# Brain Imaging Data Structure Specification

v1.7.0

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# Contents

# The Brain Imaging Data Structure

The Brain Imaging Data Structure (BIDS) is a simple and intuitive way to organize and describe data.

This document defines the BIDS specification, which provides many details to help implement the standard. It includes the core specification as well as many extensions to specific brain imaging modalities, and increasingly also to other kinds of data.

If BIDS is new to you, and you would like to learn more about how to adapt your own datasets to match the BIDS specification, we recommend exploring the BIDS Starter Kit. Alternatively, to get started please read the introduction to the specification.

For an overview of the BIDS ecosystem, visit the BIDS homepage. The entire specification can also be downloaded as PDF.

# Introduction

## Motivation

Neuroimaging experiments result in complicated data that can be arranged in many different ways. So far there is no consensus how to organize and share data obtained in neuroimaging experiments. Even two researchers working in the same lab can opt to arrange their data in a different way. Lack of consensus (or a standard) leads to misunderstandings and time wasted on rearranging data or rewriting scripts expecting certain structure. Here we describe a simple and easy-to-adopt way of organising 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. To understand the organisation of the files and their format you will only need to refer them to this document. This is especially important if you are running your own lab and anticipate more than one person working on the same data over time. By using BIDS you will save time trying to understand and reuse data acquired by a graduate student or postdoc that has already left the lab.
- There are a growing number of data analysis software packages that can understand data organised according to BIDS (see the up to date list).
- Databases such as OpenNeuro.org accept datasets organised according to BIDS. If you ever plan to share your data publicly (nowadays some journals require this) you can minimize the additional time and energy spent on publication, and speed up the curation process by using BIDS to structure and describe your data right after acquisition.
- Validation tools such as the BIDS Validator can check your dataset integrity and help you easily spot missing values.

BIDS was heavily inspired by the format used internally by the OpenfMRI repository that is now known as OpenNeuro.org, and has been supported by the International Neuroinformatics Coordinating Facility (INCF) and the INCF Neuroimaging Data Sharing (NIDASH) Task Force. While working on BIDS we consulted many neuroscientists to make sure it covers most common experiments, but at the same time is intuitive and easy to adopt. The specification is intentionally based on simple file formats and folder structures to reflect current lab practices and make it accessible to a wide range of scientists coming from different backgrounds.

## Extensions

The BIDS specification can be extended in a backwards compatible way and will evolve over time. This is accomplished through community-driven BIDS Extension Proposals (BEPs). For more information about the BEP process, see Extending the BIDS specification.

# Citing BIDS

When referring to BIDS in context of academic literature, please cite one or more of the publications listed below. We RECOMMEND that you cite the original publication on BIDS and additionally the publication regarding the datatype you were using (for example, EEG, MEG, iEEG, if available).

For example:

> The data used in the study were organized using the Brain Imaging Data Structure (Gorgolewski, K., Auer, T., Calhoun, V. et al., 2016) with the extension for EEG data (Pernet, C.R., Appelhoff, S., Gorgolewski, K.J. et al., 2019).

## Original publication

- Gorgolewski, K.J., Auer, T., Calhoun, V.D., Craddock, R.C., Das, S., Duff, E.P., Flandin, G., Ghosh, S.S., Glatard, T., Halchenko, Y.O., Handwerker, D.A., Hanke, M., Keator, D., Li, X., Michael, Z., Maumet, C., Nichols, B.N., Nichols, T.E., Pellman, J., Poline, J.-B., Rokem, A., Schaefer, G., Sochat, V., Triplett, W., Turner, J.A., Varoquaux, G., Poldrack, R.A. (2016). The brain imaging data structure, a format for organizing and describing outputs of neuroimaging experiments. Scientific Data, 3 (160044). doi:10.1038/sdata.2016.44

## Datatype specific publications

### EEG

- Pernet, C. R., Appelhoff, S., Gorgolewski, K.J., Flandin, G., Phillips, C., Delorme, A., Oostenveld, R. (2019). EEG-BIDS, an extension to the brain imaging data structure for electroencephalography. Scientific data, 6 (103). doi:10.1038/s41597-019-0104-8

### iEEG

- Holdgraf, C., Appelhoff, S., Bickel, S., Bouchard, K., D'Ambrosio, S., David, O., Devinsky, O., Dichter, B., Flinker, A., Foster, B. L., Gorgolewski, K. J., Groen, I., Groppe, D., Gunduz, A., Hamilton, L., Honey, C. J., Jas, M., Knight, R., Lauchaux, J.-P., Lau, J. C., Lee-Messer, C., Lundstrom, B. N., Miller, K. J., Ojemann, J. G., Oostenveld, R., Petridou, N., Piantoni, G., Pigorini, A., Pouratian, N., Ramsey, N. F., Stolk, A., Swann, N. C., Tadel, F., Voytek, B., Wandell, B. A., Winawer, J., Whitaker, K., Zehl, L., Hermes, D. (2019). iEEG-BIDS, extending the Brain Imaging Data Structure specification to human intracranial electrophysiology. Scientific data, 6 (102). doi:10.1038/s41597-019-0105-7

### MEG

- Niso Galan, J.G., Gorgolewski, K.J., Bock, E., Brooks, T.L., Flandin, G., Gramfort, A., Henson, R.N., Jas, M., Litvak, V., Moreau, J., Oostenveld, R., Schoffelen, J.-M., Tadel, F., Wexler, J., Baillet, S. (2018). MEG-BIDS, the brain imaging data structure extended to magnetoencephalography. Scientific Data, 5 (180110). doi:10.1038/sdata.2018.110

### PET

- Knudsen GM, Ganz M, Appelhoff S, Boellaard R, Bormans G, Carson RE, Catana C, Doudet D, Gee AD, Greve DN, Gunn RN, Halldin C, Herscovitch P, Huang H, Keller SH, Lammertsma AA, Lanzenberger R, Liow JS, Lohith TG, Lubberink M, Lyoo CH, Mann JJ, Matheson GJ, Nichols TE, Nørgaard M, Ogden T, Parsey R, Pike VW, Price J, Rizzo G, Rosa-Neto P, Schain M, Scott PJH, Searle G, Slifstein M, Suhara T, Talbot PS, Thomas A, Veronese M, Wong DF, Yaqub M, Zanderigo F, Zoghbi

S, Innis RB. (2020). Guidelines for Content and Format of PET Brain Data in Publications and in Archives: A Consensus Paper. Journal of Cerebral Blood Flow and Metabolism, 2020 Aug; 40(8): 1576-1585. doi:10.1177/0271678X20905433

Genetics

- Clara Moreau, Martineau Jean-Louis, Ross Blair, Christopher Markiewicz, Jessica Turner, Vince Calhoun, Thomas Nichols, Cyril Pernet (2020). The genetics-BIDS extension: Easing the search for genetic data associated with human brain imaging. GigaScience, 9 (10). doi:10.1093/gigascience/giaa104

## Research Resource Identifier (RRID)

BIDS has also a Research Resource Identifier (RRID), which you can also include in your citations in addition to relevant publications (see above):

- `RRID:SCR_016124`

# Common principles

## Definitions

The keywords ”MUST”, ”MUST NOT”, ”REQUIRED”, ”SHALL”, ”SHALL NOT”, ”SHOULD”, ”SHOULD NOT”, ”RECOMMENDED”, ”MAY”, and ”OPTIONAL” in this document are to be interpreted as described in [RFC2119].

Throughout this specification we use a list of terms and abbreviations. To avoid misunderstanding we clarify them here.

1. Dataset - a set of neuroimaging and behavioral data acquired for a purpose of a particular study. A dataset consists of data acquired from one or more subjects, possibly from multiple sessions.
2. Subject - a person or animal participating in the study. Used interchangeably with term Participant.
3. Session - a logical grouping of neuroimaging and behavioral data consistent across subjects. Session can (but doesn’t have to) be synonymous to a visit in a longitudinal study. In general, subjects will stay in the scanner during one session. However, for example, if a subject has to leave the scanner room and then be re-positioned on the scanner bed, the set of MRI acquisitions will still be considered as a session and match sessions acquired in other subjects. Similarly, in situations where different data types are obtained over several visits (for example fMRI on one day followed by DWI the day after) those can be grouped in one session. Defining multiple sessions is appropriate when several identical or similar data acquisitions are planned and performed on all -or most- subjects, often in the case of some intervention between sessions (for example, training). In the PET context, a session may also indicate a group of related scans, taken in one or more visits.
4. Sample - a sample pertaining to a subject such as tissue, primary cell or cell-free sample. The `sample-<label>` key/value pair is used to distinguish between different samples from the same subject. The label MUST be unique per subject and is RECOMMENDED to be unique throughout the dataset.
5. Data acquisition - a continuous uninterrupted block of time during which a brain scanning instrument was acquiring data according to particular scanning sequence/protocol.
6. Data type - a functional group of different types of data. BIDS defines the following data types:
    (a) `func` (task based and resting state functional MRI)
    (b) `dwi` (diffusion weighted imaging)
    (c) `fmap` (field inhomogeneity mapping data such as field maps)
    (d) `anat` (structural imaging such as T1, T2, PD, and so on)
    (e) `perf` (perfusion)

   (f) `meg` (magnetoencephalography)
   (g) `eeg` (electroencephalography)
   (h) `ieeg` (intracranial electroencephalography)
   (i) `beh` (behavioral)
   (j) `pet` (positron emission tomography)
   (k) `micr` (microscopy)

   Data files are contained in a directory named for the data type. In raw datasets, the data type directory is nested inside subject and (optionally) session directories.

7. Task - a set of structured activities performed by the participant. Tasks are usually accompanied by stimuli and responses, and can greatly vary in complexity. For the purpose of this specification we consider the so-called "resting state" a task. In the context of brain scanning, a task is always tied to one data acquisition. Therefore, even if during one acquisition the subject performed multiple conceptually different behaviors (with different sets of instructions) they will be considered one (combined) task.

8. Event - something that happens or may be perceived by a test subject as happening at a particular instant during the recording. Events are most commonly associated with on- or offset of stimulus presentations, or with the distinct marker of on- or offset of a subject's response or motor action. Other events may include unplanned incidents (for example, sudden onset of noise and vibrations due to construction work, laboratory device malfunction), changes in task instructions (for example, switching the response hand), or experiment control parameters (for example, changing the stimulus presentation rate over experimental blocks), and noted data feature occurrences (for example, a recording electrode producing noise). In BIDS, each event has an onset time and duration. Note that not all tasks will have recorded events (for example, "resting state").

9. Run - an uninterrupted repetition of data acquisition that has the same acquisition parameters and task (however events can change from run to run due to different subject response or randomized nature of the stimuli). Run is a synonym of a data acquisition. Note that "uninterrupted" may look different by modality due to the nature of the recording. For example, in MRI or [MEG] (04-modality-specific-files/02-magnetoencephalography.md), if a subject leaves the scanner, the acquisition must be restarted. For some types of PET acquisitions, a subject may leave and re-enter the scanner without interrupting the scan.

10. Modality - the category of brain data recorded by a file. For MRI data, different pulse sequences are considered distinct modalities, such as `T1w`, `bold` or `dwi`. For passive recording techniques, such as EEG, MEG or iEEG, the technique is sufficiently uniform to define the modalities `eeg`, `meg` and `ieeg`. When applicable, the modality is indicated in the suffix. The modality may overlap with, but should not be confused with the data type.

11. **`<index>`** - a nonnegative integer, possibly prefixed with arbitrary number of 0s for consistent indentation, for example, it is `01` in `run-01` following `run-<index>` specification.

12. **`<label>`** - an alphanumeric value, possibly prefixed with arbitrary number of 0s for consistent indentation, for example, it is `rest` in `task-rest` following `task-<label>` specification. Note that labels MUST not collide when casing is ignored (see Case collision intolerance).

13. **`suffix`** - an alphanumeric value, located after the `key-value_` pairs (thus after the final `_`), right before the File extension, for example, it is `eeg` in `sub-05_task-matchingpennies_eeg.vhdr`.

14. File extension - a portion of the filename after the left-most period (`.`) preceded by any other alphanumeric. For example, `.gitignore` does not have a file extension, but the file extension of `test.nii.gz` is `.nii.gz`. Note that the left-most period is included in the file extension.

15. DEPRECATED - A "deprecated" entity or metadata field SHOULD NOT be used in the generation of new datasets. It remains in the standard in order to preserve the interpretability of existing datasets. Validating software SHOULD warn when deprecated practices are detected and provide a suggestion for updating the dataset to preserve the curator's intent.

## Compulsory, optional, and additional data and metadata

The following standard describes a way of arranging data and writing down metadata for a subset of neuroimaging experiments. Some aspects of the standard are compulsory. For example a particular filename format is required when storing structural scans. Some aspects are regulated but optional. For example a T2 volume does not need to be included, but when it is available it should be saved under a particular filename specified in the standard. This standard aspires to describe a majority of datasets, but acknowledges that there will be cases that do not fit. In such cases one can include additional files and subfolders to the existing folder structure following common sense. For example one may want to include eye tracking data in a vendor specific format that is not covered by this standard. The most sensible place to put it is next to the continuous recording file with the same naming scheme but different extensions. The solutions will change from case to case and publicly available datasets will be reviewed to include common data types in the future releases of the BIDS specification.

## File name structure

A filename consists of a chain of entities, or key-value pairs, a suffix and an extension. Two prominent examples of entities are `subject` and `session`.

For a data file that was collected in a given `session` from a given `subject`, the filename MUST begin with the string `sub-<label>_ses-<label>`. If the `session` level is omitted in the folder structure, the filename MUST begin with the string `sub-<label>`, without `ses-<label>`.

Note that `sub-<label>` corresponds to the `subject` entity because it has the `sub-` ”key” and`<label>` ”value”, where `<label>` would in a real data file correspond to a unique identifier of that subject, such as `01`. The same holds for the `session` entity with its `ses-` key and its `<label>` value.

The extra session layer (at least one `/ses-<label>` subfolder) SHOULD be added for all subjects if at least one subject in the dataset has more than one session. If a `/ses-<label>` subfolder is included as part of the directory hierarchy, then the same `ses-<label>` key/value pair MUST also be included as part of the filenames themselves. Acquisition time of session can be defined in the sessions file.

A chain of entities, followed by a suffix, connected by underscores (`_`) produces a human readable filename, such as `sub-01_task-rest_eeg.edf`. It is evident from the filename alone that the file contains resting state data from subject `01`. The suffix `eeg` and the extension `.edf` depend on the imaging modality and the data format and indicate further details of the file’s contents.

Entities within a filename MUST be unique. For example, the following filename is not valid because it uses the `acq` entity twice: `sub-01_acq-laser_acq-uneven_electrodes.tsv`

In cases where entities duplicate metadata, the presence of an entity should not be used as a replacement for the corresponding metadata field. For instance, in echo-planar imaging MRI, the `dir-<label>` entity MAY be used to distinguish files with different phase-encoding directions, but the file’s `PhaseEncodingDirection` can only be specified as metadata.

A summary of all entities in BIDS and the order in which they MUST be specified is available in the entity table in the appendix.

### Entity-linked file collections

An entity-linked file collection is a set of files that are related to each other based on a repetitive acquisition of sequential data by changing acquisition parameters one (or multiple) at a time or by being inherent components of the same data. Entity-linked collections are identified by a common suffix, indicating the group of files that should be considered a logical unit. Within each collection, files MUST be distinguished from each other by at least one entity (for example, `echo`) that corresponds to an altered acquisition parameter (`EchoTime`) or that defines a component relationship (for example, `part`). Note that these entities MUST be described by the specification and the parameter changes they declare MUST NOT invalidate the definition of the accompanying suffix. For example, the use of the `echo` entity along with the `T1w` suffix casts doubt on the validity of the identified contrast weighting. Provided the conditions above are satisfied, any suffix (such as `bold`) can identify an entity-linked file collection, although certain suffixes are exclusive for this purpose (for example, `MP2RAGE`). Use cases concerning this convention are compiled in the file collections appendix. This convention is mainly intended for but not limited to MRI modalities.

### Case collision intolerance

File name components are case sensitive, but collisions MUST be avoided when casing is ignored. For example, a dataset cannot contain both `sub-s1` and `sub-S1`, as the labels would collide on a case-insensitive filesystem. Additionally, because the suffix `eeg` is defined, then the suffix `EEG` will not be added to future versions of the standard.

## Source vs. raw vs. derived data

BIDS was originally designed to describe and apply consistent naming conventions to raw (unprocessed or minimally processed due to file format conversion) data. During analysis such data will be transformed and partial as well as final results will be saved. Derivatives of the raw data (other than products of DICOM to NIfTI conversion) 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. See Storage of derived datasets for more on organizing derivatives.

Similar rules apply to source data, which is defined as data before harmonization, reconstruction, and/or file format conversion (for example, E-Prime event logs or DICOM files). Storing actual source files with the data is preferred over links to external source repositories to maximize long term preservation, which would suffer if an external repository would not be available anymore. This specification currently does not go into the details of recommending a particular naming scheme for including different types of source data (such as the raw event logs or parameter files, before conversion to BIDS). However, in the case that these data are to be included:

1. These data MUST be kept in separate `sourcedata` folder with a similar folder structure as presented below for the BIDS-managed data. For example: `sourcedata/sub-01/ses-pre/func/sub-01_ses-pre_task-rest_bold.dicom.tgz` or `sourcedata/sub-01/ses-pre/func/MyEvent.sce`.
2. A README file SHOULD be found at the root of the `sourcedata` folder or the `derivatives` folder, or both. This file should describe the nature of the raw data or the derived data. We RECOMMEND including the PDF print-out with the actual sequence parameters generated by the scanner in the `sourcedata` folder.

Alternatively one can organize their data in the following way

```
my_dataset-1/
   sourcedata/
      sub-01/
      sub-02/
      ...
   ...
   derivatives/
      pipeline_1/
      pipeline_2/
      ...
```

In this example, where `sourcedata` and `derivatives` are not nested inside `rawdata`, only the `rawdata` subfolder needs to be a BIDS-compliant dataset. The subfolders of `derivatives` MAY be BIDS-compliant derivatives datasets (see Non-compliant derivatives for further discussion). This specification does not prescribe anything about the contents of `sourcedata` folders in the above example - nor does it prescribe the `sourcedata`, `derivatives`, or `rawdata` folder names. The above example is just a convention that can be useful for organizing raw, source, and derived data while maintaining BIDS compliance of the raw data folder. When using this convention it is RECOMMENDED to set the `SourceDatasets` field in `dataset_description.json` of each subfolder of `derivatives` to:

```
{
  "SourceDatasets": [ {"URL": "file://../../rawdata/"} ]
}
```

## Storage of derived datasets

Derivatives can be stored/distributed in two ways:

1. Under a `derivatives/` subfolder in the root of the source BIDS dataset folder to make a clear distinction between raw data and results of data processing. A data processing pipeline will typically have a dedicated directory under which it stores all of its outputs. Different components of a pipeline can, however, also be stored under different subfolders. There are few restrictions on the directory names; it is RECOMMENDED to use the format `<pipeline>-<variant>` in cases where it is anticipated that the same pipeline will output more than one variant (for example, `AFNI-blurring` and `AFNI-noblurring`). For the sake of consistency, the subfolder name SHOULD be the `GeneratedBy.Name` field in `data_description.json`, optionally followed by a hyphen and a suffix (see Derived dataset and pipeline description).

   Example of derivatives with one directory per pipeline:

   ```
   <dataset>/derivatives/fmriprep-v1.4.1/sub-0001
   <dataset>/derivatives/spm/sub-0001
   <dataset>/derivatives/vbm/sub-0001
   ```

   Example of a pipeline with split derivative directories:

   ```
   <dataset>/derivatives/spm-preproc/sub-0001
   <dataset>/derivatives/spm-stats/sub-0001
   ```

   Example of a pipeline with nested derivative directories:

   ```
   <dataset>/derivatives/spm-preproc/sub-0001
   <dataset>/derivatives/spm-preproc/derivatives/spm-stats/sub-0001
   ```

2. As a standalone dataset independent of the source (raw or derived) BIDS dataset. This way of specifying derivatives is particularly useful when the source dataset is provided with read-only access, for publishing derivatives as independent bodies of work, or for describing derivatives that were created from more than one source dataset. The `sourcedata/` subdirectory MAY be used to include the source dataset(s) that were used to generate the derivatives. Likewise, any code used to generate the derivatives from the source data MAY be included in the `code/` subdirectory.

   Example of a derivative dataset including the raw dataset as source:

```
my_processed_data/
   code/
      processing_pipeline-1.0.0.img
      hpc_submitter.sh
      ...
```

```
    sourcedata/
       sub-01/
       sub-02/
       ...
    sub-01/
    sub-02/
    ...
```

Throughout this specification, if a section applies particularly to derivatives, then Case 1 will be assumed for clarity in templates and examples, but removing `/derivatives/<pipeline>` from the template name will provide the equivalent for Case 2. In both cases, every derivatives dataset is considered a BIDS dataset and must include a `dataset_description.json` file at the root level (see Dataset description). Consequently, files should be organized to comply with BIDS to the full extent possible (that is, unless explicitly contradicted for derivatives). Any subject-specific derivatives should be housed within each subject's directory; if session-specific derivatives are generated, they should be deposited under a session subdirectory within the corresponding subject directory; and so on.

### Non-compliant derivatives

Nothing in this specification should be interpreted to disallow the storage/distribution of non-compliant derivatives of BIDS datasets. In particular, if a BIDS dataset contains a `derivatives/` sub-directory, the contents of that directory may be a heterogeneous mix of BIDS Derivatives datasets and non-compliant derivatives.

## File Formation specification

### Imaging files

All imaging data MUST be stored using the NIfTI file format. We RECOMMEND using compressed NIfTI files (.nii.gz), either version 1.0 or 2.0. Imaging data SHOULD be converted to the NIfTI format using a tool that provides as much of the NIfTI header information (such as orientation and slice timing information) as possible. Since the NIfTI standard offers limited support for the various image acquisition parameters available in DICOM files, we RECOMMEND that users provide additional meta information extracted from DICOM files in a sidecar JSON file (with the same filename as the `.nii[.gz]` file, but with a `.json` extension). Extraction of BIDS compatible metadata can be performed using dcm2niix and dicm2nii DICOM to NIfTI converters. The BIDS-validator will check for conflicts between the JSON file and the data recorded in the NIfTI header.

### Tabular files

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.

Example:

```
onset   duration    response_time   correct stop_trial  go_trial
```

```
200 200 0   n/a n/a n/a
```

Note: The TSV examples in this document (like the one above this note) are occasionally formatted using space characters instead of tabs to improve human readability. Directly copying and then pasting these examples from the specification for use in new BIDS datasets can lead to errors and is discouraged.

Tabular files MAY be optionally accompanied by a simple data dictionary in the form of a JSON object within a JSON file. The JSON files containing the data dictionaries MUST have the same name as their corresponding tabular files but with `.json` extensions. If a data dictionary is provided, it MAY contain one or more fields describing the columns found in the TSV file (in addition to any other metadata one wishes to include that describe the file as a whole). Note that if a field name included in the data dictionary matches a column name in the TSV file, then that field MUST contain a description of the corresponding column, using an object containing the following fields:

| Key name | Requirement Level | Data type | Description |
|---|---|---|---|
| LongName | OPTIONAL | string | Long (unabbreviated) name of the column. |
| Description | RECOMMENDED | string | Free-form natural language description. The description of the column. |
| Levels | RECOMMENDED | object of strings | For categorical variables: An object of possible values (keys) and their descriptions (values). |
| Units | RECOMMENDED | string | Measurement units for the associated file. SI units in CMIXF formatting are RECOMMENDED (see Units). |
| TermURL | RECOMMENDED | string | URL pointing to a formal definition of this type of data in an ontology available on the web. |
| HED | OPTIONAL | string or object of strings | Hierarchical Event Descriptor (HED) information, see: Appendix III for details. |

Please note that while both `Units` and `Levels` are RECOMMENDED, typically only one of these two fields would be specified for describing a single TSV file column.

Example:

```
{
  "test": {
    "LongName": "Education level",
    "Description": "Education level, self-rated by participant",
    "Levels": {
      "1": "Finished primary school",
      "2": "Finished secondary school",
      "3": "Student at university",
```

```
      "4": "Has degree from university"
    }
  },
  "bmi": {
    "LongName": "Body mass index",
    "Units": "kg/m^2",
    "TermURL": "https://purl.bioontology.org/ontology/SNOMEDCT/60621009"
  }
}
```

### Key/value files (dictionaries)

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/, and at https://tools.ietf.org/html/std90. 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 (for example, `SamplingFrequency`, 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.

Example of a hypothetical `*_bold.json` file, accompanying a `*_bold.nii` file:

```
{
  "RepetitionTime": 3,
  "Instruction": "Lie still and keep your eyes open"
}
```

Example of a hypothetical `*_events.json` file, accompanying an `*_events.tsv` file. Note that the JSON file contains a key describing an arbitrary column `stim_presentation_side` in the TSV file it accompanies. See task events section for more information.

```
{
  "stim_presentation_side": {
    "Levels": {
      "1": "stimulus presented on LEFT side",
      "2": "stimulus presented on RIGHT side"
    }
  }
}
```

## The Inheritance Principle

1. Any metadata file (such as `.json`, `.bvec` or `.tsv`) MAY be defined at any directory level.
2. For a given data file, any metadata file is applicable to that data file if:

   (a) It is stored at the same directory level or higher;
   (b) The metadata and the data filenames possess the same suffix;
   (c) The metadata filename does not include any entity absent from the data filename.

3. A metadata file MUST NOT have a filename that would be otherwise applicable to some data file based on rules 2.b and 2.c but is made inapplicable based on its location in the directory structure as per rule 2.a.

4. There MUST NOT be multiple metadata files applicable to a data file at one level of the directory hierarchy.

5. If multiple metadata files satisfy criteria 2.a-c above:

   (a) For tabular files and other simple metadata files (for instance, `bvec` / `bval` files for diffusion MRI), accessing metadata associated with a data file MUST consider only the applicable file that is lowest in the filesystem hierarchy.

   (b) For JSON files, key-values are loaded from files from the top of the directory hierarchy downwards, such that key-values from the top level are inherited by all data files at lower levels to which it is applicable unless overridden by a value for the same key present in another metadata file at a lower level (though it is RECOMMENDED to minimize the extent of such overrides).

Corollaries:

1. As per rule 3, metadata files applicable only to a specific participant / session MUST be defined in or below the directory corresponding to that participant / session; similarly, a metadata file that is applicable to multiple participants / sessions MUST NOT be placed within a directory corresponding to only one such participant / session.

2. It is permissible for a single metadata file to be applicable to multiple data files at that level of the hierarchy or below. Where such metadata content is consistent across multiple data files, it is RECOMMENDED to store metadata in this way, rather than duplicating that metadata content across multiple metadata files.

3. Where multiple applicable JSON files are loaded as per rule 5.b, key-values can only be overwritten by files lower in the filesystem hierarchy; the absence of a key-value in a later file does not imply the ”unsetting” of that field (indeed removal of existing fields is not possible).

Example 1: Demonstration of inheritance principle

```
sub-01/
    func/
        sub-01_task-rest_acq-default_bold.nii.gz
        sub-01_task-rest_acq-longtr_bold.nii.gz
        sub-01_task-rest_acq-longtr_bold.json
task-rest_bold.json
```

Contents of file `task-rest_bold.json`:

```
{
    "EchoTime": 0.040,
    "RepetitionTime": 1.0
}
```

Contents of file `sub-01/func/sub-01_task-rest_acq-longtr_bold.json`:

```
{
    "RepetitionTime": 3.0
}
```

When reading image `sub-01/func/sub-01_task-rest_acq-default_bold.nii.gz`, only metadata file `task-rest_bold.json` is read; file `sub-01/func/sub-01_task-rest_acq-long` is inapplicable as it contains entity ”`acq-longtr`” that is absent from the image path (rule 2.c). When reading image `sub-01/func/sub-01_task-rest_acq-longtr_bold.nii.gz`, metadata file `task-rest_bold.json` at the top level is read first, followed by file `sub-01/func/sub-01_task-rest_acq-longtr_bold.json` at the bottom level (rule 5.b); the value for field ”`RepetitionTime`” is therefore overridden to the value `3.0`. The value for field ”`EchoTime`” remains applicable to that image, and is not unset by its absence in the metadata file at the lower level (rule 5.b; corollary 3).

Example 2: Impermissible use of multiple metadata files at one directory level (rule 4)

```
sub-01/
   ses-test/
      anat/
         sub-01_ses-test_T1w.nii.gz
      func/
         sub-01_ses-test_task-overtverbgeneration_run-1_bold.nii.gz
         sub-01_ses-test_task-overtverbgeneration_run-2_bold.nii.gz
         sub-01_ses-test_task-overtverbgeneration_bold.json
         sub-01_ses-test_task-overtverbgeneration_run-2_bold.json
```

Example 3: Modification of filesystem structure from Example 2 to satisfy inheritance principle requirements

```
sub-01/
   ses-test/
      sub-01_ses-test_task-overtverbgeneration_bold.json
      anat/
         sub-01_ses-test_T1w.nii.gz
      func/
         sub-01_ses-test_task-overtverbgeneration_run-1_bold.nii.gz
         sub-01_ses-test_task-overtverbgeneration_run-2_bold.nii.gz
         sub-01_ses-test_task-overtverbgeneration_run-2_bold.json
```

Example 4: Single metadata file applying to multiple data files (corollary 2)

```
sub-01/
   anat/
   func/
      sub-01_task-xyz_acq-test1_run-1_bold.nii.gz
      sub-01_task-xyz_acq-test1_run-2_bold.nii.gz
      sub-01_task-xyz_acq-test1_bold.json
```

## Participant names and other labels

BIDS allows for custom user-defined `<label>`s and `<index>`es for example, for naming of participants, sessions, acquisition schemes. Note that they MUST consist only of allowed characters as described in Definitions above. In `<index>`es we RECOMMEND using zero padding (for example, `01` instead of `1` if you have more than nine subjects) to make alphabetical sorting more intuitive. Note that zero padding SHOULD NOT be used to merely maintain uniqueness of `<index>`es.

Please note that a given label or index is distinct from the "prefix" it refers to. For example `sub-01` refers to the `sub` entity (a subject) with the label `01`. The `sub-` prefix is not part of the subject label, but must be included in filenames (similarly to other key names).

## Specification of paths

Several metadata fields in BIDS require the specification of paths, that is, a string of characters used to uniquely identify a location in a directory structure. For example the `IntendedFor` or `AssociatedEmptyroom` metadata fields.

Throughout BIDS all such paths MUST be specified using the slash character (`/`), regardless of the operating system that a particular dataset is curated on or used on.

Paths SHOULD NOT be absolute local paths, because these might break when a dataset is used on a different machine. It is RECOMMENDED that all paths specified in a BIDS dataset are relative paths, as specified in the respective descriptions of metadata fields that require the use of paths.

## Uniform Resource Indicator

A Uniform Resource Indicator (URI) is a string referring to a resource and SHOULD have the form `<scheme>:[//<authority>]<path>[?<query>][#<fragment>]`, as specified in RFC 3986. This applies to URLs and other common URIs, including Digital Object Identifiers (DOIs), which may be fully specified as `doi:<path>`, for example, doi:10.5281/zenodo.3686061. A given resource may have multiple URIs. When selecting URIs to add to dataset metadata, it is important to consider specificity and persistence.

Several fields are designated for DOIs, for example, `DatasetDOI` in `dataset_description.json`. DOI values SHOULD be fully specified URIs such as `doi:10.18112/openneuro.ds00000` Bare DOIs such as `10.18112/openneuro.ds000001.v1.0.0` are DEPRECATED.

## Units

All units SHOULD be specified as per International System of Units (abbreviated as SI, from the French Système international (d'unités)) and can be SI units or SI derived units. In case there are valid reasons to deviate from SI units or SI derived units, the units MUST be specified in the sidecar JSON file. In case data is expressed in SI units or SI derived units, the units MAY be specified in the sidecar JSON file. In case non-standard prefixes are added to SI or non-SI units, these non-standard prefixed units MUST be specified in the JSON file. See Appendix V for a list of standard units and prefixes. Note also that for the formatting of SI units, the CMIXF-12 convention for encoding units is RECOMMENDED. CMIXF provides a consistent system for all units and prefix symbols with only basic characters, avoiding symbols that can cause text encoding problems; for example the CMIXF formatting for "micro volts" is `uV`, "degrees Celsius" is `oC` and "Ohm" is `Ohm`. See Appendix V for more information.

For additional rules, see below:

- Elapsed time SHOULD be expressed in seconds. Please note that some DICOM parameters have been traditionally expressed in milliseconds. Those need to be converted to seconds.

- Frequency SHOULD be expressed in Hertz.
- Arbitrary units SHOULD be indicated with the string `"arbitrary"`.

Describing dates and timestamps:

- Date time information MUST be expressed in the following format `YYYY-MM-DDThh:mm:ss[.000000][Z]` (year, month, day, hour (24h), minute, second, optional fractional seconds, and optional UTC time indicator). This is almost equivalent to the RFC3339 "date-time" format, with the exception that UTC indicator `Z` is optional and non-zero UTC offsets are not indicated. If `Z` is not indicated, time zone is always assumed to be the local time of the dataset viewer. No specific precision is required for fractional seconds, but the precision SHOULD be consistent across the dataset. For example `2009-06-15T13:45:30`.
- Time stamp information MUST be expressed in the following format: `hh:mm:ss[.000000]` For example `13:45:30`.
- Note that, depending on local ethics board policy, date time information may not need to be fully detailed. For example, it is permissible to set the time to `00:00:00` if reporting the exact recording time is undesirable. However, for privacy protection reasons, it is RECOMMENDED to shift dates, as described below, without completely removing time information, as time information can be useful for research purposes.
- Dates can be shifted by a random number of days for privacy protection reasons. To distinguish real dates from shifted dates, is is RECOMMENDED to set shifted dates to the year 1925 or earlier. Note that some data formats do not support arbitrary recording dates. For example, the EDF data format can only contain recording dates after 1985. For longitudinal studies dates MUST be shifted by the same number of days within each subject to maintain the interval information. For example: `1867-06-15T13:45:30`
- WARNING: The Neuromag/Elekta/MEGIN file format for MEG (`.fif`) does not support recording dates earlier than `1902` roughly. Some analysis software packages (for example, MNE-Python) handle their data as `.fif` internally and will break if recording dates are specified prior to `1902`, even if the original data format is not `.fif`. See MEG-file-formats for more information.
- Age SHOULD be given as the number of years since birth at the time of scanning (or first scan in case of multi session datasets). Using higher accuracy (weeks) should in general be avoided due to privacy protection, unless when appropriate given the study goals, for example, when scanning babies.

# Directory structure

## Single session example

This is an example of the folder and file structure. Because there is only one session, the session level is not required by the format. For details on individual files see descriptions in the next section:

```
sub-control01/
   anat/
      sub-control01_T1w.nii.gz
      sub-control01_T1w.json
      sub-control01_T2w.nii.gz
      sub-control01_T2w.json
   func/
      sub-control01_task-nback_bold.nii.gz
      sub-control01_task-nback_bold.json
```

```
            sub-control01_task-nback_events.tsv
            sub-control01_task-nback_physio.tsv.gz
            sub-control01_task-nback_physio.json
            sub-control01_task-nback_sbref.nii.gz
        dwi/
            sub-control01_dwi.nii.gz
            sub-control01_dwi.bval
            sub-control01_dwi.bvec
        fmap/
            sub-control01_phasediff.nii.gz
            sub-control01_phasediff.json
            sub-control01_magnitude1.nii.gz
    code/
        deface.py
    derivatives/
    README
    participants.tsv
    dataset_description.json
    CHANGES
```

## Unspecified data

Additional files and folders containing raw data MAY be added as needed for special cases. All non-standard file entities SHOULD conform to BIDS-style naming conventions, including alphabetic entities and suffixes and alphanumeric labels/indices. Non-standard suffixes SHOULD reflect the nature of the data, and existing entities SHOULD be used when appropriate. For example, an ASSET calibration scan might be named `sub-01_acq-ASSET_calibration.nii.gz`.

Non-standard files and directories should be named with care. Future BIDS efforts may standardize new entities and suffixes, changing the meaning of filenames and setting requirements on their contents or metadata. Validation and parsing tools MAY treat the presence of non-standard files and directories as an error, so consult the details of these tools for mechanisms to suppress warnings or provide interpretations of your filenames.

# Modality agnostic files

## Dataset description

Templates:

- `dataset_description.json`
- `README`
- `CHANGES`
- `LICENSE`

### `dataset_description.json`

The file `dataset_description.json` is a JSON file describing the dataset. Every dataset MUST include this file with the following fields:

| Key name | Requirement Level | Data type | Description |
|---|---|---|---|
| Name | REQUIRED | string | Name of the dataset. |
| BIDSVersion | REQUIRED | string | The version of the BIDS standard that was used. |
| HEDVersion | RECOMMENDED | string | If HED tags are used: The version of the HED schema used to validate HED tags for study. |
| DatasetType | RECOMMENDED | string | The interpretation of the dataset. For backwards compatibility, the default value is `"raw"`. Must be one of: `"raw"`, `"derivative"`. |

| Key name | Requirement Level | Data type | Description |
|---|---|---|---|
| License | RECOMMENDED | string | The license for the dataset. The use of license name abbreviations is RECOMMENDED for specifying a license (see Appendix II). The corresponding full license text MAY be specified in an additional `LICENSE` file. |
| Authors | OPTIONAL | array of strings | List of individuals who contributed to the creation/curation of the dataset. |
| Acknowledgements | OPTIONAL | string | Text acknowledging contributions of individuals or institutions beyond those listed in Authors or Funding. |
| HowToAcknowledge | OPTIONAL | string | Text containing instructions on how researchers using this dataset should acknowledge the original authors. This field can also be used to define a publication that should be cited in publications that use the dataset. |
| Funding | OPTIONAL | array of strings | List of sources of funding (grant numbers). |
| EthicsApprovals | OPTIONAL | array of strings | List of ethics committee approvals of the research protocols and/or protocol identifiers. |
| ReferencesAndLinks | OPTIONAL | array of strings | List of references to publications that contain information on the dataset. A reference may be textual or a URI. |
| DatasetDOI | OPTIONAL | string | The Digital Object Identifier of the dataset (not the corresponding paper). DOIs SHOULD be expressed as a valid URI; bare DOIs such as `10.0.2.3/dfjj.10` are URI. |
| GeneratedBy | RECOMMENDED | array of objects | Used to specify provenance of the dataset. |
| SourceDatasets | RECOMMENDED | array of objects | Used to specify the locations and relevant attributes of all source datasets. Valid keys in each object include `"URL"`, `"DOI"` (see URI), and `"Version"` with string values. |

Each object in the `GeneratedBy` array includes the following REQUIRED, RECOMMENDED and OPTIONAL keys:

| Key name | Requirement level | Data type | Description |
|---|---|---|---|
| Name | REQUIRED | string | Name of the pipeline or process that generated the outputs. Use `"Manual"` to indicate the derivatives were generated by hand, or adjusted manually after an initial run of an automated pipeline. |
| Version | RECOMMENDED | string | Version of the pipeline. |
| Description | OPTIONAL | string | Plain-text description of the pipeline or process that generated the outputs. RECOMMENDED if `Name` is `"Manual"`. |
| CodeURL | OPTIONAL | string | URL where the code used to generate the dataset may be found. |
| Container | OPTIONAL | object | Used to specify the location and relevant attributes of software container image used to produce the dataset. Valid keys in this object include `Type`, `Tag` and `URI` with string values. |

Example:

```
{
  "Name": "The mother of all experiments",
  "BIDSVersion": "1.6.0",
  "DatasetType": "raw",
  "License": "CC0",
  "Authors": [
    "Paul Broca",
    "Carl Wernicke"
  ],
  "Acknowledgements": "Special thanks to Korbinian Brodmann for help in formatting this dataset in BIDS. We thank Alan Lloyd Hodgkin and Andrew Huxley
  "HowToAcknowledge": "Please cite this paper: https://www.ncbi.nlm.nih.gov/pubmed/001012092119281",
  "Funding": [
    "National Institute of Neuroscience Grant F378236MFH1",
    "National Institute of Neuroscience Grant 5RMZ0023106"
  ],
  "EthicsApprovals": [
    "Army Human Research Protections Office (Protocol ARL-20098-10051, ARL 12-040, and ARL 12-041)"
```

```
  ],
  "ReferencesAndLinks": [
    "https://www.ncbi.nlm.nih.gov/pubmed/001012092119281",
    "Alzheimer A., & Kraepelin, E. (2015). Neural correlates of presenile dementia in humans. Journal of Neuroscientific Data, 2, 234001. doi:1920.8/j
  ],
  "DatasetDOI": "doi:10.0.2.3/dfjj.10",
  "HEDVersion": "8.0.0",
  "GeneratedBy": [
    {
      "Name": "reproin",
      "Version": "0.6.0",
      "Container": {
        "Type": "docker",
        "Tag": "repronim/reproin:0.6.0"
      }
    }
  ],
  "SourceDatasets": [
    {
      "URL": "s3://dicoms/studies/correlates",
      "Version": "April 11 2011"
    }
  ]
}
```

### Derived dataset and pipeline description

As for any BIDS dataset, a `dataset_description.json` file MUST be found at the top level of every derived dataset: `<dataset>/derivatives/<pipeline_name>/dataset_descripti`

In contrast to raw BIDS datasets, derived BIDS datasets MUST include a `GeneratedBy` key:

| Key name | Requirement Level | Data type | Description |
|---|---|---|---|
| GeneratedBy | REQUIRED | array of objects | Used to specify provenance of the dataset. |

If a derived dataset is stored as a subfolder of the raw dataset, then the `Name` field of the first `GeneratedBy` object MUST be a substring of the derived dataset folder name. That is, in a directory `<dataset>/derivatives/<pipeline>[-<variant>]/`, the first `GeneratedBy` object should have a `Name` of `<pipeline>`.

Example:

```
{
  "Name": "FMRIPREP Outputs",
  "BIDSVersion": "1.6.0",
  "DatasetType": "derivative",
  "GeneratedBy": [
    {
      "Name": "fmriprep",
      "Version": "1.4.1",
      "Container": {
        "Type": "docker",
        "Tag": "poldracklab/fmriprep:1.4.1"
        }
    },
    {
      "Name": "Manual",
      "Description": "Re-added RepetitionTime metadata to bold.json files"
    }
  ],
  "SourceDatasets": [
    {
      "DOI": "doi:10.18112/openneuro.ds000114.v1.0.1",
      "URL": "https://openneuro.org/datasets/ds000114/versions/1.0.1",
      "Version": "1.0.1"
    }
  ]
}
```

## `README`

Every BIDS dataset SHOULD come with a free form text file (`README`) describing the dataset in more detail. The `README` file MUST be either in ASCII or UTF-8 encoding. A guideline for creating a good `README` file can be found in the bids-starter-kit.

## `CHANGES`

Version history of the dataset (describing changes, updates and corrections) MAY be provided in the form of a `CHANGES` text file. This file MUST follow the CPAN Changelog convention. The `CHANGES` file MUST be either in ASCII or UTF-8 encoding.

Example:

```
1.0.1 2015-08-27
  - Fixed slice timing information.
```

```
1.0.0 2015-08-17
  - Initial release.
```

### `LICENSE`

A `LICENSE` file MAY be provided in addition to the short specification of the used license in the `dataset_description.json` `"License"` field. The `"License"` field and `LICENSE` file MUST correspond. The `LICENSE` file MUST be either in ASCII or UTF-8 encoding.

## Participants file

Template:

```
participants.tsv
participants.json
```

The purpose of this RECOMMENDED file is to describe properties of participants such as age, sex, handedness, species and strain. 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.

The RECOMMENDED `species` column SHOULD be a binomial species name from the NCBI Taxonomy (for examples `homo sapiens`, `mus musculus`, `rattus norvegicus`). For backwards compatibility, if `species` is absent, the participant is assumed to be `homo sapiens`.

Commonly used optional columns in `participants.tsv` files are `age`, `sex`, `handedness`, `strain`, and `strain_rrid`. We RECOMMEND to make use of these columns, and in case that you do use them, we RECOMMEND to use the following values for them:

| Column name | Requirement Level | Data type | Description |
|---|---|---|---|
| participant_id | REQUIRED | string | A participant identifier of the form `sub-<label>`, matching a participant entity found in the dataset. There MUST be exactly one row for each participant. |
| species | RECOMMENDED | string | The `species` column SHOULD be a binomial species name from the NCBI Taxonomy (for example, `homo sapiens`, `mus musculus`, `rattus norvegicus`). For backwards compatibility, if `species` is absent, the participant is assumed to be `homo sapiens`. |
| age | RECOMMENDED | number | Numeric value in years (float or integer value). |

| Column name | Requirement Level | Data type | Description |
|---|---|---|---|
| sex | RECOMMENDED | string | String value indicating phenotypical sex, one of ”male”, ”female”, ”other”.For ”male”, use one of these values: `male`, `m`, `M`, `MALE`, `Male`.For ”female”, use one of these values: `female`, `f`, `F`, `FEMALE`, `Female`.For ”other”, use one of these values: `other`, `o`, `O`, `OTHER`, `Other`. Must be one of: `"male"`, `"m"`, `"M"`, `"MALE"`, `"Male"`, `"female"`, `"f"`, `"F"`, `"FEMALE"`, `"Female"`, `"other"`, `"o"`, `"O"`, `"OTHER"`, `"Other"`, `"n/a"`. |
| handedness | RECOMMENDED | string | String value indicating one of ”left”, ”right”, ”ambidextrous”.For ”left”, use one of these values: `left`, `l`, `L`, `LEFT`, `Left`.For ”right”, use one of these values: `right`, `r`, `R`, `RIGHT`, `Right`.For ”ambidextrous”, use one of these values: `ambidextrous`, `a`, `A`, `AMBIDEXTROUS`, `Ambidextrous`. Must be one of: `"left"`, `"l"`, `"L"`, `"LEFT"`, `"Left"`, `"right"`, `"r"`, `"R"`, `"RIGHT"`, `"Right"`, `"ambidextrous"`, `"a"`, `"A"`, `"AMBIDEXTROUS"`, `"Ambidextrous"`, `"n/a"`. |
| strain | RECOMMENDED | string | For species different from `homo sapiens`, string value indicating the strain of the species, for example: `C57BL/6J`. |
| strain_rrid | RECOMMENDED | string | For species different from `homo sapiens`, research resource identifier (RRID) of the strain of the species, for example: `RRID:IMSR_JAX:000664`. |

Throughout BIDS you can indicate missing values with `n/a` (for ”not available”).

`participants.tsv` example:

```
participant_id age sex handedness group
```

```
sub-01 34 M right read
sub-02 12 F right write
sub-03 33 F n/a read
```

It is RECOMMENDED to accompany each `participants.tsv` file with a sidecar `participants.json` file to describe the TSV column names and properties of their values (see also the section on tabular files). Such sidecar files are needed to interpret the data, especially so when optional columns are defined beyond `age`, `sex`, `handedness`, `species`, `strain`, and `strain_rrid`, such as `group` in this example, or when a different age unit is needed (for example, gestational weeks). If no `units` is provided for age, it will be assumed to be in years relative to date of birth.

`participants.json` example:

```
{
    "age": {
        "Description": "age of the participant",
        "Units": "years"
    },
    "sex": {
        "Description": "sex of the participant as reported by the participant",
        "Levels": {
            "M": "male",
            "F": "female"
        }
    },
    "handedness": {
        "Description": "handedness of the participant as reported by the participant",
        "Levels": {
            "left": "left",
            "right": "right"
        }
    },
    "group": {
        "Description": "experimental group the participant belonged to",
        "Levels": {
            "read": "participants who read an inspirational text before the experiment",
            "write": "participants who wrote an inspirational text before the experiment"
        }
    }
}
```

## Samples file

Template:

`samples.tsv`
`samples.json`

The purpose of this file is to describe properties of samples, indicated by the `sample` entity. This file is REQUIRED if `sample-<label>` is present in any filename within the dataset. Each sample MUST be described by one and only one row.

| Column name | Requirement Level | Data type | Description |
|---|---|---|---|
| sample_id | REQUIRED | string | A sample identifier of the form `sample-<label>`, matching a sample entity found in the dataset. The combination of `sample_id` and `participant_id` MUST be unique. |
| participant_id | REQUIRED | string | A participant identifier of the form `sub-<label>`, matching a participant entity found in the dataset. The combination of `sample_id` and `participant_id` MUST be unique. |
| sample_type | REQUIRED | string | Biosample type defined by ENCODE Biosample Type. Must be one of: `"cell line"`, `"in vitro differentiated cells"`, `"primary cell"`, `"cell-free sample"`, `"cloning host"`, `"tissue"`, `"whole organisms"`, `"organoid"`, `"technical sample"`. |
| pathology | RECOMMENDED | string | String value describing the pathology of the sample or type of control. When different from `healthy`, pathology SHOULD be specified. The pathology may be specified in either `samples.tsv` or `sessions.tsv`, depending on whether the pathology changes over time. |
| derived_from | RECOMMENDED | string | `sample-<label>` key/value pair from which a sample is derived, for example a slice of tissue (`sample-02`) derived from a block of tissue (`sample-01`). |

`samples.tsv` example:

```
sample_id participant_id sample_type derived_from
sample-01 sub-01 tissue n/a
sample-02 sub-01 tissue sample-01
sample-03 sub-01 tissue sample-01
sample-04 sub-02 tissue n/a
sample-05 sub-02 tissue n/a
```

It is RECOMMENDED to accompany each `samples.tsv` file with a sidecar `samples.json` file to describe the TSV column names and properties of their values (see also the section on tabular files).

`samples.json` example:

```
{
    "sample_type": {
        "Description": "type of sample from ENCODE Biosample Type (https://www.encodeproject.org/profiles/biosample_type)",
    },
    "derived_from": {
        "Description": "sample_id from which the sample is derived"
    }
}
```

## Phenotypic and assessment data

Template:

```
phenotype/
    <measurement_tool_name>.tsv
    <measurement_tool_name>.json
```

Optional: Yes

If the dataset includes multiple sets of participant level measurements (for example responses from multiple questionnaires) they can be split into individual files separate from `participants.tsv`.

Each of the measurement files MUST be kept in a `/phenotype` directory placed at the root of the BIDS dataset and MUST end with the `.tsv` extension. File names SHOULD be chosen to reflect the contents of the file. For example, the "Adult ADHD Clinical Diagnostic Scale" could be saved in a file called `/phenotype/acds_adult.tsv`.

