvec
 - sub-02/
 - sub-03/
 - sub-04/

Transparency - Other people (*including future you*) can easily see what each file contains based on the file names



How does this support open science and reproducibility?

- my_dataset/
 - participants.tsv
 - sub-01/
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 - sub-01_task-rest_bold.nii.gz
 - sub-01_task-rest_bold.json
 - dwi/
 - sub-01_dwi.nii.gz
 - sub-01_dwi.json
 - sub-01_dwi.bval
 - □ sub-01_dwi.bvec
 - sub-02/
 - sub-03/
 - sub-04/

Transparency - Other people (including future you)
can easily see what each file
contains based on the file names

Predictability - Standardization allows easy access with scripts, which facilitates standardization of processing/analysis

(mriqc) (fmriprep)

(BIDS allows you to use both of these very easily.

See links on final slide!)



How does this support open science and reproducibility?

- my_dataset/
 - participants.tsv
 - sub-01/
 - anat/
 - sub-01_T1w.nii.gz
 - func/
 - sub-01_task-rest_bold.nii.gz
 - sub-01_task-rest_bold.json
 - __dwi/
 - sub-01_dwi.nii.gz
 - sub-01_dwi.json
 - sub-01_dwi.bval
 - □ sub-01_dwi.bvec
 - sub-02/
 - sub-03/
 - sub-04/

- **Transparency** Other people (*including future you*) can easily see what each file contains based on the file names
- Predictability Standardization allows easy access with scripts, which facilitates standardization of processing/analysis
- Provenance Including task timing, acquisition parameters, etc. provides the context of the data alongside the data themselves



BIAC MyStudy/ Data/ Anat/ 19540101 00001/ bia6 00001 001.nii.gz bia6 00001 001.bxh 19540102 00002/ bia6 00002 001.nii.gz bia6 00002 001.bxh bia6 00002 100.nii.gz bia6 00002 100.bxh Func/ 19540101 00001/ bia6 00001 003 01.nii.gz bia6 00001 003 01.bxh bia6 00001 003 02.nii.gz bia6 00001 003 02.bxh 19540102 00002/ bia6 00002 003 01.nii.gz bia6 00002 003 01.bxh

bia6_00002_004_01.nii.gz bia6_00002_004_01.bxh

BIDS



Goal

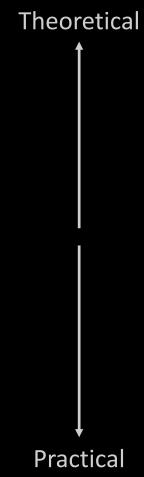
Make it as easy as possible to convert data from BIAC into BIDS

What is BIDS and why is it useful?

What does bxh2bids do?

How does bxh2bids work?

Short bxh2bids demo



Anat/ 19540101 00001/ bia6 00001 001.nii.gz bia6 00001 00(1.bxh) 19540102 00002/ bia6_00002_001.nii.gz bia6 00002 00(1.bxh) bia6 00002 100.nii.gz bia6 00002 100.bxh Func/ 19540101 00001/ bia6 00001 003 01.nii.gz bia6 00001 003 0 .. bxh bia6 00001 004 01.nii.gz bia6 00001 004 01.bxh 19540102 00002/ bia6 00002 003 01.nii.gz bia6 00002 003 01.bxh bia6 00002 004 01.nii.gz bia6 00002 004 01.bxh

bxh2bids

Locate .bxh files

```
my dataset/
  participants.tsv
   sub-01/
      □anat/
         Sub-01_T1w.nii.gz
     func/
         sub-01_task-rest_bold.nii.gz
         sub-01_task-rest_bold.json
     □ dwi/
         sub-01_dwi.nii.gz
         sub-01 dwi.json
         sub-01_dwi.bval
         □ sub-01 dwi.bvec
    ☐sub-02/
     |sub-03
    sub-04/
```

Func/ 19540101 00001/ bia6 00001 003 01.nii.gz bia6 00001 003 01.bxh

bxh2bids

For each .bxh file:

