RaBIDS

Rapid analysis pipeline using the Brain Imaging Data Structure

Manual – v0.2

Christian Paret – 2020

RG Psychobiologie of Selfregulation

Department of Psychosomatic and Psychotherapeutic Medicine

Central Institute of Mental Health

christian.paret@zi-mannheim.de

1   Inhalt

2   Software requirements

Tested with Matlab 2020a and SPM12 v7219 on a Windows-10 machine. Tested with dicom images from a PrismaFit Siemens scanner and experiment logfiles produced with Presentation software (neurobehavioral systems) version 18-20. Uses Microsoft Excel 2010.

3   Before you start measuring

3.1   Naming MRI sequences

An MRI measurement protocol can consist of several MRI series. For example, you may administer two functional tasks in one session, and the technical assistant (MTA) will start an echoplanar imaging (EPI) sequence for each task-run by selecting the corresponding tab at the MRI computer. It is recommended to assign unique names to each of these MRI series by changing the name of this tab. Ask the MTA to do this when you set up the sequence. You should also have information ready on the number of images per sequence.Name your MRI sequence and use this name to identify each MRI series

3.1.1   Define subject ID to make it RaBIDS compatible

The subject ID is a series of characters or numbers used to identify a study participant. The subject ID + session ID allow unambiguous identification of a measurement. For example:

- Subject ID: sub-02
- Session ID: ses-01

    (The naming format of Subject and Session ID is arbitrary, as can be seen below)

→ Unique ID for identification of this measurement: sub-02ses-01

You need to use the unique ID to register the participant at the MRI scanner. The name of your Presentation logfiles needs to begin with the unique ID.

If you have multiple sessions you need to make sure that the session identifier comes as a suffix to the subject code as shown above (I call this the the "session suffix"). E.g. for subject named "sub-02", session 1, following unique IDs are allowed:

- sub-02ses-01 ("ses-01" is the session suffix)
- sub-0201 ("01" is the session suffix)
- 0201 ("01" is the session suffix)
- Etc.

You should NOT put the session identifier anywhere else than at the end of the unique ID! That is, the following unique IDs CANNOT be processed with the RaBIDS software, because it may incorrectly interpret your input:

- ses01sub02
- 01sub02 (where "01" is the session)
- 0102 (where "01" is the session)
- Etc.

3.2   Exporting data from the MRI scanner

The person operating the experiment and MRI machine should export data to the data exchange server in the following structure:

    A) Presentation logfiles:
- [Your project folder on hobbes]
  - sourcedata
    - [Subject ID; recommended to begin with prefix "sub-"] (e.g. sub-01, sub-02, sub-03, …, sub-99)
      - [Session ID; recommended to begin with prefix "ses-"] (e.g. ses-pre, ses-post, ses-fu, ses-01,…)
        - *Save logfiles here* (e.g. "sub02ses01_task-emo.log")

    B) MRI images:
- [Your project folder on hobbes]
  - dicomdir
    - [Subject ID; recommended to begin with prefix "sub-"] (e.g. sub-01, sub-02, sub-03, …, sub-99)

- [Session ID; recommended to begin with prefix
  "ses-"] (e.g. ses-pre, ses-post, ses-fu, ses-01,…)
  - *Save MRI images here*

The session-level can be skipped in case there is only one session per subject.

4   Getting started

4.1   Download additional software

4.1.1   SPM

https://www.fil.ion.ucl.ac.uk/spm/software/spm12/

4.1.2   dicm2nii

We use dicm2nii (version 2020.10.08) provided by Xiangrui Li for importing dicoms to nifti-format. RaBIDS is actually a wrapper to automatically apply the dicm2nii function to neuroimaging data.

https://github.com/xiangruili/dicm2nii

- For automated production of .json files during dicom import: open dicm2nii GUI and select option "save json file". This is needed to receive a BIDS-compatible data set

5   Import a dataset into BIDS format

It is recommended to do the tutorial before using RaBIDS the first time for your own data.

5.1   Sourcedata

Sourcedata is all data other than dicom data that is recorded in the context of a functional MRI measurement (Gorgolewski et al., 2016). You need to populate this folder according to the BIDS structure (adhere to the structure above for saving Presentations logfiles to your local project directory). RaBIDS expects your Presentation logfiles to be located here.

