

RaBIDS

Rapid and **a**utomated conversion of neuroimaging data to **BIDS**

Manual

CAVE: Major changes were necessary with v0.4 with the new dicom format provided by Siemens. The tutorial is not compatible with v0.4.

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1 Inhalt

2	Change log.....	4
3	Requirements and limitations.....	4
3.1	Software.....	4
3.2	Scanner	5
3.3	Fieldmaps.....	Fehler! Textmarke nicht definiert.
4	Before you start measuring	5
4.1	Naming MRI sequences.....	5
4.1.1	Define subject ID to make it RaBIDS compatible	5
4.2	Exporting data from the MRI scanner	6
5	Getting started	7
5.1	Download additional software.....	7
5.1.1	SPM.....	7
5.1.2	dicm2nii.....	7
6	Import a dataset into BIDS format	Fehler! Textmarke nicht definiert.
6.1	Sourcedata	8
6.2	Dicom images	Fehler! Textmarke nicht definiert.
6.3	Fill the datasheet.....	8
6.3.1	ObjectType: add path	9
6.3.2	ObjectType: data_analysis_path	9
6.3.3	ObjectType: data exchange path	9
6.3.4	ObjectType: sourcedata path.....	9
6.3.5	ObjectType: dicoms	9
6.3.6	ObjectType: subject info	9
6.3.7	ObjectType: add sub prefix	10
6.3.8	ObjectType: MR scanner	10
6.3.9	ObjectType: MRI series	10
6.3.10	ObjectType: series info	12
6.3.11	ObjectType: general suffix.....	12
6.3.12	ObjectType: session ID	13
6.3.13	ObjectType: session info.....	13

6.3.14	ObjectType: first image	13
6.3.15	ObjectType: write scan protocol.....	14
6.3.16	ObjectType: overwrite import	14
6.3.17	ObjectTypes: overwrite sots	14
6.4	Import dataset	14
6.5	Define Stimulus Onset Times (SOTS).....	14
6.5.1	Condition	15
6.5.2	Log ID.....	16
6.5.3	Logfile ID format.....	16
6.5.4	Contrast.....	17
6.6	Create SOTS file	18
7	RaBIDS Warnings	18
8	Appendix.....	19
8.1	Datasheet file (/code/RaBIDS_templates/datasheet.xlsx).....	20
8.2	Conditions-file (/code/RaBIDS_templates/conditions_TaskName.xlsx)	22

2 Change log

2022/05/16:

- 1) New contrast type implemented. Previous contrast type description is invalid (previous contrast type ‘t’ changed to ‘tcon’).
- 2) Best practice recommendation added to section “fill the datasheet”: A sustainable approach to define paths for SPM-analysis.

2023/04/13:

- 1) Create_sots function updated, read-excel function should be less error-prone.
- 2) Conditions_TaskName.xlsx file: SplitCondition option added. If selected, SOTs-files have two stimulus onset functions per condition.
- 3) Conditions_TaskName.xlsx file, fields ContrastPlus1 and ContrastMinus1: with v0.3 it is possible to define more than one condition for each field.

2025/09/02:

Major changes. Most important:

1. Now dcm2niix is used for dicom import to nifti
2. Bugs in the definition of fieldmap B0-images were fixed
3. Import of DWI images was added

3 Requirements and limitations

3.1 Software

Tested with Matlab 2023a and SPM12 v7219 on a Windows-10 machine. To use the automatic creation of stimulus onset time (SOT) files (including events.tsv files required for BIDS validation), experiment logfiles need to be produced with Presentation software

(neurobehavioral systems) version 18 or later. Microsoft Excel 2010 is used to generate input data tables.

3.2 Scanner

Tested with dicom images from a PrismaFit Siemens scanner running syngo XA60.

4 Before you start measuring

4.1 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

4.1.1 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 “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.

4.2 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:

4.2.1 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”)

4.2.2 MRI images with Siemens syngo VE versions (deprecated):

- [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.