Locate image data

```
my dataset/
  participants.tsv
   sub-01/
      □anat/
         sub-01_T1w.nii.gz
      func/
         sub-01_task-rest_bold.nii.gz
         sub-01_task-rest_bold.json
     □dwi/
         sub-01_dwi.nii.gz
         sub-01 dwi.json
         sub-01_dwi.bval
         □ sub-01 dwi.bvec
    sub-02/
    \_sub-03/
    sub-04/
```

Func/ 19540101 00001/ bia6 00001 003 01.nii.gz bia6 00001 003 01.bxh

bxh2bids

For each .bxh file:

- Locate image data
- Determine BIDS Type

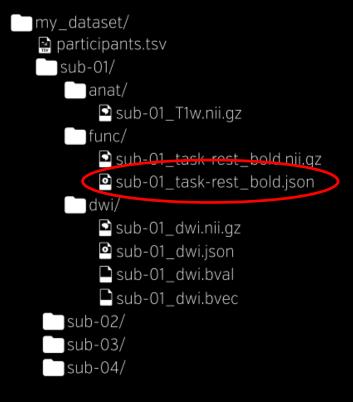
```
my dataset/
  participants.tsv
   sub-01/
      □anat/
         🔁 sub-01_T1w.nii.gz
        lfunc/
         sub-01_task-rest_bold.nii.gz
         sub-01_task-rest_bold.json
      □ dwi/
         sub-01_dwi.nii.gz
         sub-01 dwi.json
         sub-01_dwi.bval
         sub-01_dwi.bvec
    sub-02/
    \_sub-03/
    sub-04/
```

Func/ 19540101 00001/ bia6 00001 003 01.nii.gz bia6 00001 003 01.bxh

bxh2bids

For each .bxh file:

- Locate image data
- Determine BIDS Type
- Create json file

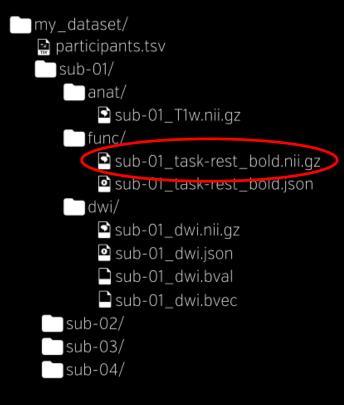


Func/ 19540101 00001/ bia6 00001 003 01.nii.gz bia6 00001 003 01.bxh

bxh2bids

For each .bxh file:

- Locate image data
- Determine BIDS Type
- Create json file
- Rename/copy image



Func/ 19540101 00001/ bia6 00001 003 01.nii.gz bia6 00001 003 01.bxh

bxh2bids

For each .bxh file:

- Locate image data
- Determine BIDS Type
- Create json file
- Rename/copy image

If Functional:

Rename/Copy event .tsv file

```
my dataset/
  participants.tsv
   sub-01/
      □ anat/
         sub-01_T1w.nii.gz
      func/
         sub-01_task-rest_bold.nii.gz
         sub-01_task-rest_bold.json
     □ dwi/
         sub-01_dwi.nii.gz
         sub-01 dwi.json
         sub-01_dwi.bval
         □ sub-01 dwi.bvec
    ☐sub-02/
    \_sub-03/
    sub-04/
```

bxh2bids

For each .bxh file:

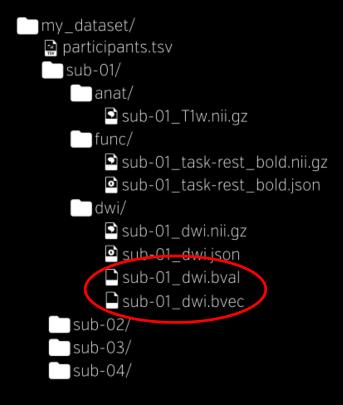
- Locate image data
- Determine BIDS Type
- Create json file
- Rename/copy image

If Functional:

 Rename/Copy event .tsv file

If DWI:

 Extract bvals and bvecs into files



Thanks to John Powers

...with a little help.

User

For each BIAC session:

- Fill out .json template with BIDS sub, ses, and run labels.
- If functional task, create a .tsv file.