The files can include an arbitrary set of columns, but one of them MUST be `participant_id` and the entries of that column MUST correspond to the subjects in the BIDS dataset and `participants.tsv` file.

As with all other tabular data, the additional phenotypic information files MAY be accompanied by a JSON file describing the columns in detail (see Tabular files).

In addition to the column descriptions, the JSON file MAY contain the following fields:

| Key name | Requirement Level | Data type | Description |
|---|---|---|---|
| MeasurementToolMetadata | OPTIONAL | object | A description of the measurement tool as a whole. Contains two fields: `"Description"` and `"TermURL"`. `"Description"` is a free text description of the measurement tool. `"TermURL"` is a URL to an entity in an ontology corresponding to this tool. |
| Derivative | OPTIONAL | boolean | Indicates that values in the corresponding column are transformations of values from other columns (for example a summary score based on a subset of items in a questionnaire). Must be one of: `"true"`, `"false"`. |

As an example, consider the contents of a file called `phenotype/acds_adult.json`:

```
{
  "MeasurementToolMetadata": {
    "Description": "Adult ADHD Clinical Diagnostic Scale V1.2",
    "TermURL": "https://www.cognitiveatlas.org/task/id/trm_5586ff878155d"
  },
  "adhd_b": {
    "Description": "B. CHILDHOOD ONSET OF ADHD (PRIOR TO AGE 7)",
    "Levels": {
      "1": "YES",
      "2": "NO"
    }
  },
  "adhd_c_dx": {
    "Description": "As child met A, B, C, D, E and F diagnostic criteria",
    "Levels": {
      "1": "YES",
      "2": "NO"
    }
  }
}
```

Please note that in this example `MeasurementToolMetadata` includes information about the questionnaire and `adhd_b` and `adhd_c_dx` correspond to individual columns.

In addition to the keys available to describe columns in all tabular files (`LongName`, `Description`, `Levels`, `Units`, and `TermURL`) the `participants.json` file as well as phenotypic files can also include column descriptions with a `Derivative` field that, when set to true, indicates that values in the corresponding column is a transformation of values from other columns (for example a summary score based on a subset of items in a questionnaire).

## Scans file

Template:

```
sub-<label>/
    [ses-<label>/]
        sub-<label>[_ses-<label>]_scans.tsv
        sub-<label>[_ses-<label>]_scans.json
```

Optional: Yes

The purpose of this file is to describe timing and other properties of each imaging acquisition sequence (each run file) within one session.

Each neural recording file SHOULD be described by exactly one row. Some recordings consist of multiple parts, that span several files, for example through `echo-`, `part-`, or `split-` entities. Such recordings MUST be documented with one row per file.

| Column name | Requirement Level | Data type | Description |
|---|---|---|---|
| filename | REQUIRED | string | Relative paths to files. There MUST be exactly one row for each file. |
| acq_time | OPTIONAL | string | Acquisition time refers to when the first data point in each run was acquired. Furthermore, if this header is provided, the acquisition times of all files from the same recording MUST be identical. Datetime format and their anonymization are described in Units. |

Additional fields can include external behavioral measures relevant to the scan. For example vigilance questionnaire score administered after a resting state scan. All such included additional fields SHOULD be documented in an accompanying `_scans.json` file that describes these fields in detail (see Tabular files).

Example `_scans.tsv`:

```
filename    acq_time
func/sub-control01_task-nback_bold.nii.gz   1877-06-15T13:45:30
func/sub-control01_task-motor_bold.nii.gz   1877-06-15T13:55:33
meg/sub-control01_task-rest_split-01_meg.nii.gz 1877-06-15T12:15:27
meg/sub-control01_task-rest_split-02_meg.nii.gz 1877-06-15T12:15:27
```

## Sessions file

Template:

```
sub-<label>/
    sub-<label>_sessions.tsv
```

Optional: Yes

In case of multiple sessions there is an option of adding additional `sessions.tsv` files describing variables changing between sessions. In such case one file per participant SHOULD be added. These files MUST include a `session_id` column and describe each session by one and only one row. Column names in `sessions.tsv` files MUST be different from group level participant key column names in the `participants.tsv` file.

| Column name | Requirement Level | Data type | Description |
|---|---|---|---|
| session_id | REQUIRED | string | A session identifier of the form `ses-<label>`, matching a session found in the dataset. There MUST be exactly one row for each session. |
| acq_time | OPTIONAL | string | Acquisition time refers to when the first data point of the first run was acquired. Datetime format and their anonymization are described in Units. |
| pathology | RECOMMENDED | string | String value describing the pathology of the sample or type of control. When different from `healthy`, pathology SHOULD be specified. The pathology may be specified in either `samples.tsv` or `sessions.tsv`, depending on whether the pathology changes over time. |

`_sessions.tsv` example:

```
session_id  acq_time    systolic_blood_pressure
ses-predrug 2009-06-15T13:45:30 120
ses-postdrug    2009-06-16T13:45:30 100
ses-followup    2009-06-17T13:45:30 110
```

## Code

Template: `code/*`

Source code of scripts that were used to prepare the dataset MAY be stored here. Examples include anonymization or defacing of the data, or the conversion from the format of the source data to the BIDS format (see source vs. raw vs. derived data). Extra care should be taken to avoid including original IDs or any identifiable information with the source code. There are no limitations or recommendations on the language and/or code organization of these scripts at the moment.

# Magnetic Resonance Imaging

## Common metadata fields

MR Data described in the following sections share the following RECOMMENDED metadata fields (stored in sidecar JSON files). MRI acquisition parameters are divided into several categories based on ”A checklist for fMRI acquisition methods reporting in the literature” (article, checklist) by Ben Inglis.

### Scanner Hardware

| Key name | Requirement Level | Data type | Description |
|---|---|---|---|
| Manufacturer | RECOMMENDED | string | Manufacturer of the equipment that produced the measurements. Corresponds to DICOM Tag 0008, 0070 `Manufacturer`. |
| ManufacturersModelName | RECOMMENDED | string | Manufacturer’s model name of the equipment that produced the measurements. Corresponds to DICOM Tag 0008, 1090 `Manufacturers Model Name`. |
| DeviceSerialNumber | RECOMMENDED | string | The serial number of the equipment that produced the measurements. A pseudonym can also be used to prevent the equipment from being identifiable, so long as each pseudonym is unique within the dataset. Corresponds to DICOM Tag 0018, 1000 `DeviceSerialNumber`. |

| Key name | Requirement Level | Data type | Description |
|---|---|---|---|
| StationName | RECOMMENDED | string | Institution defined name of the machine that produced the measurements. Corresponds to DICOM Tag 0008, 1010 `Station Name`. |
| SoftwareVersions | RECOMMENDED | string | Manufacturer's designation of software version of the equipment that produced the measurements. Corresponds to DICOM Tag 0018, 1020 `Software Versions`. |
| HardcopyDeviceSoftwareVersion | DEPRECATED | string | Manufacturer's designation of the software of the device that created this Hardcopy Image (the printer). Corresponds to DICOM Tag 0018, 101A `Hardcopy Device Software Version`. |
| MagneticFieldStrength | RECOMMENDED, but REQUIRED for Arterial Spin Labeling | number | Nominal field strength of MR magnet in Tesla. Corresponds to DICOM Tag 0018, 0087 `Magnetic Field Strength`. |
| ReceiveCoilName | RECOMMENDED | string | Information describing the receiver coil. Corresponds to DICOM Tag 0018, 1250 `Receive Coil Name`, although not all vendors populate that DICOM Tag, in which case this field can be derived from an appropriate private DICOM field. |
| ReceiveCoilActiveElements | RECOMMENDED | string | Information describing the active/selected elements of the receiver coil. This does not correspond to a tag in the DICOM ontology. The vendor-defined terminology for active coil elements can go in this field. See an example below the table. |
| GradientSetType | RECOMMENDED | string | It should be possible to infer the gradient coil from the scanner model. If not, for example because of a custom upgrade or use of a gradient insert set, then the specifications of the actual gradient coil should be reported independently. |

| Key name | Requirement Level | Data type | Description |
|---|---|---|---|
| MRTransmitCoilSequence | RECOMMENDED | string | This is a relevant field if a non-standard transmit coil is used. Corresponds to DICOM Tag 0018, 9049 `MR Transmit Coil Sequence`. |
| MatrixCoilMode | RECOMMENDED | string | (If used) A method for reducing the number of independent channels by combining in analog the signals from multiple coil elements. There are typically different default modes when using un-accelerated or accelerated (for example, `"GRAPPA"`, `"SENSE"`) imaging. |
| CoilCombinationMethod | RECOMMENDED | string | Almost all fMRI studies using phased-array coils use root-sum-of-squares (rSOS) combination, but other methods exist. The image reconstruction is changed by the coil combination method (as for the matrix coil mode above), so anything non-standard should be reported. |

Example for `ReceiveCoilActiveElements`:

For Siemens, coil channels are typically not activated/selected individually, but rather in pre-defined selectable ”groups” of individual channels, and the list of the ”groups” of elements that are active/selected in any given scan populates the `Coil String` entry in Siemens’ private DICOM fields (for example, `HEA;HEP` for the Siemens standard 32 ch coil when both the anterior and posterior groups are activated). This is a flexible field that can be used as most appropriate for a given vendor and coil to define the ”active” coil elements. Since individual scans can sometimes not have the intended coil elements selected, it is preferable for this field to be populated directly from the DICOM for each individual scan, so that it can be used as a mechanism for checking that a given scan was collected with the intended coil elements selected

## Sequence Specifics

| Key name | Requirement Level | Data type | Description |
|---|---|---|---|
| PulseSequenceType | RECOMMENDED | string | A general description of the pulse sequence used for the scan (for example, `"MPRAGE"`, `"Gradient Echo EPI"`, `"Spin Echo EPI"`, `"Multiband gradient echo EPI"`). |

| Key name | Requirement Level | Data type | Description |
|---|---|---|---|
| ScanningSequence | RECOMMENDED | string or array of strings | Description of the type of data acquired. Corresponds to DICOM Tag 0018, 0020 `Scanning Sequence`. |
| SequenceVariant | RECOMMENDED | string or array of strings | Variant of the ScanningSequence. Corresponds to DICOM Tag 0018, 0021 `Sequence Variant`. |
| ScanOptions | RECOMMENDED | string or array of strings | Parameters of ScanningSequence. Corresponds to DICOM Tag 0018, 0022 `Scan Options`. |
| SequenceName | RECOMMENDED | string | Manufacturer's designation of the sequence name. Corresponds to DICOM Tag 0018, 0024 `Sequence Name`. |
| PulseSequenceDetails | RECOMMENDED | string | Information beyond pulse sequence type that identifies the specific pulse sequence used (for example, `"Standard Siemens Sequence distributed with the VB17 software"`, `"Siemens WIP ### version #.##,"` or `"Sequence written by X using a version compiled on MM/DD/YYYY"`). |
| NonlinearGradientCorrection | RECOMMENDED, but REQUIRED if PET data are present | boolean | Boolean stating if the image saved has been corrected for gradient nonlinearities by the scanner sequence. Must be one of: `"true"`, `"false"`. |
| MRAcquisitionType | RECOMMENDED, but REQUIRED for Arterial Spin Labeling | string | Type of sequence readout. Corresponds to DICOM Tag 0018, 0023 `MR Acquisition Type`. Must be one of: `"2D"`, `"3D"`. |
| MTState | RECOMMENDED | boolean | Boolean stating whether the magnetization transfer pulse is applied. Corresponds to DICOM Tag 0018, 9020 `Magnetization Transfer`. Must be one of: `"true"`, `"false"`. |
| MTOffsetFrequency | RECOMMENDED if the MTstate is `True`. | number | The frequency offset of the magnetization transfer pulse with respect to the central H1 Larmor frequency in Hertz (Hz). |

| Key name | Requirement Level | Data type | Description |
|---|---|---|---|
| MTPulseBandwidth | RECOMMENDED if the MTstate is `True`. | number | The excitation bandwidth of the magnetization transfer pulse in Hertz (Hz). |
| MTNumberOfPulses | RECOMMENDED if the MTstate is `True`. | number | The number of magnetization transfer RF pulses applied before the readout. |
| MTPulseShape | RECOMMENDED if the MTstate is `True`. | string | Shape of the magnetization transfer RF pulse waveform. The value `"GAUSSHANN"` refers to a Gaussian pulse with a Hanning window. The value `"SINCHANN"` refers to a sinc pulse with a Hanning window. The value `"SINCGAUSS"` refers to a sinc pulse with a Gaussian window. Must be one of: `"HARD"`, `"GAUSSIAN"`, `"GAUSSHANN"`, `"SINC"`, `"SINCHANN"`, `"SINCGAUSS"`, `"FERMI"`. |
| MTPulseDuration | RECOMMENDED if the MTstate is `True`. | number | Duration of the magnetization transfer RF pulse in seconds. |
| SpoilingState | RECOMMENDED | boolean | Boolean stating whether the pulse sequence uses any type of spoiling strategy to suppress residual transverse magnetization. Must be one of: `"true"`, `"false"`. |
| SpoilingType | RECOMMENDED if the SpoilingState is `True`. | string | Specifies which spoiling method(s) are used by a spoiled sequence. Must be one of: `"RF"`, `"GRADIENT"`, `"COMBINED"`. |
| SpoilingRFPhaseIncrement | RECOMMENDED if the SpoilingType is `"RF"` or `"COMBINED"`. | number | The amount of incrementation described in degrees, which is applied to the phase of the excitation pulse at each TR period for achieving RF spoiling. |
| SpoilingGradientMoment | RECOMMENDED if the SpoilingType is `"GRADIENT"` or `"COMBINED"`. | number | Zeroth moment of the spoiler gradient lobe in millitesla times second per meter (mT.s/m). |
| SpoilingGradientDuration | RECOMMENDED if the SpoilingType is `"GRADIENT"` or `"COMBINED"`. | number | The duration of the spoiler gradient lobe in seconds. The duration of a trapezoidal lobe is defined as the summation of ramp-up and plateau times. |

### In-Plane Spatial Encoding

| Key name | Requirement Level | Data type | Description |
|---|---|---|---|
| NumberShots | RECOMMENDED | number or array of numbers | The number of RF excitations needed to reconstruct a slice or volume (may be referred to as partition). Please mind that this is not the same as Echo Train Length which denotes the number of k-space lines collected after excitation in a multi-echo readout. The data type array is applicable for specifying this parameter before and after the k-space center is sampled. Please see `"NumberShots"` metadata field in the qMRI appendix for corresponding calculations. |
| ParallelReductionFactorInPlane | RECOMMENDED | number | The parallel imaging (for instance, GRAPPA) factor. Use the denominator of the fraction of k-space encoded for each slice. For example, 2 means half of k-space is encoded. Corresponds to DICOM Tag 0018, 9069 `Parallel Reduction Factor In-plane`. |
| ParallelAcquisitionTechnique | RECOMMENDED | string | The type of parallel imaging used (for example `"GRAPPA"`, `"SENSE"`). Corresponds to DICOM Tag 0018, 9078 `Parallel Acquisition Technique`. |
| PartialFourier | RECOMMENDED | number | The fraction of partial Fourier information collected. Corresponds to DICOM Tag 0018, 9081 `Partial Fourier`. |
| PartialFourierDirection | RECOMMENDED | string | The direction where only partial Fourier information was collected. Corresponds to DICOM Tag 0018, 9036 `Partial Fourier Direction`. |

| Key name | Requirement Level | Data type | Description |
|---|---|---|---|
| PhaseEncodingDirection | RECOMMENDED | string | The letters `i`, `j`, `k` correspond to the first, second and third axis of the data in the NIFTI file. The polarity of the phase encoding is assumed to go from zero index to maximum index unless `-` sign is present (then the order is reversed - starting from the highest index instead of zero). `PhaseEncodingDirection` is defined as the direction along which phase is was modulated which may result in visible distortions. Note that this is not the same as the DICOM term `InPlanePhaseEncodingDirection` which can have `ROW` or `COL` values. This parameter is REQUIRED if corresponding fieldmap data is present or when using multiple runs with different phase encoding directions (which can be later used for field inhomogeneity correction).Must be one of: `"i"`, `"j"`, `"k"`, `"i-"`, `"j-"`, `"k-"`. |

| Key name | Requirement Level | Data type | Description |
|---|---|---|---|
| EffectiveEchoSpacing | RECOMMENDED | number | The ”effective” sampling interval, specified in seconds, between lines in the phase-encoding direction, defined based on the size of the reconstructed image in the phase direction. It is frequently, but incorrectly, referred to as ”dwell time” (see the `"DwellTime"` parameter for actual dwell time). It is required for unwarping distortions using field maps. Note that beyond just in-plane acceleration, a variety of other manipulations to the phase encoding need to be accounted for properly, including partial fourier, phase oversampling, phase resolution, phase field-of-view and interpolation. 2 This parameter is REQUIRED if corresponding fieldmap data is present.Must be a number greater than 0. |
| TotalReadoutTime | RECOMMENDED | number | This is actually the ”effective” total readout time, defined as the readout duration, specified in seconds, that would have generated data with the given level of distortion. It is NOT the actual, physical duration of the readout train. If `"EffectiveEchoSpacing"` has been properly computed, it is just `EffectiveEchoSpacing * (ReconMatrixPE - 1)`. 3 This parameter is REQUIRED if corresponding ’field/distortion’ maps acquired with opposing phase encoding directions are present (see Case 4: Multiple phase encoded directions). |

| Key name | Requirement Level | Data type | Description |
|---|---|---|---|
| MixingTime | RECOMMENDED | number | In the context of a stimulated- and spin-echo 3D EPI sequence for B1+ mapping, corresponds to the interval between spin- and stimulated-echo pulses. In the context of a diffusion-weighted double spin-echo sequence, corresponds to the interval between two successive diffusion sensitizing gradients, specified in seconds. |

2Conveniently, for Siemens data, this value is easily obtained as `1 / (BWPPPE * ReconMatrixPE)`, where BWPPPE is the ”BandwidthPerPixelPhaseEncode” in DICOM Tag 0019, 1028 and ReconMatrixPE is the size of the actual reconstructed data in the phase direction (which is NOT reflected in a single DICOM Tag for all possible aforementioned scan manipulations). See here and here

3We use the time between the center of the first ”effective” echo and the center of the last ”effective” echo, sometimes called the ”FSL definition”.

## Timing Parameters

| Key name | Requirement Level | Data type | Description |
|---|---|---|---|
| EchoTime | RECOMMENDED, but REQUIRED if corresponding fieldmap data is present, or the data comes from a multi echo sequence or Arterial Spin Labeling | number or array of numbers | The echo time (TE) for the acquisition, specified in seconds. Corresponds to DICOM Tag 0018, 0081 `Echo Time` (please note that the DICOM term is in milliseconds not seconds). The data type number may apply to files from any MRI modality concerned with a single value for this field, or to the files in a file collection where the value of this field is iterated using the file collection. The data type array provides a value for each volume in a 4D dataset and should only be used when the volume timing is critical for interpretation of the data, such as in file collection or variable echo time fMRI sequences. |

| Key name | Requirement Level | Data type | Description |
|---|---|---|---|
| InversionTime | RECOMMENDED | number | The inversion time (TI) for the acquisition, specified in seconds. Inversion time is the time after the middle of inverting RF pulse to middle of excitation pulse to detect the amount of longitudinal magnetization. Corresponds to DICOM Tag 0018, 0082 `Inversion Time` (please note that the DICOM term is in milliseconds not seconds). Must be a number greater than 0. |
| SliceTiming | RECOMMENDED, but REQUIRED for sparse sequences that do not have the `DelayTime` field set, and Arterial Spin Labeling with `MRAcquisitionType` set on `2D`. | array of numbers | The time at which each slice was acquired within each volume (frame) of the acquisition. Slice timing is not slice order -- rather, it is a list of times containing the time (in seconds) of each slice acquisition in relation to the beginning of volume acquisition. The list goes through the slices along the slice axis in the slice encoding dimension (see below). Note that to ensure the proper interpretation of the `"SliceTiming"` field, it is important to check if the OPTIONAL `SliceEncodingDirection` exists. In particular, if `"SliceEncodingDirection"` is negative, the entries in `"SliceTiming"` are defined in reverse order with respect to the slice axis, such that the final entry in the `"SliceTiming"` list is the time of acquisition of slice 0. Without this parameter slice time correction will not be possible. |

| Key name | Requirement Level | Data type | Description |
|---|---|---|---|
| SliceEncodingDirection | RECOMMENDED | string | The axis of the NIfTI data along which slices were acquired, and the direction in which `"SliceTiming"` is defined with respect to. `i`, `j`, `k` identifiers correspond to the first, second and third axis of the data in the NIfTI file. A `-` sign indicates that the contents of `"SliceTiming"` are defined in reverse order - that is, the first entry corresponds to the slice with the largest index, and the final entry corresponds to slice index zero. When present, the axis defined by `"SliceEncodingDirection"` needs to be consistent with the `slice_dim` field in the NIfTI header. When absent, the entries in `"SliceTiming"` must be in the order of increasing slice index as defined by the NIfTI header. Must be one of: `"i"`, `"j"`, `"k"`, `"i-"`, `"j-"`, `"k-"`. |
| DwellTime | RECOMMENDED | number | Actual dwell time (in seconds) of the receiver per point in the readout direction, including any oversampling. For Siemens, this corresponds to DICOM field 0019, 1018 (in ns). This value is necessary for the optional readout distortion correction of anatomicals in the HCP Pipelines. It also usefully provides a handle on the readout bandwidth, which isn't captured in the other metadata tags. Not to be confused with `"EffectiveEchoSpacing"`, and the frequent mislabeling of echo spacing (which is spacing in the phase encoding direction) as ”dwell time” (which is spacing in the readout direction). |

## RF & Contrast

| Key name | Requirement Level | Data type | Description |
|---|---|---|---|
| FlipAngle | RECOMMENDED, but REQUIRED if `LookLocker` is set `true` | number or array of numbers | Flip angle (FA) for the acquisition, specified in degrees. Corresponds to: DICOM Tag 0018, 1314 `Flip Angle`. The data type number may apply to files from any MRI modality concerned with a single value for this field, or to the files in a file collection where the value of this field is iterated using the file collection. The data type array provides a value for each volume in a 4D dataset and should only be used when the volume timing is critical for interpretation of the data, such as in file collection or variable flip angle fMRI sequences. |
| NegativeContrast | OPTIONAL | boolean | `true` or `false` value specifying whether increasing voxel intensity (within sample voxels) denotes a decreased value with respect to the contrast suffix. This is commonly the case when Cerebral Blood Volume is estimated via usage of a contrast agent in conjunction with a T2* weighted acquisition protocol. Must be one of: `"true"`, `"false"`. |

## Slice Acceleration

| Key name | Requirement Level | Data type | Description |
|---|---|---|---|
| MultibandAccelerationFactor | RECOMMENDED | number | The multiband factor, for multiband acquisitions. |

## Anatomical landmarks

Useful for multimodal co-registration with MEG, (S)EEG, TMS, and so on.

| Key name | Requirement Level | Data type | Description |
|---|---|---|---|
| AnatomicalLandmarkCoordinates | RECOMMENDED | object of arrays | Key:value pairs of any number of additional anatomical landmarks and their coordinates in voxel units (where first voxel has index 0,0,0) relative to the associated anatomical MRI (for example, `{"AC": [127,119,149], "PC": [128,93,141], "IH": [131,114,206]}`, or `{"NAS": [127,213,139], "LPA": [52,113,96], "RPA": [202,113,91]}`). Each array MUST contain three numeric values corresponding to x, y, and z axis of the coordinate system in that exact order. |

## Echo-Planar Imaging and B0 mapping

Echo-Planar Imaging (EPI) schemes typically used in the acquisition of diffusion and functional MRI may also be intended for estimating the B0 field nonuniformity inside the scanner (in other words, mapping the field) without the acquisition of additional MRI schemes such as gradient-recalled echo (GRE) sequences that are stored under the `fmap/` folder of the BIDS structure.

The modality labels `dwi` (under `dwi/`), `bold` (under `func/`), `asl` (under `perf/`), `sbref` (under `dwi/`, `func/` or `perf/`), and any modality under `fmap/` are allowed to encode the MR protocol intent for fieldmap estimation using the following metadata:

| Key name | Requirement Level | Data type | Description |
|---|---|---|---|
| B0FieldIdentifier | RECOMMENDED | string or array of strings | The presence of this key states that this particular 3D or 4D image MAY be used for fieldmap estimation purposes. Each `"B0FieldIdentifier"` MUST be a unique string within one participant's tree, shared only by the images meant to be used as inputs for the estimation of a particular instance of the B0 field estimation. It is RECOMMENDED to derive this identifier from DICOM Tags, for example, DICOM tag 0018, 1030 `Protocol Name`, or DICOM tag 0018, 0024 `Sequence Name` when the former is not defined (for example, in GE devices.) |
| B0FieldSource | RECOMMENDED | string or array of strings | At least one existing `"B0FieldIdentifier"` defined by images in the participant's tree. This field states the B0 field estimation designated by the `"B0FieldIdentifier"` that may be used to correct the dataset for distortions caused by B0 inhomogeneities. `"B0FieldSource"` and `"B0FieldIdentifier"` MAY both be present for images that are used to estimate their own B0 field, for example, in ”pepolar” acquisitions. |

## Institution information

| Key name | Requirement Level | Data type | Description |
|---|---|---|---|
| InstitutionName | RECOMMENDED | string | The name of the institution in charge of the equipment that produced the measurements. Corresponds to DICOM Tag 0008, 0080 `InstitutionName`. |

| Key name | Requirement Level | Data type | Description |
|---|---|---|---|
| InstitutionAddress | RECOMMENDED | string | The address of the institution in charge of the equipment that produced the measurements. Corresponds to DICOM Tag 0008, 0081 `InstitutionAddress`. |
| InstitutionalDepartmentName | RECOMMENDED | string | The department in the institution in charge of the equipment that produced the measurements. Corresponds to DICOM Tag 0008, 1040 `Institutional Department Name`. |

When adding additional metadata please use the CamelCase version of DICOM ontology terms whenever possible. See also recommendations on JSON files.

## Anatomy imaging data

Template:

```
sub-<label>/
    [ses-<label>/]
        anat/
            sub-<label>[_ses-<label>][_acq-<label>][_ce-<label>][_rec-<label>][_run-<index>][_part-<mag|phase|real|imag>]_<suffix>.json
            sub-<label>[_ses-<label>][_acq-<label>][_ce-<label>][_rec-<label>][_run-<index>][_part-<mag|phase|real|imag>]_<suffix>.nii[.gz]
            sub-<label>[_ses-<label>][_acq-<label>][_ce-<label>][_rec-<label>][_run-<index>]_<suffix>.json
            sub-<label>[_ses-<label>][_acq-<label>][_ce-<label>][_rec-<label>][_run-<index>]_<suffix>.nii[.gz]
            sub-<label>[_ses-<label>][_acq-<label>][_ce-<label>][_rec-<label>][_run-<index>][_mod-<label>]_defacemask.json
            sub-<label>[_ses-<label>][_acq-<label>][_ce-<label>][_rec-<label>][_run-<index>][_mod-<label>]_defacemask.nii[.gz]
            sub-<label>[_ses-<label>][_acq-<label>][_ce-<label>][_rec-<label>][_run-<index>]_echo-<index>[_part-<mag|phase|real|imag>]_MEGRE.json
            sub-<label>[_ses-<label>][_acq-<label>][_ce-<label>][_rec-<label>][_run-<index>]_echo-<index>[_part-<mag|phase|real|imag>]_MEGRE.nii[.gz]
            sub-<label>[_ses-<label>][_acq-<label>][_ce-<label>][_rec-<label>][_run-<index>]_echo-<index>[_part-<mag|phase|real|imag>]_MESE.json
            sub-<label>[_ses-<label>][_acq-<label>][_ce-<label>][_rec-<label>][_run-<index>]_echo-<index>[_part-<mag|phase|real|imag>]_MESE.nii[.gz]
            sub-<label>[_ses-<label>][_acq-<label>][_ce-<label>][_rec-<label>][_run-<index>][_echo-<index>]_flip-<index>[_part-<mag|phase|real|imag>]_V
            sub-<label>[_ses-<label>][_acq-<label>][_ce-<label>][_rec-<label>][_run-<index>][_echo-<index>]_flip-<index>[_part-<mag|phase|real|imag>]_V
            sub-<label>[_ses-<label>][_acq-<label>][_ce-<label>][_rec-<label>][_run-<index>]_inv-<index>[_part-<mag|phase|real|imag>]_IRT1.json
            sub-<label>[_ses-<label>][_acq-<label>][_ce-<label>][_rec-<label>][_run-<index>]_inv-<index>[_part-<mag|phase|real|imag>]_IRT1.nii[.gz]
            sub-<label>[_ses-<label>][_acq-<label>][_ce-<label>][_rec-<label>][_run-<index>][_echo-<index>][_flip-<index>]_inv-<index>[_part-<mag|phase
            sub-<label>[_ses-<label>][_acq-<label>][_ce-<label>][_rec-<label>][_run-<index>][_echo-<index>][_flip-<index>]_inv-<index>[_part-<mag|phase
            sub-<label>[_ses-<label>][_acq-<label>][_ce-<label>][_rec-<label>][_run-<index>][_echo-<index>]_flip-<index>_mt-<on|off>[_part-<mag|phase|r
            sub-<label>[_ses-<label>][_acq-<label>][_ce-<label>][_rec-<label>][_run-<index>][_echo-<index>]_flip-<index>_mt-<on|off>[_part-<mag|phase|r
            sub-<label>[_ses-<label>][_acq-<label>][_ce-<label>][_rec-<label>][_run-<index>][_echo-<index>]_flip-<index>_mt-<on|off>[_part-<mag|phase|r
```

```
sub-<label>[_ses-<label>][_acq-<label>][_ce-<label>][_rec-<label>][_run-<index>][_echo-<index>]_flip-<index>_mt-<on|off>[_part-<mag|phase|r
sub-<label>[_ses-<label>][_acq-<label>][_ce-<label>][_rec-<label>][_run-<index>]_mt-<on|off>[_part-<mag|phase|real|imag>]_MTR.json
sub-<label>[_ses-<label>][_acq-<label>][_ce-<label>][_rec-<label>][_run-<index>]_mt-<on|off>[_part-<mag|phase|real|imag>]_MTR.nii[.gz]
```

Currently supported non-parametric structural MR images include:

| Name | `suffix` | Description |
|---|---|---|
| T1-weighted image | T1w | In arbitrary units (arbitrary). The contrast of these images is mainly determined by spatial variations in the longitudinal relaxation time of the imaged specimen. In spin-echo sequences this contrast is achieved at relatively short repetition and echo times. To achieve this weighting in gradient-echo images, again, short repetition and echo times are selected; however, at relatively large flip angles. Another common approach to increase T1 weighting in gradient-echo images is to add an inversion preparation block to the beginning of the imaging sequence (for example, `TurboFLASH` or `MP-RAGE`). |
| T2-weighted image | T2w | In arbitrary units (arbitrary). The contrast of these images is mainly determined by spatial variations in the (true) transverse relaxation time of the imaged specimen. In spin-echo sequences this contrast is achieved at relatively long repetition and echo times. Generally, gradient echo sequences are not the most suitable option for achieving T2 weighting, as their contrast natively depends on T2-star rather than on T2. |
| Proton density (PD) weighted image | PDw | In arbitrary units (arbitrary). The contrast of these images is mainly determined by spatial variations in the spin density (1H) of the imaged specimen. In spin-echo sequences this contrast is achieved at short repetition and long echo times. In a gradient-echo acquisition, PD weighting dominates the contrast at long repetition and short echo times, and at small flip angles. |

| Name | `suffix` | Description |
|---|---|---|
| T2star weighted image | T2starw | In arbitrary units (arbitrary). The contrast of these images is mainly determined by spatial variations in the (observed) transverse relaxation time of the imaged specimen. In spin-echo sequences, this effect is negated as the excitation is followed by an inversion pulse. The contrast of gradient-echo images natively depends on T2-star effects. However, for T2-star variation to dominate the image contrast, gradient-echo acquisitions are carried out at long repetition and echo times, and at small flip angles. |
| Fluid attenuated inversion recovery image | FLAIR | In arbitrary units (arbitrary). Structural images with predominant T2 contribution (also known as T2-FLAIR), in which signal from fluids (for example, CSF) is nulled out by adjusting inversion time, coupled with notably long repetition and echo times. |
| Inplane T1 | inplaneT1 | In arbitrary units (arbitrary). T1 weighted structural image matched to a functional (task) image. |
| Inplane T2 | inplaneT2 | In arbitrary units (arbitrary). T2 weighted structural image matched to a functional (task) image. |
| PD and T2 weighted image | PDT2 | In arbitrary units (arbitrary). PDw and T2w images acquired using a dual echo FSE sequence through view sharing process (Johnson et al. 1994). |
| Homogeneous (flat) T1-weighted MP2RAGE image | UNIT1 | In arbitrary units (arbitrary). UNIT1 images are REQUIRED to use this suffix regardless of the method used to generate them. Note that although this image is T1-weighted, regions without MR signal will contain white salt-and-pepper noise that most segmentation algorithms will fail on. Therefore, it is important to dissociate it from `T1w`. Please see `MP2RAGE` specific notes in the qMRI appendix for further information. |
| Angiogram | angio | Magnetic resonance angiography sequences focus on enhancing the contrast of blood vessels (generally arteries, but sometimes veins) against other tissue types. |

If the structural images included in the dataset were defaced (to protect identity of participants) one MAY provide the binary mask that was used to remove facial features in the form of `_defacemask` files. In such cases, the OPTIONAL `mod-<label>` key/value pair corresponds to modality suffix, such as T1w or inplaneT1, referenced by the defacemask image. For example, `sub-01_mod-T1w_defacemask.nii.gz`.

If several scans with the same acquisition parameters are acquired in the same session, they MUST be indexed with the `run-<index>` entity: `_run-1`, `_run-2`, `_run-3`, and so on (only nonnegative integers are allowed as run labels).

If different entities apply, such as a different session indicated by `ses-<label>`, or different acquisition parameters indicated by `acq-<label>`, then `run` is not needed to distinguish the scans and MAY be omitted.

The OPTIONAL `acq-<label>` key/value pair corresponds to a custom label the user MAY use to distinguish a different set of parameters used for acquiring the same modality. For example this should be used when a study includes two T1w images - one full brain low resolution and one restricted field of view but high resolution. In such case two files could have the following names: `sub-01_acq-highres_T1w.nii.gz` and `sub-01_acq-lowres_T1w.nii.gz`, however the user is free to choose any other label than `highres` and `lowres` as long as they are consistent across subjects and sessions. In case different sequences are used to record the same modality (for example, RARE and FLASH for T1w) this field can also be used to make that distinction. At what level of detail to make the distinction (for example, just between RARE and FLASH, or between RARE, FLASH, and FLASHsubsampled) remains at the discretion of the researcher.

Similarly the OPTIONAL `ce-<label>` key/value can be used to distinguish sequences using different contrast enhanced images. The label is the name of the contrast agent. The key `ContrastBolusIngredient` MAY be also be added in the JSON file, with the same label.

Some meta information about the acquisition MAY be provided in an additional JSON file. See Common metadata fields for a list of terms and their definitions. There are also some OPTIONAL JSON fields specific to anatomical scans:

| Key name | Requirement Level | Data type | Description |
|---|---|---|---|
| ContrastBolusIngredient | OPTIONAL | string | Active ingredient of agent. Corresponds to DICOM Tag 0018, 1048 `Contrast/Bolus Ingredient`. Must be one of: `"IODINE"`, `"GADOLINIUM"`, `"CARBON DIOXIDE"`, `"BARIUM"`, `"XENON"`. |

| Key name | Requirement Level | Data type | Description |
|---|---|---|---|
| RepetitionTimeExcitation | OPTIONAL | number | The interval, in seconds, between two successive excitations. [DICOM Tag 0018, 0080](http://dicomlookup.com/lookup.asp?sw=Tnumber&q=(0018,0080) best refers to this parameter. This field may be used together with the `"RepetitionTimePreparation"` for certain use cases, such as MP2RAGE. Use `RepetitionTimeExcitation` (in combination with `"RepetitionTimePreparation"` if needed) for anatomy imaging data rather than `"RepetitionTime"` as it is already defined as the amount of time that it takes to acquire a single volume in the task imaging data section. Must be a number greater than or equal to 0. |
| RepetitionTimePreparation | OPTIONAL | number or array of numbers | The interval, in seconds, that it takes a preparation pulse block to re-appear at the beginning of the succeeding (essentially identical) pulse sequence block. The data type number may apply to files from any MRI modality concerned with a single value for this field. The data type array provides a value for each volume in a 4D dataset and should only be used when the volume timing is critical for interpretation of the data, such as in ASL. |

The `part-<label>` key/value pair is used to indicate which component of the complex representation of the MRI signal is represented in voxel data. This entity is associated with the DICOM Tag `0008, 9208`. Allowed label values for this entity are `phase`, `mag`, `real` and `imag`, which are typically used in `part-mag`/`part-phase` or `part-real`/`part-imag` pairs of files. For example:

```
sub-01/
   anat/
      sub-01_part-mag_T1w.nii.gz
      sub-01_part-mag_T1w.json
```

```
        sub-01_part-phase_T1w.nii.gz
        sub-01_part-phase_T1w.json
```

Phase images MAY be in radians or in arbitrary units. The sidecar JSON file MUST include the units of the `phase` image. The possible options are `rad` or `arbitrary`.

For example, for `sub-01_part-phase_T1w.json`:

```
{
   "Units": "rad"
}
```

When there is only a magnitude image of a given type, the `part` key MAY be omitted.

Similarly, the OPTIONAL `rec-<label>` key/value can be used to distinguish different reconstruction algorithms (for example ones using motion correction).

Structural MR images whose intensity is represented in a non-arbitrary scale constitute parametric maps. Currently supported parametric maps include:

| Name | `suffix` | Description |
|---|---|---|
| Longitudinal relaxation time image | T1map | In seconds (s). T1 maps are REQUIRED to use this suffix regardless of the method used to generate them. See this interactive book on T1 mapping for further reading on T1-mapping. |
| Longitudinal relaxation rate image | R1map | In seconds-1 (1/s). R1 maps (R1 = 1/T1) are REQUIRED to use this suffix regardless of the method used to generate them. |
| True transverse relaxation time image | T2map | In seconds (s). T2 maps are REQUIRED to use this suffix regardless of the method used to generate them. |
| True transverse relaxation rate image | R2map | In seconds-1 (1/s). R2 maps (R2 = 1/T2) are REQUIRED to use this suffix regardless of the method used to generate them. |
| Observed transverse relaxation time image | T2starmap | In seconds (s). T2-star maps are REQUIRED to use this suffix regardless of the method used to generate them. |
| Observed transverse relaxation rate image | R2starmap | In seconds-1 (1/s). R2-star maps (R2star = 1/T2star) are REQUIRED to use this suffix regardless of the method used to generate them. |
| Proton density image | PDmap | In arbitrary units (arbitrary). PD maps are REQUIRED to use this suffix regardless of the method used to generate them. |

| Name | `suffix` | Description |
|---|---|---|
| Magnetization transfer ratio image | MTRmap | In arbitrary units (arbitrary). MTR maps are REQUIRED to use this suffix regardless of the method used to generate them. MTRmap intensity values are RECOMMENDED to be represented in percentage in the range of 0-100%. |
| Magnetization transfer saturation image | MTsat | In arbitrary units (arbitrary). MTsat maps are REQUIRED to use this suffix regardless of the method used to generate them. |
| T1 in rotating frame (T1 rho) image | T1rho | In seconds (s). T1-rho maps are REQUIRED to use this suffix regardless of the method used to generate them. |
| Myelin water fraction image | MWFmap | In arbitrary units (arbitrary). MWF maps are REQUIRED to use this suffix regardless of the method used to generate them. MWF intensity values are RECOMMENDED to be represented in percentage in the range of 0-100%. |
| Macromolecular tissue volume (MTV) image | MTVmap | In arbitrary units (arbitrary). MTV maps are REQUIRED to use this suffix regardless of the method used to generate them. |
| Combined PD/T2 image | PDT2map | In arbitrary units (arbitrary). Combined PD/T2 maps are REQUIRED to use this suffix regardless of the method used to generate them. |
| Quantitative susceptibility map (QSM) | Chimap | In parts per million (ppm). QSM allows for determining the underlying magnetic susceptibility of tissue (Chi) (Wang & Liu, 2014). Chi maps are REQUIRED to use this suffix regardless of the method used to generate them. |
| RF transmit field image | TB1map | In arbitrary units (arbitrary). Radio frequency (RF) transmit (B1+) field maps are REQUIRED to use this suffix regardless of the method used to generate them. TB1map intensity values are RECOMMENDED to be represented as percent multiplicative factors such that FlipAngleeffective = B1+intensity*FlipAnglenominal . |

| Name | `suffix` | Description |
|---|---|---|
| RF receive sensitivity map | RB1map | In arbitrary units (arbitrary). Radio frequency (RF) receive (B1-) sensitivity maps are REQUIRED to use this suffix regardless of the method used to generate them. RB1map intensity values are RECOMMENDED to be represented as percent multiplicative factors such that Amplitudeeffective = B1-intensity*Amplitudeideal. |
| Observed signal amplitude (S0) image | S0map | In arbitrary units (arbitrary). For a multi-echo (typically fMRI) sequence, S0 maps index the baseline signal before exponential (T2-star) signal decay. In other words: the exponential of the intercept for a linear decay model across log-transformed echos. For more information, please see, for example, the tedana documentation. S0 maps are RECOMMENDED to use this suffix if derived from an ME-FMRI dataset. |
| Equilibrium magnetization (M0) map | M0map | In arbitrary units (arbitrary). A common quantitative MRI (qMRI) fitting variable that represents the amount of magnetization at thermal equilibrium. M0 maps are RECOMMENDED to use this suffix if generated by qMRI applications (for example, variable flip angle T1 mapping). |

Parametric images listed in the table above are typically generated by processing a file collection. Please visit the file collections appendix to see the list of suffixes available for quantitative MRI (qMRI) applications associated with these maps. For any other details on the organization of parametric maps, their recommended metadata fields, and the application specific entity or metadata requirement levels of file collections that can generate them, visit the qMRI appendix.

## Deprecated suffixes

Some suffixes that were available in versions of the specification prior to 1.5.0 have been deprecated. These suffixes are ambiguous and have been superseded by more precise conventions. Therefore, they are not recommended for use in new datasets. They are, however, still valid suffixes, to maintain backwards compatibility.

The following suffixes are valid, but SHOULD NOT be used for new BIDS compatible datasets (created after version 1.5.0.):

| Name | `suffix` | Description |
|---|---|---|
| T2* image | T2star | Ambiguous, may refer to a parametric image or to a conventional image. Change: Replaced by `T2starw` or `T2starmap`. |

| Name | `suffix` | Description |
|---|---|---|
| Fast-Low-Angle-Shot image | FLASH | FLASH (Fast-Low-Angle-Shot) is a vendor-specific implementation for spoiled gradient echo acquisition. It is commonly used for rapid anatomical imaging and also for many different qMRI applications. When used for a single file, it does not convey any information about the image contrast. When used in a file collection, it may result in conflicts across filenames of different applications. Change: Removed from suffixes. |
| Proton density image | PD | Ambiguous, may refer to a parametric image or to a conventional image. Change: Replaced by `PDw` or `PDmap`. |

## Task (including resting state) imaging data

Currently supported image contrasts include:

| Name | `suffix` | Description |
|---|---|---|
| Blood-Oxygen-Level Dependent image | bold | Blood-Oxygen-Level Dependent contrast (specialized T2* weighting) |
| Cerebral blood volume image | cbv | Cerebral Blood Volume contrast (specialized T2* weighting or difference between T1 weighted images) |
| Phase image | phase | DEPRECATED. Phase information associated with magnitude information stored in BOLD contrast. This suffix should be replaced by the DEPRECATED in conjunction with the `bold` suffix. |

Template:

```
sub-<label>/
    [ses-<label>/]
        func/
            sub-<label>[_ses-<label>]_task-<label>[_acq-<label>][_ce-<label>][_rec-<label>][_dir-<label>][_run-<index>][_echo-<index>][_part-<mag|phase
            sub-<label>[_ses-<label>]_task-<label>[_acq-<label>][_ce-<label>][_rec-<label>][_dir-<label>][_run-<index>][_echo-<index>][_part-<mag|phase
            sub-<label>[_ses-<label>]_task-<label>[_acq-<label>][_ce-<label>][_rec-<label>][_dir-<label>][_run-<index>][_echo-<index>][_part-<mag|phase
            sub-<label>[_ses-<label>]_task-<label>[_acq-<label>][_ce-<label>][_rec-<label>][_dir-<label>][_run-<index>][_echo-<index>][_part-<mag|phase
            sub-<label>[_ses-<label>]_task-<label>[_acq-<label>][_ce-<label>][_rec-<label>][_dir-<label>][_run-<index>][_echo-<index>][_part-<mag|phase
```

```
sub-<label>[_ses-<label>]_task-<label>[_acq-<label>][_ce-<label>][_rec-<label>][_dir-<label>][_run-<index>][_echo-<index>][_part-<mag|phase
sub-<label>[_ses-<label>]_task-<label>[_acq-<label>][_ce-<label>][_rec-<label>][_dir-<label>][_run-<index>][_echo-<index>]_phase.json
sub-<label>[_ses-<label>]_task-<label>[_acq-<label>][_ce-<label>][_rec-<label>][_dir-<label>][_run-<index>][_echo-<index>]_phase.nii[.gz]
sub-<label>[_ses-<label>]_task-<label>[_acq-<label>][_ce-<label>][_rec-<label>][_dir-<label>][_run-<index>]_events.json
sub-<label>[_ses-<label>]_task-<label>[_acq-<label>][_ce-<label>][_rec-<label>][_dir-<label>][_run-<index>]_events.tsv
sub-<label>[_ses-<label>]_task-<label>[_acq-<label>][_ce-<label>][_rec-<label>][_dir-<label>][_run-<index>][_recording-<label>]_physio.json
sub-<label>[_ses-<label>]_task-<label>[_acq-<label>][_ce-<label>][_rec-<label>][_dir-<label>][_run-<index>][_recording-<label>]_physio.tsv.
sub-<label>[_ses-<label>]_task-<label>[_acq-<label>][_ce-<label>][_rec-<label>][_dir-<label>][_run-<index>][_recording-<label>]_stim.json
sub-<label>[_ses-<label>]_task-<label>[_acq-<label>][_ce-<label>][_rec-<label>][_dir-<label>][_run-<index>][_recording-<label>]_stim.tsv.gz
```

Functional imaging consists of techniques that support rapid temporal repetition. This includes but is not limited to task based fMRI as well as resting state fMRI, which is treated like any other task. For task based fMRI a corresponding task events file (see below) MUST be provided (please note that this file is not necessary for resting state scans). For multiband acquisitions, one MAY also save the single-band reference image as type `sbref` (for example, `sub-control01_task-nback_sbref.nii.gz`).

Each task has a unique label that MUST only consist of letters and/or numbers (other characters, including spaces and underscores, are not allowed) with the `task-<label>` key/value pair. Those labels MUST be consistent across subjects and sessions.

If more than one run of the same task has been acquired the `run-<index>` key/value pair MUST be used: `_run-1`, `_run-2`, `_run-3`, and so on. If only one run was acquired the `run-<index>` can be omitted. In the context of functional imaging a run is defined as the same task, but in some cases it can mean different set of stimuli (for example randomized order) and participant responses.

The OPTIONAL `acq-<label>` key/value pair corresponds to a custom label one may use to distinguish different set of parameters used for acquiring the same task. For example this should be used when a study includes two resting state images - one single band and one multiband. In such case two files could have the following names: `sub-01_task-rest_acq-singleband_bold.nii.gz` and `sub-01_task-rest_acq-multiband_bold.nii.gz`, however the user is MAY choose any other label than `singleband` and `multiband` as long as they are consistent across subjects and sessions and consist only of the legal label characters.

Similarly the OPTIONAL `ce-<label>` key/value can be used to distinguish sequences using different contrast enhanced images. The label is the name of the contrast agent. The key ContrastBolusIngredient MAY be also be added in the JSON file, with the same label.

Similarly the OPTIONAL `rec-<label>` key/value can be used to distinguish different reconstruction algorithms (for example ones using motion correction).

Similarly the OPTIONAL `dir-<label>` and `rec-<label>` key/values can be used to distinguish different phase-encoding directions and reconstruction algorithms (for example ones using motion correction). See `fmap` Case 4 for more information on `dir` field specification.

Multi-echo data MUST be split into one file per echo using the `echo-<index>` key-value pair. For example:

```
sub-01/
   func/
      sub-01_task-cuedSGT_run-1_echo-1_bold.nii.gz
      sub-01_task-cuedSGT_run-1_echo-1_bold.json
      sub-01_task-cuedSGT_run-1_echo-2_bold.nii.gz
      sub-01_task-cuedSGT_run-1_echo-2_bold.json
      sub-01_task-cuedSGT_run-1_echo-3_bold.nii.gz
      sub-01_task-cuedSGT_run-1_echo-3_bold.json
```

Please note that the `<index>` denotes the number/index (in the form of a nonnegative integer) of the echo not the echo time value which needs to be stored in the field EchoTime of the separate JSON file.

Complex-valued data MUST be split into one file for each data type. For BOLD data, there are separate suffixes for magnitude (`_bold`) and phase (`_phase`) data, but the `_phase` suffix is deprecated. Newly generated datasets SHOULD NOT use the `_phase` suffix, and the suffix will be removed from the specification in the next major release. For backwards compatibility, `_phase` is considered equivalent to `_part-phase_bold`. When the `_phase` suffix is not used, each file shares the same name with the exception of the `part-<mag|phase>` or `part-<real|imag>` key/value.

For example:

```
sub-01/
   func/
      sub-01_task-cuedSGT_part-mag_bold.nii.gz
      sub-01_task-cuedSGT_part-mag_bold.json
      sub-01_task-cuedSGT_part-phase_bold.nii.gz
      sub-01_task-cuedSGT_part-phase_bold.json
      sub-01_task-cuedSGT_part-mag_sbref.nii.gz
      sub-01_task-cuedSGT_part-mag_sbref.json
      sub-01_task-cuedSGT_part-phase_sbref.nii.gz
      sub-01_task-cuedSGT_part-phase_sbref.json
```

Some meta information about the acquisition MUST be provided in an additional JSON file.