4.2.3 MRI images with Siemens syngo XA

The naming schemes of directories differ from institution to institution (and maybe from scanner to scanner). Therefore, there is no general recommendation how to structure files. Rather, you will need to adapt some code in the RaBIDS functions to accommodate the structure.

5 Getting started

5.1 Download additional software

5.1.1 SPM

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

5.1.2 dcm2niix

Download the latest version of dcm2niix from <https://github.com/rordenlab/dcm2niix>.

6 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.

6.1 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 seven columns named “ObjectType, Description, UserInput, RunNumber, MinImages, MaxImages, UsageNotes”. Your input is required to the fields “UserInput, RunNumber, MinImages, MaxImages”. Never change the “ObjectType” fields. You may enter notes in the UsageNotes column (ignored by the program).

Best practice recommendation: Map the project directory, define paths relative to the mapped project directory. Here is an example: the absolute path to the data analysis directory of project “BOLDpro5” is given by: `\\zi.local\flstorage\dep_psm\group_psm\Projects\BOLDpro5\Data_analysis`. We mapped the research-group directory to drive “Y”. Hence, the relative path is given by: `“Y:\Projects\BOLDpro5\Data_analysis”`. Why is this important? You should know that SPM saves meta-data about the images, including the absolute paths. When something with regards to your file structure changes after your analysis was done, SPM is no longer be able to access the images. Worst case is that you need to change path definition, delete old results, and redo first-level analysis. Why should my filestructure change? There are several reasons: your IT administrator may change it (actually happened to us recently) or you may want to repeat your analysis on a different computer. In any case, you can easily recreate the file structure and map drive Y.

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

6.1.1 ObjectType: add path

Absolute path to software used by RaBIDS (see 5.1).

6.1.2 ObjectType: executable

Absolute path to software dcm2niix.

6.1.3 ObjectType: data_analysis_path

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

6.1.4 ObjectType: data exchange path

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

6.1.5 ObjectType: sourcedata path

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

6.1.6 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”. For Siemens syngo XA60 (and later versions) there is a “Siemens_MA” option for images acquired at Central Institute of Mental Health, Mannheim.

6.1.7 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 registered 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).

6.1.8 ObjectType: add sub 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”.

6.1.9 ObjectType: add ses prefix

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

6.1.10 ObjectType: MR scanner

Not yet implemented

6.1.11 ObjectType: MRI series

Assign TaskName to MRI series. 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: $\text{MinImages} \leq \text{number of images in the scan} \leq \text{MaxImages}$. The program cannot deal with more than one series with the exact same name (series info, see 6.1.12) and overlapping ranges of number of volumes.

Functional scans

Usage: functional [*task label*] (*B0 Field Source label*)

Task name: Arbitrary label of the functional task

B0 Field Source: Arbitrary label of a fielmap scan that should be used for distortion correction of this task run. B0 Field Identifier and the corresponding B0 Field Source need to be assigned the same name.

Example: functional [reappraisal] (fmap0)

It is also required to populate the RunNumber column (e.g. 1).

Fieldmaps

Phase-difference image:

Usage: fieldmap phasediff [task-task label_run-run number] (B0 Field Identifier label)

Task label: Arbitrary label of the functional task

Run number: 1 or higher

B0 Field Identifier label: Arbitrary label of a fieldmap scan that should be used for distortion correction of a task run. B0 Field Identifier and the corresponding B0 Field Source need to be assigned the same name.

Example: fieldmap phasediff [task-reappraisal_run-1] [task-reappraisal_run-2] (fmap0)

Note: Add one or more task runs, each task-run needs to be framed by square brackets. The information in square brackets will be written to the json metadata-file accompanying the phase-difference nifti image (field “IntendedFor”). This is an alternative way to mark field maps that should be used for distortion correction of functional scans.