5.2   Dicom images

You have two options:

-   Import dicom MRI images directly from a data exchange server without copy-pasting it to your local project directory. This works as long as you use the data structure suggested above for exporting data from the scanner site.
-   Create a directory called "dicomdir" in your project directory. Copy-paste all dicoms to this directory. You do not need to sort them into subdirectories. This option will slow down the import process for large datasets, because RaBIDS lists all content of the dicomdir directory.

5.3   Fill the datasheet

Go to directory dataset\code\RaBIDS templates (or see Appendix). Copy the file datasheet.xlsx to the directory dataset\code, which you have created in your local project directory. The Excel-table has six colomns named "ObjectType, Description, UserInput, MinImages, MaxImages, UsageNotes". Your input is required to the fields "UserInput, MinImages, MaxImages". Never change the "ObjectType" fields. You may enter notes in the UsageNotes colomn (ignored by the program).

Don't forget to save your input everytime before running RaBIDS_1_Import (e.g. by pressing keys Ctrl+S)!

5.3.1   ObjectType: add path

Absolute path to software used by RaBIDS (see 4.1).

5.3.2   ObjectType: data_analysis_path

Parent directory of dataset-directory (probably your local project directory).

5.3.3   ObjectType: data exchange path

Define path to the directory called "dicomdir" containing the dicom MRI images of your study on the data exchange server.

5.3.4   ObjectType: sourcedata path

Define path to the directory called "sourcedata" containing the Presentation logfiles of your study.

5.3.5   ObjectType: dicoms

Explain how your dicoms are saved: if they are all mixed in one directory enter "allinone", if they were exported in a BIDS-similar directory structure (see above), enter "BIDS".

5.3.6   ObjectType: subject info

Duplicate the subject info row as many times as you have subjects to analyse. You can also just analyze a subset of your sample. Input the exact name of each subject as it has been registrated in the scanner and in the Presentation logfile. Note that lower case letters used for registration at the scanner are automatically translated to uppercase in Siemens-file names. You need to type the file name exactly as you registered the subject, that is, including lower case letters (this information is still present in the meta-data and will be used by the RaBIDS program).

5.3.7   ObjectType: add prefix

For BIDS compatibility, each subject name needs to begin with "sub-". If you have not yet adopted this format, write "yes" in the "user input" field, otherwise "no".

5.3.8   ObjectType: MRI series

Assign TaskName to MRI series ("rest" for resting state scan, "anat" for anatomical scan, e.g. "emoreg" for emotion regulation task, "fieldmap phasediff"[1] for phase-difference fieldmaps and "fieldmap magnitude" for magnitude fieldmaps). You may consult the recent BIDS manual to find inspiration for an appropriate label for your functional task. For each MRI series you need to define "MinImages" and "MaxImages". The program only uses the scan if the number of images is within the given range: MinImages ≤ number of images in the scan ≤ MaxImages. The program cannot deal with scans with more than one series with the exact name (series info, see 5.3.9) and overlapping ranges of number of volumes.

5.3.9   ObjectType: series info

This is the name of the MRI series as it has been labeled at the MR computer.
Example: this is an example path to an anatomical sequence at our Siemens-scanner (PrismaFit): \\USER\psm\EFPNFB\Tag1\t1_mpr_ns_sag_pat2_iso_asy.
Highlighted in purple = project directory; yellow = series info.

5.3.10   ObjectType: general suffix

The general suffix corresponds to the project name at the MR scanner. This ObjectType needs to be set according to the name of the scan, see example below.
Note, that the general suffix can take value underscore (i.e., "_"). For our Siemens-scanners at the Central Institute, use the value starting after "MR." and ending before ".RUNNING-SCAN-NUMBER".

Example: this is an example path to an anatomical sequence at our Siemens-scanner (PrismaFit): \\USER\psm\EFPNFB\Tag1\t1_mpr_ns_sag_pat2_iso_asy.
Highlighted in purple = project directory; yellow = series info.

The export-dicom tool uses the first two sub-directories to USER to create a general suffix in the dicom name, i.e. "psm" and "EFPNFB". The first volume of the mprage scan for subject EFP01 is called:

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[1] CAVE: Double-check whether import of fieldmap phase/phasedifference images works! Phase/phasedifference maps might not be recognized correctly.

EFP01.MR.PSM_EFPNFB.0006.0001.2018.05.14.13.00.47.560079.855171.IMA

Highlighted text in cyan=subject name; purple = general suffix; text in yellow = series number of scan; green = running number of scan in this series.