## Required fields

| Key name | Requirement Level | Data type | Description |
|---|---|---|---|
| RepetitionTime | REQUIRED | number | The time in seconds between the beginning of an acquisition of one volume and the beginning of acquisition of the volume following it (TR). When used in the context of functional acquisitions this parameter best corresponds to DICOM Tag 0020, 0110: the ”time delta between images in a dynamic of functional set of images” but may also be found in DICOM Tag 0018, 0080: ”the period of time in msec between the beginning of a pulse sequence and the beginning of the succeeding (essentially identical) pulse sequence”. This definition includes time between scans (when no data has been acquired) in case of sparse acquisition schemes. This value MUST be consistent with the ’pixdim[4]’ field (after accounting for units stored in ’xyzt_units’ field) in the NIfTI header. This field is mutually exclusive with VolumeTiming. Must be a number greater than 0. |
| VolumeTiming | REQUIRED | array of numbers | The time at which each volume was acquired during the acquisition. It is described using a list of times referring to the onset of each volume in the BOLD series. The list must have the same length as the BOLD series, and the values must be non-negative and monotonically increasing. This field is mutually exclusive with `"RepetitionTime"` and `"DelayTime"`. If defined, this requires acquisition time (TA) be defined via either `"SliceTiming"` or `"AcquisitionDuration"` be defined. |

| Key name | Requirement Level | Data type | Description |
|---|---|---|---|
| TaskName | REQUIRED | string | Name of the task. No two tasks should have the same name. The task label included in the file name is derived from this `"TaskName"` field by removing all non-alphanumeric (`[a-zA-Z0-9]`) characters. For example `"TaskName"` `"faces n-back"` will correspond to task label `facesnback`. A RECOMMENDED convention is to name resting state task using labels beginning with `rest`. |

For the fields described above and in the following section, the term ”Volume” refers to a reconstruction of the object being imaged (for example, brain or part of a brain). In case of multiple channels in a coil, the term ”Volume” refers to a combined image rather than an image from each coil.

## Other RECOMMENDED metadata

### Timing Parameters

| Key name | Requirement Level | Data type | Description |
|---|---|---|---|
| NumberOfVolumesDiscardedByScanner | RECOMMENDED | integer | Number of volumes (”dummy scans”) discarded by the scanner (as opposed to those discarded by the user post hoc) before saving the imaging file. For example, a sequence that automatically discards the first 4 volumes before saving would have this field as 4. A sequence that does not discard dummy scans would have this set to 0. Please note that the onsets recorded in the `events.tsv` file should always refer to the beginning of the acquisition of the first volume in the corresponding imaging file - independent of the value of `"NumberOfVolumesDiscardedByScanner"` field. Must be a number greater than or equal to 0. |

| Key name | Requirement Level | Data type | Description |
|---|---|---|---|
| NumberOfVolumesDiscardedByUser | RECOMMENDED | integer | Number of volumes ("dummy scans") discarded by the user before including the file in the dataset. If possible, including all of the volumes is strongly recommended. Please note that the onsets recorded in the `events.tsv` file should always refer to the beginning of the acquisition of the first volume in the corresponding imaging file - independent of the value of `"NumberOfVolumesDiscardedByUser"` field. Must be a number greater than or equal to 0. |
| DelayTime | RECOMMENDED | number | User specified time (in seconds) to delay the acquisition of data for the following volume. If the field is not present it is assumed to be set to zero. Corresponds to Siemens CSA header field `lDelayTimeInTR`. This field is REQUIRED for sparse sequences using the `"RepetitionTime"` field that do not have the `"SliceTiming"` field set to allowed for accurate calculation of "acquisition time". This field is mutually exclusive with `"VolumeTiming"`. |
| AcquisitionDuration | RECOMMENDED, but REQUIRED for sequences that are described with the `VolumeTiming` field and that do not have the `SliceTiming` field set to allow for accurate calculation of "acquisition time" | number | Duration (in seconds) of volume acquisition. Corresponds to DICOM Tag 0018, 9073 `Acquisition Duration`. This field is mutually exclusive with `"RepetitionTime"`. Must be a number greater than 0. |

| Key name | Requirement Level | Data type | Description |
|---|---|---|---|
| DelayAfterTrigger | RECOMMENDED | number | Duration (in seconds) from trigger delivery to scan onset. This delay is commonly caused by adjustments and loading times. This specification is entirely independent of `"NumberOfVolumesDiscardedByScanner"` or `"NumberOfVolumesDiscardedByUser"`, as the delay precedes the acquisition. |

The following table recapitulates the different ways that specific fields have to be populated for functional sequences. Note that all these options can be used for non sparse sequences but that only options B, D and E are valid for sparse sequences.

| | **`RepetitionTime`** | **`SliceTiming`** | **`AcquisitionDuration`** | **`DelayTime`** | **`VolumeTiming`** |
|---|---|---|---|---|---|
| option A | [ X ] | | [ ] | | [ ] |
| option B | [ ] | [ X ] | | [ ] | [ X ] |
| option C | [ ] | | [ X ] | [ ] | [ X ] |
| option D | [ X ] | [ X ] | [ ] | | [ ] |
| option E | [ X ] | | [ ] | [ X ] | [ ] |

Legend

- [ X ] --> MUST be defined
- ☐ --> MUST NOT be defined
- empty cell --> MAY be specified

fMRI task information

| Key name | Requirement Level | Data type | Description |
|---|---|---|---|
| Instructions | RECOMMENDED | string | Text of the instructions given to participants before the recording. This is especially important in context of resting state recordings and distinguishing between eyes open and eyes closed paradigms. |
| TaskDescription | RECOMMENDED | string | Longer description of the task. |

| Key name | Requirement Level | Data type | Description |
|---|---|---|---|
| CogAtlasID | RECOMMENDED | string | URI of the corresponding Cognitive Atlas Task term. |
| CogPOID | RECOMMENDED | string | URI of the corresponding CogPO term. |

See Common metadata fields for a list of additional terms and their definitions.

Example:

```
sub-01/
   func/
      sub-control01_task-nback_bold.json
```

```
{
   "TaskName": "N Back",
   "RepetitionTime": 0.8,
   "EchoTime": 0.03,
   "FlipAngle": 78,
   "SliceTiming": [0.0, 0.2, 0.4, 0.6, 0.0, 0.2, 0.4, 0.6, 0.0, 0.2, 0.4, 0.6, 0.0, 0.2, 0.4, 0.6],
   "MultibandAccelerationFactor": 4,
   "ParallelReductionFactorInPlane": 2,
   "PhaseEncodingDirection": "j",
   "InstitutionName": "Stanford University",
   "InstitutionAddress": "450 Serra Mall, Stanford, CA 94305-2004, USA",
   "DeviceSerialNumber": "11035",
   "B0FieldSource": ["phasediff_fmap0", "pepolar_fmap0"]
}
```

If this information is the same for all participants, sessions and runs it can be provided in `task-<label>_bold.json` (in the root directory of the dataset). However, if the information differs between subjects/runs it can be specified in the `sub-<label>/func/sub-<label>_task-<label>[_acq-<label>][_run-<index>]_bold.json` file. If both files are specified fields from the file corresponding to a particular participant, task and run takes precedence.

## Diffusion imaging data

Several example datasets contain diffusion imaging data formatted using this specification and that can be used for practical guidance when curating a new dataset:

- `genetics_ukbb`
- `eeg_rest_fmri`
- `ds114`
- `ds000117`

Diffusion-weighted imaging data acquired for a participant. Currently supported image types include:

| Name | `suffix` | Description |
|---|---|---|
| Diffusion-weighted image | dwi | Diffusion-weighted imaging contrast (specialized T2 weighting). |
| Single-band reference image | sbref | Single-band reference for one or more multi-band `dwi` images. |

Template:

```
sub-<label>/
    [ses-<label>/]
        dwi/
            sub-<label>[_ses-<label>][_acq-<label>][_dir-<label>][_run-<index>][_part-<mag|phase|real|imag>]_dwi.bval
            sub-<label>[_ses-<label>][_acq-<label>][_dir-<label>][_run-<index>][_part-<mag|phase|real|imag>]_dwi.bvec
            sub-<label>[_ses-<label>][_acq-<label>][_dir-<label>][_run-<index>][_part-<mag|phase|real|imag>]_dwi.json
            sub-<label>[_ses-<label>][_acq-<label>][_dir-<label>][_run-<index>][_part-<mag|phase|real|imag>]_dwi.nii[.gz]
            sub-<label>[_ses-<label>][_acq-<label>][_dir-<label>][_run-<index>][_part-<mag|phase|real|imag>]_sbref.json
            sub-<label>[_ses-<label>][_acq-<label>][_dir-<label>][_run-<index>][_part-<mag|phase|real|imag>]_sbref.nii[.gz]
            sub-<label>[_ses-<label>][_acq-<label>][_dir-<label>][_run-<index>][_part-<mag|phase|real|imag>][_recording-<label>]_physio.json
            sub-<label>[_ses-<label>][_acq-<label>][_dir-<label>][_run-<index>][_part-<mag|phase|real|imag>][_recording-<label>]_physio.tsv.gz
            sub-<label>[_ses-<label>][_acq-<label>][_dir-<label>][_run-<index>][_part-<mag|phase|real|imag>][_recording-<label>]_stim.json
            sub-<label>[_ses-<label>][_acq-<label>][_dir-<label>][_run-<index>][_part-<mag|phase|real|imag>][_recording-<label>]_stim.tsv.gz
```

If more than one run of the same acquisition and direction has been acquired, the `run-<index>` key/value pair MUST be used: `_run-1`, `_run-2`, `_run-3` (and so forth.) When there is only one scan of a given acquisition and direction, the run key MAY be omitted. The `run-<index>` key/value pair is RECOMMENDED to encode the splits of multipart DWI scans (see below.)

The OPTIONAL `acq-<label>` key/value pair corresponds to a custom label the user may use to distinguish different sets of parameters.

The OPTIONAL `dir-<label>` key/value pair corresponds to a custom label the user may use to distinguish different sets of phase-encoding directions.

Combining multi- and single-band acquisitions. The single-band reference image MAY be stored with suffix `sbref` (for example, `dwi/sub-control01_sbref.nii[.gz]`) as long as the image has no corresponding gradient information (`[*_]dwi.bval` and `[*_]dwi.bvec` sidecar files) to be stored.

Otherwise, if some gradient information is associated to the single-band diffusion image and a multi-band diffusion image also exists, the `acq-<label>` key/value pair MUST be used to distinguish both images. In such a case, two files could have the following names: `sub-01_acq-singleband_dwi.nii.gz` and `sub-01_acq-multiband_dwi.nii.gz`. The user is free to choose any other label than `singleband` and `multiband`, as long as they are consistent across subjects and sessions.

### REQUIRED gradient orientation information

The REQUIRED gradient orientation information corresponding to a DWI acquisition MUST be stored using `[*_]dwi.bval` and `[*_]dwi.bvec` pairs of files. The `[*_]dwi.bval` and `[*_]dwi.bvec` files MAY be saved on any level of the directory structure and thus define those values for all sessions and/or subjects in one place (see the inheritance principle).

As an exception to the common principles that parameters are constant across runs, the gradient table information (stored within the `[*_]dwi.bval` and `[*_]dwi.bvec` files) MAY change across DWI runs.

Gradient orientation file formats. The `[*_]dwi.bval` and `[*_]dwi.bvec` files MUST follow the FSL format: The `[*_]dwi.bvec` file contains 3 rows with N space-delimited floating-point numbers (corresponding to the N volumes in the corresponding NIfTI file.) The first row contains the x elements, the second row contains the y elements and the third row contains the z elements of a unit vector in the direction of the applied diffusion gradient, where the i-th elements in each row correspond together to the i-th volume, with `[0,0,0]` for non-diffusion-weighted (also called b=0 or low-b) volumes. Following the FSL format for the `[*_]dwi.bvec` specification, the coordinate system of the b vectors MUST be defined with respect to the coordinate system defined by the header of the corresponding `_dwi` NIfTI file and not the scanner's device coordinate system (see Coordinate systems). The most relevant limitation imposed by this choice is that the gradient information cannot be directly stored in this format if the scanner generates b-vectors in scanner coordinates.

Example of `[*_]dwi.bvec` file, with N=6, with two b=0 volumes in the beginning:

```
0 0 0.021828 -0.015425 -0.70918 -0.2465
0 0 0.80242 0.22098 -0.00063106 0.1043
0 0 -0.59636 0.97516 -0.70503 -0.96351
```

The `[*_]dwi.bval` file contains the b-values (in s/mm2) corresponding to the volumes in the relevant NIfTI file), with 0 designating b=0 volumes, space-delimited.

Example of `[*_]dwi.bval` file, corresponding to the previous `[*_]dwi.bvec` example:

```
0 0 2000 2000 1000 1000
```

### Multipart (split) DWI schemes

Some MR schemes cannot be acquired directly by some scanner devices, requiring to generate several DWI runs that were originally meant to belong in a single one. For instance, some GE scanners cannot collect more than ≈160 volumes in a single run under fast-changing gradients, so acquiring HCP-style diffusion images will require splitting the DWI scheme in several runs. Because researchers will generally optimize the data splits, these will likely not be able to be directly concatenated. BIDS permits defining arbitrary groupings of these multipart scans with the following metadata:

| Key name | Requirement Level | Data type | Description |
|---|---|---|---|
| MultipartID | REQUIRED | string | A unique (per participant) label tagging DWI runs that are part of a multipart scan. |

JSON example:

```
{
  "MultipartID": "dwi_1"
}
```

For instance, if there are two phase-encoding directions (`AP`, `PA`), and two runs each, and the intent of the researcher is that all of them are part of a unique multipart scan, then they will tag all four runs with the same `MultipartID` (shown at the right-hand side of the file listing):

```
sub-1/
   dwi                                # MultipartID/
      sub-1_dir-AP_run-1_dwi.nii.gz  # dwi_1
      sub-1_dir-AP_run-2_dwi.nii.gz  # dwi_1
      sub-1_dir-PA_run-1_dwi.nii.gz  # dwi_1
      sub-1_dir-PA_run-2_dwi.nii.gz  # dwi_1
```

If, conversely, the researcher wanted to store two multipart scans, one possibility is to combine matching phase-encoding directions:

```
sub-1/
   dwi                                # MultipartID/
      sub-1_dir-AP_run-1_dwi.nii.gz  # dwi_1
      sub-1_dir-AP_run-2_dwi.nii.gz  # dwi_1
      sub-1_dir-PA_run-1_dwi.nii.gz  # dwi_2
      sub-1_dir-PA_run-2_dwi.nii.gz  # dwi_2
```

Alternatively, the researcher's intent could be combining opposed phase-encoding runs instead:

```
sub-1/
   dwi                                # MultipartID/
      sub-1_dir-AP_run-1_dwi.nii.gz  # dwi_1
      sub-1_dir-AP_run-2_dwi.nii.gz  # dwi_2
      sub-1_dir-PA_run-1_dwi.nii.gz  # dwi_1
      sub-1_dir-PA_run-2_dwi.nii.gz  # dwi_2
```

The `MultipartID` metadata MAY be used with the `acq-<label>` key/value pair, for example:

```
sub-1/
   dwi                                    # MultipartID/
      sub-1_acq-shell1_run-1_dwi.nii.gz  # dwi_1
      sub-1_acq-shell1_run-2_dwi.nii.gz  # dwi_2
      sub-1_acq-shell2_run-1_dwi.nii.gz  # dwi_1
      sub-1_acq-shell2_run-2_dwi.nii.gz  # dwi_2
```

## Other RECOMMENDED metadata

The `PhaseEncodingDirection` and `TotalReadoutTime` metadata fields are RECOMMENDED to enable the correction of geometrical distortions with fieldmap information. See Common metadata fields for a list of additional terms that can be included in the corresponding JSON file.

JSON example:

```
{
  "PhaseEncodingDirection": "j-",
  "TotalReadoutTime": 0.095,
  "B0FieldSource": ["phasediff_fmap0", "pepolar_fmap0"]
}
```

## Arterial Spin Labeling perfusion data

Several example ASL datasets have been formatted using this specification and can be used for practical guidance when curating a new dataset.

Template:

```
sub-<label>/
    [ses-<label>/]
        perf/
            sub-<label>[_ses-<label>][_acq-<label>][_rec-<label>][_dir-<label>][_run-<index>]_asl.json
            sub-<label>[_ses-<label>][_acq-<label>][_rec-<label>][_dir-<label>][_run-<index>]_asl.nii[.gz]
            sub-<label>[_ses-<label>][_acq-<label>][_rec-<label>][_dir-<label>][_run-<index>]_m0scan.json
            sub-<label>[_ses-<label>][_acq-<label>][_rec-<label>][_dir-<label>][_run-<index>]_m0scan.nii[.gz]
            sub-<label>[_ses-<label>][_acq-<label>][_rec-<label>][_dir-<label>][_run-<index>]_aslcontext.json
            sub-<label>[_ses-<label>][_acq-<label>][_rec-<label>][_dir-<label>][_run-<index>]_aslcontext.tsv
            sub-<label>[_ses-<label>][_acq-<label>][_rec-<label>][_run-<index>]_asllabeling.jpg
            sub-<label>[_ses-<label>][_acq-<label>][_rec-<label>][_dir-<label>][_run-<index>][_recording-<label>]_physio.json
            sub-<label>[_ses-<label>][_acq-<label>][_rec-<label>][_dir-<label>][_run-<index>][_recording-<label>]_physio.tsv.gz
            sub-<label>[_ses-<label>][_acq-<label>][_rec-<label>][_dir-<label>][_run-<index>][_recording-<label>]_stim.json
            sub-<label>[_ses-<label>][_acq-<label>][_rec-<label>][_dir-<label>][_run-<index>][_recording-<label>]_stim.tsv.gz
```

The complete ASL time series should be stored as a 4D NIfTI file in the original acquisition order, accompanied by two ancillary files: `*_asl.json` and `*_aslcontext.tsv`.

### `*_aslcontext.tsv`

The `*_aslcontext.tsv` table consists of a single column of labels identifying the `volume_type` of each volume in the corresponding `*_asl.nii[.gz]` file. Volume types are defined in the following table, based on DICOM Tag 0018, 9257 `ASL Context`. Note that the volume_types `control` and `label` within BIDS only serve to specify the magnetization state of the blood and thus the ASL subtraction order. See Appendix XII - ASL for more information on `control` and `label`.

| volume_type | Definition |
|---|---|
| control | The control image is acquired in the exact same way as the label image, except that the magnetization of the blood flowing into the imaging region has not been inverted. |

| volume_type | Definition |
|---|---|
| label | The label image is acquired in the exact same way as the control image, except that the blood magnetization flowing into the imaging region has been inverted. |
| m0scan | The M0 image is a calibration image, used to estimate the equilibrium magnetization of blood. |
| deltam | The deltaM image is a perfusion-weighted image, obtained by the subtraction of `control` - `label`. |
| cbf | The cerebral blood flow (CBF) image is produced by dividing the deltaM by the M0, quantified into `mL/100g/min` (See also doi:10.1002/mrm.25197). |

If the `control` and `label` images are not available, their derivative `deltam` should be stored within the `*_asl.nii[.gz]` and specified in the `*_aslcontext.tsv` instead. If the `deltam` is not available, `cbf` should be stored within the `*_asl.nii[.gz]` and specified in the `*_aslcontext.tsv`. When `cbf` is stored within the `*_asl.nii[.gz]`, its units need to be specified in the `*_asl.json` as well. Note that the raw images, including the `m0scan`, may also be used for quality control. See Appendix XII - ASL for examples of the three possible cases, in order of decreasing preference.

### Scaling

The `*_asl.nii.gz` and `*_m0scan.nii.gz` should contain appropriately scaled data, and no additional scaling factors are allowed other than the scale slope in the respective NIfTI headers.

### M0

The `m0scan` can either be stored inside the 4D ASL time-series NIfTI file or as a separate NIfTI file, depending on whether it was acquired within the ASL time-series or as a separate scan. These and other M0 options are specified in the REQUIRED `M0Type` field of the `*_asl.json` file. It can also be stored under `fmap/sub-<label>[_ses-<label>][_acq-<label>][_ce-<label>]_dir-<label>[_run-<index>]_m0scan.nii[.gz]`, when the pepolar approach is used.

### `*_asl.json` file

Depending on the method used for ASL acquisition ((P)CASL or PASL) different metadata fields are applicable. Additionally, some common metadata fields are REQUIRED for the `*_asl.json`: `MagneticFieldStrength`, `MRAcquisitionType`, `EchoTime`, `SliceTiming` in case `MRAcquisitionType` is defined as 2D, `RepetitionTimePreparation`, and `FlipAngle` in case `LookLocker` is `true`. See Appendix XII - ASL for more information on the most common ASL sequences.

Common metadata fields applicable to both (P)CASL and PASL

| Key name | Requirement Level | Data type | Description |
|---|---|---|---|
| ArterialSpinLabelingType | REQUIRED | string | The arterial spin labeling type. Must be one of: `"CASL"`, `"PCASL"`, `"PASL"`. |

| Key name | Requirement Level | Data type | Description |
|---|---|---|---|
| PostLabelingDelay | REQUIRED | number or array of numbers | This is the postlabeling delay (PLD) time, in seconds, after the end of the labeling (for `"CASL"` or `"PCASL"`) or middle of the labeling pulse (for `"PASL"`) until the middle of the excitation pulse applied to the imaging slab (for 3D acquisition) or first slice (for 2D acquisition). Can be a number (for a single-PLD time series) or an array of numbers (for multi-PLD and Look-Locker). In the latter case, the array of numbers contains the PLD of each volume, namely each `control` and `label`, in the acquisition order. Any image within the time-series without a PLD, for example an `m0scan`, is indicated by a zero. Based on DICOM Tags 0018, 9079 `Inversion Times` and 0018, 0082 `InversionTime`. |
| BackgroundSuppression | REQUIRED | boolean | Boolean indicating if background suppression is used. Must be one of: `"true"`, `"false"`. |
| M0Type | REQUIRED | string | Describes the presence of M0 information. `"Separate"` means that a separate `*_m0scan.nii[.gz]` is present. `"Included"` means that an m0scan volume is contained within the current `*_asl.nii[.gz]`. `"Estimate"` means that a single whole-brain M0 value is provided. `"Absent"` means that no specific M0 information is present. Must be one of: `"Separate"`, `"Included"`, `"Estimate"`, `"Absent"`. |
| TotalAcquiredPairs | REQUIRED | number | The total number of acquired `control-label` pairs. A single pair consists of a single `control` and a single `label` image. Must be a number greater than 0. |

| Key name | Requirement Level | Data type | Description |
|---|---|---|---|
| VascularCrushing | RECOMMENDED | boolean | Boolean indicating if Vascular Crushing is used. Corresponds to DICOM Tag 0018, 9259 `ASL Crusher Flag`. Must be one of: `"true"`, `"false"`. |
| AcquisitionVoxelSize | RECOMMENDED | array of numbers | An array of numbers with a length of 3, in millimeters. This parameter denotes the original acquisition voxel size, excluding any inter-slice gaps and before any interpolation or resampling within reconstruction or image processing. Any point spread function effects, for example due to T2-blurring, that would decrease the effective resolution are not considered here. |
| M0Estimate | OPTIONAL, but REQUIRED when `M0Type` is defined as `Estimate` | number | A single numerical whole-brain M0 value (referring to the M0 of blood), only if obtained externally (for example retrieved from CSF in a separate measurement). Must be a number greater than 0. |
| BackgroundSuppressionNumberPulses | OPTIONAL, RECOMMENDED if `BackgroundSuppression` is `true` | number | The number of background suppression pulses used. Note that this excludes any effect of background suppression pulses applied before the labeling. Must be a number greater than or equal to 0. |
| BackgroundSuppressionPulseTime | OPTIONAL, RECOMMENDED if `BackgroundSuppression` is `true` | array of numbers | Array of numbers containing timing, in seconds, of the background suppression pulses with respect to the start of the labeling. In case of multi-PLD with different background suppression pulse times, only the pulse time of the first PLD should be defined. |

| Key name | Requirement Level | Data type | Description |
|---|---|---|---|
| VascularCrushingVENC | OPTIONAL, RECOMMENDED if `VascularCrushing` is `true` | number or array of numbers | The crusher gradient strength, in centimeters per second. Specify either one number for the total time-series, or provide an array of numbers, for example when using QUASAR, using the value zero to identify volumes for which `VascularCrushing` was turned off. Corresponds to DICOM Tag 0018, 925A `ASL Crusher Flow Limit`. |
| LabelingOrientation | RECOMMENDED | array of numbers | Orientation of the labeling plane (`(P)CASL`) or slab (`PASL`). The direction cosines of a normal vector perpendicular to the ASL labeling slab or plane with respect to the patient. Corresponds to DICOM Tag 0018, 9255 `ASL Slab Orientation`. |
| LabelingDistance | RECOMMENDED | number | Distance from the center of the imaging slab to the center of the labeling plane (`(P)CASL`) or the leading edge of the labeling slab (`PASL`), in millimeters. If the labeling is performed inferior to the isocenter, this number should be negative. Based on DICOM macro C.8.13.5.14. |
| LabelingLocationDescription | RECOMMENDED | string | Description of the location of the labeling plane (`"CASL"` or `"PCASL"`) or the labeling slab (`"PASL"`) that cannot be captured by fields `LabelingOrientation` or `LabelingDistance`. May include a link to an anonymized screenshot of the planning of the labeling slab/plane with respect to the imaging slab or slices `*_asllabeling.jpg`. Based on DICOM macro C.8.13.5.14. |
| LookLocker | OPTIONAL | boolean | Boolean indicating if a Look-Locker readout is used. Must be one of: `"true"`, `"false"`. |

| Key name | Requirement Level | Data type | Description |
|---|---|---|---|
| LabelingEfficiency | OPTIONAL | number | Labeling efficiency, specified as a number between zero and one, only if obtained externally (for example phase-contrast based). Must be a number greater than 0. |

(P)CASL-specific metadata fields

These fields can only be used when `ArterialSpinLabelingType` is `"CASL"` or `"PCASL"`. See Appendix XII - ASL for more information on the (P)CASL sequence and the Labeling Pulse fields.

| Key name | Requirement Level | Data type | Description |
|---|---|---|---|
| LabelingDuration | REQUIRED | number or array of numbers | Total duration of the labeling pulse train, in seconds, corresponding to the temporal width of the labeling bolus for `"PCASL"` or `"CASL"`. In case all control-label volumes (or deltam or CBF) have the same `LabelingDuration`, a scalar must be specified. In case the control-label volumes (or deltam or cbf) have a different `"LabelingDuration"`, an array of numbers must be specified, for which any `m0scan` in the timeseries has a `"LabelingDuration"` of zero. In case an array of numbers is provided, its length should be equal to the number of volumes specified in `*_aslcontext.tsv`. Corresponds to DICOM Tag 0018, 9258 `ASL Pulse Train Duration`. |
| PCASLType | RECOMMENDED if `ArterialSpinLabelingType` is `"PCASL"` | string | The type of gradient pulses used in the `control` condition. Must be one of: `"balanced"`, `"unbalanced"`. |
| CASLType | RECOMMENDED if `ArterialSpinLabelingType` is `"CASL"` | string | Describes if a separate coil is used for labeling. Must be one of: `"single-coil"`, `"double-coil"`. |
| LabelingPulseAverageGradient | RECOMMENDED | number | The average labeling gradient, in milliteslas per meter. Must be a number greater than 0. |

| Key name | Requirement Level | Data type | Description |
|---|---|---|---|
| LabelingPulseMaximumGradient | RECOMMENDED | number | The maximum amplitude of the gradient switched on during the application of the labeling RF pulse(s), in milliteslas per meter. Must be a number greater than 0. |
| LabelingPulseAverageB1 | RECOMMENDED | number | The average B1-field strength of the RF labeling pulses, in microteslas. As an alternative, `"LabelingPulseFlipAngle"` can be provided. Must be a number greater than 0. |
| LabelingPulseDuration | RECOMMENDED | number | Duration of the individual labeling pulses, in milliseconds. Must be a number greater than 0. |
| LabelingPulseFlipAngle | RECOMMENDED | number | The flip angle of a single labeling pulse, in degrees, which can be given as an alternative to `"LabelingPulseAverageB1"`. Must be a number greater than 0 and less than or equal to 360. |
| LabelingPulseInterval | RECOMMENDED | number | Delay between the peaks of the individual labeling pulses, in milliseconds. Must be a number greater than 0. |

PASL-specific metadata fields

These fields can only be used when `ArterialSpinLabelingType` is `PASL`. See Appendix XII - ASL for more information on the PASL sequence and the BolusCutOff fields.

| Key name | Requirement Level | Data type | Description |
|---|---|---|---|
| BolusCutOffFlag | REQUIRED | boolean | Boolean indicating if a bolus cut-off technique is used. Corresponds to DICOM Tag 0018, 925C `ASL Bolus Cut-off Flag`. Must be one of: `"true"`, `"false"`. |
| PASLType | RECOMMENDED | string | Type of the labeling pulse of the `PASL` labeling, for example `"FAIR"`, `"EPISTAR"`, or `"PICORE"`. |

| Key name | Requirement Level | Data type | Description |
|---|---|---|---|
| LabelingSlabThickness | RECOMMENDED | number | Thickness of the labeling slab in millimeters. For non-selective FAIR a zero is entered. Corresponds to DICOM Tag 0018, 9254 `ASL Slab Thickness`. Must be a number greater than 0. |
| BolusCutOffDelayTime | OPTIONAL, REQUIRED if `BolusCutOffFlag` is `true` | number or array of numbers | Duration between the end of the labeling and the start of the bolus cut-off saturation pulse(s), in seconds. This can be a number or array of numbers, of which the values must be non-negative and monotonically increasing, depending on the number of bolus cut-off saturation pulses. For Q2TIPS, only the values for the first and last bolus cut-off saturation pulses are provided. Based on DICOM Tag 0018, 925F `ASL Bolus Cut-off Delay Time`. |
| BolusCutOffTechnique | OPTIONAL, REQUIRED if `BolusCutOffFlag` is `true` | string | Name of the technique used, for example `"Q2TIPS"`, `"QUIPSS"`, `"QUIPSSII"`. Corresponds to DICOM Tag 0018, 925E `ASL Bolus Cut-off Technique`. |

### `m0scan` metadata fields

Some common metadata fields are REQUIRED for the `*_m0scan.json`: `EchoTime`, `RepetitionTimePreparation`, and `FlipAngle` in case `LookLocker` is `true`.

| Key name | Requirement Level | Data type | Description |
|---|---|---|---|
| IntendedFor | REQUIRED | string or array of strings | The paths to files for which the associated file is intended to be used. Contains one or more filenames with paths relative to the participant subfolder. Paths need to use forward slashes instead of backward slashes, regardless of operating system. This is used to refer to the ASL time series for which the `*_m0scan.nii[.gz]` is intended. |
| AcquisitionVoxelSize | RECOMMENDED | array of numbers | An array of numbers with a length of 3, in millimeters. This parameter denotes the original acquisition voxel size, excluding any inter-slice gaps and before any interpolation or resampling within reconstruction or image processing. Any point spread function effects, for example due to T2-blurring, that would decrease the effective resolution are not considered here. |

The following table recapitulates the ASL field dependencies. If Source field (column 1) contains the Value specified in column 2, then the Requirements in column 4 are imposed on the Dependent fields in column 3. See Appendix XII for this information in the form of flowcharts.

| Source field | Value | Dependent field | Requirements |
|---|---|---|---|
| MRAcquisitionType | 2D / 3D | SliceTiming | [X] / [] |
| LookLocker | true | FlipAngle | [X] |
| ArterialSpinLabelingType | PCASL | LabelingDuration | [X] |
| ArterialSpinLabelingType | PASL | BolusCutOffFlag | [X] |
| BolusCutOffFlag | true / false | BolusCutOffDelayTime | [X] / [] |
| BolusCutOffFlag | true / false | BolusCutOffTechnique | [X] / [] |
| M0Type | Separate | */perf/ | contains `*_m0scan.nii[.gz]` and `*_m0scan.json` |
| M0Type | Included | *_aslcontext.tsv | contains m0scan |
| M0Type | Estimate | M0Estimate | [X] |
| `*_aslcontext.tsv` | cbf | Units | [X] |

Legend

- [ X ] --> MUST be defined
☐ --> MUST NOT be defined

## Fieldmap data

Data acquired to correct for B0 inhomogeneities can come in different forms. The current version of this standard considers four different scenarios:

1. Phase-difference map
2. Two phase maps
3. Direct field mapping
4. ”PEpolar” fieldmaps

These four different types of field mapping strategies can be encoded using the following image types:

| Name | `suffix` | Description |
|---|---|---|
| Magnitude | magnitude | Field-mapping MR schemes such as gradient-recalled echo (GRE) generate a Magnitude image to be used for anatomical reference. Requires the existence of Phase, Phase-difference or Fieldmap maps. |
| Magnitude | magnitude1 | Magnitude map generated by GRE or similar schemes, associated with the first echo in the sequence. |
| Magnitude | magnitude2 | Magnitude map generated by GRE or similar schemes, associated with the second echo in the sequence. |
| Phase | phase1 | Phase map generated by GRE or similar schemes, associated with the first echo in the sequence. |
| Phase | phase2 | Phase map generated by GRE or similar schemes, associated with the second echo in the sequence. |
| Phase-difference | phasediff | Some scanners subtract the `phase1` from the `phase2` map and generate a unique `phasediff` file. For instance, this is a common output for the built-in fieldmap sequence of Siemens scanners. |
| Fieldmap | fieldmap | Some MR schemes such as spiral-echo imaging (SEI) sequences are able to directly provide maps of the B0 field inhomogeneity. |
| EPI | epi | The phase-encoding polarity (PEpolar) technique combines two or more Spin Echo EPI scans with different phase encoding directions to estimate the underlying inhomogeneity/deformation map. |

Two OPTIONAL entities, following more general rules of the specification, are allowed across all the four scenarios:

- The OPTIONAL `run-<index>` key/value pair corresponds to a one-based index to distinguish multiple fieldmaps with the same parameters.
- The OPTIONAL `acq-<label>` key/value pair corresponds to a custom label the user may use to distinguish different set of parameters.

## Expressing the MR protocol intent for fieldmaps

Fieldmaps are typically acquired with the purpose of correcting one or more EPI scans under `dwi/`, `func/`, or `perf/` for distortions derived from B0 nonuniformity.

### Using `B0FieldIdentifier` metadata

The general purpose `B0FieldIdentifier` MRI metadata is RECOMMENDED for the prescription of the B0 field estimation intent of the original acquisition protocol. `B0FieldIdentifier` and `B0FieldSource` duplicate the capabilities of the original `IntendedFor` approach (see below), while permitting more complex use cases. It is RECOMMENDED to use both approaches to maintain compatibility with tools that support older datasets.

### Using `IntendedFor` metadata

Fieldmap data MAY be linked to the specific scan(s) it was acquired for by filling the `IntendedFor` field in the corresponding JSON file.

| Key name | Requirement Level | Data type | Description |
|---|---|---|---|
| IntendedFor | OPTIONAL | string or array of strings | The paths to files for which the associated file is intended to be used. Contains one or more filenames with paths relative to the participant subfolder. Paths need to use forward slashes instead of backward slashes, regardless of operating system. This field is OPTIONAL, and in case the fieldmaps do not correspond to any particular scans, it does not have to be filled. |

For example:

```
{
   "IntendedFor": [
        "ses-pre/func/sub-01_ses-pre_task-motor_run-1_bold.nii.gz",
        "ses-pre/func/sub-01_ses-pre_task-motor_run-2_bold.nii.gz"
    ]
}
```

## Types of fieldmaps

### Case 1: Phase-difference map and at least one magnitude image

Example datasets containing that type of fieldmap can be found here:

- `7t_trt`
- `genetics_ukbb`
- `ds000117`

Template:

```
sub-<label>/
    [ses-<label>/]
        fmap/
            sub-<label>[_ses-<label>][_acq-<label>][_run-<index>]_magnitude1.json
            sub-<label>[_ses-<label>][_acq-<label>][_run-<index>]_magnitude1.nii[.gz]
            sub-<label>[_ses-<label>][_acq-<label>][_run-<index>]_magnitude2.json
            sub-<label>[_ses-<label>][_acq-<label>][_run-<index>]_magnitude2.nii[.gz]
            sub-<label>[_ses-<label>][_acq-<label>][_run-<index>]_phasediff.json
            sub-<label>[_ses-<label>][_acq-<label>][_run-<index>]_phasediff.nii[.gz]
```

where the REQUIRED `_phasediff` image corresponds to the phase-drift map between echo times, the REQUIRED `_magnitude1` image corresponds to the shorter echo time, and the OPTIONAL `_magnitude2` image to the longer echo time.

Required fields:

| Key name | Requirement Level | Data type | Description |
|---|---|---|---|
| EchoTime1 | REQUIRED | number | The time (in seconds) when the first (shorter) echo occurs. Must be a number greater than 0. |
| EchoTime2 | REQUIRED | number | The time (in seconds) when the second (longer) echo occurs. Must be a number greater than 0. |

In this particular case, the sidecar JSON file `sub-<label>[_ses-<label>][_acq-<label>][_run-<index>]_phasediff.json` MUST define the time of two echos used to map the phase and finally calculate the phase-difference map. For example:

```
{
   "EchoTime1": 0.00600,
   "EchoTime2": 0.00746,
   "B0FieldIdentifier": "phasediff_fmap0"
}
```

### Case 2: Two phase maps and two magnitude images

Similar to case 1, but instead of a precomputed phase-difference map, two separate phase images and two magnitude images corresponding to first and second echos are available.

Template:

```
sub-<label>/
    [ses-<label>/]
        fmap/
            sub-<label>[_ses-<label>][_acq-<label>][_run-<index>]_magnitude1.json
            sub-<label>[_ses-<label>][_acq-<label>][_run-<index>]_magnitude1.nii[.gz]
            sub-<label>[_ses-<label>][_acq-<label>][_run-<index>]_magnitude2.json
            sub-<label>[_ses-<label>][_acq-<label>][_run-<index>]_magnitude2.nii[.gz]
            sub-<label>[_ses-<label>][_acq-<label>][_run-<index>]_phase1.json
            sub-<label>[_ses-<label>][_acq-<label>][_run-<index>]_phase1.nii[.gz]
            sub-<label>[_ses-<label>][_acq-<label>][_run-<index>]_phase2.json
            sub-<label>[_ses-<label>][_acq-<label>][_run-<index>]_phase2.nii[.gz]
```

Required fields:

| Key name | Requirement Level | Data type | Description |
|---|---|---|---|
| EchoTime | REQUIRED | number | The time (in seconds) when the echo corresponding to this map was acquired. Must be a number greater than 0. |

Each phase map has a corresponding sidecar JSON file to specify its corresponding `EchoTime`. For example, `sub-<label>[_ses-<label>][_acq-<label>][_run-<index>]_phase2.js` may read:

```
{
   "EchoTime": 0.00746,
   "B0FieldIdentifier": "phases_fmap0"
}
```

### Case 3: Direct field mapping

In some cases (for example GE), the scanner software will directly reconstruct a B0 field map along with a magnitude image used for anatomical reference.

Template:

```
sub-<label>/
    [ses-<label>/]
        fmap/
```

```
            sub-<label>[_ses-<label>][_acq-<label>][_run-<index>]_fieldmap.json
            sub-<label>[_ses-<label>][_acq-<label>][_run-<index>]_fieldmap.nii[.gz]
            sub-<label>[_ses-<label>][_acq-<label>][_run-<index>]_magnitude.json
            sub-<label>[_ses-<label>][_acq-<label>][_run-<index>]_magnitude.nii[.gz]
```

Required fields:

| Key name | Requirement Level | Data type | Description |
|---|---|---|---|
| Units | REQUIRED | string | Measurement units for the associated file. SI units in CMIXF formatting are RECOMMENDED (see Units). Fieldmaps must be in units of Hertz (`"Hz"`), radians per second (`"rad/s"`), or Tesla (`"T"`). |

For example:

```
{
   "Units": "rad/s",
   "IntendedFor": "func/sub-01_task-motor_bold.nii.gz",
   "B0FieldIdentifier": "b0map_fmap0"
}
```

See Using `IntendedFor` metadata for details on the `IntendedFor` field.

Case 4: Multiple phase encoded directions (”pepolar”)

An example dataset containing that type of fieldmap can be found here:

- `ieeg_visual_multimodal`

The phase-encoding polarity (PEpolar) technique combines two or more Spin Echo EPI scans with different phase encoding directions to estimate the distortion map corresponding to the nonuniformities of the B0 field. These `*_epi.nii[.gz]` - or `*_m0scan.nii[.gz]` for arterial spin labeling perfusion data - files can be 3D or 4D -- in the latter case, all timepoints share the same scanning parameters. Examples of software tools using these kinds of images are FSL TOPUP, AFNI `3dqwarp`, and SPM.

Template:

```
sub-<label>/
    [ses-<label>/]
        fmap/
            sub-<label>[_ses-<label>][_acq-<label>][_ce-<label>]_dir-<label>[_run-<index>]_epi.json
            sub-<label>[_ses-<label>][_acq-<label>][_ce-<label>]_dir-<label>[_run-<index>]_epi.nii[.gz]
```

The `dir-<label>` entity is REQUIRED for these files. This key-value pair MUST be used in addition to the REQUIRED `PhaseEncodingDirection` metadata field (see File name structure).

Required fields:

| Key name | Requirement Level | Data type | Description |
|---|---|---|---|
| PhaseEncodingDirection | REQUIRED | string | The letters `i`, `j`, `k` correspond to the first, second and third axis of the data in the NIFTI file. The polarity of the phase encoding is assumed to go from zero index to maximum index unless `-` sign is present (then the order is reversed - starting from the highest index instead of zero). `PhaseEncodingDirection` is defined as the direction along which phase is was modulated which may result in visible distortions. Note that this is not the same as the DICOM term `InPlanePhaseEncodingDirection` which can have `ROW` or `COL` values. Must be one of: `"i"`, `"j"`, `"k"`, `"i-"`, `"j-"`, `"k-"`. |
| TotalReadoutTime | REQUIRED | number | This is actually the ”effective” total readout time, defined as the readout duration, specified in seconds, that would have generated data with the given level of distortion. It is NOT the actual, physical duration of the readout train. If `"EffectiveEchoSpacing"` has been properly computed, it is just `EffectiveEchoSpacing * (ReconMatrixPE - 1)`. |

For example:

```
{
   "PhaseEncodingDirection": "j-",
   "TotalReadoutTime": 0.095,
   "IntendedFor": "func/sub-01_task-motor_bold.nii.gz",
```

```
   "B0FieldIdentifier": "pepolar_fmap0"
}
```

See Using `IntendedFor` metadata for details on the `IntendedFor` field.

As for other EPI sequences, these field mapping sequences may have any of the in-plane spatial encoding metadata keys. However, please note that `PhaseEncodingDirection` and `TotalReadoutTime` keys are REQUIRED for these field mapping sequences.

# Magnetoencephalography

Support for Magnetoencephalography (MEG) was developed as a BIDS Extension Proposal. Please see Citing BIDS on how to appropriately credit this extension when referring to it in the context of the academic literature.

The following example MEG datasets have been formatted using this specification and can be used for practical guidance when curating a new dataset.

- `multimodal MEG and MRI`

Further datasets are available from the BIDS examples repository.

## MEG recording data

Template:

```
sub-<label>/
    [ses-<label>/]
        meg/
            sub-<label>[_ses-<label>]_task-<label>[_acq-<label>][_run-<index>][_proc-<label>][_split-<index>]_meg.<extension>
            sub-<label>[_ses-<label>]_task-<label>[_acq-<label>][_run-<index>][_proc-<label>][_split-<index>]_meg.json
            sub-<label>[_ses-<label>]_acq-<calibration>_meg.dat
            sub-<label>[_ses-<label>]_acq-<crosstalk>_meg.fif
            sub-<label>[_ses-<label>][_task-<label>][_acq-<label>][_space-<label>]_markers.mrk
            sub-<label>[_ses-<label>][_task-<label>][_acq-<label>][_space-<label>]_markers.sqd
            sub-<label>[_ses-<label>]_task-<label>[_acq-<label>][_run-<index>]_events.json
            sub-<label>[_ses-<label>]_task-<label>[_acq-<label>][_run-<index>]_events.tsv
            sub-<label>[_ses-<label>]_task-<label>[_acq-<label>][_run-<index>][_proc-<label>][_recording-<label>]_physio.json
            sub-<label>[_ses-<label>]_task-<label>[_acq-<label>][_run-<index>][_proc-<label>][_recording-<label>]_physio.tsv.gz
            sub-<label>[_ses-<label>]_task-<label>[_acq-<label>][_run-<index>][_proc-<label>][_recording-<label>]_stim.json
            sub-<label>[_ses-<label>]_task-<label>[_acq-<label>][_run-<index>][_proc-<label>][_recording-<label>]_stim.tsv.gz
```

Unprocessed MEG data MUST be stored in the native file format of the MEG instrument with which the data was collected. With the MEG specification of BIDS, we wish to promote the adoption of good practices in the management of scientific data. Hence, the emphasis is not to impose a new, generic data format for the modality, but rather to standardize the way data is stored in repositories. Further, there is currently no widely accepted standard file format for MEG, but major software applications, including free and open-source solutions for MEG data analysis, provide readers of such raw files.

Some software readers may skip important metadata that is specific to MEG system manufacturers. It is therefore RECOMMENDED that users provide additional meta information extracted from the manufacturer raw data files in a sidecar JSON file. This allows for easy searching and indexing of key metadata elements without the need to parse files in proprietary data format. Other relevant files MAY be included alongside the MEG data; examples are provided below.

This template is for MEG data of any kind, including but not limited to task-based, resting-state, and noise recordings. If multiple Tasks were performed within a single Run, the task description can be set to `task-multitask`. The `*_meg.json` file SHOULD contain details on the Tasks.

Some manufacturers' data storage conventions use folders which contain data files of various nature: for example, CTF's `.ds` format, or BTi/4D's data folder. Yet other manufacturers split their files once they exceed a certain size limit. For example Neuromag/Elekta/Megin, which can produce several files for a single recording. Both `some_file.fif` and `some_file-1.fif` would belong to a single recording. In BIDS, the `split` entity is RECOMMENDED to deal with split files. If there are multiple parts of a recording and the optional `scans.tsv` is provided, remember to list all files separately in `scans.tsv` and that the entries for the `acq_time` column in `scans.tsv` MUST all be identical, as described in Scans file.

Another manufacturer-specific detail pertains to the KIT/Yokogawa/Ricoh system, which saves the MEG sensor coil positions in a separate file with two possible filename extensions (`.sqd`, `.mrk`). For these files, the `markers` suffix MUST be used. For example: `sub-01_task-nback_markers.sqd`

Please refer to Appendix VI for general information on how to deal with such manufacturer specifics and to see more examples.

The `proc-<label>` entity is analogous to the `rec-<label>` entity for MRI, and denotes a variant of a file that was a result of particular processing performed on the device. This is useful for files produced in particular by Elekta's MaxFilter (for example, sss, tsss, trans, quat, mc), which some installations impose to be run on raw data prior to analysis. Such processing steps are needed for example because of active shielding software corrections that have to be performed to before the MEG data can actually be exploited.

## Recording EEG simultaneously with MEG

Note that if EEG is recorded with a separate amplifier, it SHOULD be stored separately under a new `/eeg` data type (see the EEG specification).

If however EEG is recorded simultaneously with the same MEG system, it MAY be stored under the `/meg` data type. In that case, it SHOULD have the same sampling frequency as MEG (see `SamplingFrequency` field below). Furthermore, the EEG sensor coordinates SHOULD be specified using MEG-specific coordinate systems (see coordinates section below and coordinates section).