For each study:

Fill out a "run"
 python script with
 data input/output
 information

```
my dataset/
  participants.tsv
   sub-01/
      □anat/
          sub-01_T1w.nii.gz
      func/
          sub-01_task-rest_bold.nii.gz
          sub-01_task-rest_bold.json
      □ dwi/
          sub-01_dwi.nii.gz
          sub-01 dwi.json
         sub-01_dwi.bval
          □ sub-01 dwi.bvec
    \_sub-02/
     |sub-03
    sub-04/
```

```
Anat/

19540101_00001/

bia6_00001_001.nii.gz

bia6_00001_001.bxh

19540102_00002/

bia6_00002_001.nii.gz

bia6_00002_100.nii.gz

bia6_00002_100.bxh

Func/

19540101_00001/

bia6_00001_003_01.nii.gz

bia6_00001_003_01.bxh
```

bia6 00001 004 01.nii.gz

bia6_00002_003_01.nii.gz bia6_00002_003_01.bxh bia6_00002_004_01.nii.gz bia6_00002_004_01.bxh

bia6 00001 004 01.bxh

19540102 00002/

...with a little help.

User

For each BIAC session:

- Fill out .json template with BIDS sub, ses, and run labels.
- If functBut fear not!

sub-01 task-rest_bold.nii.gz After initial set-up, getting a new session task-rest_bold.json into BIDS takes only about 5 min.

> Fill out .json template with basic directory info (input, output,

🖭 sub-01 dwi.json sub-01_dwi.bval sub-01 dwi.bvec

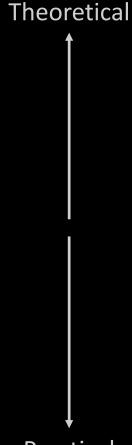
sub-01_T1w.nii.gz

What is BIDS and why is it useful?

What does bxh2bids do?

How does bxh2bids work?

Short bxh2bids demo



Practical

Getting the Code

Available on Github: https://github.com/jlgraner/bxh2bids

- Click the "Clone or Download" button
- Save as a .zip, then unzip it

OR

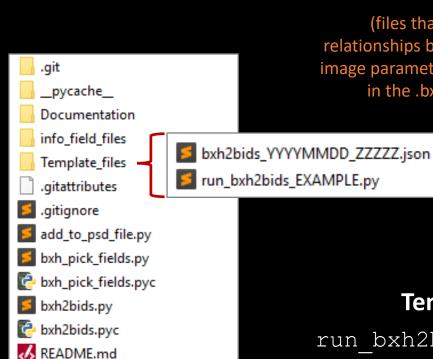
Clone via git:

"git clone https://github.com/jlgraner/bxh2bids"

Things Inside the Zip

Python Scripts

bxh2bids.py: library containing the functions that actually do things bxh pick fields.py: function that pulls BIDS-relevant info. from .bxh files



requirements.txt

setup.py

run autobxh2bids EXAMPLE.py

(files that store image parameters and fields in the .bxh files)

relationships between BIDS —— "Translation" Files

anat info fields.json func info fields.json dwi info fields.json psd types.json

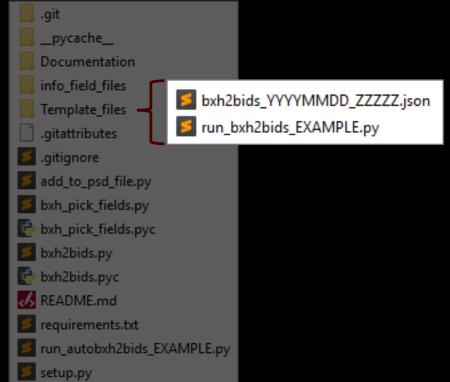
Template Files 🔸

run bxh2bids EXAMPLE.py bxh2bids YYYYMMDD ZZZZ.json (files that store information BIDS needs to know but that isn't in the .bxh files)

Things Inside the Zip (That You'd Care About)

bxh2bids_YYYYMMDD_ZZZZ.json: Session information file template. You'll need one edited and renamed copy of this for each imaging session.

run_bxh2bids_EXAMPLE.py: Script that runs everything. You'll need one edited and renamed copy for each study.