Fieldmap magnitude image:

Usage: fieldmap magnitude

DWI

Usage: dwi [name of acquisition] (phase encoding direction)

Name of acquisition: arbitrary name to append to file label (acq-XXX)

Phase encoding direction: PA or AP, to append to file label (dir-XX)

Example: dwi [cmrr] (AP)

Anatomical

Usage: anat [suffix] (scan number)

Suffix (optional): It may happen that export creates multiple dicom outputs from a single scan (example below). In this case, suffix defines the series to import.

Scan number (optional, but mandatory if suffix defined): Series nr of dicom output for import.

t1_mp2rage_sag_INV1_5_MR	05.09.2025 15:25	File folder
t1_mp2rage_sag_INV2_6_MR	05.09.2025 15:26	File folder
t1_mp2rage_sag_UNI-DEN_7_MR	05.09.2025 15:26	File folder
t1_mp2rage_sag_UNI-DEN_MPR_cor_9_MR	05.09.2025 15:27	File folder
t1_mp2rage_sag_UNI-DEN_MPR_cor_ND_15_MR	05.09.2025 15:27	File folder
t1_mp2rage_sag_UNI-DEN_MPR_tra_8_MR	05.09.2025 15:27	File folder
t1_mp2rage_sag_UNI-DEN_MPR_tra_ND_14_MR	05.09.2025 15:28	File folder
t1_mp2rage_sag_UNI-DEN_ND_13_MR	05.09.2025 15:28	File folder

Figure: example of multiple dicom output received for a MP2RAGE scan. Here, we want to import series nr. 7 (t1_mp2rage_sag_UNI-DEN_7_MR), where suffix is “UNI-DEN” and series nr. is “7”.

6.1.12 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.

6.1.13 ObjectType: general suffix

Siemens with syngo XA60 and later

Leave empty.

Siemens MR systems with older software versions

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:

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.

6.1.14 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 4.1.1 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”).

6.1.15 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.

6.1.16 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. Declare the first image (e.g. x=5) in “MinImages”; x-1 images will be discarded in firstlevel analysis. The create-SOTS step is based on x and will use x as timepoint 0 to reference event times of the stimulation protocol.

6.1.17 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.

6.1.18 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.

6.1.19 ObjectTypes: overwrite sots

Allow to overwrite existing sots of subject/session.

6.2 Import dataset

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

6.3 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 6.1.11; e.g. “conditions_emoreg.xlsx”).

6.3.1 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 column 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 an 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.

SplitCondition

If selected, the first half of events (early events) and the second half of events (late events) of a condition are represented in separate stimulus functions. If there is an uneven number of events for the condition, the stimulus in the middle will not be included in any of the stimulus functions. SplitCondition can take values 0, 1, 2, where: 0 and 1 = a single stimulus function for all events of the condition; and 2 = two stimulus functions will be produced (ConditionName_early, ConditionName_late). Values > 2 are undefined and will output a warning message to the command window.

6.3.2 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” column.

6.3.3 Logfile ID format

- ‘BIDS’: logfile name format is: “sub-SUBJECTNUMBER_session-SESSIONNUMBER_LogID.log” (see 4.2A)

- ‘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” column. Logfiles are found in the sourcedata directory.

6.3.4 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 column 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

Define the type of contrast. You can select between t-contrast (tcon) or effects-of-interest f-contrast (eoi). Dependent from the selection there are different values expected for the ContrastPlus1 and ContrastMinus1 fields (see below). It is recommended to define Contrast 1 as eoi.

Must be one of the following:

- tcon
- eoi

ContrastPlus1

If this is a t-contrast (see ContrastType):

Enter the condition(s) that you want to contrast against another condition(s) (i.e. $\text{ContrastPlus1} > \text{ContrastMinus1}$). Enter the conditions that you want to include in the contrast, separated with semicolons (e.g., face; control).

If this is a eoi f-contrast (see ContrastType):

Enter the conditions that you want to include in the effects of interest f-contrast, separated with semicolons (e.g., face; control). The eoi may be used to adjust for, e.g. in functional connectivity analysis or in signal timecourse analysis (e.g. SPM's VOI tool).