## Sidecar JSON (`*_meg.json`)

Generic fields MUST be present:

| Key name | Requirement Level | Data type | Description |
|---|---|---|---|
| TaskName | REQUIRED | string | Name of the task. No two tasks should have the same name. The task label included in the file name is derived from this `"TaskName"` field by removing all non-alphanumeric (`[a-zA-Z0-9]`) characters. For example `"TaskName"` `"faces n-back"` will correspond to task label `facesnback`. A RECOMMENDED convention is to name resting state task using labels beginning with `rest`. |

SHOULD be present: For consistency between studies and institutions, we encourage users to extract the values of these fields from the actual raw data. Whenever possible, please avoid using ad-hoc wording.

| Key name | Requirement Level | Data type | Description |
|---|---|---|---|
| InstitutionName | RECOMMENDED | string | The name of the institution in charge of the equipment that produced the measurements. |
| InstitutionAddress | RECOMMENDED | string | The address of the institution in charge of the equipment that produced the measurements. |
| InstitutionalDepartmentName | RECOMMENDED | string | The department in the institution in charge of the equipment that produced the measurements. |
| Manufacturer | RECOMMENDED | string | Manufacturer of the equipment that produced the measurements. For MEG scanners, this must be one of: `"CTF"`, `"Elekta/Neuromag"`, `"BTi/4D"`, `"KIT/Yokogawa"`, `"ITAB"`, `"KRISS"`, `"Other"`. See Appendix VII for preferred names. |
| ManufacturersModelName | RECOMMENDED | string | Manufacturer's model name of the equipment that produced the measurements. See Appendix VII for preferred names. |

| Key name | Requirement Level | Data type | Description |
|---|---|---|---|
| SoftwareVersions | RECOMMENDED | string | Manufacturer's designation of software version of the equipment that produced the measurements. |
| TaskDescription | RECOMMENDED | string | Longer description of the task. |
| Instructions | RECOMMENDED | string | Text of the instructions given to participants before the recording. This is especially important in context of resting state recordings and distinguishing between eyes open and eyes closed paradigms. |
| CogAtlasID | RECOMMENDED | string | URI of the corresponding Cognitive Atlas Task term. |
| CogPOID | RECOMMENDED | string | URI of the corresponding CogPO term. |
| DeviceSerialNumber | RECOMMENDED | string | The serial number of the equipment that produced the measurements. A pseudonym can also be used to prevent the equipment from being identifiable, so long as each pseudonym is unique within the dataset. |

Specific MEG fields MUST be present:

| Key name | Requirement Level | Data type | Description |
|---|---|---|---|
| SamplingFrequency | REQUIRED | number | Sampling frequency (in Hz) of all the data in the recording, regardless of their type (for example, `2400`). The sampling frequency of data channels that deviate from the main sampling frequency SHOULD be specified in the `channels.tsv` file. |
| PowerLineFrequency | REQUIRED | number or `"n/a"` | Frequency (in Hz) of the power grid at the geographical location of the instrument (for example, `50` or `60`). |

| Key name | Requirement Level | Data type | Description |
|---|---|---|---|
| DewarPosition | REQUIRED | string | Position of the dewar during the MEG scan: `"upright"`, `"supine"` or `"degrees"` of angle from vertical: for example on CTF systems, `"upright=15°, supine=90°"`. |
| SoftwareFilters | REQUIRED | object of objects or `"n/a"` | Object of temporal software filters applied, or `"n/a"` if the data is not available. Each key:value pair in the JSON object is a name of the filter and an object in which its parameters are defined as key:value pairs (for example, `{"Anti-aliasing filter": {"half-amplitude cutoff (Hz)": 500, "Roll-off": "6dB/Octave"}}`). |
| DigitizedLandmarks | REQUIRED | boolean | `true` or `false` value indicating whether anatomical landmark points (fiducials) are contained within this recording. Must be one of: `"true"`, `"false"`. |
| DigitizedHeadPoints | REQUIRED | boolean | `true` or `false` value indicating whether head points outlining the scalp/face surface are contained within this recording. Must be one of: `"true"`, `"false"`. |

SHOULD be present:

| Key name | Requirement Level | Data type | Description |
|---|---|---|---|
| MEGChannelCount | RECOMMENDED | integer | Number of MEG channels (for example, `275`). Must be a number greater than or equal to 0. |
| MEGREFChannelCount | RECOMMENDED | integer | Number of MEG reference channels (for example, `23`). For systems without such channels (for example, Neuromag Vectorview), `MEGREFChannelCount` should be set to `0`. Must be a number greater than or equal to 0. |

| Key name | Requirement Level | Data type | Description |
|---|---|---|---|
| EEGChannelCount | RECOMMENDED | integer | Number of EEG channels recorded simultaneously (for example, `21`). Must be a number greater than or equal to 0. |
| ECOGChannelCount | RECOMMENDED | integer | Number of ECoG channels. Must be a number greater than or equal to 0. |
| SEEGChannelCount | RECOMMENDED | integer | Number of SEEG channels. Must be a number greater than or equal to 0. |
| EOGChannelCount | RECOMMENDED | integer | Number of EOG channels. Must be a number greater than or equal to 0. |
| ECGChannelCount | RECOMMENDED | integer | Number of ECG channels. Must be a number greater than or equal to 0. |
| EMGChannelCount | RECOMMENDED | integer | Number of EMG channels. Must be a number greater than or equal to 0. |
| MiscChannelCount | RECOMMENDED | integer | Number of miscellaneous analog channels for auxiliary signals. Must be a number greater than or equal to 0. |
| TriggerChannelCount | RECOMMENDED | integer | Number of channels for digital (TTL bit level) triggers. Must be a number greater than or equal to 0. |
| RecordingDuration | RECOMMENDED | number | Length of the recording in seconds (for example, `3600`). |
| RecordingType | RECOMMENDED | string | Defines whether the recording is `"continuous"`, `"discontinuous"`, or `"epoched"`, where `"epoched"` is limited to time windows about events of interest (for example, stimulus presentations or subject responses). Must be one of: `"continuous"`, `"epoched"`, `"discontinuous"`. |
| EpochLength | RECOMMENDED | number | Duration of individual epochs in seconds (for example, `1`) in case of epoched data. If recording was continuous or discontinuous, leave out the field. Must be a number greater than or equal to 0. |
| ContinuousHeadLocalization | RECOMMENDED | boolean | `true` or `false` value indicating whether continuous head localisation was performed. Must be one of: `"true"`, `"false"`. |

| Key name | Requirement Level | Data type | Description |
|---|---|---|---|
| HeadCoilFrequency | RECOMMENDED | number or array of numbers | List of frequencies (in Hz) used by the head localisation coils ('HLC' in CTF systems, 'HPI' in Elekta, 'COH' in BTi/4D) that track the subject's head position in the MEG helmet (for example, `[293, 307, 314, 321]`). |
| MaxMovement | RECOMMENDED | number | Maximum head movement (in mm) detected during the recording, as measured by the head localisation coils (for example, `4.8`). |
| SubjectArtefactDescription | RECOMMENDED | string | Freeform description of the observed subject artefact and its possible cause (for example, `"Vagus Nerve Stimulator"`, `"non-removable implant"`). If this field is set to `"n/a"`, it will be interpreted as absence of major source of artifacts except cardiac and blinks. |
| AssociatedEmptyRoom | RECOMMENDED | array of strings or string | Relative path in BIDS folder structure to empty-room file associated with the subject's MEG recording. The path needs to use forward slashes instead of backward slashes (for example, "sub-emptyroom/ses-/meg/sub-emptyroom_ses-_task-noise_run-_meg.ds"). |
| HardwareFilters | RECOMMENDED | object of objects or `"n/a"` | Object of temporal hardware filters applied, or `"n/a"` if the data is not available. Each key:value pair in the JSON object is a name of the filter and an object in which its parameters are defined as key:value pairs. For example, `{"Highpass RC filter": {"Half amplitude cutoff (Hz)": 0.0159, "Roll-off": "6dB/Octave"}}`. |

Specific EEG fields (if recorded with MEG, see Recording EEG simultaneously with MEG SHOULD be present:

| Key name | Requirement Level | Data type | Description |
|---|---|---|---|
| EEGPlacementScheme | OPTIONAL | string | Placement scheme of EEG electrodes. Either the name of a standardized placement system (for example, `"10-20"`) or a list of standardized electrode names (for example, `["Cz", "Pz"]`). |
| CapManufacturer | OPTIONAL | string | Name of the cap manufacturer (for example, `"EasyCap"`). |
| CapManufacturersModelName | OPTIONAL | string | Manufacturer's designation of the EEG cap model (for example, `"actiCAP 64 Ch Standard-2"`). |
| EEGReference | OPTIONAL | string | General description of the reference scheme used and (when applicable) of location of the reference electrode in the raw recordings (for example, `"left mastoid"`, `"Cz"`, `"CMS"`). If different channels have a different reference, this field should have a general description and the channel specific reference should be defined in the `channels.tsv` file. |

Example:

```
{
   "InstitutionName": "Stanford University",
   "InstitutionAddress": "450 Serra Mall, Stanford, CA 94305-2004, USA",
   "Manufacturer": "CTF",
   "ManufacturersModelName": "CTF-275",
   "DeviceSerialNumber": "11035",
   "SoftwareVersions": "Acq 5.4.2-linux-20070507",
   "PowerLineFrequency": 60,
   "SamplingFrequency": 2400,
   "MEGChannelCount": 270,
   "MEGREFChannelCount": 26,
   "EEGChannelCount": 0,
   "EOGChannelCount": 2,
   "ECGChannelCount": 1,
   "EMGChannelCount": 0,
```

```
    "DewarPosition": "upright",
  "SoftwareFilters": {
    "SpatialCompensation": {"GradientOrder": "3rd"}
  },
  "RecordingDuration": 600,
  "RecordingType": "continuous",
  "EpochLength": 0,
  "TaskName": "rest",
  "ContinuousHeadLocalization": true,
  "HeadCoilFrequency": [1470,1530,1590],
  "DigitizedLandmarks": true,
  "DigitizedHeadPoints": true
}
```

Note that the date and time information SHOULD be stored in the Study key file (`scans.tsv`), see Scans file. Date time information MUST be expressed as indicated in Units

## Channels description (`*_channels.tsv`)

Template:

```
sub-<label>/
    [ses-<label>/]
        meg/
            sub-<label>[_ses-<label>]_task-<label>[_acq-<label>][_run-<index>][_proc-<label>]_channels.json
            sub-<label>[_ses-<label>]_task-<label>[_acq-<label>][_run-<index>][_proc-<label>]_channels.tsv
```

This file is RECOMMENDED as it provides easily searchable information across BIDS datasets. For example for general curation, response to queries, or for batch analysis. To avoid confusion, the channels SHOULD be listed in the order they appear in the MEG data file. Any number of additional columns MAY be added to provide additional information about the channels. Missing values MUST be indicated with `"n/a"`.

The columns of the channels description table stored in `*_channels.tsv` are:

MUST be present in this specific order:

| Column name | Requirement Level | Data type | Description |
|---|---|---|---|
| name | REQUIRED | string | Label of the channel. |

| Column name | Requirement Level | Data type | Description |
|---|---|---|---|
| type | REQUIRED | string | Type of channel; MUST use the channel types listed below. Note that the type MUST be in upper-case. Must be one of: `"MEGMAG"`, `"MEGGRADAXIAL"`, `"MEGGRADPLANAR"`, `"MEGREFMAG"`, `"MEGREFGRADAXIAL"`, `"MEGREFGRADPLANAR"`, `"MEGOTHER"`, `"EEG"`, `"ECOG"`, `"SEEG"`, `"DBS"`, `"VEOG"`, `"HEOG"`, `"EOG"`, `"ECG"`, `"EMG"`, `"TRIG"`, `"AUDIO"`, `"PD"`, `"EYEGAZE"`, `"PUPIL"`, `"MISC"`, `"SYSCLOCK"`, `"ADC"`, `"DAC"`, `"HLU"`, `"FITERR"`, `"OTHER"`. |
| units | REQUIRED | string | Physical unit of the value represented in this channel, for example, `V` for Volt, or `fT/cm` for femto Tesla per centimeter (see Units). |

SHOULD be present:

| Column name | Requirement Level | Data type | Description |
|---|---|---|---|
| description | OPTIONAL | string | Brief free-text description of the channel, or other information of interest. |
| sampling_frequency | OPTIONAL | number | Sampling rate of the channel in Hz. |
| low_cutoff | OPTIONAL | number or `"n/a"` | Frequencies used for the high-pass filter applied to the channel in Hz. If no high-pass filter applied, use `n/a`. |
| high_cutoff | OPTIONAL | number or `"n/a"` | Frequencies used for the low-pass filter applied to the channel in Hz. If no low-pass filter applied, use `n/a`. Note that hardware anti-aliasing in A/D conversion of all MEG/EEG electronics applies a low-pass filter; specify its frequency here if applicable. |
| notch | OPTIONAL | number or `"n/a"` | Frequencies used for the notch filter applied to the channel, in Hz. If no notch filter applied, use `n/a`. |

| Column name | Requirement Level | Data type | Description |
|---|---|---|---|
| software_filters | OPTIONAL | string or `"n/a"` | List of temporal and/or spatial software filters applied (for example, `SSS`, `SpatialCompensation`). Note that parameters should be defined in the general MEG sidecar .json file. Indicate `n/a` in the absence of software filters applied. |
| status | OPTIONAL | string | Data quality observed on the channel. A channel is considered `bad` if its data quality is compromised by excessive noise. If quality is unknown, then a value of `n/a` may be used. Description of noise type SHOULD be provided in `[status_description]`. Must be one of: `"good"`, `"bad"`, `"n/a"`. |
| status_description | OPTIONAL | string | Freeform text description of noise or artifact affecting data quality on the channel. It is meant to explain why the channel was declared bad in `[status]`. |

Example:

```
name type units description sampling_frequency low_cutoff high_cutoff notch software_filters status
UDIO001 TRIG V analogue trigger 1200 0.1 300 0 n/a good
MLC11 MEGGRADAXIAL T sensor 1st-order grad 1200 0 n/a 50 SSS bad
```

Restricted keyword list for field `type`. Note that upper-case is REQUIRED:

| Keyword | Description |
|---|---|
| MEGMAG | MEG magnetometer |
| MEGGRADAXIAL | MEG axial gradiometer |
| MEGGRADPLANAR | MEG planargradiometer |
| MEGREFMAG | MEG reference magnetometer |
| MEGREFGRADAXIAL | MEG reference axial gradiometer |
| MEGREFGRADPLANAR | MEG reference planar gradiometer |
| MEGOTHER | Any other type of MEG sensor |
| EEG | Electrode channel |
| ECOG | Electrode channel |

| Keyword | Description |
|---|---|
| SEEG | Electrode channel |
| DBS | Electrode channel |
| VEOG | Vertical EOG (electrooculogram) |
| HEOG | Horizontal EOG |
| EOG | Generic EOG channel |
| ECG | ElectroCardioGram (heart) |
| EMG | ElectroMyoGram (muscle) |
| TRIG | System Triggers |
| AUDIO | Audio signal |
| PD | Photodiode |
| EYEGAZE | Eye Tracker gaze |
| PUPIL | Eye Tracker pupil diameter |
| MISC | Miscellaneous |
| SYSCLOCK | System time showing elapsed time since trial started |
| ADC | Analog to Digital input |
| DAC | Digital to Analog output |
| HLU | Measured position of head and head coils |
| FITERR | Fit error signal from each head localization coil |
| OTHER | Any other type of channel |

Example of free text for field `description`:

- stimulus, response, vertical EOG, horizontal EOG, skin conductance, sats, intracranial, eyetracker

Example:

```
name type units description
VEOG VEOG V vertical EOG
FDI EMG V left first dorsal interosseous
UDIO001 TRIG V analog trigger signal
UADC001 AUDIO V envelope of audio signal presented to participant
```

## Coordinate System JSON (`*_coordsystem.json`)

Template:

```
sub-<label>/
    [ses-<label>/]
        meg/
```

`sub-<label>[_ses-<label>][_acq-<label>]_coordsystem.json`

OPTIONAL. A JSON document specifying the coordinate system(s) used for the MEG, EEG, head localization coils, and anatomical landmarks.

MEG and EEG sensors:

| Key name | Requirement Level | Data type | Description |
|---|---|---|---|
| MEGCoordinateSystem | REQUIRED | string | Defines the coordinate system for the MEG sensors. See Appendix VIII for a list of restricted keywords for coordinate systems. If `"Other"`, provide definition of the coordinate system in `"MEGCoordinateSystemDescription"`. Must be one of: `"CTF"`, `"ElektaNeuromag"`, `"4DBti"`, `"KitYokogawa"`, `"ChietiItab"`, `"Other"`, `"CapTrak"`, `"EEGLAB"`, `"EEGLAB-HJ"`, `"Other"`, `"ICBM452AirSpace"`, `"ICBM452Warp5Space"`, `"IXI549Space"`, `"fsaverage"`, `"fsaverageSym"`, `"fsLR"`, `"MNIColin27"`, `"MNI152Lin"`, `"MNI152NLin2009aSym"`, `"MNI152NLin2009bSym"`, `"MNI152NLin2009cSym"`, `"MNI152NLin2009aAsym"`, `"MNI152NLin2009bAsym"`, `"MNI152NLin2009cAsym"`, `"MNI152NLin6Sym"`, `"MNI152NLin6ASym"`, `"MNI305"`, `"NIHPD"`, `"OASIS30AntsOASISAnts"`, `"OASIS30Atropos"`, `"Talairach"`, `"UNCInfant"`, `"fsaverage3"`, `"fsaverage4"`, `"fsaverage5"`, `"fsaverage6"`, `"fsaveragesym"`, `"UNCInfant0V21"`, `"UNCInfant1V21"`, `"UNCInfant2V21"`, `"UNCInfant0V22"`, `"UNCInfant1V22"`, `"UNCInfant2V22"`, `"UNCInfant0V23"`, `"UNCInfant1V23"`, `"UNCInfant2V23"`. |

| Key name | Requirement Level | Data type | Description |
|---|---|---|---|
| MEGCoordinateUnits | REQUIRED | string | Units of the coordinates of `"MEGCoordinateSystem"`. Must be one of: `"m"`, `"mm"`, `"cm"`, `"n/a"`. |
| MEGCoordinateSystemDescription | OPTIONAL, but REQUIRED if `MEGCoordinateSystem` is `Other` | string | Free-form text description of the coordinate system. May also include a link to a documentation page or paper describing the system in greater detail. |

| Key name | Requirement Level | Data type | Description |
|---|---|---|---|
| EEGCoordinateSystem | OPTIONAL | string | Defines the coordinate system for the EEG sensors.See Appendix VIII for a list of restricted keywords for coordinate systems. If `"Other"`, provide definition of the coordinate system in `EEGCoordinateSystemDescription`. See Appendix VIII. Preferably the same as the `MEGCoordinateSystem`.Must be one of: `"CTF"`, `"ElektaNeuromag"`, `"4DBti"`, `"KitYokogawa"`, `"ChietiItab"`, `"Other"`, `"CapTrak"`, `"EEGLAB"`, `"EEGLAB-HJ"`, `"Other"`, `"ICBM452AirSpace"`, `"ICBM452Warp5Space"`, `"IXI549Space"`, `"fsaverage"`, `"fsaverageSym"`, `"fsLR"`, `"MNIColin27"`, `"MNI152Lin"`, `"MNI152NLin2009aSym"`, `"MNI152NLin2009bSym"`, `"MNI152NLin2009cSym"`, `"MNI152NLin2009aAsym"`, `"MNI152NLin2009bAsym"`, `"MNI152NLin2009cAsym"`, `"MNI152NLin6Sym"`, `"MNI152NLin6ASym"`, `"MNI305"`, `"NIHPD"`, `"OASIS30AntsOASISAnts"`, `"OASIS30Atropos"`, `"Talairach"`, `"UNCInfant"`, `"fsaverage3"`, `"fsaverage4"`, `"fsaverage5"`, `"fsaverage6"`, `"fsaveragesym"`, `"UNCInfant0V21"`, `"UNCInfant1V21"`, `"UNCInfant2V21"`, `"UNCInfant0V22"`, `"UNCInfant1V22"`, `"UNCInfant2V22"`, `"UNCInfant0V23"`, `"UNCInfant1V23"`, `"UNCInfant2V23"`. |
| EEGCoordinateUnits | OPTIONAL | string | Units of the coordinates of `EEGCoordinateSystem`. Must be one of: `"m"`, `"mm"`, `"cm"`, `"n/a"`. |

| Key name | Requirement Level | Data type | Description |
|---|---|---|---|
| EEGCoordinateSystemDescription | OPTIONAL, but REQUIRED if `EEGCoordinateSystem` is `Other` | string | Free-form text description of the coordinate system. May also include a link to a documentation page or paper describing the system in greater detail. See Recording EEG simultaneously with MEG. |

Head localization coils:

| Key name | Requirement Level | Data type | Description |
|---|---|---|---|
| HeadCoilCoordinates | OPTIONAL | object of arrays | Key:value pairs describing head localization coil labels and their coordinates, interpreted following the `HeadCoilCoordinateSystem` (for example, `{"NAS": [12.7,21.3,13.9], "LPA": [5.2,11.3,9.6], "RPA": [20.2,11.3,9.1]}`). Note that coils are not always placed at locations that have a known anatomical name (for example, for Elekta, Yokogawa systems); in that case generic labels can be used (for example, `{"coil1": [12.2,21.3,12.3], "coil2": [6.7,12.3,8.6], "coil3": [21.9,11.0,8.1]}`). Each array MUST contain three numeric values corresponding to x, y, and z axis of the coordinate system in that exact order. |

| Key name | Requirement Level | Data type | Description |
|---|---|---|---|
| HeadCoilCoordinateSystem | OPTIONAL | string | Defines the coordinate system for the head coils. See Appendix VIII for a list of restricted keywords for coordinate systems. If `"Other"`, provide definition of the coordinate system in `HeadCoilCoordinateSystemDescription`. Must be one of: `"CTF"`, `"ElektaNeuromag"`, `"4DBti"`, `"KitYokogawa"`, `"ChietiItab"`, `"Other"`, `"CapTrak"`, `"EEGLAB"`, `"EEGLAB-HJ"`, `"Other"`, `"ICBM452AirSpace"`, `"ICBM452Warp5Space"`, `"IXI549Space"`, `"fsaverage"`, `"fsaverageSym"`, `"fsLR"`, `"MNIColin27"`, `"MNI152Lin"`, `"MNI152NLin2009aSym"`, `"MNI152NLin2009bSym"`, `"MNI152NLin2009cSym"`, `"MNI152NLin2009aAsym"`, `"MNI152NLin2009bAsym"`, `"MNI152NLin2009cAsym"`, `"MNI152NLin6Sym"`, `"MNI152NLin6ASym"`, `"MNI305"`, `"NIHPD"`, `"OASIS30AntsOASISAnts"`, `"OASIS30Atropos"`, `"Talairach"`, `"UNCInfant"`, `"fsaverage3"`, `"fsaverage4"`, `"fsaverage5"`, `"fsaverage6"`, `"fsaveragesym"`, `"UNCInfant0V21"`, `"UNCInfant1V21"`, `"UNCInfant2V21"`, `"UNCInfant0V22"`, `"UNCInfant1V22"`, `"UNCInfant2V22"`, `"UNCInfant0V23"`, `"UNCInfant1V23"`, `"UNCInfant2V23"`. |
| HeadCoilCoordinateUnits | OPTIONAL | string | Units of the coordinates of `HeadCoilCoordinateSystem`. Must be one of: `"m"`, `"mm"`, `"cm"`, `"n/a"`. |

| Key name | Requirement Level | Data type | Description |
|---|---|---|---|
| HeadCoilCoordinateSystemDescription | OPTIONAL, but REQUIRED if `HeadCoilCoordinateSystem` is `Other` | string | Free-form text description of the coordinate system. May also include a link to a documentation page or paper describing the system in greater detail. |

Digitized head points:

| Key name | Requirement Level | Data type | Description |
|---|---|---|---|
| DigitizedHeadPoints | OPTIONAL | boolean | `true` or `false` value indicating whether head points outlining the scalp/face surface are contained within this recording. Must be one of: `"true"`, `"false"`. |

| Key name | Requirement Level | Data type | Description |
|---|---|---|---|
| DigitizedHeadPointsCoordinateSystem | OPTIONAL | string | Defines the coordinate system for the digitized head points. See Appendix VIII for a list of restricted keywords for coordinate systems. If `"Other"`, provide definition of the coordinate system in `"DigitizedHeadPointsCoordinateSystemDescript` Must be one of: `"CTF"`, `"ElektaNeuromag"`, `"4DBti"`, `"KitYokogawa"`, `"ChietiItab"`, `"Other"`, `"CapTrak"`, `"EEGLAB"`, `"EEGLAB-HJ"`, `"Other"`, `"ICBM452AirSpace"`, `"ICBM452Warp5Space"`, `"IXI549Space"`, `"fsaverage"`, `"fsaverageSym"`, `"fsLR"`, `"MNIColin27"`, `"MNI152Lin"`, `"MNI152NLin2009aSym"`, `"MNI152NLin2009bSym"`, `"MNI152NLin2009cSym"`, `"MNI152NLin2009aAsym"`, `"MNI152NLin2009bAsym"`, `"MNI152NLin2009cAsym"`, `"MNI152NLin6Sym"`, `"MNI152NLin6ASym"`, `"MNI305"`, `"NIHPD"`, `"OASIS30AntsOASISAnts"`, `"OASIS30Atropos"`, `"Talairach"`, `"UNCInfant"`, `"fsaverage3"`, `"fsaverage4"`, `"fsaverage5"`, `"fsaverage6"`, `"fsaveragesym"`, `"UNCInfant0V21"`, `"UNCInfant1V21"`, `"UNCInfant2V21"`, `"UNCInfant0V22"`, `"UNCInfant1V22"`, `"UNCInfant2V22"`, `"UNCInfant0V23"`, `"UNCInfant1V23"`, `"UNCInfant2V23"`. |
| DigitizedHeadPointsCoordinateUnits | OPTIONAL | string | Units of the coordinates of `"DigitizedHeadPointsCoordinateSystem"`. Must be one of: `"m"`, `"mm"`, `"cm"`, `"n/a"`. |

| Key name | Requirement Level | Data type | Description |
|---|---|---|---|
| DigitizedHeadPointsCoordinateSystemDe | OPTIONAL, but REQUIRED if `DigitizedHeadPointsCoordinateSystem` is `Other` | string | Free-form text description of the coordinate system. May also include a link to a documentation page or paper describing the system in greater detail. |

Anatomical MRI:

| Key name | Requirement Level | Data type | Description |
|---|---|---|---|
| IntendedFor | OPTIONAL | string or array of strings | The paths to files for which the associated file is intended to be used. Contains one or more filenames with paths relative to the participant subfolder. Paths need to use forward slashes instead of backward slashes, regardless of operating system. This is used to identify the structural MRI(s), possibly of different types if a list is specified, to be used with the MEG recording. |

Anatomical landmarks:

| Key name | Requirement Level | Data type | Description |
|---|---|---|---|
| AnatomicalLandmarkCoordinates | OPTIONAL | object of arrays | Key:value pairs of the labels and 3-D digitized locations of anatomical landmarks, interpreted following the `"AnatomicalLandmarkCoordinateSystem"` (for example, `{"NAS": [12.7,21.3,13.9], "LPA": [5.2,11.3,9.6], "RPA": [20.2,11.3,9.1]}`. Each array MUST contain three numeric values corresponding to x, y, and z axis of the coordinate system in that exact order. |

| Key name | Requirement Level | Data type | Description |
|---|---|---|---|
| AnatomicalLandmarkCoordinateSystem | OPTIONAL | string | Defines the coordinate system for the anatomical landmarks. See Appendix VIII for a list of restricted keywords for coordinate systems. If `"Other"`, provide definition of the coordinate system in `"AnatomicalLandmarkCoordinateSystemDescripti` Preferably the same as the `MEGCoordinateSystem`.Must be one of: `"CTF"`, `"ElektaNeuromag"`, `"4DBti"`, `"KitYokogawa"`, `"ChietiItab"`, `"Other"`, `"CapTrak"`, `"EEGLAB"`, `"EEGLAB-HJ"`, `"Other"`, `"ICBM452AirSpace"`, `"ICBM452Warp5Space"`, `"IXI549Space"`, `"fsaverage"`, `"fsaverageSym"`, `"fsLR"`, `"MNIColin27"`, `"MNI152Lin"`, `"MNI152NLin2009aSym"`, `"MNI152NLin2009bSym"`, `"MNI152NLin2009cSym"`, `"MNI152NLin2009aAsym"`, `"MNI152NLin2009bAsym"`, `"MNI152NLin2009cAsym"`, `"MNI152NLin6Sym"`, `"MNI152NLin6ASym"`, `"MNI305"`, `"NIHPD"`, `"OASIS30AntsOASISAnts"`, `"OASIS30Atropos"`, `"Talairach"`, `"UNCInfant"`, `"fsaverage3"`, `"fsaverage4"`, `"fsaverage5"`, `"fsaverage6"`, `"fsaveragesym"`, `"UNCInfant0V21"`, `"UNCInfant1V21"`, `"UNCInfant2V21"`, `"UNCInfant0V22"`, `"UNCInfant1V22"`, `"UNCInfant2V22"`, `"UNCInfant0V23"`, `"UNCInfant1V23"`, `"UNCInfant2V23"`. |
| AnatomicalLandmarkCoordinateUnits | OPTIONAL | string | Units of the coordinates of `"AnatomicalLandmarkCoordinateSystem"`. Must be one of: `"m"`, `"mm"`, `"cm"`, `"n/a"`. |

| Key name | Requirement Level | Data type | Description |
|---|---|---|---|
| AnatomicalLandmarkCoordinateSystemDescription | OPTIONAL, but REQUIRED if `AnatomicalLandmarkCoordinateSystem` is `Other` | string | Free-form text description of the coordinate system. May also include a link to a documentation page or paper describing the system in greater detail. |

It is also RECOMMENDED that the MRI voxel coordinates of the actual anatomical landmarks for co-registration of MEG with structural MRI are stored in the `AnatomicalLandmarkCoordinates` field in the JSON sidecar of the corresponding T1w MRI anatomical data of the subject seen in the MEG session (see Anatomy Imaging Data).

For example: `"sub-01/ses-mri/anat/sub-01_ses-mri_acq-mprage_T1w.json"`

In principle, these locations are those of absolute anatomical markers. However, the marking of NAS, LPA and RPA is more ambiguous than that of for example, AC and PC. This may result in some variability in their 3-D digitization from session to session, even for the same participant. The solution would be to use only one T1w file and populate the `AnatomicalLandmarkCoordinates` field with session-specific labels for example, ”NAS-session1”: `[127,213,139]`,”NAS-session2”: `[123,220,142]`.

Fiducials information:

| Key name | Requirement Level | Data type | Description |
|---|---|---|---|
| FiducialsDescription | OPTIONAL | string | Free-form text description of how the fiducials such as vitamin-E capsules were placed relative to anatomical landmarks, and how the position of the fiducials were measured (for example, `"both with Polhemus and with T1w MRI"`). |

For more information on the definition of anatomical landmarks, please visit: http://www.fieldtriptoolbox.org/faq/how_are_the_lpa_and_rpa_points_defined

For more information on typical coordinate systems for MEG-MRI coregistration: http://www.fieldtriptoolbox.org/faq/how_are_the_different_head_and_mri_coordinate_systems_defined, or: http://neuroimage.usc.edu/brainstorm/CoordinateSystems

## Landmark photos (`*_photo.jpg`)

Photos of the anatomical landmarks and/or head localization coils (`*_photo.jpg`)

Template:

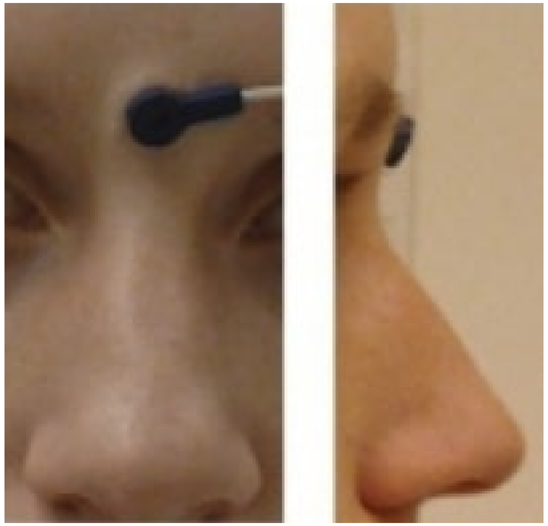
```
sub-<label>/
    [ses-<label>/]
```

```
        meg/
            sub-<label>[_ses-<label>][_acq-<label>]_photo.jpg
```

Photos of the anatomical landmarks and/or head localization coils on the subject's head are RECOMMENDED. If the coils are not placed at the location of actual anatomical landmarks, these latter may be marked with a piece of felt-tip taped to the skin. Please note that the photos may need to be cropped or blurred to conceal identifying features prior to sharing, depending on the terms of the consent given by the participant.

The `acq-<label>` entity can be used to indicate acquisition of different photos of the same face (or other body part in different angles to show, for example, the location of the nasion (NAS) as opposed to the right periauricular point (RPA)).

Example of the NAS fiducial placed between the eyebrows, rather than at the actual anatomical nasion: `sub-0001_ses-001_acq-NAS_photo.jpg`



## Head shape and electrode description (`*_headshape.<ext>`)

Template:

```
sub-<label>/
    [ses-<label>/]
        meg/
            sub-<label>[_ses-<label>][_acq-<label>]_headshape.<extension>
```

This file is RECOMMENDED.

The 3-D locations of points that describe the head shape and/or EEG electrode locations can be digitized and stored in separate files. The `acq-<label>` entity can be used when more than one type of digitization in done for a session, for example when the head points are in a separate file from the EEG locations. These files are stored in the specific format of the 3-D digitizer's manufacturer (see Appendix VI).

Example:

```
sub-control01/
   ses-01/
      sub-control01_ses-01_acq-HEAD_headshape.pos
      sub-control01_ses-01_acq-EEG_headshape.pos
```

Note that the `*_headshape` file(s) is shared by all the runs and tasks in a session. If the subject needs to be taken out of the scanner and the head-shape has to be updated, then for MEG it could be considered to be a new session.

## Empty-room MEG recordings

Empty-room MEG recordings capture the environmental and recording system's noise. In the context of BIDS it is RECOMMENDED to perform an empty-room recording for each experimental session. It is RECOMMENDED to store the empty-room recording inside a subject folder named `sub-emptyroom`. The label for the `task-<label>` entity in the empty-room recording SHOULD be set to `noise`. If a `session-<label>` entity is present, its label SHOULD be the date of the empty-room recording in the format `YYYYMMDD`, that is `ses-YYYYMMDD`. The `scans.tsv` file containing the date and time of the acquisition SHOULD also be included. The rationale is that this naming scheme will allow users to easily retrieve the empty-room recording that best matches a particular experimental session, based on date and time of the recording. It should be possible to query empty-room recordings just like usual subject recordings, hence all metadata sidecar files (such as the `channels.tsv`) file SHOULD be present as well.

Example:

```
sub-control01/
sub-control02/
sub-emptyroom/
   ses-20170801/
      sub-emptyroom_ses-20170801_scans.tsv
      meg/
         sub-emptyroom_ses-20170801_task-noise_meg.ds
         sub-emptyroom_ses-20170801_task-noise_meg.json
         sub-emptyroom_ses-20170801_task-noise_channels.tsv
```

# Electroencephalography

Support for Electroencephalography (EEG) was developed as a BIDS Extension Proposal. Please see Citing BIDS on how to appropriately credit this extension when referring to it in the context of the academic literature.

Several example EEG datasets have been formatted using this specification and can be used for practical guidance when curating a new dataset.

## EEG recording data

Template:

```
sub-<label>/
    [ses-<label>/]
        eeg/
            sub-<label>[_ses-<label>]_task-<label>[_acq-<label>][_run-<index>]_eeg.<extension>
            sub-<label>[_ses-<label>]_task-<label>[_acq-<label>][_run-<index>]_eeg.json
            sub-<label>[_ses-<label>]_task-<label>[_acq-<label>][_run-<index>]_events.json
            sub-<label>[_ses-<label>]_task-<label>[_acq-<label>][_run-<index>]_events.tsv
            sub-<label>[_ses-<label>]_task-<label>[_acq-<label>][_run-<index>][_recording-<label>]_physio.json
            sub-<label>[_ses-<label>]_task-<label>[_acq-<label>][_run-<index>][_recording-<label>]_physio.tsv.gz
            sub-<label>[_ses-<label>]_task-<label>[_acq-<label>][_run-<index>][_recording-<label>]_stim.json
            sub-<label>[_ses-<label>]_task-<label>[_acq-<label>][_run-<index>][_recording-<label>]_stim.tsv.gz
```

The EEG community uses a variety of formats for storing raw data, and there is no single standard that all researchers agree on. For BIDS, EEG data MUST be stored in one of the following formats:

| Format | Extension(s) | Description |
|---|---|---|
| European data format | `.edf` | Each recording consists of a single `.edf` file. `edf+` files are permitted. The capital `.EDF` extension MUST NOT be used. |

| Format | Extension(s) | Description |
|---|---|---|
| BrainVision Core Data Format | `.vhdr`, `.vmrk`, `.eeg` | Each recording consists of a `.vhdr`, `.vmrk`, `.eeg` file triplet. |
| EEGLAB | `.set`, `.fdt` | The format used by the MATLAB toolbox EEGLAB. Each recording consists of a `.set` file with an optional `.fdt` file. |
| Biosemi | `.bdf` | Each recording consists of a single `.bdf` file. `bdf+` files are permitted. The capital `.BDF` extension MUST NOT be used. |

It is RECOMMENDED to use the European data format, or the BrainVision data format. It is furthermore discouraged to use the other accepted formats over these RECOMMENDED formats, particularly because there are conversion scripts available in most commonly used programming languages to convert data into the RECOMMENDED formats. The data in their original format, if different from the supported formats, can be stored in the `/sourcedata` directory.

The original data format is especially valuable in case conversion elicits the loss of crucial metadata specific to manufacturers and specific EEG systems. We also encourage users to provide additional meta information extracted from the manufacturer specific data files in the sidecar JSON file. Other relevant files MAY be included alongside the original EEG data in `/sourcedata`.

Note the RecordingType, which depends on whether the data stream on disk is interrupted or not. Continuous data is by definition 1 segment without interruption. Epoched data consists of multiple segments that all have the same length (for example, corresponding to trials) and that have gaps in between. Discontinuous data consists of multiple segments of different length, for example due to a pause in the acquisition.

Note that for proper documentation of EEG recording metadata it is important to understand the difference between electrode and channel: An EEG electrode is attached to the skin, whereas a channel is the combination of the analog differential amplifier and analog-to-digital converter that result in a potential (voltage) difference that is stored in the EEG dataset. We employ the following short definitions:

- Electrode = A single point of contact between the acquisition system and the recording site (for example, scalp, neural tissue, …). Multiple electrodes can be organized as caps (for EEG), arrays, grids, leads, strips, probes, shafts, and so on.
- Channel = A single analog-to-digital converter in the recording system that regularly samples the value of a transducer, which results in the signal being represented as a time series in the digitized data. This can be connected to two electrodes (to measure the potential difference between them), a magnetic field or magnetic gradient sensor, temperature sensor, accelerometer, and so on.

Although the reference and ground electrodes are often referred to as channels, they are in most common EEG systems not recorded by themselves. Therefore they are not represented as channels in the data. The type of referencing for all channels and optionally the location of the reference electrode and the location of the ground electrode MAY be specified.

## Sidecar JSON (`*_eeg.json`)

Generic fields MUST be present:

| Key name | Requirement Level | Data type | Description |
|---|---|---|---|
| TaskName | REQUIRED | string | Name of the task. No two tasks should have the same name. The task label included in the file name is derived from this `"TaskName"` field by removing all non-alphanumeric (`[a-zA-Z0-9]`) characters. For example `"TaskName"` `"faces n-back"` will correspond to task label `facesnback`. A RECOMMENDED convention is to name resting state task using labels beginning with `rest`. |

SHOULD be present: For consistency between studies and institutions, we encourage users to extract the values of these fields from the actual raw data. Whenever possible, please avoid using ad hoc wording.

| Key name | Requirement Level | Data type | Description |
|---|---|---|---|
| InstitutionName | RECOMMENDED | string | The name of the institution in charge of the equipment that produced the measurements. |
| InstitutionAddress | RECOMMENDED | string | The address of the institution in charge of the equipment that produced the measurements. |
| InstitutionalDepartmentName | RECOMMENDED | string | The department in the institution in charge of the equipment that produced the measurements. |
| Manufacturer | RECOMMENDED | string | Manufacturer of the equipment that produced the measurements. |
| ManufacturersModelName | RECOMMENDED | string | Manufacturer’s model name of the equipment that produced the measurements. |
| SoftwareVersions | RECOMMENDED | string | Manufacturer’s designation of software version of the equipment that produced the measurements. |
| TaskDescription | RECOMMENDED | string | Longer description of the task. |

| Key name | Requirement Level | Data type | Description |
|---|---|---|---|
| Instructions | RECOMMENDED | string | Text of the instructions given to participants before the recording. This is especially important in context of resting state recordings and distinguishing between eyes open and eyes closed paradigms. |
| CogAtlasID | RECOMMENDED | string | URI of the corresponding Cognitive Atlas Task term. |
| CogPOID | RECOMMENDED | string | URI of the corresponding CogPO term. |
| DeviceSerialNumber | RECOMMENDED | string | The serial number of the equipment that produced the measurements. A pseudonym can also be used to prevent the equipment from being identifiable, so long as each pseudonym is unique within the dataset. |

Specific EEG fields MUST be present:

| Key name | Requirement Level | Data type | Description |
|---|---|---|---|
| EEGReference | REQUIRED | string | General description of the reference scheme used and (when applicable) of location of the reference electrode in the raw recordings (for example, `"left mastoid"`, `"Cz"`, `"CMS"`). If different channels have a different reference, this field should have a general description and the channel specific reference should be defined in the `channels.tsv` file. |
| SamplingFrequency | REQUIRED | number | Sampling frequency (in Hz) of all the data in the recording, regardless of their type (for example, `2400`). The sampling frequency of data channels that deviate from the main sampling frequency SHOULD be specified in the `channels.tsv` file. |

| Key name | Requirement Level | Data type | Description |
|---|---|---|---|
| PowerLineFrequency | REQUIRED | number or `"n/a"` | Frequency (in Hz) of the power grid at the geographical location of the instrument (for example, `50` or `60`). |
| SoftwareFilters | REQUIRED | object of objects or `"n/a"` | Object of temporal software filters applied, or `"n/a"` if the data is not available. Each key:value pair in the JSON object is a name of the filter and an object in which its parameters are defined as key:value pairs (for example, `{"Anti-aliasing filter": {"half-amplitude cutoff (Hz)": 500, "Roll-off": "6dB/Octave"}}`). |

SHOULD be present:

| Key name | Requirement Level | Data type | Description |
|---|---|---|---|
| CapManufacturer | RECOMMENDED | string | Name of the cap manufacturer (for example, `"EasyCap"`). |
| CapManufacturersModelName | RECOMMENDED | string | Manufacturer's designation of the EEG cap model (for example, `"actiCAP 64 Ch Standard-2"`). |
| EEGChannelCount | RECOMMENDED | integer | Number of EEG channels recorded simultaneously (for example, `21`). Must be a number greater than or equal to 0. |
| ECGChannelCount | RECOMMENDED | integer | Number of ECG channels. Must be a number greater than or equal to 0. |
| EMGChannelCount | RECOMMENDED | integer | Number of EMG channels. Must be a number greater than or equal to 0. |
| EOGChannelCount | RECOMMENDED | integer | Number of EOG channels. Must be a number greater than or equal to 0. |
| MiscChannelCount | RECOMMENDED | integer | Number of miscellaneous analog channels for auxiliary signals. Must be a number greater than or equal to 0. |
| TriggerChannelCount | RECOMMENDED | integer | Number of channels for digital (TTL bit level) triggers. Must be a number greater than or equal to 0. |

| Key name | Requirement Level | Data type | Description |
|---|---|---|---|
| RecordingDuration | RECOMMENDED | number | Length of the recording in seconds (for example, `3600`). |
| RecordingType | RECOMMENDED | string | Defines whether the recording is `"continuous"`, `"discontinuous"`, or `"epoched"`, where `"epoched"` is limited to time windows about events of interest (for example, stimulus presentations or subject responses). Must be one of: `"continuous"`, `"epoched"`, `"discontinuous"`. |
| EpochLength | RECOMMENDED | number | Duration of individual epochs in seconds (for example, `1`) in case of epoched data. If recording was continuous or discontinuous, leave out the field. Must be a number greater than or equal to 0. |
| EEGGround | RECOMMENDED | string | Description of the location of the ground electrode (for example, `"placed on right mastoid (M2)"`). |
| HeadCircumference | RECOMMENDED | number | Circumference of the participant's head, expressed in cm (for example, `58`). Must be a number greater than 0. |
| EEGPlacementScheme | RECOMMENDED | string | Placement scheme of EEG electrodes. Either the name of a standardized placement system (for example, `"10-20"`) or a list of standardized electrode names (for example, `["Cz", "Pz"]`). |
| HardwareFilters | RECOMMENDED | object of objects or `"n/a"` | Object of temporal hardware filters applied, or `"n/a"` if the data is not available. Each key:value pair in the JSON object is a name of the filter and an object in which its parameters are defined as key:value pairs. For example, `{"Highpass RC filter": {"Half amplitude cutoff (Hz)": 0.0159, "Roll-off": "6dB/Octave"}}`. |

| Key name | Requirement Level | Data type | Description |
|---|---|---|---|
| SubjectArtefactDescription | RECOMMENDED | string | Freeform description of the observed subject artefact and its possible cause (for example, `"Vagus Nerve Stimulator"`, `"non-removable implant"`). If this field is set to `"n/a"`, it will be interpreted as absence of major source of artifacts except cardiac and blinks. |

Example:

```
{
  "TaskName":"Seeing stuff",
  "TaskDescription":"Subjects see various images for which phase, amplitude spectrum, and color vary continuously",
  "Instructions":"Your task is to detect images when they appear for the 2nd time, only then press the response button with your right/left hand (count
  "InstitutionName":"The world best university, 10 Beachfront Avenue, Papeete",
  "SamplingFrequency":2400,
  "Manufacturer":"Brain Products",
  "ManufacturersModelName":"BrainAmp DC",
  "CapManufacturer":"EasyCap",
  "CapManufacturersModelName":"M1-ext",
  "EEGChannelCount":87,
  "EOGChannelCount":2,
  "ECGChannelCount":1,
  "EMGChannelCount":0,
  "MiscChannelCount":0,
  "TriggerChannelCount":1,
  "PowerLineFrequency":50,
  "EEGPlacementScheme":"10 percent system",
  "EEGReference":"single electrode placed on FCz",
  "EEGGround":"placed on AFz",
  "SoftwareFilters":{
    "Anti-aliasing filter":{
      "half-amplitude cutoff (Hz)": 500,
      "Roll-off": "6dB/Octave"
    }
  },
  "HardwareFilters":{
    "ADC's decimation filter (hardware bandwidth limit)":{
```

```
      "-3dB cutoff point (Hz)":480,
      "Filter order sinc response":5
    }
  },
  "RecordingDuration":600,
  "RecordingType":"continuous"
}
```

Note that the date and time information SHOULD be stored in the Study key file (`scans.tsv`). Date time information MUST be expressed as indicated in Units

## Channels description (`*_channels.tsv`)

Template:

```
sub-<label>/
    [ses-<label>/]
        eeg/
            sub-<label>[_ses-<label>]_task-<label>[_acq-<label>][_run-<index>]_channels.json
            sub-<label>[_ses-<label>]_task-<label>[_acq-<label>][_run-<index>]_channels.tsv
```

This file is RECOMMENDED as it provides easily searchable information across BIDS datasets. For example for general curation, response to queries, or for batch analysis. To avoid confusion, the channels SHOULD be listed in the order they appear in the EEG data file. Any number of additional columns MAY be added to provide additional information about the channels.

Note that electrode positions SHOULD NOT be added to this file, but to `*_electrodes.tsv`. Furthermore, the entries in `*_electrodes.tsv` and `*_channels.tsv` do not have to match exactly, as for example in the case of recording a single `EOG` channel from a bipolar referencing scheme of two electrodes, or a data channel originating from an auxiliary, non-electrode device. That is, in most cases `*_electrodes.tsv` will have more entries than `*_channels.tsv`. See the examples for `*_channels.tsv` below, and for `*_electrodes.tsv` in ”Electrodes description”.

The columns of the channels description table stored in `*_channels.tsv` are:

MUST be present in this specific order:

| Column name | Requirement Level | Data type | Description |
|---|---|---|---|
| name | REQUIRED | string | Label of the channel. |

| Column name | Requirement Level | Data type | Description |
|---|---|---|---|
| type | REQUIRED | string | Type of channel; MUST use the channel types listed below. Note that the type MUST be in upper-case. Must be one of: `"MEGMAG"`, `"MEGGRADAXIAL"`, `"MEGGRADPLANAR"`, `"MEGREFMAG"`, `"MEGREFGRADAXIAL"`, `"MEGREFGRADPLANAR"`, `"MEGOTHER"`, `"EEG"`, `"ECOG"`, `"SEEG"`, `"DBS"`, `"VEOG"`, `"HEOG"`, `"EOG"`, `"ECG"`, `"EMG"`, `"TRIG"`, `"AUDIO"`, `"PD"`, `"EYEGAZE"`, `"PUPIL"`, `"MISC"`, `"SYSCLOCK"`, `"ADC"`, `"DAC"`, `"HLU"`, `"FITERR"`, `"OTHER"`. |
| units | REQUIRED | string | Physical unit of the value represented in this channel, for example, `V` for Volt, or `fT/cm` for femto Tesla per centimeter (see Units). |

SHOULD be present:

| Column name | Requirement Level | Data type | Description |
|---|---|---|---|
| description | OPTIONAL | string | Brief free-text description of the channel, or other information of interest. |
| sampling_frequency | OPTIONAL | number | Sampling rate of the channel in Hz. |
| reference | OPTIONAL | string | Name of the reference electrode(s). This column is not needed when it is common to all channels. In that case the reference electrode(s) can be specified in `*_eeg.json` as `EEGReference`). |
| low_cutoff | OPTIONAL | number or `"n/a"` | Frequencies used for the high-pass filter applied to the channel in Hz. If no high-pass filter applied, use `n/a`. |

| Column name | Requirement Level | Data type | Description |
|---|---|---|---|
| high_cutoff | OPTIONAL | number or `"n/a"` | Frequencies used for the low-pass filter applied to the channel in Hz. If no low-pass filter applied, use `n/a`. Note that hardware anti-aliasing in A/D conversion of all MEG/EEG electronics applies a low-pass filter; specify its frequency here if applicable. |
| notch | OPTIONAL | number or `"n/a"` | Frequencies used for the notch filter applied to the channel, in Hz. If no notch filter applied, use `n/a`. |
| status | OPTIONAL | string | Data quality observed on the channel. A channel is considered `bad` if its data quality is compromised by excessive noise. If quality is unknown, then a value of `n/a` may be used. Description of noise type SHOULD be provided in `[status_description]`. Must be one of: `"good"`, `"bad"`, `"n/a"`. |
| status_description | OPTIONAL | string | Freeform text description of noise or artifact affecting data quality on the channel. It is meant to explain why the channel was declared bad in `[status]`. |

Restricted keyword list for field `type` in alphabetic order (shared with the MEG and iEEG modality; however, only the types that are common in EEG data are listed here). Note that upper-case is REQUIRED:

| Keyword | Description |
|---|---|
| AUDIO | Audio signal |
| EEG | Electroencephalogram channel |
| EOG | Generic electrooculogram (eye), different from HEOG and VEOG |
| ECG | Electrocardiogram (heart) |
| EMG | Electromyogram (muscle) |
| EYEGAZE | Eye tracker gaze |
| GSR | Galvanic skin response |
| HEOG | Horizontal EOG (eye) |
| MISC | Miscellaneous |
| PPG | Photoplethysmography |

| Keyword | Description |
|---|---|
| PUPIL | Eye tracker pupil diameter |
| REF | Reference channel |
| RESP | Respiration |
| SYSCLOCK | System time showing elapsed time since trial started |
| TEMP | Temperature |
| TRIG | System triggers |
| VEOG | Vertical EOG (eye) |

Example of free-form text for field `description`

- n/a, stimulus, response, skin conductance, battery status

### Example `channels.tsv`

See also the corresponding `electrodes.tsv` example.

```
name     type  units  description                      reference     status  status_description
VEOG     VEOG  uV     left eye                         VEOG-, VEOG+  good    n/a
FDI      EMG   uV     left first dorsal interosseous   FDI-, FDI+    good    n/a
Cz       EEG   uV     n/a                              REF           bad     high frequency noise
UADC001  MISC  n/a    envelope of audio signal         n/a           good    n/a
```

## Electrodes description (`*_electrodes.tsv`)

Template:

```
sub-<label>/
    [ses-<label>/]
        eeg/
            sub-<label>[_ses-<label>][_acq-<label>][_space-<label>]_electrodes.json
            sub-<label>[_ses-<label>][_acq-<label>][_space-<label>]_electrodes.tsv
```

File that gives the location of EEG electrodes. Note that coordinates are expected in cartesian coordinates according to the `EEGCoordinateSystem` and `EEGCoordinateUnits` fields in `*_coordsystem.json`. If an `*_electrodes.tsv` file is specified, a `*_coordsystem.json` file MUST be specified as well. The order of the required columns in the `*_electrodes.tsv` file MUST be as listed below.