run_bxh2bids.py

"Out of the box"

```
#COPY OF THE bxh2bids DIRECTORY AS A STRING.

bxh2bids_dir = "DIRECTORY CONTAINING YOUR bxh2bids.py FILE"

sys.path.append(bxh2bids_dir)

import bxh2bids as b2b

#The sessions you wish to put into BIDS format right now

to_run = [

"YYYYYMMDD_ZZZZZ'
]

#Set information about your study sessions

source_study_dir="PATH CONTAINING YOUR 'Data' DIRECTORY"

target_study_dir="WHERE YOU WANT THE BIDS DATA TO BE WRITTEN. THE LAST ELEMENT OF THE PATH WILL BE THE STUDY NAME."

log_dir="DIRECTORY WHERE YOU WANT THIS SCRIPT TO WRITE LOG FILES"

ses_info_dir="DIRECTORY WHERE YOU WILL STORE YOUR SESSION INFO FILES"
```

Ready to run

bxh2bids_SESSION_INFO.json

Create a directory to house copies of this outside the repository.

You'll need one of these per session.

"Out of the box"

bxh2bids_19540101_00001.json

Ready to run

Example Functional Event .tsv File

It is up to the user* to create these to match the BIDS specification.

The first 2 columns (onset, duration) are required; other optional columns are specified in the BIDS spec.

						_
onset	duration	n trial_t	ype	stim_in	fo	response_time
8.27	2.90	arrow cor	rect	0.47282		
11.30	2.90	arrow cor	rect	0.33608		
14.33	2.90	arrow cor				
17.52	5.01	negMemCue	CEN	SORED	n/a	
	10.01					
32.55	5.02	negVRate	4	2.9466		
37.78	5.00	negARate	4	1.2226		
	2.90	arrow cor	rect	0.60232		
55.86	2.90	arrow cor	rect	0.37413		
	2.90		rect	0.32297		
62.00	5.01	negMemCue	CEN	SORED	n/a	
67.01	10.01	negStratCue	DIS	TRACT	n/a	
77.03	5.02	negVRate	4	2.1837		
82.26		negARate	4	1.0129		
94.31	2.90	arrow cor	rect	0.39248		
97.34	2.90	arrow Non-	e	None		
100.38	2.90	arrow cor	rect	0.44316		
103.48	5.01	negMemCue	CEN	SORED	n/a	
108.49	10.01	negStratCue	DIS	TRACT	n/a	
118.51	5.02	negVRate	4	2.2781		
123.74	5.00	negARate	4	0.74089		
137.81	2.90	arrow cor	rect	0.46613		
140.84	2.90	arrow cor	rect	0.45588		
143.87	2.90	arrow cor	rect	0.3679		
146.97	5.01	neuMemCue	CEN	SORED	n/a	
151.99	10.01	neuStratCue	FLO	w n/a		
	5.02	neuVRate	4	1.2277		
167.24	5.00	neuARate	4	0.74964		
182.29		arrow cor	rect	0.47444		

*John G. has some code to convert FSL condition files to a BIDS .tsv.

Thanks to Leonard Faul

Logistical Summary

Initial Setup (~30 min)

https://github.com/jlgraner/bxh2bids
run_bxh2bids_EXAMPLE.py
bxh2bids_YYYYMMDD_ZZZZZZ.json
Copy and edit

Things to do for each BIAC session (each unique YYYYMMDD_##### directory) (~5 min)

Event .tsv files bxh2bids_YYYYMMDD_ZZZZZZ.json file Create

When you want to run it

run_bxh2bids_MYSTUDY.py - Edit session list
"python -m run_bxh2bids_MYSTUDY"

Useful Links

bxh2bids: https://github.com/jlgraner/bxh2bids

BIDS main site: http://bids.neuroimaging.io

BIDS validator: http://incf.github.io/bids-validator/

BIDS spec: http://bids.neuroimaging.io/bids_spec1.0.2.pdf

mriqc: http://mriqc.readthedocs.io/en/latest/

fmriprep: http://fmriprep.readthedocs.io/en/latest/