ContrastMinus1

If this is a t-contrast (see ContrastType):

This condition is contrasted against the condition entered in the ContrastPlus1 field.

Leave empty to estimate ContrastPlus1>implicit baseline. Enter the conditions that you want to include in the contrast, separated with semicolons (e.g., face; control).

If this is a eoi f-contrast (see ContrastType):

Leave empty; entries will be ignored.

6.4 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.

7 RaBIDS Warnings

For RaBIDS warning messages in the command window refer to the document "RaBIDS Warning Reference.pdf".

8 *Appendix*

8.1 Datasheet file (example) (/code/RaBIDS_templates/datasheet_MA.xlsx)

ObjectType	Description	UserInput	RunNumber	MinImages	MaxImages	UsageNotes
add path	SPM	C:\Program Files\MATLAB\toolboxes\spm12_mit_conn21		0	0	Define path t
add path	functions	.\RaBIDS functions		0	0	
executable	dcm2niix	E:\dcm2niix\dcm2niix.exe		0	0	Define path t
data analysis path	e.g. your project directory	W:\group_psm\BrainSTEADy_data_analysis\Neuroimaging		0	0	Define path t
data exchange path	path to your project's dicom directory on hobbess	W:\group_psm\BrainSTEADy_data_analysis\Neuroimaging\dicoms		0	0	Define path t
sourcedata path	path to logfiles	not defined		0	0	Define path t
dicoms	how to expect dicom files?	Siemens_TB				Choose "allin
subject info	subject ID	TB101				
add sub prefix	add 'sub-' to subject ID	yes				
add ses prefix	add 'ses-' to session ID	yes				
subject info	subject ID	TB103				
add sub prefix	add 'sub-' to subject ID	yes				
add ses prefix	add 'ses-' to session ID	yes				
subject info	subject ID	TB105				
add sub prefix	add 'sub-' to subject ID	yes				
add ses prefix	add 'ses-' to session ID	yes				
MRI series	TaskName and define min-max	dwi [cmrr] (AP)	1	36	36	
series info	MRI series ID	dwi_ses-base_acq-cmrr_task-rest_run-01_dir-AP				
MRI series	TaskName and define min-max	dwi [cmrr] (PA)	1	36	36	
series info	MRI series ID	dwi_ses-base_acq-cmrr_task-rest_run-02_dir-PA				
MRI series	TaskName and define min-max	functional [neurofeedback]	1	430	430	
series info	MRI series ID	ep2d_NFB_run1				
MRI series	TaskName and define min-max	functional [neurofeedback]	2	430	430	
series info	MRI series ID	ep2d_NFB_run2				
MRI series	TaskName and define min-max	anat		1	1	
series info	MRI series ID	MPRAGE_1iso_G2				
MRI series	TaskName and define min-max	fieldmap magnitude		2	2	
series info	MRI series ID	gre_field_mapping				
MRI series	TaskName and define min-max	fieldmap phasediff [task-neurofeedback_run-1] [task-neurofeedback_run-2]		1	1	UserInput: yc
series info	MRI series ID	gre_field_mapping				
general suffix	general suffix to find MR images					if no session
session ID	first session ID	V2				
session info	first session suffix	none				
first image	This volume will be used as t0 for stimulus onset timing					
write scan protocol	saves scan protocol to dicom directory	yes				
overwrite import	overwrite existing session directory	no				
overwrite sots	overwrite existing sots files (...multicond.mat)	yes				

8.2 Conditions-file (/code/RaBIDS_templates/conditions_TaskName.xlsx)

	Name	OnsetID	Duration	OffsetID	SplitCondition	ContrastType	ContrastPlus1	ContrastMinus1
Condition1								
Condition2								
Logfile ID format	BIDS			none				
Log ID	*							
Contrast1						eoi		
Contrast2						tcon		