MUST be present in this specific order:

| Column name | Requirement Level | Data type | Description |
|---|---|---|---|
| name | REQUIRED | string | Name of the electrode contact point. |
| x | REQUIRED | number | Recorded position along the x-axis. |
| y | REQUIRED | number | Recorded position along the y-axis. |
| z | REQUIRED | number or `"n/a"` | Recorded position along the z-axis. |

SHOULD be present:

| Column name | Requirement Level | Data type | Description |
|---|---|---|---|
| type | RECOMMENDED | string | Type of the electrode (for example, cup, ring, clip-on, wire, needle). |
| material | RECOMMENDED | string | Material of the electrode (for example, `Tin`, `Ag/AgCl`, `Gold`). |
| impedance | RECOMMENDED | number | Impedance of the electrode, units MUST be in `kOhm`. |

### Example `electrodes.tsv`

See also the corresponding `electrodes.tsv` example.

```
name    x        y         z        type     material
VEOG+   n/a      n/a       n/a      cup      Ag/AgCl
VEOG-   n/a      n/a       n/a      cup      Ag/AgCl
FDI+    n/a      n/a       n/a      cup      Ag/AgCl
FDI-    n/a      n/a       n/a      cup      Ag/AgCl
GND     -0.0707  0.0000    -0.0707  clip-on  Ag/AgCl
Cz      0.0000   0.0714    0.0699   cup      Ag/AgCl
REF     -0.0742  -0.0200   -0.0100  cup      Ag/AgCl
```

The `acq-<label>` key/value pair can be used to indicate acquisition of the same data. For example, this could be the recording of electrode positions with a different electrode position recording device, or repeated digitization before and after the recording.

## Coordinate System JSON (`*_coordsystem.json`)

Template:

```
sub-<label>/
    [ses-<label>/]
        eeg/
```

```
sub-<label>[_ses-<label>][_acq-<label>][_space-<label>]_coordsystem.json
```

A `*_coordsystem.json` file is used to specify the fiducials, the location of anatomical landmarks, and the coordinate system and units in which the position of electrodes and landmarks is expressed. The `*_coordsystem.json` is REQUIRED if the optional `*_electrodes.tsv` is specified. If a corresponding anatomical MRI is available, the locations of landmarks and fiducials according to that scan should also be stored in the `*_T1w.json` file which goes alongside the MRI data.

For disambiguation, we employ the following definitions for fiducials and anatomical landmarks respectively:

- Fiducials are objects with a well defined location used to facilitate the localization of electrodes and co-registration with other geometric data such as the participant's own T1 weighted magnetic resonance head image, a T1 weighted template head image, or a spherical head model. Commonly used fiducials are vitamin-E pills, which show clearly in an MRI, or reflective spheres that are localized with an infrared optical tracking system.
- Anatomical landmarks are locations on a research subject such as the nasion, which is the intersection of the frontal bone and two nasal bones of the human skull.

Fiducials are typically used in conjunction with anatomical landmarks. An example would be the placement of vitamin-E pills on top of anatomical landmarks, or the placement of LEDs on the nasion and preauricular points to triangulate the position of other LED-lit electrodes on a research subject's head.

- For more information on the definition of anatomical landmarks, please visit: https://www.fieldtriptoolbox.org/faq/how_are_the_lpa_and_rpa_points_defined
- For more information on coordinate systems for coregistration, please visit: https://www.fieldtriptoolbox.org/faq/how_are_the_different_head_and_mri_coordinate_systems_defined

General fields:

| Key name | Requirement Level | Data type | Description |
|---|---|---|---|
| IntendedFor | OPTIONAL | string or array of strings | The paths to files for which the associated file is intended to be used. Contains one or more filenames with paths relative to the participant subfolder. Paths need to use forward slashes instead of backward slashes, regardless of operating system. This identifies the MRI or CT scan associated with the electrodes, landmarks, and fiducials. |

Fields relating to the EEG electrode positions:

| Key name | Requirement Level | Data type | Description |
|---|---|---|---|
| EEGCoordinateSystem | REQUIRED | string | Defines the coordinate system for the EEG sensors.See Appendix VIII for a list of restricted keywords for coordinate systems. If `"Other"`, provide definition of the coordinate system in `EEGCoordinateSystemDescription`. Must be one of: `"CTF"`, `"ElektaNeuromag"`, `"4DBti"`, `"KitYokogawa"`, `"ChietiItab"`, `"Other"`, `"CapTrak"`, `"EEGLAB"`, `"EEGLAB-HJ"`, `"Other"`, `"ICBM452AirSpace"`, `"ICBM452Warp5Space"`, `"IXI549Space"`, `"fsaverage"`, `"fsaverageSym"`, `"fsLR"`, `"MNIColin27"`, `"MNI152Lin"`, `"MNI152NLin2009aSym"`, `"MNI152NLin2009bSym"`, `"MNI152NLin2009cSym"`, `"MNI152NLin2009aAsym"`, `"MNI152NLin2009bAsym"`, `"MNI152NLin2009cAsym"`, `"MNI152NLin6Sym"`, `"MNI152NLin6ASym"`, `"MNI305"`, `"NIHPD"`, `"OASIS30AntsOASISAnts"`, `"OASIS30Atropos"`, `"Talairach"`, `"UNCInfant"`, `"fsaverage3"`, `"fsaverage4"`, `"fsaverage5"`, `"fsaverage6"`, `"fsaveragesym"`, `"UNCInfant0V21"`, `"UNCInfant1V21"`, `"UNCInfant2V21"`, `"UNCInfant0V22"`, `"UNCInfant1V22"`, `"UNCInfant2V22"`, `"UNCInfant0V23"`, `"UNCInfant1V23"`, `"UNCInfant2V23"`. |
| EEGCoordinateUnits | REQUIRED | string | Units of the coordinates of `EEGCoordinateSystem`. Must be one of: `"m"`, `"mm"`, `"cm"`, `"n/a"`. |

| Key name | Requirement Level | Data type | Description |
|---|---|---|---|
| EEGCoordinateSystemDescription | RECOMMENDED, but REQUIRED if `EEGCoordinateSystem` is `"Other"` | string | Free-form text description of the coordinate system. May also include a link to a documentation page or paper describing the system in greater detail. |

Fields relating to the position of fiducials measured during an EEG session/run:

| Key name | Requirement Level | Data type | Description |
|---|---|---|---|
| FiducialsDescription | OPTIONAL | string | Free-form text description of how the fiducials such as vitamin-E capsules were placed relative to anatomical landmarks, and how the position of the fiducials were measured (for example, `"both with Polhemus and with T1w MRI"`). |
| FiducialsCoordinates | RECOMMENDED | object of arrays | Key:value pairs of the labels and 3-D digitized position of anatomical landmarks, interpreted following the `"FiducialsCoordinateSystem"` (for example, `{"NAS": [12.7,21.3,13.9], "LPA": [5.2,11.3,9.6], "RPA": [20.2,11.3,9.1]}`). Each array MUST contain three numeric values corresponding to x, y, and z axis of the coordinate system in that exact order. |

| Key name | Requirement Level | Data type | Description |
|---|---|---|---|
| FiducialsCoordinateSystem | RECOMMENDED | string | Defines the coordinate system for the fiducials. Preferably the same as the `"EEGCoordinateSystem"`. See Appendix VIII for a list of restricted keywords for coordinate systems. If `"Other"`, provide definition of the coordinate system in `"FiducialsCoordinateSystemDescription"`. Must be one of: `"CTF"`, `"ElektaNeuromag"`, `"4DBti"`, `"KitYokogawa"`, `"ChietiItab"`, `"Other"`, `"CapTrak"`, `"EEGLAB"`, `"EEGLAB-HJ"`, `"Other"`, `"ICBM452AirSpace"`, `"ICBM452Warp5Space"`, `"IXI549Space"`, `"fsaverage"`, `"fsaverageSym"`, `"fsLR"`, `"MNIColin27"`, `"MNI152Lin"`, `"MNI152NLin2009aSym"`, `"MNI152NLin2009bSym"`, `"MNI152NLin2009cSym"`, `"MNI152NLin2009aAsym"`, `"MNI152NLin2009bAsym"`, `"MNI152NLin2009cAsym"`, `"MNI152NLin6Sym"`, `"MNI152NLin6ASym"`, `"MNI305"`, `"NIHPD"`, `"OASIS30AntsOASISAnts"`, `"OASIS30Atropos"`, `"Talairach"`, `"UNCInfant"`, `"fsaverage3"`, `"fsaverage4"`, `"fsaverage5"`, `"fsaverage6"`, `"fsaveragesym"`, `"UNCInfant0V21"`, `"UNCInfant1V21"`, `"UNCInfant2V21"`, `"UNCInfant0V22"`, `"UNCInfant1V22"`, `"UNCInfant2V22"`, `"UNCInfant0V23"`, `"UNCInfant1V23"`, `"UNCInfant2V23"`. |
| FiducialsCoordinateUnits | RECOMMENDED | string | Units in which the coordinates that are listed in the field `"FiducialsCoordinateSystem"` are represented. Must be one of: `"m"`, `"mm"`, `"cm"`, `"n/a"`. |

| Key name | Requirement Level | Data type | Description |
|---|---|---|---|
| FiducialsCoordinateSystemDescription | RECOMMENDED, but REQUIRED if `FiducialsCoordinateSystem` is `"Other"` | string | Free-form text description of the coordinate system. May also include a link to a documentation page or paper describing the system in greater detail. |

Fields relating to the position of anatomical landmark measured during an EEG session/run:

| Key name | Requirement Level | Data type | Description |
|---|---|---|---|
| AnatomicalLandmarkCoordinates | RECOMMENDED | object of arrays | Key:value pairs of the labels and 3-D digitized locations of anatomical landmarks, interpreted following the `"AnatomicalLandmarkCoordinateSystem"` (for example, `{"NAS": [12.7,21.3,13.9], "LPA": [5.2,11.3,9.6], "RPA": [20.2,11.3,9.1]}`. Each array MUST contain three numeric values corresponding to x, y, and z axis of the coordinate system in that exact order. |

| Key name | Requirement Level | Data type | Description |
|---|---|---|---|
| AnatomicalLandmarkCoordinateSystem | RECOMMENDED | string | Defines the coordinate system for the anatomical landmarks. See Appendix VIII for a list of restricted keywords for coordinate systems. If `"Other"`, provide definition of the coordinate system in `"AnatomicalLandmarkCoordinateSystemDescripti` Preferably the same as the `EEGCoordinateSystem`.Must be one of: `"CTF"`, `"ElektaNeuromag"`, `"4DBti"`, `"KitYokogawa"`, `"ChietiItab"`, `"Other"`, `"CapTrak"`, `"EEGLAB"`, `"EEGLAB-HJ"`, `"Other"`, `"ICBM452AirSpace"`, `"ICBM452Warp5Space"`, `"IXI549Space"`, `"fsaverage"`, `"fsaverageSym"`, `"fsLR"`, `"MNIColin27"`, `"MNI152Lin"`, `"MNI152NLin2009aSym"`, `"MNI152NLin2009bSym"`, `"MNI152NLin2009cSym"`, `"MNI152NLin2009aAsym"`, `"MNI152NLin2009bAsym"`, `"MNI152NLin2009cAsym"`, `"MNI152NLin6Sym"`, `"MNI152NLin6ASym"`, `"MNI305"`, `"NIHPD"`, `"OASIS30AntsOASISAnts"`, `"OASIS30Atropos"`, `"Talairach"`, `"UNCInfant"`, `"fsaverage3"`, `"fsaverage4"`, `"fsaverage5"`, `"fsaverage6"`, `"fsaveragesym"`, `"UNCInfant0V21"`, `"UNCInfant1V21"`, `"UNCInfant2V21"`, `"UNCInfant0V22"`, `"UNCInfant1V22"`, `"UNCInfant2V22"`, `"UNCInfant0V23"`, `"UNCInfant1V23"`, `"UNCInfant2V23"`. |
| AnatomicalLandmarkCoordinateUnits | RECOMMENDED | string | Units of the coordinates of `"AnatomicalLandmarkCoordinateSystem"`. Must be one of: `"m"`, `"mm"`, `"cm"`, `"n/a"`. |

| Key name | Requirement Level | Data type | Description |
|---|---|---|---|
| AnatomicalLandmarkCoordinateSystemI | RECOMMENDED, but REQUIRED if `AnatomicalLandmarkCoordinateSystem` is `"Other"` | string | Free-form text description of the coordinate system. May also include a link to a documentation page or paper describing the system in greater detail. |

If the position of anatomical landmarks is measured using the same system or device used to measure electrode positions, and if thereby the anatomical landmarks are expressed in the same coordinates, the coordinates of the anatomical landmarks can be specified in `electrodes.tsv`. The same applies to the coordinates of the fiducials.

Anatomical landmarks or fiducials measured on an anatomical MRI that match the landmarks or fiducials during an EEG session/run, must be stored separately in the corresponding `*_T1w.json` or `*_T2w.json` file and should be expressed in voxels (starting from `[0, 0, 0]`).

Example:

```
{
  "IntendedFor":"/sub-01/ses-01/anat/sub-01_T1w.nii",
  "EEGCoordinateSystem":"Other",
  "EEGCoordinateUnits":"mm",
  "EEGCoordinateSystemDescription":"RAS orientation: Origin halfway between LPA and RPA, positive x-axis towards RPA, positive y-axis orthogonal to x-a
  "FiducialsDescription":"Electrodes and fiducials were digitized with Polhemus, fiducials were recorded as the centre of vitamin E capsules sticked or
}
```

## Landmark photos (`*_photo.jpg`)

Photos of the anatomical landmarks and/or fiducials.

Template:

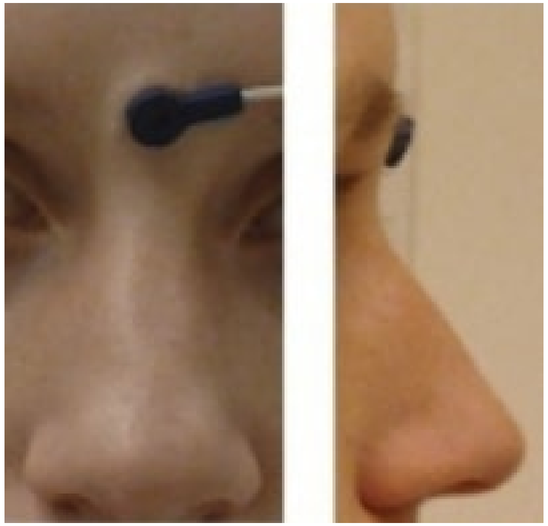
```
sub-<label>/
    [ses-<label>/]
        eeg/
            sub-<label>[_ses-<label>][_acq-<label>]_photo.jpg
```

Photos of the anatomical landmarks and/or fiducials are OPTIONAL. Please note that the photos may need to be cropped or blurred to conceal identifying features prior to sharing, depending on the terms of the consent given by the participant.

The `acq-<label>` key/value pair can be used to indicate acquisition of different photos of the same face (or other body part in different angles to show, for example, the location of the nasion (NAS) as opposed to the right periauricular point (RPA).

Example:

Picture of a NAS fiducial placed between the eyebrows, rather than at the actual anatomical nasion: `sub-0001_ses-001_acq-NAS_photo.jpg`



# Intracranial Electroencephalography

Support Intracranial Electroencephalography (iEEG) was developed as a BIDS Extension Proposal. Please see Citing BIDS on how to appropriately credit this extension when referring to it in the context of the academic literature.

Several example iEEG datasets have been formatted using this specification and can be used for practical guidance when curating a new dataset.

## iEEG recording data

Template:

```
sub-<label>/
    [ses-<label>/]
        ieeg/
            sub-<label>[_ses-<label>]_task-<label>[_acq-<label>][_run-<index>]_ieeg.<extension>
            sub-<label>[_ses-<label>]_task-<label>[_acq-<label>][_run-<index>]_ieeg.json
            sub-<label>[_ses-<label>]_task-<label>[_acq-<label>][_run-<index>]_events.json
            sub-<label>[_ses-<label>]_task-<label>[_acq-<label>][_run-<index>]_events.tsv
            sub-<label>[_ses-<label>]_task-<label>[_acq-<label>][_run-<index>][_recording-<label>]_physio.json
            sub-<label>[_ses-<label>]_task-<label>[_acq-<label>][_run-<index>][_recording-<label>]_physio.tsv.gz
            sub-<label>[_ses-<label>]_task-<label>[_acq-<label>][_run-<index>][_recording-<label>]_stim.json
            sub-<label>[_ses-<label>]_task-<label>[_acq-<label>][_run-<index>][_recording-<label>]_stim.tsv.gz
```

The iEEG community uses a variety of formats for storing raw data, and there is no single standard that all researchers agree on. For BIDS, iEEG data MUST be stored in one of the following formats:

| Format | Extension(s) | Description |
|---|---|---|
| European data format | `.edf` | Each recording consists of a `.edf` single file. `edf+` files are permitted. The capital `.EDF` extension MUST NOT be used. |

| Format | Extension(s) | Description |
|---|---|---|
| BrainVision Core Data Format | `.vhdr`, `.vmrk`, `.eeg` | Each recording consists of a `.vhdr`, `.vmrk`, `.eeg` file triplet. |
| EEGLAB | `.set`, `.fdt` | The format used by the MATLAB toolbox EEGLAB. Each recording consists of a `.set` file with an optional `.fdt` file. |
| Neurodata Without Borders | `.nwb` | Each recording consists of a single `.nwb` file. |
| MEF3 | `.mefd` | Each recording consists of a `.mefd` directory. |

It is RECOMMENDED to use the European data format, or the BrainVision data format. It is furthermore discouraged to use the other accepted formats over these RECOMMENDED formats, particularly because there are conversion scripts available in most commonly used programming languages to convert data into the RECOMMENDED formats.

Future versions of BIDS may extend this list of supported file formats. File formats for future consideration MUST have open access documentation, MUST have open source implementation for both reading and writing in at least two programming languages and SHOULD be widely supported in multiple software packages. Other formats that may be considered in the future should have a clear added advantage over the existing formats and should have wide adoption in the BIDS community.

The data format in which the data was originally stored is especially valuable in case conversion elicits the loss of crucial metadata specific to manufacturers and specific iEEG systems. We also encourage users to provide additional meta information extracted from the manufacturer-specific data files in the sidecar JSON file. Other relevant files MAY be included alongside the original iEEG data in the `/sourcedata` directory.

Note the RecordingType, which depends on whether the data stream on disk is interrupted or not. Continuous data is by definition 1 segment without interruption. Epoched data consists of multiple segments that all have the same length (for example, corresponding to trials) and that have gaps in between. Discontinuous data consists of multiple segments of different length, for example due to a pause in the acquisition.

### Terminology: Electrodes vs. Channels

For proper documentation of iEEG recording metadata it is important to understand the difference between electrode and channel: an iEEG electrode is placed on or in the brain, whereas a channel is the combination of the analog differential amplifier and analog-to-digital converter that result in a potential (voltage) difference that is stored in the iEEG dataset. We employ the following short definitions:

- Electrode = A single point of contact between the acquisition system and the recording site (for example, scalp, neural tissue, …). Multiple electrodes can be organized as arrays, grids, leads, strips, probes, shafts, caps (for EEG), and so forth.
- Channel = A single analog-to-digital converter in the recording system that regularly samples the value of a transducer, which results in the signal being represented as a time series in the digitized data. This can be connected to two electrodes (to measure the potential difference between them), a magnetic field or magnetic gradient sensor, temperature sensor, accelerometer, and so forth.

Although the reference and ground electrodes are often referred to as channels, they are in most common iEEG systems not recorded by themselves. Therefore they are not represented as channels in the data. The type of referencing for all channels and optionally the location of the reference electrode and the location of the ground electrode MAY be specified.

### Sidecar JSON (`*_ieeg.json`)

For consistency between studies and institutions, we encourage users to extract the values of metadata fields from the actual raw data. Whenever possible, please avoid using ad hoc wording.

Generic fields MUST be present:

| Key name | Requirement Level | Data type | Description |
|---|---|---|---|
| TaskName | REQUIRED | string | Name of the task. No two tasks should have the same name. The task label included in the file name is derived from this `"TaskName"` field by removing all non-alphanumeric (`[a-zA-Z0-9]`) characters. For example `"TaskName"` `"faces n-back"` will correspond to task label `facesnback`. A RECOMMENDED convention is to name resting state task using labels beginning with `rest`. |

Note that the `TaskName` field does not have to be a ”behavioral task” that subjects perform, but can reflect some information about the conditions present when the data was acquired (for example, `"rest"`, `"sleep"`, or `"seizure"`).

SHOULD be present: For consistency between studies and institutions, we encourage users to extract the values of these fields from the actual raw data. Whenever possible, please avoid using ad hoc wording.

| Key name | Requirement Level | Data type | Description |
|---|---|---|---|
| InstitutionName | RECOMMENDED | string | The name of the institution in charge of the equipment that produced the measurements. |
| InstitutionAddress | RECOMMENDED | string | The address of the institution in charge of the equipment that produced the measurements. |
| InstitutionalDepartmentName | RECOMMENDED | string | The department in the institution in charge of the equipment that produced the measurements. |
| Manufacturer | RECOMMENDED | string | Manufacturer of the equipment that produced the measurements. For example, `"TDT"`, `"Blackrock"`. |

| Key name | Requirement Level | Data type | Description |
|---|---|---|---|
| ManufacturersModelName | RECOMMENDED | string | Manufacturer's model name of the equipment that produced the measurements. |
| SoftwareVersions | RECOMMENDED | string | Manufacturer's designation of software version of the equipment that produced the measurements. |
| TaskDescription | RECOMMENDED | string | Longer description of the task. |
| Instructions | RECOMMENDED | string | Text of the instructions given to participants before the recording. This is especially important in context of resting state recordings and distinguishing between eyes open and eyes closed paradigms. |
| CogAtlasID | RECOMMENDED | string | URI of the corresponding Cognitive Atlas Task term. |
| CogPOID | RECOMMENDED | string | URI of the corresponding CogPO term. |
| DeviceSerialNumber | RECOMMENDED | string | The serial number of the equipment that produced the measurements. A pseudonym can also be used to prevent the equipment from being identifiable, so long as each pseudonym is unique within the dataset. |

Specific iEEG fields MUST be present:

| Key name | Requirement Level | Data type | Description |
|---|---|---|---|
| iEEGReference | REQUIRED | string | General description of the reference scheme used and (when applicable) of location of the reference electrode in the raw recordings (for example, `"left mastoid"`, `"bipolar"`, `"T01"` for electrode with name T01, `"intracranial electrode on top of a grid, not included with data"`, `"upside down electrode"`). If different channels have a different reference, this field should have a general description and the channel specific reference should be defined in the `channels.tsv` file. |
| SamplingFrequency | REQUIRED | number | Sampling frequency (in Hz) of all the data in the recording, regardless of their type (for example, `2400`). The sampling frequency of data channels that deviate from the main sampling frequency SHOULD be specified in the `channels.tsv` file. |
| PowerLineFrequency | REQUIRED | number or `"n/a"` | Frequency (in Hz) of the power grid at the geographical location of the instrument (for example, `50` or `60`). |
| SoftwareFilters | REQUIRED | object of objects or `"n/a"` | Object of temporal software filters applied, or `"n/a"` if the data is not available. Each key:value pair in the JSON object is a name of the filter and an object in which its parameters are defined as key:value pairs (for example, `{"Anti-aliasing filter": {"half-amplitude cutoff (Hz)": 500, "Roll-off": "6dB/Octave"}}`). |

Specific iEEG fields SHOULD be present:

| Key name | Requirement Level | Data type | Description |
|---|---|---|---|
| DCOffsetCorrection | DEPRECATED | string | A description of the method (if any) used to correct for a DC offset. If the method used was subtracting the mean value for each channel, use "mean". |
| HardwareFilters | RECOMMENDED | object of objects or `"n/a"` | Object of temporal hardware filters applied, or `"n/a"` if the data is not available. Each key:value pair in the JSON object is a name of the filter and an object in which its parameters are defined as key:value pairs. For example, `{"Highpass RC filter": {"Half amplitude cutoff (Hz)": 0.0159, "Roll-off": "6dB/Octave"}}`. |
| ElectrodeManufacturer | RECOMMENDED | string | Can be used if all electrodes are of the same manufacturer (for example, `"AD-TECH"`, `"DIXI"`). If electrodes of different manufacturers are used, please use the corresponding table in the `_electrodes.tsv` file. |
| ElectrodeManufacturersModelName | RECOMMENDED | string | If different electrode types are used, please use the corresponding table in the `_electrodes.tsv` file. |
| ECOGChannelCount | RECOMMENDED | integer | Number of ECoG channels. Must be a number greater than or equal to 0. |
| SEEGChannelCount | RECOMMENDED | integer | Number of SEEG channels. Must be a number greater than or equal to 0. |
| EEGChannelCount | RECOMMENDED | integer | Number of EEG channels recorded simultaneously (for example, `21`). Must be a number greater than or equal to 0. |
| EOGChannelCount | RECOMMENDED | integer | Number of EOG channels. Must be a number greater than or equal to 0. |
| ECGChannelCount | RECOMMENDED | integer | Number of ECG channels. Must be a number greater than or equal to 0. |
| EMGChannelCount | RECOMMENDED | integer | Number of EMG channels. Must be a number greater than or equal to 0. |
| MiscChannelCount | RECOMMENDED | integer | Number of miscellaneous analog channels for auxiliary signals. Must be a number greater than or equal to 0. |

| Key name | Requirement Level | Data type | Description |
|---|---|---|---|
| TriggerChannelCount | RECOMMENDED | integer | Number of channels for digital (TTL bit level) triggers. Must be a number greater than or equal to 0. |
| RecordingDuration | RECOMMENDED | number | Length of the recording in seconds (for example, `3600`). |
| RecordingType | RECOMMENDED | string | Defines whether the recording is `"continuous"`, `"discontinuous"`, or `"epoched"`, where `"epoched"` is limited to time windows about events of interest (for example, stimulus presentations or subject responses). Must be one of: `"continuous"`, `"epoched"`, `"discontinuous"`. |
| EpochLength | RECOMMENDED | number | Duration of individual epochs in seconds (for example, `1`) in case of epoched data. If recording was continuous or discontinuous, leave out the field. Must be a number greater than or equal to 0. |
| iEEGGround | RECOMMENDED | string | Description of the location of the ground electrode (`"placed on right mastoid (M2)"`). |
| iEEGPlacementScheme | RECOMMENDED | string | Freeform description of the placement of the iEEG electrodes. Left/right/bilateral/depth/surface (for example, `"left frontal grid and bilateral hippocampal depth"` or `"surface strip and STN depth"` or `"clinical indication bitemporal, bilateral temporal strips and left grid"`). |
| iEEGElectrodeGroups | RECOMMENDED | string | Field to describe the way electrodes are grouped into strips, grids or depth probes. For example, `"grid1: 10x8 grid on left temporal pole, strip2: 1x8 electrode strip on xxx"`. |

| Key name | Requirement Level | Data type | Description |
|---|---|---|---|
| SubjectArtefactDescription | RECOMMENDED | string | Freeform description of the observed subject artefact and its possible cause (for example, `"Vagus Nerve Stimulator"`, `"non-removable implant"`). If this field is set to `"n/a"`, it will be interpreted as absence of major source of artifacts except cardiac and blinks. |

Specific iEEG fields MAY be present:

| Key name | Requirement Level | Data type | Description |
|---|---|---|---|
| ElectricalStimulation | OPTIONAL | boolean | Boolean field to specify if electrical stimulation was done during the recording (options are `true` or `false`). Parameters for event-like stimulation should be specified in the `events.tsv` file. Must be one of: `"true"`, `"false"`. |
| ElectricalStimulationParameters | OPTIONAL | string | Free form description of stimulation parameters, such as frequency or shape. Specific onsets can be specified in the events.tsv file. Specific shapes can be described here in freeform text. |

Example:

```
{
  "TaskName":"visual",
  "InstitutionName":"Stanford Hospital and Clinics",
  "InstitutionAddress":"300 Pasteur Dr, Stanford, CA 94305",
  "Manufacturer":"Tucker Davis Technologies",
  "ManufacturersModelName":"n/a",
  "TaskDescription":"visual gratings and noise patterns",
  "Instructions":"look at the dot in the center of the screen and press the button when it changes color",
  "iEEGReference":"left mastoid",
  "SamplingFrequency":1000,
  "PowerLineFrequency":60,
```

```
  "SoftwareFilters":"n/a",
  "HardwareFilters":{"Highpass RC filter": {"Half amplitude cutoff (Hz)": 0.0159, "Roll-off": "6dBOctave"}},
  "ElectrodeManufacturer":"AdTech",
  "ECOGChannelCount":120,
  "SEEGChannelCount":0,
  "EEGChannelCount":0,
  "EOGChannelCount":0,
  "ECGChannelCount":0,
  "EMGChannelCount":0,
  "MiscChannelCount":0,
  "TriggerChannelCount":0,
  "RecordingDuration":233.639,
  "RecordingType":"continuous",
  "iEEGGround":"placed on the right mastoid",
  "iEEGPlacementScheme":"right occipital temporal surface",
  "ElectricalStimulation":false
}
```

Note that the date and time information SHOULD be stored in the Study key file (`scans.tsv`). Date time information MUST be expressed as indicated in Units

## Channels description (`*_channels.tsv`)

Template:

```
sub-<label>/
    [ses-<label>/]
        ieeg/
            sub-<label>[_ses-<label>]_task-<label>[_acq-<label>][_run-<index>]_channels.json
            sub-<label>[_ses-<label>]_task-<label>[_acq-<label>][_run-<index>]_channels.tsv
```

A channel represents one time series recorded with the recording system (for example, there can be a bipolar channel, recorded from two electrodes or contact points on the tissue). Although this information can often be extracted from the iEEG recording, listing it in a simple `.tsv` document makes it easy to browse or search (for example, searching for recordings with a sampling frequency of >=1000 Hz). Hence, the `channels.tsv` file is RECOMMENDED. Channels SHOULD appear in the table in the same order they do in the iEEG data file. Any number of additional columns MAY be provided to provide additional information about the channels. Note that electrode positions SHOULD NOT be added to this file but to `*_electrodes.tsv`.

The columns of the channels description table stored in `*_channels.tsv` are:

MUST be present in this specific order:

| Column name | Requirement Level | Data type | Description |
|---|---|---|---|
| name | REQUIRED | string | Label of the channel. When a corresponding electrode is specified in `_electrodes.tsv`, the name of that electrode MAY be specified here and the reference electrode name MAY be provided in the `reference` column. |
| type | REQUIRED | string | Type of channel; MUST use the channel types listed below. Note that the type MUST be in upper-case. Must be one of: `"MEGMAG"`, `"MEGGRADAXIAL"`, `"MEGGRADPLANAR"`, `"MEGREFMAG"`, `"MEGREFGRADAXIAL"`, `"MEGREFGRADPLANAR"`, `"MEGOTHER"`, `"EEG"`, `"ECOG"`, `"SEEG"`, `"DBS"`, `"VEOG"`, `"HEOG"`, `"EOG"`, `"ECG"`, `"EMG"`, `"TRIG"`, `"AUDIO"`, `"PD"`, `"EYEGAZE"`, `"PUPIL"`, `"MISC"`, `"SYSCLOCK"`, `"ADC"`, `"DAC"`, `"HLU"`, `"FITERR"`, `"OTHER"`. |
| units | REQUIRED | string | Physical unit of the value represented in this channel, for example, `V` for Volt, or `fT/cm` for femto Tesla per centimeter (see Units). |
| low_cutoff | REQUIRED | number or `"n/a"` | Frequencies used for the high-pass filter applied to the channel in Hz. If no high-pass filter applied, use `n/a`. |
| high_cutoff | REQUIRED | number or `"n/a"` | Frequencies used for the low-pass filter applied to the channel in Hz. If no low-pass filter applied, use `n/a`. Note that hardware anti-aliasing in A/D conversion of all MEG/EEG electronics applies a low-pass filter; specify its frequency here if applicable. |

SHOULD be present:

| Column name | Requirement Level | Data type | Description |
|---|---|---|---|
| reference | OPTIONAL | string or `"n/a"` | Specification of the reference (for example, `mastoid`, `ElectrodeName01`, `intracranial`, `CAR`, `other`, `n/a`). If the channel is not an electrode channel (for example, a microphone channel) use `n/a`. |
| group | OPTIONAL | string or number | Which group of channels (grid/strip/seeg/depth) this channel belongs to. This is relevant because one group has one cable-bundle and noise can be shared. This can be a name or number. Note that any groups specified in `_electrodes.tsv` must match those present here. |
| sampling_frequency | OPTIONAL | number | Sampling rate of the channel in Hz. |
| description | OPTIONAL | string | Brief free-text description of the channel, or other information of interest. |
| notch | OPTIONAL | number or `"n/a"` | Frequencies used for the notch filter applied to the channel, in Hz. If no notch filter applied, use `n/a`. |
| status | OPTIONAL | string | Data quality observed on the channel. A channel is considered `bad` if its data quality is compromised by excessive noise. If quality is unknown, then a value of `n/a` may be used. Description of noise type SHOULD be provided in `[status_description]`. Must be one of: `"good"`, `"bad"`, `"n/a"`. |
| status_description | OPTIONAL | string | Freeform text description of noise or artifact affecting data quality on the channel. It is meant to explain why the channel was declared bad in `[status]`. |

Example `sub-01_channels.tsv`:

```
name  type  units low_cutoff  high_cutoff status  status_description
LT01  ECOG  uV    300         0.11        good    n/a
LT02  ECOG  uV    300         0.11        bad     broken
```

```
H01   SEEG  uV    300         0.11        bad     line_noise
ECG1  ECG   uV    n/a         0.11        good    n/a
TR1   TRIG  n/a   n/a         n/a         good    n/a
```

Restricted keyword list for field type in alphabetic order (shared with the MEG and EEG modality; however, only types that are common in iEEG data are listed here). Note that upper-case is REQUIRED:

| Keyword | Description |
|---|---|
| EEG | Electrode channel from electroencephalogram |
| ECOG | Electrode channel from electrocorticogram (intracranial) |
| SEEG | Electrode channel from stereo-electroencephalogram (intracranial) |
| DBS | Electrode channel from deep brain stimulation electrode (intracranial) |
| VEOG | Vertical EOG (electrooculogram) |
| HEOG | Horizontal EOG |
| EOG | Generic EOG channel if HEOG or VEOG information not available |
| ECG | ElectroCardioGram (heart) |
| EMG | ElectroMyoGram (muscle) |
| TRIG | System Triggers |
| AUDIO | Audio signal |
| PD | Photodiode |
| EYEGAZE | Eye Tracker gaze |
| PUPIL | Eye Tracker pupil diameter |
| MISC | Miscellaneous |
| SYSCLOCK | System time showing elapsed time since trial started |
| ADC | Analog to Digital input |
| DAC | Digital to Analog output |
| REF | Reference channel |
| OTHER | Any other type of channel |

Example of free-form text for field `description`:

- intracranial, stimulus, response, vertical EOG, skin conductance

## Electrode description (`*_electrodes.tsv`)

Template:

```
sub-<label>/
    [ses-<label>/]
        ieeg/
```

```
sub-<label>[_ses-<label>][_acq-<label>][_space-<label>]_electrodes.json
sub-<label>[_ses-<label>][_acq-<label>][_space-<label>]_electrodes.tsv
```

File that gives the location, size and other properties of iEEG electrodes. Note that coordinates are expected in cartesian coordinates according to the `iEEGCoordinateSystem` and `iEEGCoordinateUnits` fields in `*_coordsystem.json`. If an `*_electrodes.tsv` file is specified, a `*_coordsystem.json` file MUST be specified as well.

The optional `space-<label>` entity (`*[_space-<label>]_electrodes.tsv`) can be used to indicate the way in which electrode positions are interpreted. The space `<label>` MUST be taken from one of the modality specific lists in Appendix VIII. For example for iEEG data, the restricted keywords listed under iEEG Specific Coordinate Systems are acceptable for `<label>`.

For examples:

- `_space-MNI152Lin` (electrodes are coregistred and scaled to a specific MNI template)
- `_space-Talairach` (electrodes are coregistred and scaled to Talairach space)

When referring to the `*_electrodes.tsv` file in a certain space as defined above, the `space-<label>` of the accompanying `*_coordsystem.json` MUST correspond.

For example:

```
sub-01/
   sub-01_space-Talairach_electrodes.tsv
   sub-01_space-Talairach_coordsystem.json
   ...
```

The order of the required columns in the `*_electrodes.tsv` file MUST be as listed below. The `x`, `y`, and `z` columns indicate the positions of the center of each electrode in Cartesian coordinates. Units are specified in `space-<label>_coordsystem.json`.

MUST be present in this specific order:

| Column name | Requirement Level | Data type | Description |
|---|---|---|---|
| name | REQUIRED | string | Name of the electrode contact point. |
| x | REQUIRED | number | Recorded position along the x-axis. |
| y | REQUIRED | number | Recorded position along the y-axis. |
| z | REQUIRED | number or `"n/a"` | Recorded position along the z-axis. If electrodes are in 2D space this should be a column of `n/a` values. |
| size | REQUIRED | number | Surface area of the electrode, units MUST be in `mm^2`. |

SHOULD be present:

| Column name | Requirement Level | Data type | Description |
|---|---|---|---|
| material | RECOMMENDED | string | Material of the electrode (for example, `Tin`, `Ag/AgCl`, `Gold`). |
| manufacturer | RECOMMENDED | string | The manufacturer for each electrode. Can be used if electrodes were manufactured by more than one company. |
| group | RECOMMENDED | string or number | Which group of channels (grid/strip/seeg/depth) this channel belongs to. This is relevant because one group has one cable-bundle and noise can be shared. This can be a name or number. Note that any group specified here should match a group specified in `_channels.tsv`. |
| hemisphere | RECOMMENDED | string | The hemisphere in which the electrode is placed. Must be one of: `"L"`, `"R"`. |

MAY be present:

| Column name | Requirement Level | Data type | Description |
|---|---|---|---|
| type | OPTIONAL | string | Type of the electrode (for example, cup, ring, clip-on, wire, needle). |
| impedance | OPTIONAL | number | Impedance of the electrode, units MUST be in `kOhm`. |
| dimension | OPTIONAL | string | Size of the group (grid/strip/probe) that this electrode belongs to. Must be of form `[AxB]` with the smallest dimension first (for example, `[1x8]`). |

Example:

```
name  x   y    z    size  manufacturer
LT01  19  -39  -16  2.3   Integra
LT02  23  -40  -19  2.3   Integra
H01   27  -42  -21  5     AdTech
```

## Coordinate System JSON (`*_coordsystem.json`)

Template:

```
sub-<label>/
    [ses-<label>/]
        ieeg/
            sub-<label>[_ses-<label>][_acq-<label>][_space-<label>]_coordsystem.json
```

This `_coordsystem.json` file contains the coordinate system in which electrode positions are expressed. The associated MRI, CT, X-Ray, or operative photo can also be specified.

General fields:

| Key name | Requirement Level | Data type | Description |
|---|---|---|---|
| IntendedFor | OPTIONAL | string or array of strings | The paths to files for which the associated file is intended to be used. Contains one or more filenames with paths relative to the participant subfolder. Paths need to use forward slashes instead of backward slashes, regardless of operating system. If only a surface reconstruction is available, this should point to the surface reconstruction file. Note that this file should have the same coordinate system specified in `iEEGCoordinateSystem`.<br>For example, T1:<br>`'sub-<label>/ses-<label>/anat/sub-01_T1w.nii`<br>Surface:<br>`'/derivatives/surfaces/sub-<label>/ses-<labe`<br>Operative photo:<br>`'/sub-<label>/ses-<label>/ieeg/sub-0001_ses-`<br>Talairach:<br>`'/derivatives/surfaces/sub-Talairach/ses-01/` |

Fields relating to the iEEG electrode positions:

| Key name | Requirement Level | Data type | Description |
|---|---|---|---|
| iEEGCoordinateSystem | REQUIRED | string | Defines the coordinate system for the iEEG sensors. See Appendix VIII for a list of restricted keywords for coordinate systems. If `"Other"`, provide definition of the coordinate system in `iEEGCoordinateSystemDescription`. If positions correspond to pixel indices in a 2D image (of either a volume-rendering, surface-rendering, operative photo, or operative drawing), this MUST be `"Pixels"`. For more information, see the section on Appendix VIII. Must be one of: `"Pixels"`, `"ACPC"`, `"Other"`, `"ICBM452AirSpace"`, `"ICBM452Warp5Space"`, `"IXI549Space"`, `"fsaverage"`, `"fsaverageSym"`, `"fsLR"`, `"MNIColin27"`, `"MNI152Lin"`, `"MNI152NLin2009aSym"`, `"MNI152NLin2009bSym"`, `"MNI152NLin2009cSym"`, `"MNI152NLin2009aAsym"`, `"MNI152NLin2009bAsym"`, `"MNI152NLin2009cAsym"`, `"MNI152NLin6Sym"`, `"MNI152NLin6ASym"`, `"MNI305"`, `"NIHPD"`, `"OASIS30AntsOASISAnts"`, `"OASIS30Atropos"`, `"Talairach"`, `"UNCInfant"`, `"fsaverage3"`, `"fsaverage4"`, `"fsaverage5"`, `"fsaverage6"`, `"fsaveragesym"`, `"UNCInfant0V21"`, `"UNCInfant1V21"`, `"UNCInfant2V21"`, `"UNCInfant0V22"`, `"UNCInfant1V22"`, `"UNCInfant2V22"`, `"UNCInfant0V23"`, `"UNCInfant1V23"`, `"UNCInfant2V23"`. |

| Key name | Requirement Level | Data type | Description |
|---|---|---|---|
| iEEGCoordinateUnits | REQUIRED | string | Units of the `*_electrodes.tsv`. MUST be `"pixels"` if `iEEGCoordinateSystem` is `Pixels`. Must be one of: `"m"`, `"mm"`, `"cm"`, `"pixels"`, `"n/a"`. |
| iEEGCoordinateSystemDescription | RECOMMENDED, but REQUIRED if `iEEGCoordinateSystem` is `"Other"` | string | Free-form text description of the coordinate system. May also include a link to a documentation page or paper describing the system in greater detail. |
| iEEGCoordinateProcessingDescription | RECOMMENDED | string | Has any post-processing (such as projection) been done on the electrode positions (for example, `"surface_projection"`, `"none"`). |
| iEEGCoordinateProcessingReference | RECOMMENDED | string | A reference to a paper that defines in more detail the method used to localize the electrodes and to post-process the electrode positions. |

### Recommended 3D coordinate systems

It is preferred that electrodes are localized in a 3D coordinate system (with respect to a pre- and/or post-operative anatomical MRI or CT scans or in a standard space as specified in BIDS Appendix VIII about preferred names of coordinate systems, such as ACPC).

### Allowed 2D coordinate systems

If electrodes are localized in 2D space (only x and y are specified and z is `"n/a"`), then the positions in this file MUST correspond to the locations expressed in pixels on the photo/drawing/rendering of the electrodes on the brain. In this case, `iEEGCoordinateSystem` MUST be defined as `"Pixels"`, and `iEEGCoordinateUnits` MUST be defined as `"pixels"` (note the difference in capitalization). Furthermore, the coordinates MUST be (row,column) pairs, with (0,0) corresponding to the upper left pixel and (N,0) corresponding to the lower left pixel.

### Multiple coordinate systems

If electrode positions are known in multiple coordinate systems (for example, MRI, CT and MNI), these spaces can be distinguished by the optional `space-<label>` field, see the `*_electrodes.tsv`-section for more information. Note that the `space-<label>` fields must correspond between `*_electrodes.tsv` and `*_coordsystem.json` if they refer to the same data.

Example:

```
{
    "IntendedFor": "/sub-01/ses-01/anat/sub-01_T1w.nii.gz",
```

```
    "iEEGCoordinateSystem": "ACPC",
    "iEEGCoordinateUnits": "mm",
    "iEEGCoordinateSystemDescription": "Coordinate system with the origin at anterior commissure (AC), negative y-axis going through the posterior comm
    "iEEGCoordinateProcessingDescription": "surface_projection",
    "iEEGCoordinateProcessingReference": "Hermes et al., 2010 JNeuroMeth"
}
```

## Photos of the electrode positions (`*_photo.jpg`)

Template:

```
sub-<label>/
    [ses-<label>/]
        ieeg/
            sub-<label>[_ses-<label>][_acq-<label>]_photo.jpg
```

These can include photos of the electrodes on the brain surface, photos of anatomical features or landmarks (such as sulcal structure), and fiducials. Photos can also include an X-ray picture, a flatbed scan of a schematic drawing made during surgery, or screenshots of a brain rendering with electrode positions. The photos may need to be cropped and/or blurred to conceal identifying features or entirely omitted prior to sharing, depending on obtained consent.

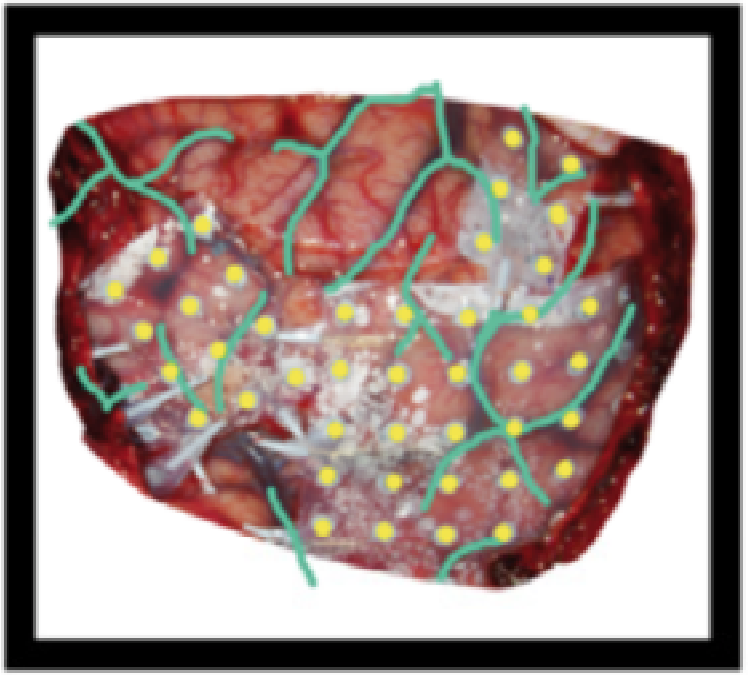
If there are photos of the electrodes, the `acq-<label>` entity should be specified with:

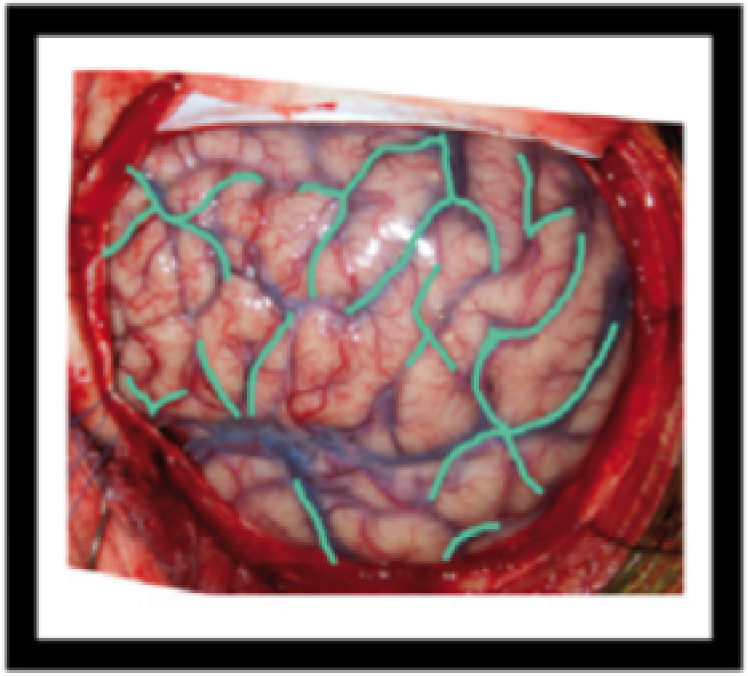
- `*_photo.jpg` in case of an operative photo
- `*_acq-xray#_photo.jpg` in case of an x-ray picture
- `*_acq-drawing#_photo.jpg` in case of a drawing or sketch of electrode placements
- `*_acq-render#_photo.jpg` in case of a rendering

The `ses-<label>` entity may be used to specify when the photo was taken.