5.3.11   ObjectType: session ID

RaBIDS assumes that subject IDs list a unique identifier for the subject (e.g. sub01) and are followed by a unique session identifier (e.g. ses02). See 3.1.1 for more information.

Each field "session ID" identifies a session (session = one series of MRI measurement typically comprising localizer and fieldmap scans, anatomical and functional scans). If your experiment has just one session per subject, you can leave the "user input" field empty. The "session info" row under the "session ID" row relates to this session and is explained below. If you have more than one session, you need to add as many "session ID" and "session info" rows as you have sessions per subject. Explain in the "UserInput" field how this particular session should be named. This input is used for naming the corresponding directory in your data structure. According to BIDS, it needs to begin with "ses-", and can be followed by e.g. "01" to name the first session (i.e. "ses-01"), or e.g. "pre" for the pre-measurement session of your clinical intervention (i.e. "ses-pre").

5.3.12   ObjectType: session info

Optional: Input the session suffix of this particular session. This is usually not needed but may be helpful/needed in some rare cases.

5.3.13   ObjectType: first image

Usually in fMRI BOLD, you start the experiment only after recording a few volumes (I usually start with the fifth scan) to exclude T1-effects in your T2*-weighted images. If you write "yes" in the "UserInput" field and declare the first image (e.g. 5) in "MinImages", the initial X-1 (e.g. 4) images will be deleted (they are not needed anymore). The program will check for the volume number in the name of the dicom image, so you don't need to be afraid that more images than intended will be deleted if you need to re-run the program on that subject/session later. Use of this feature is recommended.

5.3.14 ObjectType: write scan protocol

If user input is "yes", a scan protocol listing series number, series name and number of volumes will be written to the session directory before dicom import.

5.3.15 ObjectType: overwrite import

Write "yes" if you want to overwrite existing files in your data structure and "no" if you don't want to do it. This is helpful e.g. if you have imported some subject previously for an interim analysis, and you have collected more data meanwhile to import. In this case you can have all subjects listed in your datasheet, and RaBIDS-Import will skip those that were already imported and only work with the new ones.

5.3.16 ObjectTypes: overwrite sots

Allow to overwrite existing sots of subject/session.

5.4   Import dataset

Run the Matlab program RaBIDS_1_Import.m, which you find in the code-directory.

5.5   Define Stimulus Onset Times (SOTS)

To become BIDS compatible, your dataset needs to include "events.tsv"-files that list trial information for each task/functional scan. RaBIDS provides a solution to automatically write an events.tsv file based on the individual task logfile. In the current version, the program supports standard fMRI analysis based on stimulation protocols with stimulus blocks of flexible duration. Regressors for parametric modulation is not supported.

"RaBIDS_2_Create_SOTS.m" works on your input to the "conditions_TaskName.xlsx"-file. It produces files called "multicond.mat", which can go straightforward to SPM's first-level analysis batches. An events.tsv-file is created in addition. Output will be saved to your project directory (e.g.\dataset\sub-02\ses-01\func). Two files are generated per task:.

1. sub-02_ses-01_func_task-TaskName_multicond.mat
2. sub-02_ses-01_func_task-TaskName_events.tsv

Go to directory code/RaBIDS templates (or see Appendix). Copy "conditions_TaskName.xlsx" to the code-directory. Change the name of the Excel file according to your task:

*   conditions_TaskName.xlsx, where TaskName = the name you assigned previously in the datasheet (i.e. user input to the corresponding MRI series, see 5.3.8; e.g. "conditions_emoreg.xlsx").

5.5.1   Condition

Add a row for each condition that goes into the model. Identify each condition by counting upwards. Other than in the datasheet.xlsx table you are required to edit the items in the first colomn of the condition.xlsx table. That is, the first condition is named "Condition1", the second "Condition2", and so on.

Name

Assign a name (arbitrary) that will be used to identify this condition in the SPM-model. White spaces not allowed.

OnsetID

This is the code to identify the onset of the condition from the Presentation logfile. The program will search the logfile for entries that include the assigned OnsetID. For example, if you have entries with different name (e.g. bars1, bars4, bars5, …) that belong to the same condition, you can type 'bars', and the program will use all events that include the expression.

Duration

You may assign a fixed duration for trials of this condition type. Set duration = 0 for stimulus events that are to be modeled with a stick function (aka "onset transient"). If you don't want to use the "Duration" feature, leave the user-input field empty. See OffsetID for more information.