Example of the operative photo of ECoG electrodes (here is an annotated example in which electrodes and vasculature are marked, taken from Hermes et al., JNeuroMeth 2010).

```
sub-01/
   ses-0001/
      sub-0001_ses-01_acq-photo1_photo.jpg
      sub-0001_ses-01_acq-photo2_photo.jpg
      ...
```

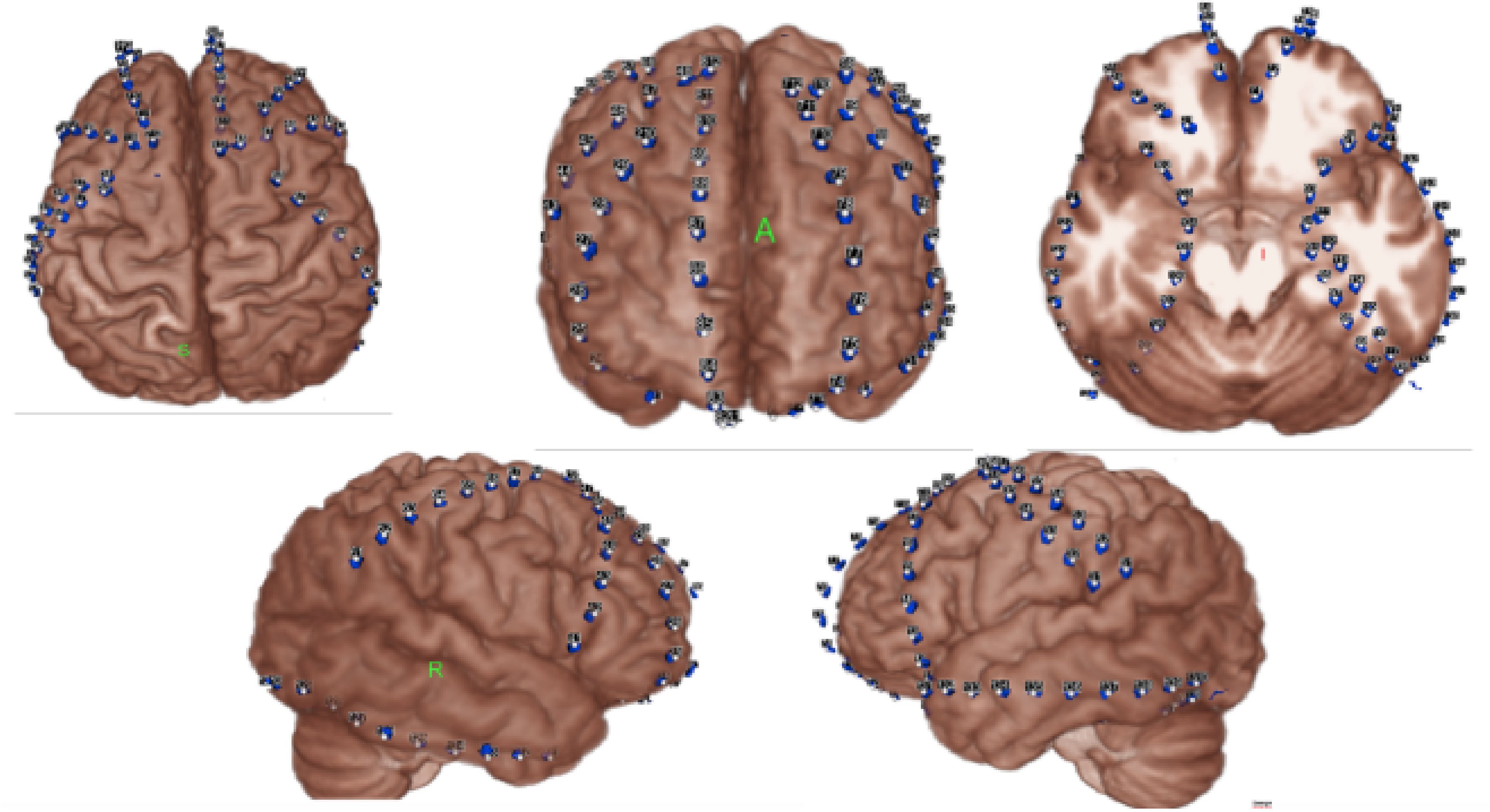




Below is an example of a volume rendering of the cortical surface with a superimposed subdural electrode implantation. This map is often provided by the EEG technician and provided to the epileptologists (for example, see Burneo JG et al.

1. doi:10.1016/j.clineuro.2014.03.020).

   `sub-0002_ses-01_acq-render_photo.jpg`



## Electrical stimulation

In case of electrical stimulation of brain tissue by passing current through the iEEG electrodes, and the electrical stimulation has an event structure (on-off, onset, duration), the `_events.tsv` file can contain the electrical stimulation parameters in addition to other events. Note that these can be intermixed with other task events. Electrical stimulation parameters can be described in columns called `electrical_stimulation_<label>`, with labels chosen by the researcher and optionally defined in more detail in an accompanying `_events.json` file (as per the main BIDS spec). Functions for complex stimulation patterns can, similar as when a video is presented, be stored in a folder in the `/stimuli/` folder. For example: `/stimuli/electrical_stimulation_functions/biphasic.tsv`

Example:

```
onset duration trial_type             electrical_stimulation_type electrical_stimulation_site electrical_stimulation_current
1.2   0.001    electrical_stimulation biphasic                    LT01-LT02                   0.005
1.3   0.001    electrical_stimulation biphasic                    LT01-LT02                   0.005
2.2   0.001    electrical_stimulation biphasic                    LT02-LT03                   0.005
4.2   1        electrical_stimulation complex                     LT02-LT03                   n/a
15.2  3        auditory_stimulus      n/a                         n/a                         n/a
```

# Task events

The purpose of this file is to describe timing and other properties of events recorded during a run. Events are, for example, stimuli presented to the participant or participant responses (see Definitions). A single event file MAY include any combination of stimulus, response, and other events. Events MAY overlap in time. Please mind that this does not imply that only so called ”event related” study designs are supported (in contrast to ”block” designs) - each ”block of events” can be represented by an individual row in the `events.tsv` file (with a long duration).

Template:

```
sub-<label>/[ses-<label>]
    <data_type>/
        <matches>_events.tsv
        <matches>_events.json
```

Where `<matches>` corresponds to task filename. For example: `sub-control01_task-nback`.

Each task events file REQUIRES a corresponding task data file. It is also possible to have a single `events.tsv` file describing events for all participants and runs (see Inheritance Principle). As with all other tabular data, `events.tsv` files MAY be accompanied by a JSON file describing the columns in detail (see Tabular Files).

The tabular files consists of one row per event and a set of REQUIRED and OPTIONAL columns:

| Column name | Requirement Level | Data type | Description |
|---|---|---|---|
| onset | REQUIRED | number | Onset (in seconds) of the event, measured from the beginning of the acquisition of the first data point stored in the corresponding task data file. Negative onsets are allowed, to account for events that occur prior to the first stored data point. For example, in case there is an in-scanner training phase that begins before the scanning sequence has started events from this sequence should have negative onset time counting down to the beginning of the acquisition of the first volume.If any data points have been discarded before forming the data file (for example, ”dummy volumes” in BOLD fMRI), a time of 0 corresponds to the first stored data point and not the first acquired data point. |
| duration | REQUIRED | number or `"n/a"` | Duration of the event (measured from onset) in seconds. Must always be either zero or positive (or `n/a` if unavailable). A ”duration” value of zero implies that the delta function or event is so short as to be effectively modeled as an impulse. |
| sample | OPTIONAL | integer | Onset of the event according to the sampling scheme of the recorded modality (that is, referring to the raw data file that the `events.tsv` file accompanies). |
| trial_type | OPTIONAL | string | Primary categorisation of each trial to identify them as instances of the experimental conditions. For example: for a response inhibition task, it could take on values `go` and `no-go` to refer to response initiation and response inhibition experimental conditions. |

| Column name | Requirement Level | Data type | Description |
|---|---|---|---|
| response_time | OPTIONAL | number or `"n/a"` | Response time measured in seconds. A negative response time can be used to represent preemptive responses and `n/a` denotes a missed response. |
| value | OPTIONAL | number or string | Marker value associated with the event (for example, the value of a TTL trigger that was recorded at the onset of the event). |
| HED | OPTIONAL | string | Hierarchical Event Descriptor (HED) Tag. See Appendix III for details. |

5 Note for MRI data: If any acquired scans have been discarded before forming the imaging data file, ensure that an `onset` of 0 corresponds to the time the first image was stored. For example in case there is an in scanner training phase that begins before the scanning sequence has started events from this sequence should have negative onset time counting down to the beginning of the acquisition of the first volume.

An arbitrary number of additional columns can be added. Those allow describing other properties of events that could be later referred in modelling and hypothesis extensions of BIDS. Note that the `trial_type` and any additional columns in a TSV file SHOULD be documented in an accompanying JSON sidecar file.

Example:

```
sub-control01/
   func/
      sub-control01_task-stopsignal_events.tsv
      sub-control01_task-stopsignal_events.json
```

Example of the content of the TSV file:

```
onset   duration    trial_type  response_time   stim_file
1.23    0.65    start   1.435   images/red_square.jpg
5.65    0.65    stop    1.739   images/blue_square.jpg
```

In the accompanying JSON sidecar, the `trial_type` column might look as follows:

```
{
    "trial_type": {
        "LongName": "Event category",
        "Description": "Indicator of type of action that is expected",
        "Levels": {
            "start": "A red square is displayed to indicate starting",
            "stop": "A blue square is displayed to indicate stopping"
        }
```

```
    }
}
```

Note that all other columns SHOULD also be described but are omitted for the sake of brevity.

For multi-echo files, the `events.tsv` file is applicable to all echos of a particular run:

```
sub-01/
   func/
      sub-01_task-cuedSGT_run-1_events.tsv
      sub-01_task-cuedSGT_run-1_echo-1_bold.nii.gz
      sub-01_task-cuedSGT_run-1_echo-2_bold.nii.gz
      sub-01_task-cuedSGT_run-1_echo-3_bold.nii.gz
```

Note: Events can also be documented in machine-actionable form using HED (Hierarchical Event Descriptor) tags. This type of documentation is particularly useful for datasets likely to be used in event-related analyses. See Hierarchical Event Descriptors for additional information and examples.

## Stimuli

Additional information about the stimuli can be added in the `events.tsv` and `events.json` files.

This can be done by using a `/stimuli` folder or by reference to a stimuli database.

### Stimuli folder

The stimulus files can be added in a `/stimuli` folder (under the root folder of the dataset; with optional subfolders) AND using a `stim_file` column in `events.tsv` mentioning which stimulus file was used for a given event,

There are no restrictions on the file formats of the stimuli files, but they should be stored in the `/stimuli` folder.

| Column name | Requirement Level | Data type | Description |
|---|---|---|---|
| stim_file | OPTIONAL | string | Represents the location of the stimulus file (such as an image, video, or audio file) presented at the given onset time. There are no restrictions on the file formats of the stimuli files, but they should be stored in the `/stimuli` folder (under the root folder of the dataset; with optional subfolders). The values under the `stim_file` column correspond to a path relative to `/stimuli`. For example `images/cat03.jpg` will be translated to `/stimuli/images/cat03.jpg`. |

### Stimuli databases

References to existing databases can also be encoded using additional columns. The following example includes references to the Karolinska Directed Emotional Faces (KDEF) database.

Example:

```
sub-control01/
   func/
      sub-control01_task-emoface_events.tsv
      sub-control01_task-emoface_events.json
```

Example of the content of the TSV file:

```
onset duration  trial_type  identifier  database  response_time
1.2 0.6 afraid  AF01AFAF  kdef  1.435
5.6 0.6 angry AM01AFAN  kdef  1.739
5.6 0.6 sad AF01ANSA  kdef  1.739
```

The `trial_type` and `identifier` columns from the `events.tsv` files might be described in the accompanying JSON sidecar as follows:

```
{
    "trial_type": {
        "LongName": "Emotion image type",
        "Description": "Type of emotional face from Karolinska database that is displayed",
        "Levels": {
            "afraid": "A face showing fear is displayed",
```

```
            "angry": "A face showing anger is displayed",
            "sad": "A face showing sadness is displayed"
        }
    },
    "identifier": {
        "LongName": "Karolinska (KDEF) database identifier",
        "Description": "ID from KDEF database used to identify the displayed image"
    }
}
```

Note that all other columns SHOULD also be described but are omitted for the sake of brevity.

### Stimulus presentation details

It is RECOMMENDED to include details of the stimulus presentation software, when applicable:

| Key name | Requirement Level | Data type | Description |
|---|---|---|---|
| StimulusPresentation | RECOMMENDED | object | Object containing key value pairs related to the software used to present the stimuli during the experiment, specifically: `"OperatingSystem"`, `"SoftwareName"`, `"SoftwareRRID"`, `"SoftwareVersion"` and `"Code"`. See table below for more information. |

The object supplied for `StimulusPresentation` SHOULD include the following key-value pairs:

| Key name | Requirement Level | Data type | Description |
|---|---|---|---|
| OperatingSystem | RECOMMENDED | string | Operating system used to run the stimuli presentation software (for formatting recommendations, see examples below this table). |
| SoftwareName | RECOMMENDED | string | Name of the software that was used to present the stimuli. |
| SoftwareRRID | RECOMMENDED | string | Research Resource Identifier of the software that was used to present the stimuli. Examples: The RRID for Psychtoolbox is 'SCR_002881', and that of PsychoPy is 'SCR_006571'. |

| Key name | Requirement Level | Data type | Description |
|---|---|---|---|
| SoftwareVersion | RECOMMENDED | string | Version of the software that was used to present the stimuli. |
| Code | RECOMMENDED | string | URI of the code used to present the stimuli. Persistent identifiers such as DOIs are preferred. If multiple versions of code may be hosted at the same location, revision-specific URIs are recommended. |

The operating system description SHOULD include the following attributes:

- type (for example, Windows, macOS, Linux)
- distribution (if applicable, for example, Ubuntu, Debian, CentOS)
- the version number (for example, 18.04.5)

Examples:

- Windows 10, Version 2004
- macOS 10.15.6
- Linux Ubuntu 18.04.5

The amount of information supplied for the `OperatingSystem` SHOULD be sufficient to re-run the code under maximally similar conditions.

The information related to stimulus presentation might be described in the accompanying JSON sidecar as follows (based on the example of the previous section):

```
{
    "trial_type": {
        "LongName":   "Emotion image type",
        "Description": "Type of emotional face from Karolinska database that is displayed",
        "Levels": {
            "afraid": "A face showing fear is displayed",
            "angry":  "A face showing anger is displayed",
            "sad":    "A face showing sadness is displayed"
        }
    },
    "identifier": {
        "LongName": "Unique identifier from Karolinska (KDEF) database",
        "Description": "ID from KDEF database used to identify the displayed image"
    },
    "StimulusPresentation": {
        "OperatingSystem": "Linux Ubuntu 18.04.5",
```

```
        "SoftwareName": "Psychtoolbox",
        "SoftwareRRID": "SCR_002881",
        "SoftwareVersion": "3.0.14",
        "Code": "doi:10.5281/zenodo.3361717"
    }
}
```

# Physiological and other continuous recordings

Example datasets with physiological data have been formatted using this specification and can be used for practical guidance when curating a new dataset:

- `7t_trt`
- `ds210`

Template:

```
sub-<label>/[ses-<label>/]
    <datatype>/
        <matches>[_recording-<label>]_physio.tsv.gz
        <matches>[_recording-<label>]_physio.json
        <matches>[_recording-<label>]_stim.tsv.gz
        <matches>[_recording-<label>]_stim.json
```

Optional: Yes

For the template directory name, `<datatype>` can correspond to any data recording modality, for example `func`, `anat`, `dwi`, `meg`, `eeg`, `ieeg`, or `beh`.

In the template filenames, the `<matches>` part corresponds to task filename before the suffix. For example for the file `sub-control01_task-nback_run-1_bold.nii.gz`, `<matches>` would correspond to `sub-control01_task-nback_run-1`.

The `recording-<label>` entity can be used to distinguish between several recording files. For example `sub-01_task-bart_recording-eyetracking_physio.tsv.gz` to contain the eyetracking data in a certain sampling frequency, and `sub-01_task-bart_recording-breathing_physio.tsv.gz` to contain respiratory measurements in a different sampling frequency.

Physiological recordings (including eyetracking) SHOULD use the `_physio` suffix, and signals related to the stimulus SHOULD use `_stim` suffix.

Physiological recordings such as cardiac and respiratory signals and other continuous measures (such as parameters of a film or audio stimuli) can be specified using two files: a gzip compressed TSV file with data (without header line) and a JSON file for storing the following metadata fields.

Note that when supplying a `*_<physio|stim>.tsv.gz` file, an accompanying `*_<physio|stim>.json` MUST be supplied as well.

| Key name | Requirement Level | Data type | Description |
|---|---|---|---|
| SamplingFrequency | REQUIRED | number | Sampling frequency (in Hz) of all the data in the recording, regardless of their type (for example, `2400`). |
| StartTime | REQUIRED | number | Start time in seconds in relation to the start of acquisition of the first data sample in the corresponding neural dataset (negative values are allowed). |
| Columns | REQUIRED | array of strings | Names of columns in file. |

Additional metadata may be included as in any TSV file to specify, for example, the units of the recorded time series. Please note that, in contrast to other TSV files in BIDS, the TSV files specified for phsyiological and other continuous recordings do not include a header line. Instead the name of columns are specified in the JSON file. This is to improve compatibility with existing software (for example, FSL, PNM) as well as to make support for other file formats possible in the future.

Example `*_physio.tsv.gz`:

```
sub-control01/
   func/
      sub-control01_task-nback_physio.tsv.gz
```

(after decompression)

```
34    110    0
44    112    0
23    100    1
```

Example `*_physio.json`:

```
sub-control01/
   func/
      sub-control01_task-nback_physio.json
```

```
{
   "SamplingFrequency": 100.0,
   "StartTime": -22.345,
   "Columns": ["cardiac", "respiratory", "trigger"],
   "cardiac": {
       "Units": "mV"
   }
}
```

## Recommendations for specific use cases

To store pulse or breathing measurements, or the scanner trigger signal, the following naming conventions SHOULD be used for the column names:

| Column name | Requirement Level | Data type | Description |
|---|---|---|---|
| cardiac | OPTIONAL | number | continuous pulse measurement |
| respiratory | OPTIONAL | number | continuous breathing measurement |
| trigger | OPTIONAL | number | continuous measurement of the scanner trigger signal |

For any other data to be specified in columns, the column names can be chosen as deemed appropriate by the researcher.

Recordings with different sampling frequencies or starting times should be stored in separate files.

If the same continuous recording has been used for all subjects (for example in the case where they all watched the same movie), one file MAY be used and placed in the root directory. For example, `task-movie_stim.tsv.gz`

For motion parameters acquired from MRI scanner side motion correction, the `_physio` suffix SHOULD be used.

For multi-echo data, a given `physio.tsv` file is applicable to all echos of a particular run. For example:

```
sub-01/
   func/
      sub-01_task-cuedSGT_run-1_physio.tsv.gz
      sub-01_task-cuedSGT_run-1_echo-1_bold.nii.gz
      sub-01_task-cuedSGT_run-1_echo-2_bold.nii.gz
      sub-01_task-cuedSGT_run-1_echo-3_bold.nii.gz
```

## Other RECOMMENDED metadata for physiological data

The following RECOMMENDED metadata can also be added in the side-car JSON files of any `*_<physio>.tsv.gz` file.

| Key name | Requirement Level | Data type | Description |
|---|---|---|---|
| Manufacturer | RECOMMENDED | string | Manufacturer of the equipment that produced the measurements. |
| ManufacturersModelName | RECOMMENDED | string | Manufacturer's model name of the equipment that produced the measurements. |
| SoftwareVersions | RECOMMENDED | string | Manufacturer's designation of software version of the equipment that produced the measurements. |

| Key name | Requirement Level | Data type | Description |
|---|---|---|---|
| DeviceSerialNumber | RECOMMENDED | string | The serial number of the equipment that produced the measurements. A pseudonym can also be used to prevent the equipment from being identifiable, so long as each pseudonym is unique within the dataset. |

# Behavioral experiments (with no neural recordings)

Template:

```
sub-<label>/
    [ses-<label>/]
        beh/
            sub-<label>[_ses-<label>]_task-<label>[_acq-<label>][_run-<index>][_recording-<label>]_physio.json
            sub-<label>[_ses-<label>]_task-<label>[_acq-<label>][_run-<index>][_recording-<label>]_physio.tsv.gz
            sub-<label>[_ses-<label>]_task-<label>[_acq-<label>][_run-<index>][_recording-<label>]_stim.json
            sub-<label>[_ses-<label>]_task-<label>[_acq-<label>][_run-<index>][_recording-<label>]_stim.tsv.gz
            sub-<label>[_ses-<label>]_task-<label>[_acq-<label>][_run-<index>]_beh.json
            sub-<label>[_ses-<label>]_task-<label>[_acq-<label>][_run-<index>]_beh.tsv
            sub-<label>[_ses-<label>]_task-<label>[_acq-<label>][_run-<index>]_events.json
            sub-<label>[_ses-<label>]_task-<label>[_acq-<label>][_run-<index>]_events.tsv
```

In addition to logs from behavioral experiments performed alongside imaging data acquisitions, one can also include data from experiments performed with no neural recordings. The results of those experiments can be stored in the `beh` folder using the same formats for event timing (`_events.tsv`), metadata (`_events.json`), physiological (`_physio.tsv.gz`, `_physio.json`) and other continuous recordings (`_stim.tsv.gz`, `_stim.json`) as for tasks performed during MRI, electrophysiological or other neural recordings. Additionally, events files that do not include the mandatory `onset` and `duration` columns can still be included, but should be labeled `_beh.tsv` rather than `_events.tsv`.

Each task has a unique label that MUST only consist of letters and/or numbers (other characters, including spaces and underscores, are not allowed) with the `task-<label>` key/value pair. Those labels MUST be consistent across subjects and sessions.

The OPTIONAL `acq-<label>` key/value pair corresponds to a custom label to distinguish different conditions present during multiple runs of the same task. For example, if a study includes runs of an n-back task, with deep brain stimulation turned on or off, the data files may be labelled `sub-01_task-nback_acq-dbson_beh.tsv` and `sub-01_task-nback_acq-dbsoff_beh.tsv`.

## RECOMMENDED metadata

In addition to the metadata that is either:

- RECOMMENDED for sidecar JSON files for tabular data, or
- REQUIRED for some data that can be found in the `beh` folder (for example `SamplingFrequency` and `StartTime` for `*_<physio|stim>.tsv.gz` files),

it is RECOMMENDED to add the following metadata to the JSON files of this folder:

| Key name | Requirement Level | Data type | Description |
|---|---|---|---|
| TaskName | RECOMMENDED | string | Name of the task. No two tasks should have the same name. The task label included in the file name is derived from this `"TaskName"` field by removing all non-alphanumeric (`[a-zA-Z0-9]`) characters. For example `"TaskName"` `"faces n-back"` will correspond to task label `facesnback`. |
| Instructions | RECOMMENDED | string | Text of the instructions given to participants before the recording. |
| TaskDescription | RECOMMENDED | string | Longer description of the task. |
| CogAtlasID | RECOMMENDED | string | URI of the corresponding Cognitive Atlas Task term. |
| CogPOID | RECOMMENDED | string | URI of the corresponding CogPO term. |
| InstitutionName | RECOMMENDED | string | The name of the institution in charge of the equipment that produced the measurements. |
| InstitutionAddress | RECOMMENDED | string | The address of the institution in charge of the equipment that produced the measurements. |
| InstitutionalDepartmentName | RECOMMENDED | string | The department in the institution in charge of the equipment that produced the measurements. |

Example of the content of a `_beh.tsv` and its accompanying `_beh.json` sidecar file:

```
trial	response	response_time	stim_file
congruent	red	1.435	images/word-red_color-red.jpg
incongruent	red	1.739	images/word-red_color-blue.jpg
```

In the accompanying JSON sidecar, the `trial` column might be documented as follows:

```
{
   "TaskName": "Stroop",
   "trial": {
```

```
      "LongName": "Trial name",
      "Description": "Indicator of the type of trial",
      "Levels": {
         "congruent": "Word and font color match.",
         "incongruent": "Word and font color do not match."
      }
   }
}
```

# Genetic Descriptor

Support genetic descriptors was developed as a BIDS Extension Proposal. Please see Citing BIDS on how to appropriately credit this extension when referring to it in the context of the academic literature.

Genetic data are typically stored in dedicated repositories, separate from imaging data. A genetic descriptor links a BIDS dataset to associated genetic data, potentially in a separate repository, with details of where to find the genetic data and the type of data available.

The following example dataset with genetics data have been formatted using this specification and can be used for practical guidance when curating a new dataset.

- `UK biobank`

## Dataset Description

Genetic descriptors are encoded as an additional, OPTIONAL entry in the `dataset_description.json` file.

Datasets linked to a genetic database entry include the following REQUIRED or OPTIONAL `dataset_description.json` keys (a dot in the key name denotes a key in a sub-object, see the example further below):

| Key name | Requirement Level | Data type | Description |
|---|---|---|---|
| Genetics.Dataset | REQUIRED | string | URI where data can be retrieved. |
| Genetics.Database | OPTIONAL | string | URI of database where the dataset is hosted. |
| Genetics.Descriptors | OPTIONAL | string or array of strings | List of relevant descriptors (for example, journal articles) for dataset using a valid URI when possible. |

Example:

```
{
  "Name": "Human Connectome Project",
```

```
  "BIDSVersion":  "1.3.0",
  "License": "CC0",
  "Authors": ["1st author", "2nd author"],
  "Funding": ["P41 EB015894/EB/NIBIB NIH HHS/United States"],
  "Genetics": {
     "Dataset": "https://www.ncbi.nlm.nih.gov/projects/gap/cgi-bin/study.cgi?study_id=phs001364.v1.p1",
     "Database": "https://www.ncbi.nlm.nih.gov/gap/",
     "Descriptors": ["doi:10.1016/j.neuroimage.2013.05.041"]
     }
}
```

## Subject naming and Participants file

If the same participants have different identifiers in the genetic and imaging datasets, the column `genetic_id` SHOULD be added to the `participants.tsv` file to associate the BIDS participant with a subject in the `Genetics.Dataset` referred to in the `dataset_description.json` file.

Information about the presence/absence of specific genetic markers MAY be duplicated in the `participants.tsv` file by adding optional columns (like `idh_mutation` in the example below). Note that optional columns MUST be further described in an accompanying `participants.json` file as described in Tabular files.

`participants.tsv` example:

```
participant_id  age sex group   genetic_id  idh_mutation
sub-control01   34  M   control 124587  yes
sub-control02   12  F   control 548936  yes
sub-patient01   33  F   patient 489634  no
```

## Genetic Information

Template:

`genetic_info.json`

The `genetic_info.json` file describes the genetic information available in the `participants.tsv` file and/or the genetic database described in `dataset_description.json`. Datasets containing the `Genetics` field in `dataset_description.json` or the `genetic_id` column in `participants.tsv` MUST include this file with the following fields:

| Key name | Requirement Level | Data type | Description |
|---|---|---|---|
| GeneticLevel | REQUIRED | string or array of strings | Describes the level of analysis. Values MUST be one of `"Genetic"`, `"Genomic"`, `"Epigenomic"`, `"Transcriptomic"`, `"Metabolomic"`, or `"Proteomic"`. |

| Key name | Requirement Level | Data type | Description |
|---|---|---|---|
| AnalyticalApproach | OPTIONAL | string or array of strings | Methodology or methodologies used to analyse the `"GeneticLevel"`. Values MUST be taken from the database of Genotypes and Phenotypes (dbGaP) under /Study/Molecular Data Type (for example, SNP Genotypes (Array) or Methylation (CpG). |
| SampleOrigin | REQUIRED | string | Describes from which tissue the genetic information was extracted. Must be one of: `"blood"`, `"saliva"`, `"brain"`, `"csf"`, `"breast milk"`, `"bile"`, `"amniotic fluid"`, `"other biospecimen"`. |
| TissueOrigin | OPTIONAL | string | Describes the type of tissue analyzed for `"SampleOrigin"` `brain`. Must be one of: `"gray matter"`, `"white matter"`, `"csf"`, `"meninges"`, `"macrovascular"`, `"microvascular"`. |
| BrainLocation | OPTIONAL | string | Refers to the location in space of the `"TissueOrigin"`. Values may be an MNI coordinate, a label taken from the Allen Brain Atlas, or layer to refer to layer-specific gene expression, which can also tie up with laminar fMRI. |
| CellType | OPTIONAL | string | Describes the type of cell analyzed. Values SHOULD come from the cell ontology. |

To ensure dataset description consistency, we recommend following Multi-omics approaches to disease by Hasin et al. 2017 to determine the `GeneticLevel:`

- `Genetic`: data report on a single genetic location (typically directly in the `participants.tsv` file)
- `Genomic`: data link to participants' genome (multiple genetic locations)
- `Epigenomic`: data link to participants' characterization of reversible modifications of DNA
- `Transcriptomic`: data link to participants RNA levels
- `Metabolomic`: data link to participants' products of cellular metabolic functions
- `Proteomic`: data link to participants peptides and proteins quantification

`genetic_info.json` example:

```
{
  "GeneticLevel": "Genomic",
```

```
  "AnalyticalApproach": ["Whole Genome Sequencing", "SNP/CNV Genotypes"],
  "SampleOrigin": "brain",
  "TissueOrigin": "gray matter",
  "CellType":  "neuron",
  "BrainLocation": "[-30 -15 10]"
}
```

# Positron Emission Tomography

Support for Positron Emission Tomography (PET) was developed as a BIDS Extension Proposal. Please see Citing BIDS on how to appropriately credit this extension when referring to it in the context of the academic literature.

Several example PET datasets have been formatted using this specification and can be used for practical guidance when curating a new dataset.

Further PET datasets are available from OpenNeuro.

## Terminology and conventions

PET-BIDS is fully consistent with the BIDS specification as a whole. However, BIDS was initially developed in the context of MRI, so some terminology may be unfamiliar to researchers from each field. This section adds clarifications to Common Principles - Definitions for the PET context, and introduces the term ”time zero” which is currently specific to PET.

1. Session - In most cases, a new session with respect to PET corresponds to a visit to the scanning site, and starts with a new injection. In situations where different data types are obtained over several visits (for example, FDG PET on one day followed by amyloid PET a couple days after) these scans may be grouped into the same session. In other datasets, a subject leaving the scanner and returning under the same injection may be considered separate sessions.
2. Run - In PET, subjects may have to leave the scanner to use the bathroom. While leaving the scanner would interrupt an MR acquisition, in PET this disruption is more appropriately considered missing data during a run.
3. Time zero - A reference point in time, to which all timestamps pertaining to a recording are relative. Time zero will most commonly be the time of injection of a radioisotope, or the time at which the first scan of an acquisition is begun. If a pharmacological within-scan challenge is performed, another time zero may be more convenient.

An overview of a common PET experiment (with blood data) can be seen in Figure 1, defined on a single time scale relative to a predefined ”time zero”.

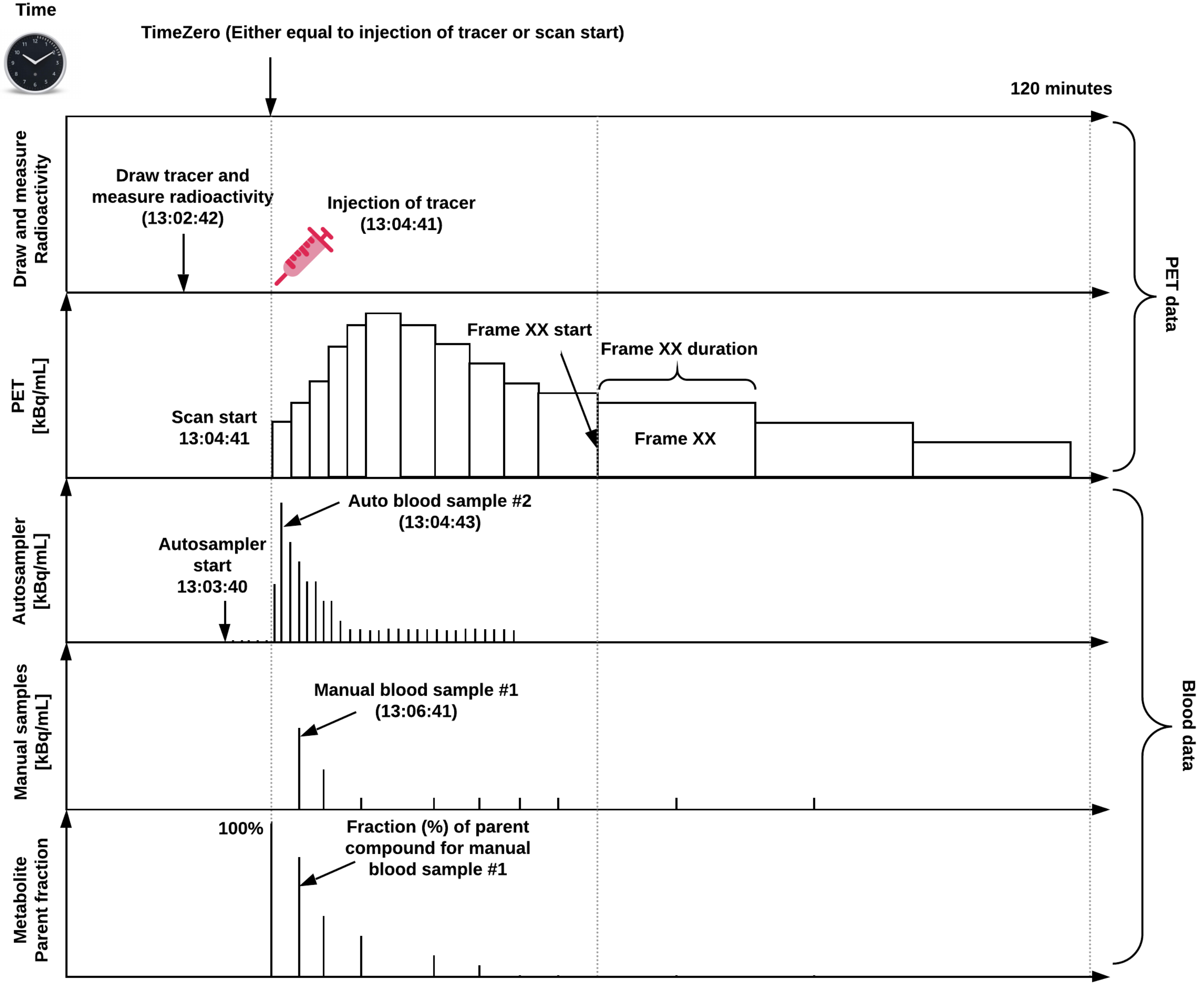

Time
TimeZero (Either equal to injection of tracer or scan start)
120 minutes
Draw and measure Radioactivity
Draw tracer and measure radioactivity (13:02:42)
Injection of tracer (13:04:41)
PET data
PET [kBq/mL]
Frame XX start
Frame XX duration
Scan start 13:04:41
Frame XX
Autosampler [kBq/mL]
Auto blood sample #2 (13:04:43)
Autosampler start 13:03:40
Manual samples [kBq/mL]
Manual blood sample #1 (13:06:41)
Blood data
Metabolite Parent fraction
100%
Fraction (%) of parent compound for manual blood sample #1

Figure 1: Overview of a common PET experiment, including blood measurements, and defined on a common time scale. Note, ”time zero” is often defined as time of injection or scan start, but if a pharmaceutical challenge is carried out during the scan, this time point may also be chosen as time zero. The injected dose, the PET data, and blood data should all be decay-corrected to time zero, but because the time of injection does not always coincide with scan start, the PET data may not always be decay-corrected to the time of injection. If this is not the case, this may be indicated in the reconstruction section (`ImageDecayCorrected` and `ImageDecayCorrectionTime`). In this example, tracer injection coincides with scan start.

# PET recording data

Template:

```
sub-<label>/
    [ses-<label>/]
        pet/
            sub-<label>[_ses-<label>][_task-<label>][_trc-<label>][_rec-<label>][_run-<index>]_pet.json
            sub-<label>[_ses-<label>][_task-<label>][_trc-<label>][_rec-<label>][_run-<index>]_pet.nii[.gz]
            sub-<label>[_ses-<label>]_task-<label>[_trc-<label>][_rec-<label>][_run-<index>]_events.json
            sub-<label>[_ses-<label>]_task-<label>[_trc-<label>][_rec-<label>][_run-<index>]_events.tsv
            sub-<label>[_ses-<label>][_task-<label>][_trc-<label>][_rec-<label>][_run-<index>][_recording-<label>]_physio.json
            sub-<label>[_ses-<label>][_task-<label>][_trc-<label>][_rec-<label>][_run-<index>][_recording-<label>]_physio.tsv.gz
            sub-<label>[_ses-<label>][_task-<label>][_trc-<label>][_rec-<label>][_run-<index>][_recording-<label>]_stim.json
            sub-<label>[_ses-<label>][_task-<label>][_trc-<label>][_rec-<label>][_run-<index>][_recording-<label>]_stim.tsv.gz
```

PET data MUST be stored in the `pet` directory. PET imaging data SHOULD be stored in 4D (or 3D, if only one volume was acquired) NIfTI files with the `_pet` suffix. Volumes MUST be stored in chronological order (the order they were acquired in).

The OPTIONAL `task-<label>` is used to indicate a task subjects were asked to perform in the scanner. Those labels MUST be consistent across subjects and sessions. For task based PET, a corresponding `task events` file MUST be provided (please note that this file is not necessary for resting scans).

The `trc-<label>` entity is used to indicate the tracer used. This entity is OPTIONAL if only one tracer is used in the study, but REQUIRED to distinguish between tracers if multiple are used. The label used is arbitrary and each file requires a separate JSON sidecar with details of the tracer used (see below). Examples are `trc-18FFDG` for fludeoxyglucose or `trc-11CPIB` for Pittsburgh compound B. Other labels are permitted, as long as they are consistent across subjects and sessions and consist only of the legal label characters.

If more than one run of the same task and acquisition (tracer) are acquired during the same session, the `run-<index>` entity MUST be used: `_run-1`, `_run-2`, `_run-3`, and so on. If only one run was acquired the `run-<index>` can be omitted.

The OPTIONAL `rec-<label>` entity is used to indicate the reconstruction method used for the image, with four reserved values:

- `acdyn`, for reconstructions with attenuation correction of dynamic data;
- `acstat`, for reconstructions with attenuation correction of static data;
- `nacdyn`, for reconstructions without attenuation correction of dynamic data;
- `nacstat`, for reconstructions without attenuation correction of static data.

Further details regarding reconstruction are in the `_pet.json` file. If multiple reconstructions of the data are made with the same type of reconstruction, a number MAY be appended to the label, for example `rec-acdyn1` and `rec-acdyn2`.

### Shared MRI data along with PET

PET and MRI images may be aggregated in the same dataset. When analyzing MRI and PET data together, it is essential to specify whether MR images have been corrected for gradient non-linearities, using the `NonLinearGradientCorrection` metadata field (see Sequence Specifics), which is REQUIRED for all MR data if PET data is also present in the dataset (see also PET-MRI correspondence). In the case of studies using combined PET/fMRI, subject-specific tasks may be carried out during the acquisition within the same session. If the same task is recorded with both modalities, the same `task-<label>` entity SHOULD be used. For further details, see Task (including resting state) imaging data.

In addition to the imaging data (`*.nii`) a `_pet.json` sidecar file MUST be provided. The included metadata are divided into sections described below.

### PET metadata

PET data MUST be described by metadata fields, stored in sidecar JSON files. These fields are derived from the recommendations in Knudsen et al. 2020, doi:10.1177/0271678X20905433, which we divide into several categories:

#### Scanner Hardware

| Key name | Requirement Level | Data type | Description |
|---|---|---|---|
| Manufacturer | REQUIRED | string | Manufacturer of the equipment that produced the measurements. Corresponds to DICOM Tag 0008, 0070 `Manufacturer`. |
| ManufacturersModelName | REQUIRED | string | Manufacturer's model name of the equipment that produced the measurements. Corresponds to DICOM Tag 0008, 1090 `Manufacturers Model Name`. |
| Units | REQUIRED | string | Measurement units for the associated file. SI units in CMIXF formatting are RECOMMENDED (see Units). SI unit for radioactivity (Becquerel) should be used (for example, `"Bq/mL"`). Corresponds to DICOM Tag 0054, 1001 `Units`. |

| Key name | Requirement Level | Data type | Description |
|---|---|---|---|
| InstitutionName | RECOMMENDED | string | The name of the institution in charge of the equipment that produced the measurements. Corresponds to DICOM Tag 0008, 0080 `InstitutionName`. |
| InstitutionAddress | RECOMMENDED | string | The address of the institution in charge of the equipment that produced the measurements. Corresponds to DICOM Tag 0008, 0081 `InstitutionAddress`. |
| InstitutionalDepartmentName | RECOMMENDED | string | The department in the institution in charge of the equipment that produced the measurements. Corresponds to DICOM Tag 0008, 1040 `Institutional Department Name`. |
| BodyPart | RECOMMENDED | string | Body part of the organ / body region scanned. Corresponds to DICOM Tag 0018, 0015 `Body Part Examined`. |

Radiochemistry

| Key name | Requirement Level | Data type | Description |
|---|---|---|---|
| TracerName | REQUIRED | string | Name of the tracer compound used (for example, `"CIMBI-36"`) |
| TracerRadionuclide | REQUIRED | string | Radioisotope labelling tracer (for example, `"C11"`). |
| InjectedRadioactivity | REQUIRED | number | Total amount of radioactivity injected into the patient (for example, `400`). For bolus-infusion experiments, this value should be the sum of all injected radioactivity originating from both bolus and infusion. Corresponds to DICOM Tag 0018, 1074 `Radionuclide Total Dose`. |
| InjectedRadioactivityUnits | REQUIRED | string | Unit format of the specified injected radioactivity (for example, `"MBq"`). |

| Key name | Requirement Level | Data type | Description |
|---|---|---|---|
| InjectedMass | REQUIRED | number or `"n/a"` | Total mass of radiolabeled compound injected into subject (for example, `10`). This can be derived as the ratio of the `"InjectedRadioactivity"` and `"MolarRadioactivity"`. For those tracers in which injected mass is not available (for example FDG) can be set to `"n/a"`). |
| InjectedMassUnits | REQUIRED | string or `"n/a"` | Unit format of the mass of compound injected (for example, `"ug"` or `"umol"`). Note this is not required for an FDG acquisition, since it is not available, and SHOULD be set to `"n/a"`. |
| SpecificRadioactivity | REQUIRED | number or `"n/a"` | Specific activity of compound injected. Note this is not required for an FDG acquisition, since it is not available, and SHOULD be set to `"n/a"`. |
| SpecificRadioactivityUnits | REQUIRED | string or `"n/a"` | Unit format of specified specific radioactivity (for example, `"Bq/g"`). Note this is not required for an FDG acquisition, since it is not available, and SHOULD be set to `"n/a"`. |
| ModeOfAdministration | REQUIRED | string | Mode of administration of the injection (for example, `"bolus"`, `"infusion"`, or `"bolus-infusion"`). |
| TracerRadLex | RECOMMENDED | string | ID of the tracer compound from the RadLex Ontology. |
| TracerSNOMED | RECOMMENDED | string | ID of the tracer compound from the SNOMED Ontology (subclass of Radioactive isotope). |
| TracerMolecularWeight | RECOMMENDED | number | Accurate molecular weight of the tracer used. |
| TracerMolecularWeightUnits | RECOMMENDED | string | Unit of the molecular weights measurement (for example, `"g/mol"`). |
| InjectedMassPerWeight | RECOMMENDED | number | Injected mass per kilogram bodyweight. |
| InjectedMassPerWeightUnits | RECOMMENDED | string | Unit format of the injected mass per kilogram bodyweight (for example, `"ug/kg"`). |

| Key name | Requirement Level | Data type | Description |
|---|---|---|---|
| SpecificRadioactivityMeasTime | RECOMMENDED | string | Time to which specific radioactivity measurement above applies in the default unit `"hh:mm:ss"`. |
| MolarActivity | RECOMMENDED | number | Molar activity of compound injected. Corresponds to DICOM Tag 0018, 1077 `Radiopharmaceutical Specific Activity`. |
| MolarActivityUnits | RECOMMENDED | string | Unit of the specified molar radioactivity (for example, `"GBq/umol"`). |
| MolarActivityMeasTime | RECOMMENDED | string | Time to which molar radioactivity measurement above applies in the default unit `"hh:mm:ss"`. |
| InfusionRadioactivity | RECOMMENDED, but REQUIRED if `ModeOfAdministration` is `bolus-infusion` | number | Amount of radioactivity infused into the patient. This value must be less than or equal to the total injected radioactivity (`"InjectedRadioactivity"`). Units should be the same as `"InjectedRadioactivityUnits"`. |
| InfusionStart | RECOMMENDED, but REQUIRED if `ModeOfAdministration` is `bolus-infusion` | number | Time of start of infusion with respect to `"TimeZero"` in the default unit seconds. |
| InfusionSpeed | RECOMMENDED, but REQUIRED if `ModeOfAdministration` is `bolus-infusion` | number | If given, infusion speed. |
| InfusionSpeedUnits | RECOMMENDED, but REQUIRED if `ModeOfAdministration` is `bolus-infusion` | string | Unit of infusion speed (for example, `"mL/s"`). |
| InjectedVolume | RECOMMENDED, but REQUIRED if `ModeOfAdministration` is `bolus-infusion` | number | Injected volume of the radiotracer in the unit `"mL"`. |
| Purity | RECOMMENDED | number | Purity of the radiolabeled compound (between 0 and 100%). Must be a number greater than or equal to 0 and less than or equal to 100. |

Pharmaceuticals

| Key name | Requirement Level | Data type | Description |
|---|---|---|---|
| PharmaceuticalName | RECOMMENDED | string | Name of pharmaceutical coadministered with tracer. |
| PharmaceuticalDoseAmount | RECOMMENDED | number or array of numbers | Dose amount of pharmaceutical coadministered with tracer. |
| PharmaceuticalDoseUnits | RECOMMENDED | string | Unit format relating to pharmaceutical dose (for example, `"mg"` or `"mg/kg"`). |
| PharmaceuticalDoseRegimen | RECOMMENDED | string | Details of the pharmaceutical dose regimen. Either adequate description or short-code relating to regimen documented elsewhere (for example, `"single oral bolus"`). |
| PharmaceuticalDoseTime | RECOMMENDED | number or array of numbers | Time of administration of pharmaceutical dose, relative to time zero. For an infusion, this should be a vector with two elements specifying the start and end of the infusion period. For more complex dose regimens, the regimen description should be complete enough to enable unambiguous interpretation of `"PharmaceuticalDoseTime"`. Unit format of the specified pharmaceutical dose time MUST be seconds. |
| Anaesthesia | OPTIONAL | string | Details of anaesthesia used, if any. |

Time

| Key name | Requirement Level | Data type | Description |
|---|---|---|---|
| TimeZero | REQUIRED | string | Time zero to which all scan and/or blood measurements have been adjusted to, in the unit ”hh:mm:ss”. This should be equal to `"InjectionStart"` or `"ScanStart"`. |
| ScanStart | REQUIRED | number | Time of start of scan with respect to `TimeZero` in the default unit seconds. |

| Key name | Requirement Level | Data type | Description |
|---|---|---|---|
| InjectionStart | REQUIRED | number | Time of start of injection with respect to `"TimeZero"` in the default unit seconds. This corresponds to DICOM Tag 0018, 1042 `Contrast/Bolus Start Time` converted to seconds relative to `"TimeZero"`. |
| FrameTimesStart | REQUIRED | array of numbers | Start times for all frames relative to `"TimeZero"` in default unit seconds. |
| FrameDuration | REQUIRED | array of numbers | Time duration of each frame in default unit seconds. This corresponds to DICOM Tag 0018, 1242 `Actual Frame Duration` converted to seconds. |
| InjectionEnd | RECOMMENDED | number | Time of end of injection with respect to `"TimeZero"` in the default unit seconds. |
| ScanDate | DEPRECATED | string | Date of scan in the format `"YYYY-MM-DD[Z]"`. This field is DEPRECATED, and this metadata SHOULD be recorded in the `acq_time` column of the corresponding DEPRECATED. |

We refer to the common principles for the standards for describing dates and timestamps, including possibilities for anonymization (see Units).

Reconstruction

| Key name | Requirement Level | Data type | Description |
|---|---|---|---|
| AcquisitionMode | REQUIRED | string | Type of acquisition of the PET data (for example, `"list mode"`). |
| ImageDecayCorrected | REQUIRED | boolean | Boolean flag specifying whether the image data have been decay-corrected. Must be one of: `"true"`, `"false"`. |
| ImageDecayCorrectionTime | REQUIRED | number | Point in time from which the decay correction was applied with respect to `"TimeZero"` in the default unit seconds. |
| ReconMethodName | REQUIRED | string | Reconstruction method or algorithm (for example, `"3d-op-osem"`). |

| Key name | Requirement Level | Data type | Description |
|---|---|---|---|
| ReconMethodParameterLabels | REQUIRED | array of strings | Names of reconstruction parameters (for example, `["subsets", "iterations"]`). |
| ReconMethodParameterUnits | REQUIRED | array of strings | Unit of reconstruction parameters (for example, `["none", "none"]`). |
| ReconMethodParameterValues | REQUIRED | array of numbers | Values of reconstruction parameters (for example, `[21, 3]`). |
| ReconFilterType | REQUIRED | string or array of strings | Type of post-recon smoothing (for example, `["Shepp"]`). |
| ReconFilterSize | REQUIRED | number or array of numbers | Kernel size of post-recon filter (FWHM) in default units `"mm"`. |
| AttenuationCorrection | REQUIRED | string | Short description of the attenuation correction method used. |
| ReconMethodImplementationVersion | RECOMMENDED | string | Identification for the software used, such as name and version. |
| AttenuationCorrectionMethodReference | RECOMMENDED | string | Reference paper for the attenuation correction method used. |
| ScaleFactor | RECOMMENDED | array of numbers | Scale factor for each frame. |
| ScatterFraction | RECOMMENDED | array of numbers | Scatter fraction for each frame (Units: 0-100%). |
| DecayCorrectionFactor | RECOMMENDED | array of numbers | Decay correction factor for each frame. |
| DoseCalibrationFactor | RECOMMENDED | number | Multiplication factor used to transform raw data (in counts/sec) to meaningful unit (Bq/ml). Corresponds to DICOM Tag 0054, 1322 `Dose Calibration Factor`. |
| PromptRate | RECOMMENDED | array of numbers | Prompt rate for each frame (same units as `Units`, for example, `"Bq/mL"`). |
| RandomRate | RECOMMENDED | array of numbers | Random rate for each frame (same units as `"Units"`, for example, `"Bq/mL"`). |
| SinglesRate | RECOMMENDED | array of numbers | Singles rate for each frame (same units as `Units`, for example, `"Bq/mL"`). |

All reconstruction-specific parameters that are not specified, but one wants to include, should go into the `ReconMethodParameterValues` field.

Example (`*_pet.json`)

```
{
  "Manufacturer": "Siemens",
  "ManufacturersModelName": "High-Resolution Research Tomograph (HRRT, CTI/Siemens)",
  "BodyPart": "Brain",
  "Units": "Bq/mL",
  "TracerName": "CIMBI-36",
  "TracerRadionuclide": "C11",
  "TracerMolecularWeight": 380.28,
  "TracerMolecularWeightUnits": "g/mol",
  "InjectedRadioactivity": 573,
  "InjectedRadioActivityUnits": "MBq",
  "InjectedMass": 0.62,
  "InjectedMassUnits": "ug",
  "SpecificRadioactivity": 929.6,
  "SpecificRadioactivityUnits": "MBq/ug",
  "ModeOfAdministration": "bolus",
  "MolarActivity": 353.51,
  "MolarActivityUnits": "GBq/umol",
  "MolarActivityMeasTime": "13:04:42",
  "TimeZero": "13:04:42",
  "ScanStart": 0,
  "InjectionStart": 0,
  "FrameTimesStart": [0, 10, 20, 30, 40, 50, 60, 80, 100, 120, 140, 160, 180, 240, 300, 360, 420, 480, 540, 660, 780, 900, 1020, 1140, 1260, 1380, 1500
  "FrameDuration": [10, 10, 10, 10, 10, 10, 20, 20, 20, 20, 20, 20, 60, 60, 60, 60, 60, 60, 120, 120, 120, 120, 120, 120, 120, 120, 300, 300, 300, 300,
  "AcquisitionMode": "list mode",
  "ImageDecayCorrected": true,
  "ImageDecayCorrectionTime": 0,
  "ReconMethodName": "3D-OSEM-PSF",
  "ReconMethodParameterLabels": ["subsets","iterations"],
  "ReconMethodParameterUnits": ["none","none"],
  "ReconMethodParameterValues": [16,10],
  "ReconFilterType": "none",
  "AttenuationCorrection": "[137Cs]transmission scan-based"
}
```

## Recommended patient data

Knudsen et al. 2020 (doi:10.1177/0271678X20905433) recommends recording participant body weight. If recorded once per participant, these data SHOULD be included in the Participants file or as Phenotypic and assessment data.

For example:

```
participant_id body_weight
sub-01 58
sub-02 96
sub-03 72
```

If multiple measurements are made, these data SHOULD be included in the Sessions file.

For example:

```
session_id body_weight
ses-01 58
ses-02 59
```

## Blood recording data

Template:

```
sub-<label>/
    [ses-<label>/]
        pet/
            sub-<label>[_ses-<label>][_task-<label>][_trc-<label>][_rec-<label>][_run-<index>]_recording-<label>_blood.json
            sub-<label>[_ses-<label>][_task-<label>][_trc-<label>][_rec-<label>][_run-<index>]_recording-<label>_blood.tsv
```

If collected, blood measurements of radioactivity are be stored in Tabular files and located in the `pet/` directory along with the corresponding PET data.

The OPTIONAL `recording` entity is used to distinguish sampling methods. For example, if an autosampler is used to record continuous blood samples, and manual measurements are also taken, then the files may have recording labels `autosampler` and `manual`, respectively. If multiple recording methods are used on the same PET acquisition, the `recording` entity MUST be used to distinguish them. All blood measurements should be reported according to a single time-scale in relation to time zero defined by the PET data (Figure 1). All definitions used below are in accordance with Innis et al. 2007 (doi:10.1038/sj.jcbfm.9600493).

Some metadata about the recording MUST be provided in an additional JSON file.

| Key name | Requirement Level | Data type | Description |
|---|---|---|---|
| PlasmaAvail | REQUIRED | boolean | Boolean that specifies if plasma measurements are available. Must be one of: `"true"`, `"false"`. |

| Key name | Requirement Level | Data type | Description |
|---|---|---|---|
| MetaboliteAvail | REQUIRED | boolean | Boolean that specifies if metabolite measurements are available. If `true`, the `metabolite_parent_fraction` column MUST be present in the corresponding `*_blood.tsv` file. Must be one of: `"true"`, `"false"`. |
| WholeBloodAvail | REQUIRED | boolean | Boolean that specifies if whole blood measurements are available. If `true`, the `whole_blood_radioactivity` column MUST be present in the corresponding `*_blood.tsv` file. Must be one of: `"true"`, `"false"`. |
| DispersionCorrected | REQUIRED | boolean | Boolean flag specifying whether the blood data have been dispersion-corrected. NOTE: not customary for manual samples, and hence should be set to `false`. Must be one of: `"true"`, `"false"`. |
| WithdrawalRate | RECOMMENDED | number | The rate at which the blood was withdrawn from the subject. The unit of the specified withdrawal rate should be in `"mL/s"`. |
| TubingType | RECOMMENDED | string | Description of the type of tubing used, ideally including the material and (internal) diameter. |
| TubingLength | RECOMMENDED | number | The length of the blood tubing, from the subject to the detector in meters. |
| DispersionConstant | RECOMMENDED | number | External dispersion time constant resulting from tubing in default unit seconds. |
| Haematocrit | RECOMMENDED | number | Measured haematocrit, meaning the volume of erythrocytes divided by the volume of whole blood. |
| BloodDensity | RECOMMENDED | number | Measured blood density. Unit of blood density should be in `"g/mL"`. |

The following metadata SHOULD or MUST be provided if corresponding flags are `true`.

| Key name | Requirement Level | Data type | Description |
|---|---|---|---|
| PlasmaFreeFraction | RECOMMENDED if `PlasmaAvail` is `true` | number | Measured free fraction in plasma, meaning the concentration of free compound in plasma divided by total concentration of compound in plasma (Units: 0-100%). Must be a number greater than or equal to 0 and less than or equal to 100. |
| PlasmaFreeFractionMethod | RECOMMENDED if `PlasmaAvail` is `true` | string | Method used to estimate free fraction. |
| MetaboliteMethod | REQUIRED if `MetaboliteAvail` is `true` | string | Method used to measure metabolites. |
| MetaboliteRecoveryCorrectionApplied | REQUIRED if `MetaboliteAvail` is `true` | boolean | Metabolite recovery correction from the HPLC, for tracers where it changes with time postinjection. If `true`, the `hplc_recovery_fractions` column MUST be present in the corresponding `*_blood.tsv` file. Must be one of: `"true"`, `"false"`. |

The following columns are defined for `_blood.tsv` files. The `time` column MUST always be the first column.

| Column name | Requirement Level | Data type | Description |
|---|---|---|---|
| time | REQUIRED | number | Time, in seconds, relative to `TimeZero` defined by the `*_pet.json`. For example, 5. |
| plasma_radioactivity | REQUIRED if `PlasmaAvail` is `true` | number | Radioactivity in plasma, in unit of plasma radioactivity (for example, `kBq/mL`). |
| metabolite_parent_fraction | REQUIRED if `MetaboliteAvail` is `true` | number | Parent fraction of the radiotracer (0-1). Must be a number greater than or equal to 0 and less than or equal to 1. |
| metabolite_polar_fraction | RECOMMENDED if `MetaboliteAvail` is `true` | number | Polar metabolite fraction of the radiotracer (0-1). Must be a number greater than or equal to 0 and less than or equal to 1. |
| hplc_recovery_fractions | REQUIRED if `MetaboliteRecoveryCorrectionApplie` is `true` | number | HPLC recovery fractions (the fraction of activity that gets loaded onto the HPLC). |

| Column name | Requirement Level | Data type | Description |
|---|---|---|---|
| whole_blood_radioactivity | REQUIRED if `WholeBloodAvail` is `true` | number | Radioactivity in whole blood samples, in unit of radioactivity measurements in whole blood samples (for example, `kBq/mL`). |

As with all tabular files, additional columns MAY be defined in `_blood.json`. For clarity, it is RECOMMENDED to include the above column definitions in `_blood.json`, as shown in the following example.

### Example blood data

**`*_recording-manual_blood.json`**:

```
{
    "PlasmaAvail": true,
    "WholeBloodAvail": true,
    "MetaboliteAvail": true,
    "MetaboliteMethod": "HPLC",
    "MetaboliteRecoveryCorrectionApplied": false,
    "DispersionCorrected": false,
    "time": {
        "Description": "Time in relation to time zero defined by the _pet.json",
        "Units": "s"
    },
    "plasma_radioactivity": {
        "Description": "Radioactivity in plasma samples. Measured using COBRA counter.",
        "Units": "kBq/mL"
    },
    "whole_blood_radioactivity": {
        "Description": "Radioactivity in whole blood samples. Measured using COBRA counter.",
        "Units": "kBq/mL"
    },
    "metabolite_parent_fraction": {
        "Description": "Parent fraction of the radiotracer.",
        "Units": "arbitrary"
    },
    "metabolite_polar_fraction": {
        "Description": "Polar metabolite fraction of the radiotracer.",
        "Units": "arbitrary"
    },
```

```
    "metabolite_lipophilic_fraction": {
        "Description": "Lipophilic metabolite fraction of the radiotracer.",
        "Units": "arbitrary"
    }
}
```

**`*_recording-manual_blood.tsv`**:

```
time plasma_radioactivity whole_blood_radioactivity metabolite_parent_fraction metabolite_polar_fraction
0    0    0    1    0
145    43.31    33.79    0.5749    0.1336
292    48.96    37.42    0.3149    0.2746
602    39.84    32.05    0.1469    0.3548
1248    37.38    31.52    0.073    0.444
1785    36.40    28.83    0.078    0.429
2390    33.13    26.32    0.061    0.453
3059    30.83    25.22    0.049    0.473
4196    27.28    21.98    0.036    0.503
5407    22.70    19.49    0.032    0.523
7193    19.71    15.70    0.02    0.559
```

# Microscopy

Support for Microscopy was developed as a BIDS Extension Proposal.

Please see Citing BIDS on how to appropriately credit this extension when referring to it in the context of the academic literature.

Microscopy datasets formatted using this specification are available on the BIDS examples repository and can be used for practical guidance when curating a new dataset.

Further Microscopy datasets are available:

- In PNG format: `data_axondeepseg_sem`
- In OME-TIFF format: `Broca's Area Light-Sheet Microscopy`

## Microscopy imaging data

Template:

```
sub-<label>/
    [ses-<label>/]
        micr/
            sub-<label>[_ses-<label>]_sample-<label>[_acq-<label>][_stain-<label>][_run-<index>][_chunk-<index>]_<suffix>.<extension>
            sub-<label>[_ses-<label>]_sample-<label>[_acq-<label>][_stain-<label>][_run-<index>][_chunk-<index>]_<suffix>.json
```

Microscopy data MUST be stored in the `micr` directory.

### File formats

The Microscopy community uses a variety of formats for storing raw data, and there is no single standard that all researchers agree on. However, a standardized file structure has been developed by the Open Microscopy Environment for whole-slide imaging with the OME-TIFF file specifications. The OME-TIFF file allows for multi-page TIFF files to store multiple image planes and supports multi-resolution pyramidal tiled images. An OME-XML data block is also embedded inside the file's header.

The BIDS standard accepts microscopy data in a number of file formats to accommodate datasets stored in 2D image formats and whole-slide imaging formats, to accommodate lossless and lossy compression, and to avoid unnecessary conversions of the original data from a non-tiled to a tiled format, or vice-versa.

Microscopy raw data MUST be stored in one of the following formats:

- Portable Network Graphics (`.png`)
- Tag Image File Format (`.tif`)
- OME-TIFF (`.ome.tif` for standard TIFF files or `.ome.btf` for BigTIFF files)

If different from PNG, TIFF or OME-TIFF, the original unprocessed data in the native format MAY be stored in the `/sourcedata` directory.

Future versions may extend this list of supported file formats, for example with the Next-Generation File Formats currently developed by OME (OME-NGFF) as a successor to OME-TIFF for better remote sharing of large datasets.

## Modality suffixes

Microscopy data currently support the following imaging modalities:

| Name | `suffix` | Description |
|---|---|---|
| Transmission electron microscopy | TEM | Transmission electron microscopy imaging data |
| Scanning electron microscopy | SEM | Scanning electron microscopy imaging data |
| Micro-CT | uCT | Micro-CT imaging data |
| Bright-field microscopy | BF | Bright-field microscopy imaging data |
| Dark-field microscopy | DF | Dark-field microscopy imaging data |
| Phase-contrast microscopy | PC | Phase-contrast microscopy imaging data |
| Differential interference contrast microscopy | DIC | Differential interference contrast microscopy imaging data |
| Fluorescence microscopy | FLUO | Fluorescence microscopy imaging data |
| Confocal microscopy | CONF | Confocal microscopy imaging data |
| Polarized-light microscopy | PLI | Polarized-light microscopy imaging data |
| Coherent anti-Stokes Raman spectroscopy | CARS | Coherent anti-Stokes Raman spectroscopy imaging data |
| 2-photon excitation microscopy | 2PE | 2-photon excitation microscopy imaging data |
| Multi-photon excitation microscopy | MPE | Multi-photon excitation microscopy imaging data |
| Super-resolution microscopy | SR | Super-resolution microscopy imaging data |
| Nonlinear optical microscopy | NLO | Nonlinear optical microscopy imaging data |
| Optical coherence tomography | OCT | Optical coherence tomography imaging data |
| Selective plane illumination microscopy | SPIM | Selective plane illumination microscopy imaging data |

## Filename entities

In the context of Microscopy, a session (`ses-<label>`) can refer to all the acquisitions between the start and the end of an imaging experiment for ex vivo imaging, or a subject lab visit for biopsy procedure and/or in vivo imaging. Consistent with other data types in BIDS, the session entity is optional.

The `sample-<label>` entity is REQUIRED for Microscopy data and is used to distinguish between different samples from the same subject. The label MUST be unique per subject and is RECOMMENDED to be unique throughout the dataset.

For example: Three brain slices (`sample-01` to `sample-03`) extracted from subject `sub-01`, imaged by scanning electron microscopy (SEM) in PNG format

```
sub-01/
   micr/
      sub-01_sample-01_SEM.png
      sub-01_sample-02_SEM.png
      sub-01_sample-03_SEM.png
      sub-01_SEM.json
```

In this example, the JSON metadata is common for all samples of `sub-01`. JSON metadata may be defined per subject or per sample as appropriate, as per the inheritance principle.

The `acq-<label>` entity corresponds to a custom label that MAY be used to distinguish a different set of parameters used for acquiring the same modality. For example, two images of the same sample acquired by bright-field microscopy (BF) in PNG format at different magnification of 40x and 60x. In such case two files could have the following names: `sub-01_sample-01_acq-40x_BF.png` and `sub-01_sample-01_acq-60x_BF.png`, however the user is free to choose any other label as long as they are consistent across subjects and sessions.

The `stain-<label>` entity MAY be used to distinguish image files from the same sample using different stains or antibodies for contrast enhancement.

For example: One brain slice (`sample-01`) extracted from subject `sub-01` with three stains (`stain-01`, `stain-02` and `stain-03`) in three separate files, imaged by selective plane illumination microscopy (SPIM) in OME-TIFF format

```
sub-01/
   micr/
      sub-01_sample-01_stain-01_SPIM.ome.tif
      sub-01_sample-01_stain-01_SPIM.json
      sub-01_sample-01_stain-02_SPIM.ome.tif
      sub-01_sample-01_stain-02_SPIM.json
      sub-01_sample-01_stain-03_SPIM.ome.tif
      sub-01_sample-01_stain-03_SPIM.json
```

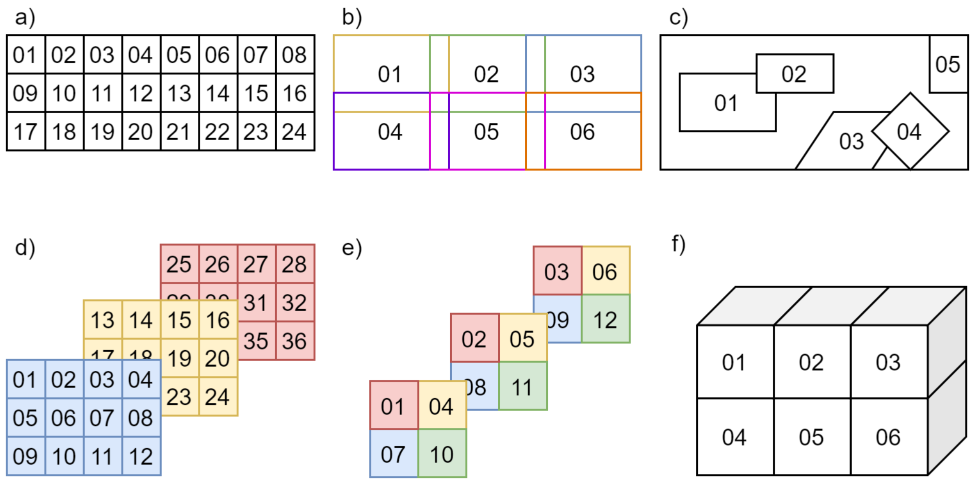
In this example, the entity stain is used to distinguish images with different stains in separate files from the same sample. In the case where a single file contains different staining in each channel, the `stain-<label>` is omitted.

Stains SHOULD be indicated in the `"SampleStaining"` key in the sidecar JSON file, although the label may be different. Description of antibodies SHOULD also be indicated in `"SamplePrimaryAntibodies"` and/or `"SampleSecondaryAntobodies"` as appropriate.

If more than one run of the same sample, acquisition and stain are acquired during the same session, the `run-<index>` entity MUST be used: `_run-1`, `_run-2`, `_run-3`, and so on. If only one run was acquired the `run-<index>` can be omitted.

The `chunk-<index>` entity is used when multiples regions (2D images or 3D volumes files) of the same physical sample are imaged with different fields of view, regardless if they overlap or not.

In some cases, the chunks can be ”ordered” and, for example, correspond to the displacement of the microscope stage. In other cases, the chunks can be different images of the same sample with no explicit spatial relation between them.



Examples of different chunks configurations can be seen in Figure 1.

Figure 1: Examples of chunks configurations.

- a) ordered 2D chunks without overlap,
- b) ordered 2D chunks with overlap,
- c) unordered 2D chunks with and without overlap,
- d) and e) ordered 2D chunks on different 3D planes,
- f) ordered 3D chunks.

For example: Four chunks (`chunk-01` to `chunk-04`) from the same brain sample (`sample-01`) of subject `sub-01`, imaged by confocal microscopy (CONF) in OME-TIFF format

```
sub-01/
   micr/
      sub-01_sample-01_chunk-01_CONF.ome.tif
      sub-01_sample-01_chunk-01_CONF.json
      sub-01_sample-01_chunk-02_CONF.ome.tif
      sub-01_sample-01_chunk-02_CONF.json
      sub-01_sample-01_chunk-03_CONF.ome.tif
      sub-01_sample-01_chunk-03_CONF.json
      sub-01_sample-01_chunk-04_CONF.ome.tif
      sub-01_sample-01_chunk-04_CONF.json
```

The index number can be assigned arbitrarily and, in the case of "ordered" chunks, the chunks' relative positions (in terms of scaling and translation) SHOULD be defined by an affine transformation matrix in the JSON sidecar file of each chunk, as described in Chunk Transformations.

In this example, the JSON metadata is different for each chunk of `sub-01_sample-01`. JSON metadata may be defined per sample or per chunk as appropriate, as per the inheritance principle.

In microscopy, many pyramidal file formats store multiple resolutions for the same acquisition. In the case where a multiple resolutions file format is converted to single resolution file format, only the higher resolution file is present in the raw data. Lower resolutions files MUST be placed under the `derivatives` folder and use the `res-<label>` entity.

For example:

```
my_dataset/
   derivatives/
      downsampled/
         sub-01/
            micr/
               sub-01_sample-01_res-4x_TEM.png
               sub-01_sample-01_res-4x_TEM.json
   sub-01/
      micr/
         sub-01_sample-01_TEM.png
         sub-01_sample-01_TEM.json
```

See Preprocessed, coregistered and/or resampled volumes for details.

## Microscopy metadata (Sidecar JSON)

Microscopy data MUST be described by metadata fields, stored in sidecar JSON files.

### Device Hardware

| Key name | Requirement Level | Data type | Description |
|---|---|---|---|
| Manufacturer | RECOMMENDED | string | Manufacturer of the equipment that produced the measurements. |
| ManufacturersModelName | RECOMMENDED | string | Manufacturer's model name of the equipment that produced the measurements. |

| Key name | Requirement Level | Data type | Description |
|---|---|---|---|
| DeviceSerialNumber | RECOMMENDED | string | The serial number of the equipment that produced the measurements. A pseudonym can also be used to prevent the equipment from being identifiable, so long as each pseudonym is unique within the dataset. |
| StationName | RECOMMENDED | string | Institution defined name of the machine that produced the measurements. |
| SoftwareVersions | RECOMMENDED | string | Manufacturer's designation of software version of the equipment that produced the measurements. |
| InstitutionName | RECOMMENDED | string | The name of the institution in charge of the equipment that produced the measurements. |
| InstitutionAddress | RECOMMENDED | string | The address of the institution in charge of the equipment that produced the measurements. |
| InstitutionalDepartmentName | RECOMMENDED | string | The department in the institution in charge of the equipment that produced the measurements. |

Image Acquisition

| Key name | Requirement Level | Data type | Description |
|---|---|---|---|
| PixelSize | REQUIRED | array of numbers | A 2- or 3-number array of the physical size of a pixel, either `[PixelSizeX, PixelSizeY]` or `[PixelSizeX, PixelSizeY, PixelSizeZ]`, where X is the width, Y the height and Z the depth. If the file format is OME-TIFF, these values need to be consistent with `PhysicalSizeX`, `PhysicalSizeY` and `PhysicalSizeZ` OME metadata fields, after converting in `PixelSizeUnits` according to `PhysicalSizeXunit`, `PhysicalSizeYunit` and `PhysicalSizeZunit` OME fields. |

| Key name | Requirement Level | Data type | Description |
|---|---|---|---|
| PixelSizeUnits | REQUIRED | string | Unit format of the specified `"PixelSize"`. MUST be one of: `"mm"` (millimeter), `"um"` (micrometer) or `"nm"` (nanometer). Must be one of: `"mm"`, `"um"`, `"nm"`. |
| Immersion | OPTIONAL | string | Lens immersion medium. If the file format is OME-TIFF, the value MUST be consistent with the `Immersion` OME metadata field. |
| NumericalAperture | OPTIONAL | number | Lens numerical aperture (for example: `1.4`). If the file format is OME-TIFF, the value MUST be consistent with the `LensNA` OME metadata field. Must be a number greater than 0. |
| Magnification | OPTIONAL | number | Lens magnification (for example: `40`). If the file format is OME-TIFF, the value MUST be consistent with the `"NominalMagnification"` OME metadata field. Must be a number greater than 0. |
| ImageAcquisitionProtocol | OPTIONAL | string | Description of the image acquisition protocol or URI (for example from protocols.io). |
| OtherAcquisitionParameters | OPTIONAL | string | Description of other relevant image acquisition parameters. |

Sample

| Key name | Requirement Level | Data type | Description |
|---|---|---|---|
| BodyPart | RECOMMENDED | string | Body part of the organ / body region scanned. From DICOM Body Part Examined (for example `"BRAIN"`). |
| BodyPartDetails | RECOMMENDED | string | Additional details about body part or location (for example: `"corpus callosum"`). |

| Key name | Requirement Level | Data type | Description |
|---|---|---|---|
| BodyPartDetailsOntology | OPTIONAL | string | URI of ontology used for BodyPartDetails (for example: `"https://www.ebi.ac.uk/ols/ontologies/uberon` |
| SampleEnvironment | RECOMMENDED | string | Environment in which the sample was imaged. MUST be one of: `"in vivo"`, `"ex vivo"` or `"in vitro"`. Must be one of: `"in vivo"`, `"ex vivo"`, `"in vitro"`. |
| SampleEmbedding | OPTIONAL | string | Description of the tissue sample embedding (for example: `"Epoxy resin"`). |
| SampleFixation | OPTIONAL | string | Description of the tissue sample fixation (for example: `"4% paraformaldehyde, 2% glutaraldehyde"`). |
| SampleStaining | RECOMMENDED | string or array of strings | Description(s) of the tissue sample staining (for example: `"Osmium"`). MAY be an array of strings if different stains are used in each channel of the file (for example: `["LFB", "PLP"]`). |
| SamplePrimaryAntibody | RECOMMENDED | string or array of strings | Description(s) of the primary antibody used for immunostaining. Either an RRID or the name, supplier and catalogue number of a commercial antibody. For non-commercial antibodies either an RRID or the host-animal and immunogen used (for examples: `"RRID:AB_2122563"` or `"Rabbit anti-Human HTR5A Polyclonal Antibody, Invitrogen, Catalog # PA1-2453"`). MAY be an array of strings if different antibodies are used in each channel of the file. |

| Key name | Requirement Level | Data type | Description |
|---|---|---|---|
| SampleSecondaryAntibody | RECOMMENDED | string or array of strings | Description(s) of the secondary antibody used for immunostaining. Either an RRID or the name, supplier and catalogue number of a commercial antibody. For non-commercial antibodies either an RRID or the host-animal and immunogen used (for examples: `"RRID:AB_228322"` or `"Goat anti-Mouse IgM Secondary Antibody, Invitrogen, Catalog # 31172"`). MAY be an array of strings if different antibodies are used in each channel of the file. |
| SliceThickness | OPTIONAL | number | Slice thickness of the tissue sample in the unit micrometers (`"um"`) (for example: `5`). Must be a number greater than 0. |
| TissueDeformationScaling | OPTIONAL | number | Estimated deformation of the tissue, given as a percentage of the original tissue size (for examples: for a shrinkage of 3%, the value is `97`; and for an expansion of 100%, the value is `200`). Must be a number greater than 0. |
| SampleExtractionProtocol | OPTIONAL | string | Description of the sample extraction protocol or URI (for example from protocols.io). |
| SampleExtractionInstitution | OPTIONAL | string | The name of the institution in charge of the extraction of the sample, if different from the institution in charge of the equipment that produced the image. |

### Chunk Transformations

Chunk transformations metadata describes the spatial relation between chunks of the same sample in an implicit coordinate system.

- The source frame of reference is the frame of reference of the associated image.
- The target frame of reference is the implicit coordinate system of the transform.
- The target frame of reference has the same units as the `PixelSizeUnits` metadata.

- The chunk transformation is described by 2 metadata fields: an affine transformation matrix and a description of the axis of the matrix.
- Other transformations should be described in derivatives.

| Key name | Requirement Level | Data type | Description |
|---|---|---|---|
| ChunkTransformationMatrix | RECOMMENDED if `<chunk-index>` is used in filenames | array of arrays | 3x3 or 4x4 affine transformation matrix describing spatial chunk transformation, for 2D and 3D respectively (for examples: `[[2, 0, 0], [0, 3, 0], [0, 0, 1]]` in 2D for 2x and 3x scaling along the first and second axis respectively; or `[[1, 0, 0, 0], [0, 2, 0, 0], [0, 0, 3, 0], [0, 0, 0, 1]]` in 3D for 2x and 3x scaling along the second and third axis respectively). Note that non-spatial dimensions like time and channel are not included in the transformation matrix. |
| ChunkTransformationMatrixAxis | REQUIRED if `ChunkTransformationMatrix` is present | array of strings | Describe the axis of the ChunkTransformationMatrix (for examples: `["X", "Y"]` or `["Z", "Y", "X"]`). |

An example of chunk transformations JSON metadata for `chunk-01` and `chunk-05` of Figure 2 is shown below:

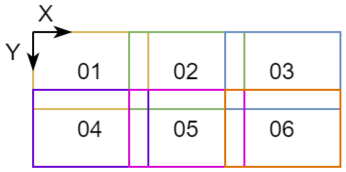


Figure 2: Example figure for chunks transformations.

In this example, there is no scaling and `chunk-01` is at the origin. `chunk-05` is translated by 5 um along `X+` and by 3 um along `Y+`.

**`*_chunk-01_<suffix>.json`**:

```
{
        "PixelSize": [1, 1],
        "PixelSizeUnits": "um",
```

```
        "ChunkTransformationMatrix": [[1, 0, 0],
                                      [0, 1, 0],
                                      [0, 0, 1]],
        "ChunkTransformationMatrixAxis": ["X", "Y"]
}
```

`*_chunk-05_<suffix>.json`:

```
{
        "PixelSize": [1, 1],
        "PixelSizeUnits": "um",
        "ChunkTransformationMatrix": [[1, 0, 5],
                                      [0, 1, 3],
                                      [0, 0, 1]],
        "ChunkTransformationMatrixAxis": ["X", "Y"]
}
```

Example of sidecar JSON file (`*_<suffix>.json`)

```
{
        "Manufacturer": "Hamamatsu",
        "ManufacturersModelName": "C9600-12",
        "PixelSize": [0.23, 0.23],
        "PixelSizeUnits": "um",
        "Magnification": 40,
        "BodyPart": "BRAIN",
        "BodyPartDetails": "corpus callosum",
        "SampleEnvironment": "ex vivo",
        "SampleFixation": "4% paraformaldehyde, 2% glutaraldehyde",
        "SampleStaining": "LFB",
        "SliceThickness": 5,
        "TissueDeformationScaling": 97
}
```

## Required Samples file

For Microscopy data, the Samples file `samples.tsv` is REQUIRED and its associated sidecar `samples.json` file is RECOMMENDED.

Additional optional columns MAY be used to describe other samples' attributes.

## Recommended Participants data

For Microscopy data, we RECOMMEND to make use of the columns `species`, `strain` and `strain_rrid` in the Participants file when applicable.

Additional optional columns MAY be used to describe other subjects' attributes.

`participants.tsv` example:

```
participant_id species strain strain_rrid
sub-01 mus musculus C57BL/6J RRID:IMSR_JAX:000664
sub-02 mus musculus C57BL/6J RRID:IMSR_JAX:000664
```

`participants.json` example:

```
{
    "species": {
        "Description": "binomial species name from the NCBI Taxonomy (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi)"
    },
    "strain": {
        "Description": "name of the strain of the species"
    },
    "strain_rrid": {
        "Description": "research resource identifier (RRID) of the strain (https://scicrunch.org/resources/Organisms/search)"
    }
}
```

## Photos of the samples (`*_photo.<extension>`)

Photos of the tissue sample, overview microscopy scans or blockface images from cutting MAY be included for visualization of large samples or to indicate the location of chunks in a sample.

Template:

```
sub-<label>/
    [ses-<label>/]
        micr/
            sub-<label>[_ses-<label>]_sample-<label>[_acq-<label>]_photo.<extension>
```

The file `<extension>` for photos MUST be either `.jpg`, `.png` or `.tif`.

The `acq-<label>` entity MAY be used to indicate acquisition of different photos of the same sample.

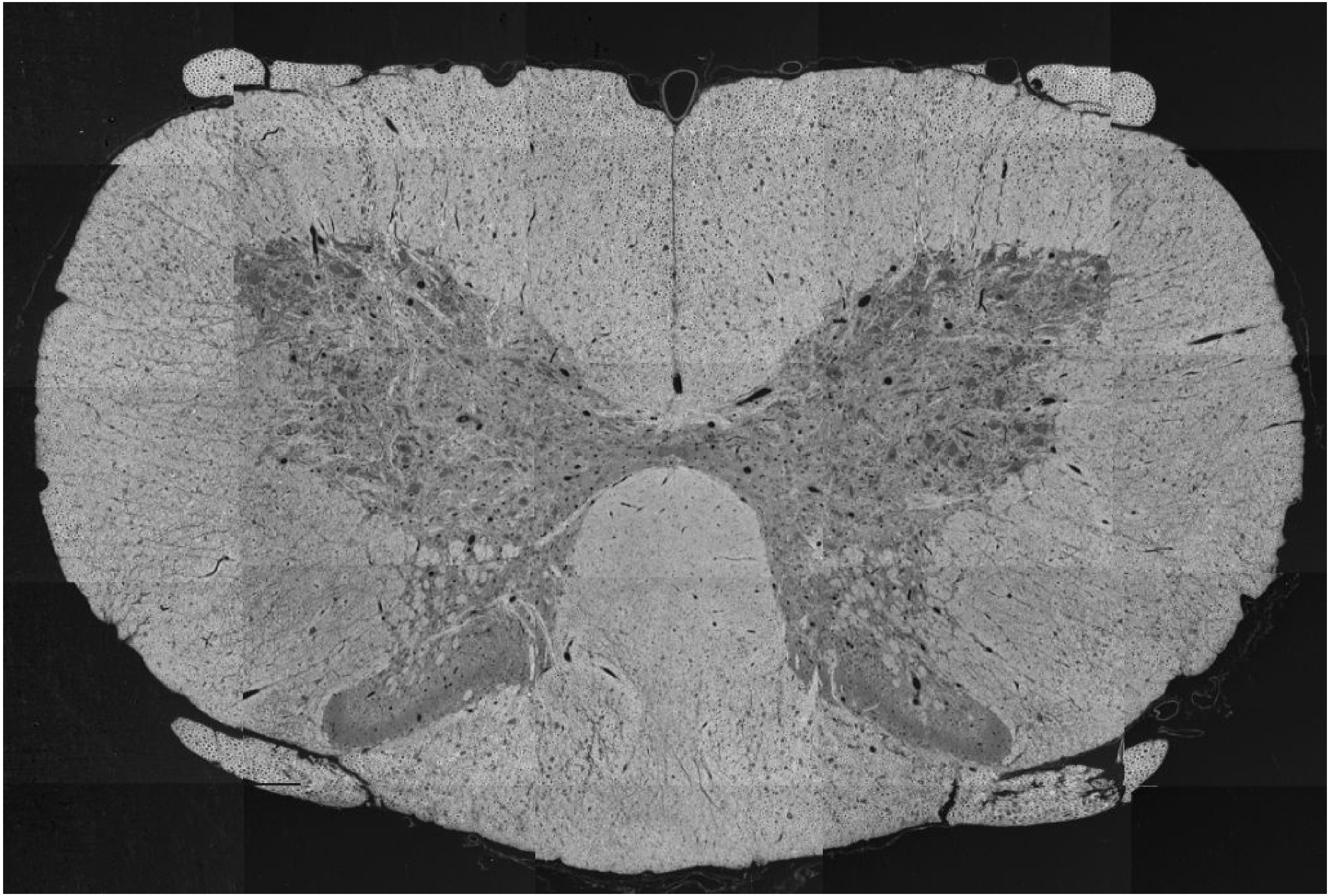
For example:

```
sub-01/
```

```
  micr/
     sub-01_sample-01_acq-1_photo.jpg
     sub-01_sample-01_acq-2_photo.jpg
```

Below is an example of a spinal cord SEM overview, modified from Zaimi et al., 2018. doi:10.1038/s41598-018-22181-4.

`sub-01_sample-01_photo.jpg`



# BIDS Derivatives

Derivatives are outputs of common processing pipelines, capturing data and meta-data sufficient for a researcher to understand and (critically) reuse those outputs in subsequent processing. Standardizing derivatives is motivated by use cases where formalized machine-readable access to processed data enables higher level processing.

The following sections cover additions to and divergences from ”raw” BIDS. Placement and naming conventions for derived datasets are addressed in Storage of derived datasets, and dataset-level metadata is included in Derived dataset and pipeline description.

## Metadata conventions

- Unless specified otherwise, individual sidecar JSON files and all metadata fields within are OPTIONAL. However, the appropriate use of these files and pertinent fields is very valuable and thus encouraged. Moreover, for some types of files, there may be one or more required metadata fields, in which case at least one metadata file containing that field must be located somewhere within the file’s hierarchy (per the Inheritance Principle).
- When chaining derivative pipelines, any JSON fields that were specified as mandatory in the input files SHOULD be propagated forward in the output file’s JSON provided they remain valid. Non-required JSON fields MAY be propagated, and are highly useful, but it is the pipeline’s responsibility to ensure that the values are still relevant and appropriate to the type of output data.

## File naming conventions

- Filenames that are permissible for a raw BIDS data type have a privileged status. Any modification of raw files must use a modified filename that does not conflict with the raw filename. Further, any files created as part of a derivative dataset must not match a permissible filename of a valid raw dataset. Stated equivalently, if any filename in a derivative dataset has a name permissible for a raw BIDS data, then that file must be an identical copy of that raw file.
- Each Derivatives filename MUST be of the form: `<source_entities>[_keyword-<value>]_<suffix>.<ext>` (where `<value>` could either be an `<index>` or a `<label>` depending on the keyword; see Definitions)
- When the derivatives chain involves outputs derived from a single raw input, `source_entities` MUST be the entire source filename, with the omission of the source suffix and extension. One exception to this rule is filename entities that are no longer relevant. Depending on the nature of the derivative file, the suffix can either be the same as the source file if that suffix is still appropriate, or a new appropriate value selected from the controlled list.

- There is no prohibition against identical filenames in different derived datasets, although users should be aware of the potential ambiguity this can create and use the sidecar JSON files to detail the specifics of individual files.
- When necessary to distinguish two files that do not otherwise have a distinguishing entity, the `_desc-<label>` keyword-value SHOULD be used. This includes the cases of needing to distinguish both differing inputs and differing outputs (for example, `_desc-T1w` and `_desc-T2w` to distinguish brain mask files derived from T1w and T2w images; or `_desc-sm4` and `_desc-sm8` to distinguish between outputs generated with two different levels of smoothing).
- When naming files that are not yet standardized, it is RECOMMENDED to use names consistent with BIDS conventions where those conventions apply. For example, if a summary statistic is derived from a given task, the file name SHOULD contain `_task-<label>`.

# Common data types and metadata

## Common file level metadata fields

Each derivative data file SHOULD be described by a JSON file provided as a sidecar or higher up in the hierarchy of the derived dataset (according to the Inheritance Principle) unless a particular derivative includes REQUIRED metadata fields, in which case a JSON file is also REQUIRED. Each derivative type defines their own set of fields, but all of them share the following (non-required) ones:

| Key name | Requirement Level | Data type | Description |
|---|---|---|---|
| Description | RECOMMENDED | string | Free-form natural language description. This describes the nature of the file. |
| Sources | OPTIONAL | array of strings | A list of files with the paths specified relative to dataset root; these files were directly used in the creation of this derivative data file. For example, if a derivative A is used in the creation of another derivative B, which is in turn used to generate C in a chain of A->B->C, C should only list B in `"Sources"`, and B should only list A in `"Sources"`. However, in case both X and Y are directly used in the creation of Z, then Z should list X and Y in `"Sources"`, regardless of whether X was used to generate Y. |
| RawSources | OPTIONAL | array of strings | A list of paths relative to dataset root pointing to the BIDS-Raw file(s) that were used in the creation of this derivative. |

### Examples

Preprocessed `bold` NIfTI file in the original coordinate space of the original run. The location of the file in the original datasets is encoded in the `RawSources` metadata, and `_desc-<label>` is used to prevent clashing with the original filename.

```
sub-01/
   func/
      sub-01_task-rest_desc-preproc_bold.nii.gz
      sub-01_task-rest_desc-preproc_bold.json
```

```
{
    "RawSources": ["sub-01/func/sub-01_task-rest_bold.nii.gz"]
}
```

If this file was generated with prior knowledge from additional sources, such as the same subject's `T1w`, then both files MAY be included in `RawSources`.

```
{
    "RawSources": [
        "sub-01/func/sub-01_task-rest_bold.nii.gz",
        "sub-01/anat/sub-01_T1w.nii.gz"
    ]
}
```

On the other hand, if a preprocessed version of the T1w image was used, and it also occurs in the derivatives, `Sources` and `RawSources` can both be specified.

```
{
    "Sources": [
        "sub-01/anat/sub-01_desc-preproc_T1w.nii.gz"
    ],
    "RawSources": [
        "sub-01/func/sub-01_task-rest_bold.nii.gz"
    ]
}
```

## Spatial references

Derivatives are often aligned to a common spatial reference to allow for the comparison of acquired data across runs, sessions, subjects or datasets. A file may indicate the spatial reference to which it has been aligned using the `space` entity and/or the `SpatialReference` metadata.

The `space` entity may take any value in Image-Based Coordinate Systems.

If the `space` entity is omitted, or the space is not in the Standard template identifiers table, then the `SpatialReference` metadata is REQUIRED.

| Key name | Requirement Level | Data type | Description |
|---|---|---|---|
| SpatialReference | RECOMMENDED if the derivative is aligned to a standard template listed in Standard template identifiers. REQUIRED otherwise. | string or object | For images with a single reference, the value MUST be a single string. For images with multiple references, such as surface and volume references, a JSON object MUST be used. |

### SpatialReference key allowed values

| Value | Description |
|---|---|
| `orig` | A (potentially unique) per-image space. Useful for describing the source of transforms from an input image to a target space. |
| URI or path | This can be used to point to a specific file. Paths are written relative to the root of the derivative dataset. |

In the case of images with multiple references, an object must link the relevant structures to reference files. If a single volumetric reference is used for multiple structures, the `VolumeReference` key MAY be used to reduce duplication. For CIFTI-2 images, the relevant structures are BrainStructure values defined in the BrainModel elements found in the CIFTI-2 header.

### Examples

Preprocessed `bold` NIfTI file in `individual` coordinate space. Please mind that in this case `SpatialReference` key is REQUIRED.

```
sub-01/
   func/
      sub-01_task-rest_space-individual_bold.nii.gz
      sub-01_task-rest_space-individual_bold.json
```

```
{
    "SpatialReference": "sub-01/anat/sub-01_desc-combined_T1w.nii.gz"
}
```

Preprocessed `bold` CIFTI-2 files that have been sampled to the fsLR surface meshes defined in the Conte69 atlas along with the MNI152NLin6Asym template. In this example, because all volumetric structures are sampled to the same reference, the `VolumeReference` key is used as a default, and only the surface references need to be specified by BrainStructure names.

```
sub-01/
   func/
      sub-01_task-rest_space-fsLR_den-91k_bold.dtseries.nii
      sub-01_task-rest_space-fsLR_den-91k_bold.json
```

```
{
    "SpatialReference": {
        "VolumeReference": "https://templateflow.s3.amazonaws.com/tpl-MNI152NLin6Asym_res-02_T1w.nii.gz",
        "CIFTI_STRUCTURE_CORTEX_LEFT": "https://github.com/mgxd/brainplot/raw/master/brainplot/Conte69_Atlas/Conte69.L.midthickness.32k_fs_LR.surf.gii"
        "CIFTI_STRUCTURE_CORTEX_RIGHT": "https://github.com/mgxd/brainplot/raw/master/brainplot/Conte69_Atlas/Conte69.R.midthickness.32k_fs_LR.surf.gii
    }
}
```

## Preprocessed or cleaned data

Template:

```
<pipeline_name>/
    sub-<label>/
        <datatype>/
            <source_entities>[_space-<space>][_desc-<label>]_<suffix>.<ext>
```

Data is considered to be preprocessed or cleaned if the data type of the input, as expressed by the BIDS `suffix`, is unchanged. By contrast, processing steps that change the number of dimensions are likely to disrupt the propagation of the input's `suffix` and generally, the outcomes of such transformation cannot be considered preprocessed or cleaned data.

Examples of preprocessing:

- Motion-corrected, temporally denoised, and transformed to MNI space BOLD series
- Inhomogeneity corrected and skull stripped T1w files
- Motion-corrected DWI files
- Time-domain filtered EEG data
- MaxFilter (for example, SSS) cleaned MEG data

The `space` entity is recommended to distinguish files with different underlying coordinate systems or registered to different reference maps. See Spatial references for details. The `desc` entity ("description") is a general purpose field with freeform values, which SHOULD be used to distinguish between multiple different versions of processing for the same input data.

Examples of preprocessed data:

```
pipeline1/
   sub-001/
      anat/
         sub-001_space-MNI305_T1w.nii.gz
         sub-001_space-MNI305_T1w.json
      func/
         sub-001_task-rest_run-1_space-MNI305_desc-preproc_bold.nii.gz
         sub-001_task-rest_run-1_space-MNI305_desc-preproc_bold.json
```

```
   pipeline2/
      sub-001/
         eeg/
            sub-001_task-listening_run-1_desc-autoannotation_events.tsv
            sub-001_task-listening_run-1_desc-autoannotation_events.json
            sub-001_task-listening_run-1_desc-filtered_eeg.edf
            sub-001_task-listening_run-1_desc-filtered_eeg.json
```

All REQUIRED metadata fields coming from a derivative file's source file(s) MUST be propagated to the JSON description of the derivative unless the processing makes them invalid (for example, if a source 4D image is averaged to create a single static volume, a `RepetitionTime` property would no longer be relevant).

# Imaging data types

This section pertains to imaging data, which characteristically have spatial extent and resolution.

## Preprocessed, coregistered and/or resampled volumes

Template:

```
<pipeline_name>/
    sub-<label>/
        <datatype>/
            <source_entities>[_space-<space>][_res-<label>][_den-<label>][_desc-<label>]_<suffix>.<ext>
```

Volumetric preprocessing does not modify the number of dimensions, and so the specifications in Preprocessed or cleaned data apply. The use of surface meshes and volumetric measures sampled to those meshes is sufficiently similar in practice to treat them equivalently.

When two or more instances of a given derivative are provided with resolution or surface sampling density being the only difference between them, then the `res` (for resolution of regularly sampled N-D data) and/or `den` (for density of non-parametric surfaces) entities SHOULD be used to avoid name conflicts. Note that only files combining both regularly sampled (for example, gridded) and surface sampled data (and their downstream derivatives) are allowed to present both `res` and `den` entities simultaneously.

Examples:

```
pipeline1/
   sub-001/
      func/
         sub-001_task-rest_run-1_space-MNI305_res-lo_bold.nii.gz
         sub-001_task-rest_run-1_space-MNI305_res-hi_bold.nii.gz
         sub-001_task-rest_run-1_space-MNI305_bold.json
```

The following metadata JSON fields are defined for preprocessed images:

| Key name | Requirement Level | Data type | Description |
|---|---|---|---|
| SkullStripped | REQUIRED | boolean | Whether the volume was skull stripped (non-brain voxels set to zero) or not. Must be one of: `"true"`, `"false"`. |
| Resolution | REQUIRED if `res` is present | string or object of strings | Specifies the interpretation of the resolution keyword. If an object is used, then the keys should be values for the `res` entity and values should be descriptions of those `res` values. |
| Density | REQUIRED if `den` is present | string or object of strings | Specifies the interpretation of the density keyword. If an object is used, then the keys should be values for the `den` entity and values should be descriptions of those `den` values. |

Example JSON file corresponding to `pipeline1/sub-001/func/sub-001_task-rest_run-1_space-MNI305_bold.json` above:

```
{
  "SkullStripped": true,
  "Resolution": {
    "hi": "Matched with high-resolution T1w (0.7mm, isotropic)",
    "lo": "Matched with original BOLD resolution (2x2x3 mm^3)"
  }
}
```

This would be equivalent to having two JSON metadata files, one corresponding to `res-lo` (`pipeline1/sub-001/func/sub-001_task-rest_run-1_space-MNI305_res-lo_bold.json`)

```
{
  "SkullStripped": true,
  "Resolution": "Matched with original BOLD resolution (2x2x3 mm^3)"
}
```

And one corresponding to `res-hi` (`pipeline1/sub-001/func/sub-001_task-rest_run-1_space-MNI305_res-hi_bold.json`):

```
{
  "SkullStripped": true,
  "Resolution": "Matched with high-resolution T1w (0.7mm, isotropic)"
}
```

Example of CIFTI-2 files (a format that combines regularly sampled data and non-parametric surfaces) having both `res` and `den` entities:

```
pipeline1/
```

```
      sub-001/
         func/
            sub-001_task-rest_run-1_space-fsLR_res-1_den-10k_bold.dtseries.nii
            sub-001_task-rest_run-1_space-fsLR_res-1_den-41k_bold.dtseries.nii
            sub-001_task-rest_run-1_space-fsLR_res-2_den-10k_bold.dtseries.nii
            sub-001_task-rest_run-1_space-fsLR_res-2_den-41k_bold.dtseries.nii
            sub-001_task-rest_run-1_space-fsLR_bold.json
```

And the corresponding `sub-001_task-rest_run-1_space-fsLR_bold.json` file:

```
{
    "SkullStripped": true,
    "Resolution": {
        "1": "Matched with MNI152NLin6Asym 1.6mm isotropic",
        "2": "Matched with MNI152NLin6Asym 2.0mm isotropic"
    },
    "Density": {
        "10k": "10242 vertices per hemisphere (5th order icosahedron)",
        "41k": "40962 vertices per hemisphere (6th order icosahedron)"
    }
}
```

## Masks

Template:

```
<pipeline_name>/
    sub-<label>/
        anat|func|dwi/
            <source_entities>[_space-<space>][_res-<label>][_den-<label>][_label-<label>][_desc-<label>]_mask.nii.gz
```

A binary (1 - inside, 0 - outside) mask in the space defined by the `space` entity. If no transformation has taken place, the value of `space` SHOULD be set to `orig`. If the mask is an ROI mask derived from an atlas, then the `label` entity) SHOULD be used to specify the masked structure (see Common image-derived labels), and the `Atlas` metadata SHOULD be defined.

JSON metadata fields:

| Key name | Requirement Level | Data type | Description |
|---|---|---|---|
| RawSources | REQUIRED | array of strings | A list of paths relative to dataset root pointing to the BIDS-Raw file(s) that were used in the creation of this derivative. |

| Key name | Requirement Level | Data type | Description |
|---|---|---|---|
| Type | RECOMMENDED | string | Short identifier of the mask. The value `"Brain"` refers to a brain mask. The value `"Lesion"` refers to a lesion mask. The value `"Face"` refers to a face mask. The value `"ROI"` refers to a region of interest mask. Must be one of: `"Brain"`, `"Lesion"`, `"Face"`, `"ROI"`. |
| Atlas | RECOMMENDED if `label` entity is defined | string | Which atlas (if any) was used to generate the mask. |
| Resolution | REQUIRED if `res` is present | string or object of strings | Specifies the interpretation of the resolution keyword. If an object is used, then the keys should be values for the `res` entity and values should be descriptions of those `res` values. |
| Density | REQUIRED if `den` is present | string or object of strings | Specifies the interpretation of the density keyword. If an object is used, then the keys should be values for the `den` entity and values should be descriptions of those `den` values. |

Examples:

```
func_loc/
   sub-001/
      func/
         sub-001_task-rest_run-1_space-MNI305_desc-PFC_mask.nii.gz
         sub-001_task-rest_run-1_space-MNI305_desc-PFC_mask.json
```

```
manual_masks/
   sub-001/
      anat/
         sub-001_desc-tumor_mask.nii.gz
         sub-001_desc-tumor_mask.json
```

## Segmentations

A segmentation is a labeling of regions of an image such that each location (for example, a voxel or a surface vertex) is identified with a label or a combination of labels. Labeled regions may include anatomical structures (such as tissue class, Brodmann area or white matter tract), discontiguous, functionally-defined networks, tumors or lesions.