OffsetID

This is the code to identify the offset of the condition in the Presentation logfile. For example, in case each trial is immediately followed by a "fixation cross" event denoted by code "fixcross" in the logfile, you may assign "fixcross" to OffsetID and leave the "Duration" field empty. If you want to use "Duration", enter some arbitrary character string (e.g. 'none'), otherwise RaBIDS_2_Create_SOTS.m will return an error.

The program will recognise the first occation of OffsetID following OnsetID to terminate a stimulus trial (see OnsetID for an example).

CAVE: If working with OffsetID it is necessary that each OnsetID event is actually followed by and OffsetID event in the logfile. If this is not the case (e.g. because the experiment ended after last OnsetID instance and OffsetID was not called again), the routine will return an error.

5.5.2   Log ID

Unique ID to identify the logfile corresponding to the task. Wildcards are allowed (i.e. use an asterisk to allow for undefined characters, e.g. *emoreg*). User input is required in the "Name" colomn.

5.5.3   Logfile ID format

- 'BIDS': logfile name format is: "sub-SUBJECTNUMBER_ses-SESSIONNUMBER_ LogID.log" (see 3.2A)
- 'free': logfile name can have any format, as long as the LogID is included. This option will not double-check whether the logfiles have the right subject name. The program searches for files with format "LogID.log" in the corresponding session directory of that subject.

User input is required in the "Name" colomn. Logfiles are found in the sourcedata directory.

5.5.4   Contrast

Add a row for each contrast that should be estimated. Identify each contrast by counting upwards. Other than in the datasheet.xlsx table you are required to edit the items in the first colomn of the condition.xlsx table. That is, the first condition is named "Contrast1", the second "Contrast2", and so on.

Name

Assign name (arbitrary) to identify the contrast in the SPM-model.

ContrastType

Only t-contrast is implemented in version v0.2. Input is ignored.

ContrastPlus1

Enter the condition that you want to contrast against another condition (i.e. ContrastPlus1 > ContrastMinus1).

ContrastMinus1

This condition is contrasted against the condition entered in the ContrastPlus1 field. Leave empty to estimate ContrastPlus1>implicit baseline.

5.6   Create SOTS file

Run matlab program RaBIDS_2_Create_SOTS.m. You are requested to input the TaskName as a character string (i.e., within inverted commas; 'TaskName') in Matlab's Command Window.

6   Appendix

6.1 Datasheet file (/code/templates/datasheet.xlsx)

ObjectType	Description	UserInput	MinImages	MaxImages
add path	SPM	C:\Program Files\spm12	0	0
add path	dicm2nii	C:\Program Files\dicm2nii	0	0
add path	saveJSONfile	.\RaBIDS other software\saveJSONfile	0	0
add path	functions	.\RaBIDS functions	0	0
data analysis path	e.g. your project directory	E:\mytrainingdata\your project directory	0	0
data exchange path	path to your project's dicom directory on hobbes	E:\mytrainingdata\data exchange server\RABIDS-example\dicomdir	0	0
sourcedata path	path to logfiles	E:\mytrainingdata\data exchange server\RABIDS-example\sourcedata	0	0
dicoms	how to expect dicom files?	BIDS		
subject info	subject ID	RABIDS01		
add prefix	add 'sub-' to subject ID	yes		
MRI series	TaskName and define min-max	TaskName	XX	XX
series info	MRI series ID	MRISeriesID		
MRI series	TaskName and define min-max	anat	XX	
series info	MRI series ID	MRISeriesID		
MRI series	TaskName and define min-max	fieldmap magnitude	XX	
series info	MRI series ID	MRISeriesID		
MRI series	TaskName and define min-max	fieldmap phasediff	XX	
series info	MRI series ID	MRISeriesID		
general suffix	general suffix to find MR images	GeneralSuffix		
session ID	first session ID	SessionID		
session info	first session suffix			
first image	first image (delete initial n-1 images)	yes		5
write scan protocol	saves scan protocol to dicom directory	yes		
overwrite import	overwrite existing session directory	yes		
overwrite sots	overwrite existing sots files (...multicond.mat)	yes		

6.2   Conditions-file (/code/templates/conditions_TaskName.xlsx)

	Name	OnsetID	Duration	OffsetID	ContrastType	ContrastPlus1	ContrastMinus1
Condition1				none			
Logfile ID format	BIDS			none			
Log ID	*						
Contrast1					t		