A discrete segmentation represents each region with a unique integer label. A probabilistic segmentation represents each region as values between 0 and 1 (inclusive) at each location in the image, and one volume/frame per structure may be concatenated in a single file.

Segmentations may be defined in a volume (labeled voxels), a surface (labeled vertices) or a combined volume/surface space.

The following section describes discrete and probabilistic segmentations of volumes, followed by discrete segmentations of surface/combined spaces. Probabilistic segmentations of surfaces are currently [unspecified][].

The following metadata fields apply to all segmentation files:

| Key name | Requirement Level | Data type | Description |
|---|---|---|---|
| Manual | OPTIONAL | boolean | Indicates if the segmentation was performed manually or via an automated process. Must be one of: `"true"`, `"false"`. |
| Atlas | OPTIONAL | string | Which atlas (if any) was used to generate the mask. |
| Resolution | REQUIRED if `res` is present | string or object of strings | Specifies the interpretation of the resolution keyword. If an object is used, then the keys should be values for the `res` entity and values should be descriptions of those `res` values. |
| Density | REQUIRED if `den` is present | string or object of strings | Specifies the interpretation of the density keyword. If an object is used, then the keys should be values for the `den` entity and values should be descriptions of those `den` values. |

## Discrete Segmentations

Discrete segmentations of brain tissue represent multiple anatomical structures (such as tissue class or Brodmann area) with a unique integer label in a 3D volume. See Common image-derived labels for a description of how integer values map to anatomical structures.

Template:

```
<pipeline_name>/
    sub-<label>/
        anat|func|dwi/
            <source_entities>[_space-<space>][_res-<label>][_den-<label>]_dseg.nii.gz
```

Example:

```
pipeline/
```

```
    sub-001/
        anat/
            sub-001_space-orig_dseg.nii.gz
            sub-001_space-orig_dseg.json
```

A segmentation can be used to generate a binary mask that functions as a discrete ”label” for a single structure. In this case, the mask suffix MUST be used, the `label` entity) SHOULD be used to specify the masked structure (see Common image-derived labels), and the `Atlas` metadata SHOULD be defined. For example:

```
pipeline/
    sub-001/
        anat/
            sub-001_space-orig_label-GM_mask.nii.gz
```

## Probabilistic Segmentations

Probabilistic segmentations of brain tissue represent a single anatomical structure with values ranging from 0 to 1 in individual 3D volumes or across multiple frames. If a single structure is included, the `label` entity SHOULD be used to specify the structure.

Template:

```
<pipeline_name>/
    sub-<label>/
        func|anat|dwi/
            <source_entities>[_space-<space>][_res-<label>][_den-<label>][_label-<label>]_probseg.nii.gz
```

Example:

```
pipeline/
    sub-001/
        anat/
            sub-001_space-orig_label-BG_probseg.nii.gz
            sub-001_space-orig_label-WM_probseg.nii.gz
```

See Common image-derived labels for reserved key values for `label`.

A 4D probabilistic segmentation, in which each frame corresponds to a different tissue class, must provide a label mapping in its JSON sidecar. For example:

```
pipeline/
    sub-001/
        anat/
            sub-001_space-orig_probseg.nii.gz
            sub-001_space-orig_probseg.json
```

The JSON sidecar MUST include the label-map key that specifies a tissue label for each volume:

```
{
    "LabelMap": [
        "BG",
        "WM",
        "GM"
        ]
}
```

Values of `label` SHOULD correspond to abbreviations defined in Common image-derived labels.

## Discrete surface segmentations

Discrete surface segmentations (sometimes called parcellations) of cortical structures MUST be stored as GIFTI label files, with the extension `.label.gii`. For combined volume/surface spaces, discrete segmentations MUST be stored as CIFTI-2 dense label files, with the extension `.dlabel.nii`.

Template:

```
<pipeline_name>/
    sub-<label>/
        anat/
            <source_entities>[_hemi-{L|R}][_space-<space>][_res-<label>][_den-<label>]_dseg.{label.gii|dlabel.nii}
```

The `hemi-<label>` entity is REQUIRED for GIFTI files storing information about a structure that is restricted to a hemibrain. For example:

```
pipeline/
   sub-001/
      anat/
         sub-001_hemi-L_dseg.label.gii
         sub-001_hemi-R_dseg.label.gii
```

The REQUIRED extension for CIFTI parcellations is `.dlabel.nii`. For example:

```
pipeline/
   sub-001/
      anat/
         sub-001_dseg.dlabel.nii
```

## Common image-derived labels

BIDS supplies a standard, generic label-index mapping, defined in the table below, that contains common image-derived segmentations and can be used to map segmentations (and parcellations) between lookup tables.

| Integer value | Description | Abbreviation (label) |
|---|---|---|
| 0 | Background | BG |
| 1 | Gray Matter | GM |
| 2 | White Matter | WM |
| 3 | Cerebrospinal Fluid | CSF |
| 4 | Bone | B |
| 5 | Soft Tissue | ST |
| 6 | Non-brain | NB |
| 7 | Lesion | L |
| 8 | Cortical Gray Matter | CGM |
| 9 | Subcortical Gray Matter | SGM |
| 10 | Brainstem | BS |
| 11 | Cerebellum | CBM |

These definitions can be overridden (or added to) by providing custom labels in a sidecar `<matches>.tsv` file, in which `<matches>` corresponds to segmentation filename.

Example:

```
pipeline/
    sub-001/
        anat/
            sub-001_space-orig_dseg.nii.gz
            sub-001_space-orig_dseg.tsv
```

Definitions can also be specified with a top-level `dseg.tsv`, which propagates to segmentations in relative subdirectories.

Example:

```
pipeline/
    dseg.tsv
    sub-001/
        anat/
            sub-001_space-orig_dseg.nii.gz
```

These TSV lookup tables contain the following columns:

| Column name | Requirement Level | Data type | Description |
|---|---|---|---|
| index | REQUIRED | integer | The label integer index. |
| name | REQUIRED | string | The unique label name. |
| abbreviation | OPTIONAL | string | The unique label abbreviation |

| Column name | Requirement Level | Data type | Description |
|---|---|---|---|
| color | OPTIONAL | string | Hexadecimal. Label color for visualization. |
| mapping | OPTIONAL | integer | Corresponding integer label in the standard BIDS label lookup. |

An example, custom `dseg.tsv` that defines three labels:

```
index   name            abbreviation    color       mapping
100     Gray Matter     GM              #ff53bb     1
101     White Matter    WM              #2f8bbe     2
102     Brainstem       BS              #36de72     11
```

The following example `dseg.tsv` defines regions that are not part of the standard BIDS labels:

```
index   name                 abbreviation
137     pars opercularis     IFGop
138     pars triangularis    IFGtr
139     pars orbitalis       IFGor
```

# Longitudinal and multi-site studies

Multiple sessions (visits) are encoded by adding an extra layer of directories and filenames in the form of a session (for example `ses-<label>`) and with a `*_sessions.tsv` file.

```
sub-control01/
   ses-predrug/
      anat/
         sub-control01_ses-predrug_T1w.nii.gz
         sub-control01_ses-predrug_T1w.json
         sub-control01_ses-predrug_T2w.nii.gz
         sub-control01_ses-predrug_T2w.json
      func/
         sub-control01_ses-predrug_task-nback_bold.nii.gz
         sub-control01_ses-predrug_task-nback_bold.json
         sub-control01_ses-predrug_task-nback_events.tsv
         sub-control01_ses-predrug_task-nback_physio.tsv.gz
         sub-control01_ses-predrug_task-nback_physio.json
         sub-control01_ses-predrug_task-nback_sbref.nii.gz
      dwi/
         sub-control01_ses-predrug_dwi.nii.gz
         sub-control01_ses-predrug_dwi.bval
         sub-control01_ses-predrug_dwi.bvec
      fmap/
         sub-control01_ses-predrug_phasediff.nii.gz
         sub-control01_ses-predrug_phasediff.json
         sub-control01_ses-predrug_magnitude1.nii.gz
      sub-control01_ses-predrug_scans.tsv
   ses-postdrug/
      func/
         sub-control01_ses-postdrug_task-nback_bold.nii.gz
```

```
            sub-control01_ses-postdrug_task-nback_bold.json
            sub-control01_ses-postdrug_task-nback_events.tsv
            sub-control01_ses-postdrug_task-nback_physio.tsv.gz
            sub-control01_ses-postdrug_task-nback_physio.json
            sub-control01_ses-postdrug_task-nback_sbref.nii.gz
         fmap/
            sub-control01_ses-postdrug_phasediff.nii.gz
            sub-control01_ses-postdrug_phasediff.json
            sub-control01_ses-postdrug_magnitude1.nii.gz
   participants.tsv
   dataset_description.json
   README
   CHANGES
```

## Multi-site or multi-center studies

This version of the BIDS specification does not explicitly cover studies with data coming from multiple sites or multiple centers (such extension is planned in BIDS `2.0`. There are however ways to model your data without any loss in terms of metadata.

### Option 1: Treat each site/center as a separate dataset

The simplest way of dealing with multiple sites is to treat data from each site as a separate and independent BIDS dataset with a separate participants.tsv and other metadata files. This way you can feed each dataset individually to BIDS Apps and everything should just work.

### Option 2: Combining sites/centers into one dataset

Alternatively you can combine data from all sites into one dataset. To identify which site each subjects comes from you can add a `site` column in the `participants.tsv` file indicating the source site. This solution allows you to analyze all of the subjects together in one dataset. One caveat is that subjects from all sites will have to have unique labels. To enforce that and improve readability you can use a subject label prefix identifying the site. For example `sub-NUY001`, `sub-MIT002`, `sub-MPG002` and so on. Remember that hyphens and underscores are not allowed in subject labels.

# BIDS Extension Proposals

The BIDS specification can be extended in a backwards compatible way and will evolve over time. This is accomplished with BIDS Extension Proposals (BEPs), which are community-driven processes (see BEP guidelines Google Doc).

On the BIDS homepage you can find a list of extension proposals that are currently being worked on.

All changes that are not backwards compatible with the current BIDS specification will be implemented in BIDS `2.0`. See the corresponding GitHub repository.

# Appendix I: Contributors

Legend (source: https://allcontributors.org/docs/en/emoji-key)

| Emoji | Represents |
|---|---|
| 💬 | Answering Questions (on the mailing list, NeuroStars, GitHub, or in person, etc.) |
| 🐛 | Bug reports |
| 📝 | Blogposts |
| 💻 | Code |
| 🖋 | Content (separate from Blogposts, for example Website news) |
| 📖 | Documentation and specification |
| 🔣 | Data (example datasets) |
| 🎨 | Design |
| 💡 | Examples (for example datasets, use `Data`) |
| 📋 | Event Organizers |
| 💵 | Financial Support |
| 🔍 | Funding/Grant Finders |
| 🤔 | Ideas & Planning |
| 🚇 | Infrastructure (hosting, build-tools, etc.) |
| 🚧 | Maintenance of the BIDS standard |
| 🧑‍🏫 | Mentoring new contributors |
| 🔌 | Plugin/utility libraries |
| 📆 | Project management |
| 👀 | Reviewed Pull Requests |
| 🔧 | Tools |
| 🌍 | Translation |
| ⚠️ | Tests |
| ✅ | Tutorials |
| 📢 | Talks |
| 📓 | User testing (of new features, tools, etc.) |

| Emoji | Represents |
|---|---|
| 📹 | Videos |

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# Appendix II: Licenses

This section lists a number of common licenses for datasets and defines suggested abbreviations for use in the dataset metadata specifications.

Please note that this list only serves to provide some examples for possible licenses. The terms of any license should be consistent with the informed consent obtained from participants and any institutional limitations on distribution.

| Identifier | License name | Description |
|---|---|---|
| PD | Public Domain | No license required for any purpose; the work is not subject to copyright in any jurisdiction. |
| PDDL | Open Data Commons Public Domain Dedication and License | License to assign public domain like permissions without giving up the copyright. |
| CC0 | Creative Commons Zero 1.0 Universal. | Use this if you are a holder of copyright or database rights, and you wish to waive all your interests in your work worldwide. |

# Appendix III: Hierarchical Event Descriptors

Hierarchical Event Descriptors (HED) are a controlled vocabulary of terms describing events in a machine-actionable form so that algorithms can use the information without manual recoding. HED annotation can be used to describe any experimental events by combining information from the dataset's `_events.tsv` files and `_events.json` sidecars.

## HED annotations and vocabulary

A HED annotation consists of terms selected from a controlled hierarchical vocabulary (the HED schema). Individual terms are comma-separated and may be grouped using parentheses to indicate association. See https://www.hedtags.org/display_hed.html to view the HED schema and the HED documentation for additional resources.

Starting with HED version 8.0.0, HED allows users to annotate using individual terms or partial paths in the HED vocabulary (for example `Red` or `Visual-presentation`) rather than the full paths in the HED hierarchy ( `Property/Sensory-property/Sensory-attribute/Visual-attribute/Color/CSS-color/Red-color/Red` or `Property/Sensory-property/Sensory-presentation/Visual-presentation`).

HED specific tools MUST treat the short and long HED tag forms interchangeably, converting between the forms when necessary, based on the HED schema. Examples of test datasets using the various forms can be found in hed-examples/datasets on GitHub. Using the short form for tags is strongly RECOMMENDED whenever possible.

## Annotating events

Event-related data in BIDS appears in tab-separated value (`events.tsv`) files in various places in the dataset hierarchy (see Events).

`events.tsv` files MUST have `onset` and `duration` columns. Dataset curators MAY also include additional columns and define their meanings in associated JSON sidecar files (`events.json`).

Example: An excerpt from an `events.tsv` file containing three columns (`trial_type`, `response_time`, and `stim_file`) in addition to the required `onset` and `duration` columns.

```
onset   duration   trial_type   response_time stim_file
1.2     0.6        go           1.435         images/red_square.jpg
5.6     0.6        stop         1.739         images/blue_square.jpg
```

The `trial_type` column in the above example contains a limited number of distinct values (`go` and `stop`). This type of column is referred to as a categorical column, and the column's meaning can be annotated by assigning HED tags to describe each of these distinct values. The JSON sidecar provides a JSON object of annotations for these categorical values. That is, the object is a dictionary mapping the categorical values to corresponding HED annotations.

In contrast, the `response_time` and `stim_file` columns could potentially contain distinct values in every row. These columns are referred to as value columns and are annotated by creating a HED tag string to describe a general pattern for these values. The HED annotation for a value column must include a `#` placeholder, which dedicated HED tools MUST replace by the actual column value when the annotations are assembled for analysis.

Example: An accompanying `events.json` sidecar describing both categorical and value columns of the previous example. The `duration` column is also annotated as a value column.

```
{
  "Duration": {
    "LongName": "Image duration",
    "Description": "Duration of the image presentations",
    "Units": "s",
    "HED": "Duration/# s"
  },
  "trial_type": {
    "LongName": "Event category",
    "Description": "Indicator of type of action that is expected",
    "Levels": {
      "go": "A red square is displayed to indicate starting",
      "stop": "A blue square is displayed to indicate stopping"
    },
    "HED": {
          "go": "Sensory-event, Visual-presentation, ((Square, Blue),(Computer-screen, Center-of))",
          "stop": "Sensory-event, Visual-presentation, ((Square, Blue), (Computer-screen, Center-of))"
       }
   },
   "response_time": {
       "LongName": "Response time after stimulus",
       "Description": "Time from stimulus presentation until subject presses button",
       "Units": "ms",
       "HED": "(Delay/# ms, Agent-action, (Experiment-participant, (Press, Mouse-button))),"
   },
   "stim_file": {
       "LongName": "Stimulus filename",
       "Description": "Relative path of the stimulus image file",
       "HED": "Pathname/#"
   }
}
```

Dedicated HED tools MUST assemble an annotation for each event by concatenating the annotations for each column.

Example: The fully assembled annotation for the first event in the above `events.tsv` file with onset `1.2` (the first row) is:

```
Duration/0.6 s, Sensory-event, Visual-presentation,
((Square, Blue), (Computer-screen, Center-of)),
(Delay/1.435 ms, Agent-action,
(Experiment-participant, (Press, Mouse-button))),
Pathname/images/red_square.jpg
```

## Annotation using the `HED` column

Another tagging strategy is to annotate individual events directly by including a `HED` column in the `events.tsv` file. This approach is necessary when each event has annotations that are unique and do not fit into a standard set of patterns.

Some acquisition or presentation software systems directly write annotations during the experiment, and these MAY also be placed in the `HED` column of the `events.tsv` file.

Dedicated HED tools that assemble the full annotation for events treat MUST not distinguish between HED annotations extracted from `_events.json` sidecars and those appearing in the `HED` column of `_events.tsv` files. The HED strings from all sources are concatenated to form the final event annotations.

Annotations placed in sidecars are the RECOMMENDED way to annotate data using HED. These annnotations are preferred to those placed directly in the `HED` column, because they are simpler, more compact, more easily edited, and less prone to inconsistencies.

## HED and the BIDS inheritance principle

Most studies have event files whose columns contain categorical and numerical values that are similar across the recordings in the study. If possible, users should annotate these columns in a single `events.json` sidecar placed at the top level in the dataset.

If some recordings in the dataset have a column whose values deviate from a standard pattern, then the annotations for that column MUST be placed in sidecars located deeper in the dataset directory hierarchy. According to the BIDS Inheritance Principle, once a column key in a sidecar (that is, the column name found in the `events.tsv` files) is set, information about that column cannot be overridden by a sidecar appearing in a directory closer to the dataset root.

## HED schema versions

The HED vocabulary is specified by a HED schema, which delineates the allowed HED path strings. The version of HED used in tagging a dataset should be provided in the `HEDVersion` field of the `dataset_description.json` file located in the dataset root directory. This allows for a proper validation of the HED annotations (for example using the `bids-validator`).

Example: The following `dataset_description.json` file specifies that the `HED8.0.0.xml` file from the `hedxml` directory of the `hed-specification` repository on GitHub should be used to validate the study event annotations.

```
{
  "Name": "A great experiment",
  "BIDSVersion": "1.6.0",
  "HEDVersion": "8.0.0"
}
```

If you omit the `HEDVersion` field from the dataset description file, any present HED information will be validated using the latest version of the HED schema, which is bound to result in problems. Hence, it is strongly RECOMMENDED that the `HEDVersion` field be included when using HED in a BIDS dataset.

# Appendix IV: Entity table

This section compiles the entities (key-value pairs) described throughout this specification, and establishes a common order within a filename. For example, if a file has an acquisition and reconstruction label, the acquisition entity must precede the reconstruction entity. REQUIRED and OPTIONAL entities for a given file type are denoted; empty cells imply that entities MUST NOT be specified. Entity formats indicate whether the value is alphanumeric (`<label>`) or numeric (`<index>`).

A general introduction to entities is given in the section on filename structure, while entity definitions are in Appendix IX.

## Magnetic Resonance Imaging

| Entity | Subject | Session | Task | Acquisition | Contrast Enhancing Agent | Reconstruction | Phase-Encoding Direction | Run | Corresponding Modality | Echo | Flip Angle | Inversion Time | Magnetization Transfer | Part | Recording |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Format | `sub-<label>` | `sub-<label>` | `sub-<label>` | `sub-<label>` | `sub-<label>` | `sub-<label>` | `sub-<label>` | `sub-<label>` | `sub-<label>` | `sub-<label>` | `sub-<label>` | `sub-<label>` | `sub-<label>` | `sub-<label>` | `sub-<label>` |

| Entity | Subject | Session | Task | Acquisition | Contrast Enhancing Agent | Reconstruction | Phase-Encoding Direction | Run | Corresponding Modality | Echo | Flip Angle | Inversion Time | Magnetization Transfer | Part | Recording |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| anat(T1v T2w PDw T2starw FLAIR inplaneT1 inplaneT2 PDT2 angio T2star FLASH PD) | REQUIR | OPTION |  | OPTION | OPTION | OPTION |  | OPTION |  |  |  |  |  | OPTION |  |
| anat(T1map T2map T2starmap R1map R2map R2starmap PDmap MTRmap MTsat UNIT1 T1rho MWFmap MTVmap PDT2map Chimap S0map M0map) | REQUIRED | OPTIONAL |  | OPTIONAL | OPTIONAL | OPTIONAL |  | OPTIONAL |  |  |  |  |  |  |  |
| anat(defa | REQUIR | OPTION |  | OPTION | OPTION | OPTION |  | OPTION | OPTION |  |  |  |  |  |  |
| anat(MESE MEGRE) | REQUIRED | OPTIONAL |  | OPTIONAL | OPTIONAL | OPTIONAL |  | OPTIONAL |  | REQUIRED |  |  |  | OPTIONAL |  |
| anat(VF | REQUIR | OPTION |  | OPTION | OPTION | OPTION |  | OPTION |  | OPTION | REQUIR |  |  | OPTION |  |

| Entity | Subject | Session | Task | Acquisition | Contrast Enhancing Agent | Reconstruction | Phase-Encoding Direction | Run | Corresponding Modality | Echo | Flip Angle | Inversion Time | Magnetization Transfer | Part | Recording |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| anat(IRT1) | REQUIRED | OPTIONAL | | OPTIONAL | OPTIONAL | OPTIONAL | | OPTIONAL | | | | REQUIRED | | OPTIONAL | |
| anat(MP | REQUIR | OPTION. | | OPTION. | OPTION. | OPTION. | | OPTION. | | OPTION. | OPTION. | REQUIR | | OPTION. | |
| anat(MPM MTS) | REQUIRED | OPTIONAL | | OPTIONAL | OPTIONAL | OPTIONAL | | OPTIONAL | | OPTIONAL | REQUIRED | | REQUIRED | OPTIONAL | |
| anat(MT | REQUIR | OPTION. | | OPTION. | OPTION. | OPTION. | | OPTION. | | | | | REQUIR | OPTION. | |
| dwi(dwi sbref) | REQUIRED | OPTIONAL | | OPTIONAL | | | OPTIONAL | OPTIONAL | | | | | | OPTIONAL | |
| dwi(phys stim) | REQUIR | OPTION. | | OPTION. | | | OPTION. | OPTION. | | | | | | OPTION. | OPTIONAL |
| fmap(phasediff phase1 phase2 magnitude1 magnitude2 magnitude fieldmap) | REQUIRED | OPTIONAL | | OPTIONAL | | | | OPTIONAL | | | | | | | |
| fmap(epi m0scan) | REQUIR | OPTION. | | OPTION. | OPTION. | | REQUIR | OPTION. | | | | | | | |
| fmap(TB1DAM) | REQUIRED | OPTIONAL | | OPTIONAL | OPTIONAL | OPTIONAL | | OPTIONAL | | | REQUIRED | OPTIONAL | | OPTIONAL | |
| fmap(TB | REQUIR | OPTION. | | OPTION. | OPTION. | OPTION. | | OPTION. | | REQUIR | REQUIR | OPTION. | | OPTION. | |
| fmap(TB1AFI TB1TFL TB1RFM RB1COR) | REQUIRED | OPTIONAL | | OPTIONAL | OPTIONAL | OPTIONAL | | OPTIONAL | | OPTIONAL | OPTIONAL | OPTIONAL | | OPTIONAL | |
| fmap(TB | REQUIR | OPTION. | | OPTION. | OPTION. | OPTION. | | OPTION. | | OPTION. | REQUIR | REQUIR | | OPTION. | |
| fmap(TB1map RB1map) | REQUIRED | OPTIONAL | | OPTIONAL | OPTIONAL | OPTIONAL | | OPTIONAL | | | | | | | |
| func(bol cbv sbref) | REQUIR | OPTION. | REQUIR | OPTION. | OPTION. | OPTION. | OPTION. | OPTION. | | OPTION. | | | | OPTION. | |
| func(phase) | REQUIRED | OPTIONAL | REQUIRED | OPTIONAL | OPTIONAL | OPTIONAL | OPTIONAL | OPTIONAL | | OPTIONAL | | | | | |
| func(eve | REQUIR | OPTION. | REQUIR | OPTION. | OPTION. | OPTION. | OPTION. | OPTION. | | | | | | | |

| Entity | Subject | Session | Task | Acquisition | Contrast Enhancing Agent | Reconstruction | Phase-Encoding Direction | Run | Corresponding Modality | Echo | Flip Angle | Inversion Time | Magnetization Transfer | Part | Recording |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| func(physio stim) | REQUIRED | OPTIONAL | REQUIRED | OPTIONAL | OPTIONAL | OPTIONAL | OPTIONAL | OPTIONAL | | | | | | | OPTIONAL |
| perf(asl aslcontext m0scan) | REQUIR | OPTION | | OPTION | | OPTION | OPTION | OPTION | | | | | | | |
| perf(asllabeling) | REQUIRED | OPTIONAL | | OPTIONAL | | OPTIONAL | | OPTIONAL | | | | | | | |
| perf(phys stim) | REQUIR | OPTION | | OPTION | | OPTION | OPTION | OPTION | | | | | | | OPTIONAL |

## Biopotential Amplification (EEG and iEEG)

| Entity | Subject | Session | Task | Acquisition | Run | Space | Recording |
|---|---|---|---|---|---|---|---|
| Format | `sub-<label>` | `sub-<label>` | `sub-<label>` | `sub-<label>` | `sub-<label>` | `sub-<label>` | `sub-<label>` |
| eeg(coordsystem electrodes) | REQUIRED | OPTIONAL | | OPTIONAL | | OPTIONAL | |
| eeg(channels eeg events) | REQUIRED | OPTIONAL | REQUIRED | OPTIONAL | OPTIONAL | | |
| eeg(photo) | REQUIRED | OPTIONAL | | OPTIONAL | | | |
| eeg(physio stim) | REQUIRED | OPTIONAL | REQUIRED | OPTIONAL | OPTIONAL | | OPTIONAL |
| ieeg(coordsystem electrodes) | REQUIRED | OPTIONAL | | OPTIONAL | | OPTIONAL | |
| ieeg(channels events ieeg) | REQUIRED | OPTIONAL | REQUIRED | OPTIONAL | OPTIONAL | | |
| ieeg(photo) | REQUIRED | OPTIONAL | | OPTIONAL | | | |
| ieeg(physio stim) | REQUIRED | OPTIONAL | REQUIRED | OPTIONAL | OPTIONAL | | OPTIONAL |

## Magnetoencephalography (MEG)

| Entity | Subject | Session | Task | Acquisition | Run | Processed (on device) | Space | Split | Recording |
|---|---|---|---|---|---|---|---|---|---|
| Format | `sub-<label>` | `sub-<label>` | `sub-<label>` | `sub-<label>` | `sub-<label>` | `sub-<label>` | `sub-<label>` | `sub-<label>` | `sub-<label>` |
| meg(meg) | REQUIRED | OPTIONAL | REQUIRED | OPTIONAL | OPTIONAL | OPTIONAL | | OPTIONAL | |
| meg(meg) | REQUIRED | OPTIONAL | | REQUIRED | | | | | |
| meg(markers) | REQUIRED | OPTIONAL | OPTIONAL | OPTIONAL | | | OPTIONAL | | |
| meg(channels) | REQUIRED | OPTIONAL | REQUIRED | OPTIONAL | OPTIONAL | OPTIONAL | | | |
| meg(events) | REQUIRED | OPTIONAL | REQUIRED | OPTIONAL | OPTIONAL | | | | |
| meg(coordsyste headshape photo) | REQUIRED | OPTIONAL | | OPTIONAL | | | | | |
| meg(physio stim) | REQUIRED | OPTIONAL | REQUIRED | OPTIONAL | OPTIONAL | OPTIONAL | | | OPTIONAL |

## Positron Emission Tomography (PET)

| Entity | Subject | Session | Task | Tracer | Reconstruction | Run | Recording |
|---|---|---|---|---|---|---|---|
| Format | `sub-<label>` | `sub-<label>` | `sub-<label>` | `sub-<label>` | `sub-<label>` | `sub-<label>` | `sub-<label>` |
| pet(pet) | REQUIRED | OPTIONAL | OPTIONAL | OPTIONAL | OPTIONAL | OPTIONAL | |
| pet(blood) | REQUIRED | OPTIONAL | OPTIONAL | OPTIONAL | OPTIONAL | OPTIONAL | REQUIRED |
| pet(events) | REQUIRED | OPTIONAL | REQUIRED | OPTIONAL | OPTIONAL | OPTIONAL | |
| pet(physio stim) | REQUIRED | OPTIONAL | OPTIONAL | OPTIONAL | OPTIONAL | OPTIONAL | OPTIONAL |

## Behavioral Data

| Entity | Subject | Session | Task | Acquisition | Run | Recording |
|---|---|---|---|---|---|---|
| Format | `sub-<label>` | `sub-<label>` | `sub-<label>` | `sub-<label>` | `sub-<label>` | `sub-<label>` |
| beh(stim physio) | REQUIRED | OPTIONAL | REQUIRED | OPTIONAL | OPTIONAL | OPTIONAL |
| beh(events beh) | REQUIRED | OPTIONAL | REQUIRED | OPTIONAL | OPTIONAL | |

## Microscopy

| Entity | Subject | Session | Sample | Acquisition | Stain | Run | Chunk |
|---|---|---|---|---|---|---|---|
| Format | `sub-<label>` | `sub-<label>` | `sub-<label>` | `sub-<label>` | `sub-<label>` | `sub-<label>` | `sub-<label>` |
| micr(TEM SEM uCT BF DF PC DIC FLUO CONF PLI CARS 2PE MPE SR NLO OCT SPIM) | REQUIRED | OPTIONAL | REQUIRED | OPTIONAL | OPTIONAL | OPTIONAL | OPTIONAL |
| micr(photo) | REQUIRED | OPTIONAL | REQUIRED | OPTIONAL | | | |

# Appendix V: Units

As described in the Units, the specification of units SHOULD follow the International System of Units (SI, abbreviated from the French Système international (d'unités)).

The CMIXF-12 convention for encoding units is RECOMMENDED to achieve maximum portability and limited variability of representation. If a CMIXF-12 representation of a unit is not possible, the unit can be declared as custom units and defined in an accompanying JSON file, as described in the units section. Earlier versions of the BIDS standard listed the following Unicode symbols, and these are still included for backwards compatibility:

1. `U+03BC` (μ) or `U+00B5` (µ)
2. `U+03A9` (Ω) or `U+2126` (Ω)
3. `U+00B0` (°)

Note that for the first two entries in this list, two characters are permissible for each, but the first character in each entry is preferred, per Unicode rules (see the section on "Duplicated Characters" on page 11 in the unicode report).

It is RECOMMENDED that units be CMIXF-12 compliant or among these five Unicode characters. Please note the appropriate upper- or lower- casing when using CMIXF-12.

For cases that are unspecified by this appendix or the units section, the CMIXF-12 convention applies.

You can use the cmixf Python package to check whether your formatting is compliant.

Examples for CMIXF-12 (including the five unicode symbols mentioned above):

1. Different formatting of "micro Volts":
   (a) RECOMMENDED: `uV` or `µV`
   (b) NOT RECOMMENDED: `microV`, `µvolt` or `1e-6V`
2. Combinations of units:
   (a) RECOMMENDED: `V/us` for the Slew rate
   (b) NOT RECOMMENDED: `volts per microsecond`

## Unit table

| Unit name | Unit symbol | Quantity name |
|---|---|---|
| metre | m | length |
| kilogram | kg | mass |
| litre (liter) | L | volume |
| second | s | time |
| ampere | A | electric current |
| kelvin | K | thermodynamic temperature |
| mole | mol | amount of substance |
| candela | cd | luminous intensity |
| radian | rad | angle |
| steradian | sr | solid angle |
| hertz | Hz | frequency |
| newton | N | force, weight |
| pascal | Pa | pressure, stress |
| joule | J | energy, work, heat |
| watt | W | power, radiant flux |
| coulomb | C | electric charge or quantity of electricity |
| volt | V | voltage (electrical potential), emf |
| farad | F | capacitance |
| ohm | Ohm | resistance, impedance, reactance |
| siemens | S | electrical conductance |
| weber | Wb | magnetic flux |
| tesla | T | magnetic flux density |
| henry | H | inductance |
| degree Celsius | oC | temperature relative to 273.15 K |
| lumen | lm | luminous flux |
| lux | lx | illuminance |
| becquerel | Bq | radioactivity (decays per unit time) |
| gray | Gy | absorbed dose (of ionizing radiation) |
| sievert | Sv | equivalent dose (of ionizing radiation) |
| katal | kat | catalytic activity |

## Prefixes

### Multiples

| Prefix name | Prefix symbol | Factor |
|---|---|---|
| deca | da | 101 |
| hecto | h | 102 |
| kilo | k | 103 |
| mega | M | 106 |
| giga | G | 109 |
| tera | T | 1012 |
| peta | P | 1015 |
| exa | E | 1018 |
| zetta | Z | 1021 |
| yotta | Y | 1024 |

## Submultiples

| Prefix name | Prefix symbol | Factor |
|---|---|---|
| deci | d | 10-1 |
| centi | c | 10-2 |
| milli | m | 10-3 |
| micro | u | 10-6 |
| nano | n | 10-9 |
| pico | p | 10-12 |
| femto | f | 10-15 |
| atto | a | 10-18 |
| zepto | z | 10-21 |
| yocto | y | 10-24 |

# Appendix VI: MEG file formats

Each MEG system brand has specific file organization and data formats. RECOMMENDED values for `manufacturer_specific_extensions`:

| Value | Description |
|---|---|
| `ctf` | CTF (folder with `.ds` extension) |
| `fif` | Neuromag / Elekta / MEGIN and BabyMEG (file with extension `.fif`) |
| `4d` | BTi / 4D Neuroimaging (folder containing multiple files without extensions) |
| `kit` | KIT / Yokogawa / Ricoh (file with extension `.sqd`, `.con`, `.raw`, `.ave` or `.mrk`) |
| `kdf` | KRISS (file with extension `.kdf`) |
| `itab` | Chieti system (file with extension `.raw` and `.mhd`) |

Below are specifications for each system brand.

## CTF

Each experimental run with a CTF system yields a folder with a `.ds` extension, containing several files. The OPTIONAL digitized positions of the head points are usually stored in a separate `.pos` file, not necessarily within the `.ds` folder.

```
[sub-<label>[_ses-<label>]_headshape.pos]
sub-<label>[_ses-<label>]_task-<label>[_run-<index>]_meg.ds>
```

CTF's data storage is therefore via directories containing multiple files. The files contained within a `.ds` directory are named such that they match the parent directory, but preserve the original file extension (for example, `.meg4`, `.res4`). The renaming of CTF datasets SHOULD be done with a specialized software such as the CTF newDs command-line application or MNE-BIDS.

Example:

```
sub-control01/
    ses-001/
```

```
      sub-control01_ses-001_scans.tsv
      meg/
         sub-control01_ses-001_coordsystem.json
         sub-control01_ses-001_headshape.pos
         sub-control01_ses-001_task-rest_run-01_meg.ds/
         sub-control01_ses-001_task-rest_run-01_meg.json
         sub-control01_ses-001_task-rest_run-01_channels.tsv
```

To learn more about CTF's data organization: https://www.fieldtriptoolbox.org/getting_started/ctf

## Neuromag/Elekta/MEGIN

Neuromag/Elekta/MEGIN and Tristan Technologies BabyMEG data is stored as FIFF files with the extension `.fif`. The digitized positions of the head points are saved inside the FIFF file along with the MEG data, with typically no `_headshape` file.

`sub-<label>[_ses-<label>]_task-<label>[_run-<index>]_meg.fif`

### Cross-talk and fine-calibration files

In case internal active shielding (IAS) was used during acquisition, raw FIFF files need to be processed using Maxwell filtering (signal-space separation, SSS) to make the data usable. To this end, two specific files are needed: The cross-talk file, and the fine-calibration file, both of which are produced by the MaxFilter software and the work of the Neuromag/Elekta/MEGIN engineers during maintenance of the MEG acquisition system. Both files are thus specific to the site of recording and may change in the process of regular system maintenance.

In BIDS, the cross-talk and fine-calibration files are shared unmodified, including their original extensions (`.fif` for cross-talk and `.dat` for fine-calibration), but with BIDS file naming convention and by using the `acq` entity.

- cross-talk file template: `sub-<label>[_ses-<label>]_acq-crosstalk_meg.fif`
- fine-calibration file template: `sub-<label>[_ses-<label>]_acq-calibration_meg.dat`

Note that cross-talk files MUST be denoted using `acq-crosstalk` and fine-calibration files MUST be denoted using `acq-calibration`.

The cross-talk and fine-calibration data MUST be stored in the subject-level `meg` folder, which may be nested inside a `ses-<label>` folder, as shown in the following examples.

Example with single session (omitted session folder)

```
sub-01/
   meg/
      sub-01_coordsystem.json
      sub-01_task-rest_meg.fif
      sub-01_task-rest_meg.json
      sub-01_task-rest_channels.tsv
```

```
      sub-01_acq-crosstalk_meg.fif
      sub-01_acq-calibration_meg.dat
sub-02/
   meg/
      sub-02_coordsystem.json
      sub-02_task-rest_meg.fif
      sub-02_task-rest_meg.json
      sub-02_task-rest_channels.tsv
      sub-02_acq-crosstalk_meg.fif
      sub-02_acq-calibration_meg.dat
```

Example with multiple sessions

```
sub-01/
   ses-01/
      sub-01_ses-01_scans.tsv
      meg/
         sub-01_ses-01_coordsystem.json
         sub-01_ses-01_task-rest_run-01_meg.fif
         sub-01_ses-01_task-rest_run-01_meg.json
         sub-01_ses-01_task-rest_run-01_channels.tsv
         sub-01_ses-01_acq-crosstalk_meg.fif
         sub-01_ses-01_acq-calibration_meg.dat
   ses-02/
      sub-01_ses-02_scans.tsv
      meg/
         sub-01_ses-02_coordsystem.json
         sub-01_ses-02_task-rest_run-01_meg.fif
         sub-01_ses-02_task-rest_run-01_meg.json
         sub-01_ses-02_task-rest_run-01_channels.tsv
         sub-01_ses-02_acq-crosstalk_meg.fif
         sub-01_ses-02_acq-calibration_meg.dat
```

### Sharing FIFF data after signal-space separation (SSS)

After applying SSS (for example, by using the MaxFilter software), files SHOULD be renamed with the corresponding label (for example, `proc-sss`) and placed in a `derivatives` subfolder.

Example:

```
sub-control01/
   ses-001/
```

```
      meg/
         sub-control01_ses-001_task-rest_run-01_proc-sss_meg.fif
         sub-control01_ses-001_task-rest_run-01_proc-sss_meg.json
```

### Split files

In the case of long data recordings that exceed a file size of 2Gb, the `.fif` files are conventionally split into multiple parts. For example:

```
some_file.fif
some_file-1.fif
```

Each of these files has an internal pointer to the next file. This is important when renaming these split recordings to the BIDS convention. Instead of a simple renaming, files should be read in and saved under their new names with dedicated tools like MNE, which will ensure that not only the filenames, but also the internal file pointers will be updated.

It is RECOMMENDED that FIFF files with multiple parts use the `split-<index>` entity to indicate each part.

If there are multiple parts of a recording and the optional `scans.tsv` is provided, remember to list all files separately in `scans.tsv` and that the entries for the `acq_time` column in `scans.tsv` MUST all be identical, as described in Scans file.

Example:

```
sub-control01/
   ses-001/
      meg/
         sub-control01_ses-001_task-rest_run-01_split-01_meg.fif
         sub-control01_ses-001_task-rest_run-01_split-02_meg.fif
```

More information can be found under the following links:

- Neuromag/Elekta/MEGIN data organization
- BabyMEG

### Recording dates in `.fif` files

It is important to note that recording dates in `.fif` files are represented as `int32` format seconds since (or before) the Epoch (`1970-01-01T00:00:00.000000` UTC). Integers in `int32` format can encode values from -2,147,483,647 to +2,147,483,647. Due to this representation, the Neuromag/Elekta/MEGIN file format for MEG (`.fif`) does not support recording dates earlier than `1901-12-13T08:45:53.000000` UTC or later than `2038-01-19T03:14:07.000000` UTC.

## BTi/4D neuroimaging

Each experimental run on a 4D neuroimaging/BTi system results in a folder containing multiple files without extensions.

```
[sub-<label>[_ses-<label>]_headshape.pos]
sub-<label>[_ses-<label>]_task-<label>[_run-<index>]_meg>
```

One SHOULD rename/create a parent run-specific directory and keep the original files for each run inside (for example, `c,rfhp0.1Hz`, `config` and `hs_file`).

Example:

```
sub-control01/
   ses-001/
      sub-control01_ses-001_scans.tsv
      meg/
         sub-control01_ses-001_coordsystem.json
         sub-control01_ses-001_headshape.pos
         sub-control01_ses-001_task-rest_run-01_meg/
         sub-control01_ses-001_task-rest_run-01_meg.json
         sub-control01_ses-001_task-rest_run-01_channels.tsv
```

Where:

```
sub-control01_ses-001_task-rest_run-01_meg/
   config
   hs_file
   e,rfhp1.0Hz.COH
   c,rfDC
```

More about the 4D neuroimaging/BTi data organization at: https://www.fieldtriptoolbox.org/getting_started/bti

## KIT/Yokogawa/Ricoh

Each experimental run on a KIT/Yokogawa/Ricoh system yields a raw file with either `.sqd` or `.con` extension, and with its associated marker coil file(s) with either `.sqd` or `.mrk` extension. The marker coil file(s) contain coil positions in the acquisition system's native space. Head points and marker points in head space are acquired using third-party hardware.

Example:

```
sub-control01/
   ses-001/
      sub-control01_ses-001_scans.tsv
      meg/
         sub-control01_ses-001_coordsystem.json
         sub-control01_ses-001_headshape.txt
         sub-control01_ses-001_task-rest_run-01_meg
         sub-control01_ses-001_task-rest_run-01_meg.json
         sub-control01_ses-001_task-rest_run-01_channels.tsv
         sub-control01_ses-001_task-rest[_acq-<label>]_run-01_markers.<mrk,sqd>
         sub-control01_ses-001_task-rest_run-01_meg.<con,sqd>
```

To understand why both `.sqd` and `.con`, as well as both `.sqd` and `.mrk` are valid extensions, we provide a brief historical perspective on the evolution of the data format: The original extension for KIT/Yokogawa/Ricoh continuous data was `.sqd`. This was later modernized to `.con` (to denote ”continuous”). However, to preserve backwards compatibility, `.sqd` is still a valid extension for the raw, continuous data file. The original extension for KIT/Yokogawa/Ricoh marker files was `.sqd` as well. That lead to the ambiguous situation where both the raw data and the marker file(s) could end on `.sqd`. To distinguish between continuous data and marker file(s), the internal header of the files needed to be read first. For this reason, the marker file extension was later modernized to `.mrk` to better disambiguate files. However again, to preserve backwards compatibility, `.sqd` is still a valid extension for the marker file(s).

If there are multiple files with marker coils, the marker files must have the `acq-<label>` parameter and no more that two marker files may be associated with one raw data file. While the acquisition parameter can take any value, it is RECOMMENDED that if the two marker measurements occur before and after the raw data acquisition, `pre` and `post` are used to differentiate the two situations.

More about the KIT/Yokogawa/Ricoh data organization at: https://www.fieldtriptoolbox.org/getting_started/yokogawa

## KRISS

Each experimental run on the KRISS system produces a file with extension `.kdf`. Additional files can be available in the same folder: the digitized positions of the head points (`\_digitizer.txt`), the position of the center of the MEG coils (`.chn`) and the event markers (`.trg`).

```
[sub-<label>[_ses-<label>]_headshape.txt]
sub-<label>[_ses-<label>]_task-<label>[_run-<index>]_meg.kdf
sub-<label>[_ses-<label>]_task-<label>[_run-<index>]_meg.chn
sub-<label>[_ses-<label>]_task-<label>[_run-<index>]_meg.trg
sub-<label>[_ses-<label>]_task-<label>[_acq-<label>]_digitizer.txt
```

Example:

```
sub-control01/
   ses-001/
      sub-control01_ses-001_scans.tsv
      meg/
         sub-control01_ses-001_coordsystem.json
         sub-control01_ses-001_headshape.txt
         sub-control01_ses-001_task-rest_run-01_meg
         sub-control01_ses-001_task-rest_run-01_meg.json
         sub-control01_ses-001_task-rest_run-01_channels.tsv
         sub-control01_ses-001_task-rest_run-01_meg.chn
         sub-control01_ses-001_task-rest_run-01_meg.kdf
         sub-control01_ses-001_task-rest_run-01_meg.trg
         sub-control01_ses-001_task-rest_digitizer.txt
```

## ITAB

Each experimental run on a ITAB-ARGOS153 system yields a raw (`.raw`) data file plus an associated binary header file (`.mhd`). The raw data file has an ASCII header that contains detailed information about the data acquisition system, followed by binary data. The associated binary header file contains part of the information from the ASCII header, specifically the one needed to process data, plus other information on offline preprocessing performed after data acquisition (for example, sensor position relative to subject's head, head markers, stimulus information).

Example:

```
sub-control01/
   ses-001/
      meg/
         sub-control01_ses-001_coordsystem.json
         sub-control01_ses-001_headshape.txt
         sub-control01_ses-001_task-rest_run-01_meg
         sub-control01_ses-001_task-rest_run-01_meg.json
         sub-control01_ses-001_task-rest_run-01_channels.tsv
         sub-control01_ses-001_task-rest_run-01_meg.raw
         sub-control01_ses-001_task-rest_run-01_meg.raw.mhd
```

## Aalto MEG–MRI

For stand-alone MEG data, the Aalto hybrid device uses the standard `.fif` data format and follows the conventions of Elekta/Neuromag as described above. The `.fif` files may contain unreconstructed MRI data. The inclusion of MRI data and information for accurate reconstruction will be fully standardized at a later stage.

# Appendix VII: MEG systems

Preferred names of MEG systems comprise restricted keywords for Manufacturer field in the `*_meg.json` file:

- `CTF`
- `Neuromag/Elekta/Megin`
- `BTi/4D`
- `KIT/Yokogawa/Ricoh`
- `KRISS`
- `ITAB`
- `Aalto/MEG-MRI`
- `Other`

Restricted keywords for ManufacturersModelName field in the `*_meg.json` file:

| System Model Name | Manufacturer | Details |
|---|---|---|
| CTF-64 | CTF | |
| CTF-151 | CTF | https://www.ctf.com/products |
| CTF-275 | CTF | CTF-275: OMEGA 2000 |
| Neuromag-122 | Neuromag/Elekta/Megin | |
| ElektaVectorview | Neuromag/Elekta/Megin | 102 magnetometers + 204 planar gradiometers |
| ElektaTRIUX | Neuromag/Elekta/Megin | https://www.elekta.com/diagnostic-solutions/ |
| 4D-Magnes-WH2500 | BTi/4D | |
| 4D-Magnes-WH3600 | BTi/4D | |
| KIT-157 | KIT/Yokogawa | |
| KIT-160 | KIT/Yokogawa | |
| KIT-208 | KIT/Yokogawa | |
| ITAB-ARGOS153 | ITAB | |
| Aalto-MEG-MRI-YYYY/MM | Aalto/MEG-MRI | YYYY-MM (year, month; or major version) |

# Appendix VIII: Coordinate systems

## Introduction

To interpret a coordinate (x, y, z), it is required that you know (1) relative to which origin the coordinate is expressed, (2) the interpretation of the three axes, and (3) the units in which the numbers are expressed. This information is sometimes called the coordinate system.

These letters help describe the coordinate system definition:

- A/P means anterior/posterior
- L/R means left/right
- S/I means superior/inferior

For example: `RAS` means that the first dimension (X) points towards the right hand side of the head, the second dimension (Y) points towards the Anterior aspect of the head, and the third dimension (Z) points towards the top of the head. The directions are considered to be from the subject's perspective. For example, in the `RAS` coordinate system, a point to the subject's left will have a negative `x` value.

Besides coordinate systems, defined by their origin and direction of the axes, BIDS defines ”spaces” as an artificial frame of reference, created to describe different anatomies in a unifying manner (see for example, doi:10.1016/j.neuroimage.2012.01.024).

The ”space” and all coordinates expressed in this space are by design a transformation of the real world geometry, and nearly always different from the individual subject space that it stems from. An example is the Talairach-Tournoux space, which is constructed by piecewise linear scaling of an individual's brain to that of the Talairach-Tournoux 1988 atlas. In the Talairach-Tournoux space, the origin of the coordinate system is at the AC and units are expressed in mm.

The coordinate systems below all relate to neuroscience and therefore to the head or brain coordinates. $Please be aware that all data acquisition starts with ”device coordinates” (scanner), which does not have to be identical to the initial ”file format coordinates” (DICOM), which are again different from the ”head” coordinates (for example, NIFTI). Not only do device coordinate vary between hardware manufacturers, but also the head coordinates differ, mostly due to different conventions used in specific software packages developed by different (commercial or academic) groups.

# Coordinate Systems applicable to MEG, EEG, and iEEG

Generally, across the MEG, EEG, and iEEG modalities, the first two pieces of information for a coordinate system (origin and orientation) are specified in `<CoordSysType>CoordinateSystem`. The third piece of information for a coordinate system (units) are specified in `<CoordSysType>CoordinateUnits`. Here, `<CoordSysType>` can be one of the following, depending on the data that is supposed to be documented:

- `MEG`
- `EEG`
- `iEEG`
- `Fiducials`
- `AnatomicalLandmark`
- `HeadCoil`
- `DigitizedHeadPoints`

Allowed values for the `<CoordSysType>CoordinateSystem` field come from a list of restricted keywords, as listed in the sections below.

Note that `Fiducials`, `AnatomicalLandmark`, `HeadCoil`, and `DigitizedHeadPoints` `CoordSysType`s share the restricted keywords with the data modality they are shared with. For example, if an `AnatomicalLandmark` field is shared as part of an EEG dataset, the EEG-specific coordinate systems apply. However, if it is shared as part of an MEG dataset, the MEG-specific coordinate systems apply.

If no value from the list of restricted keywords fits, there is always the option to specify the value as follows:

- `Other`: Use this for other coordinate systems and specify all required details in the `<CoordSysType>CoordinateSystemDescription` field

If you believe a specific coordinate system should be added to the list of restricted keywords for MEG, EEG, or iEEG, please open a new issue on the bids-standard/bids-specification GitHub repository.

Note that the short descriptions below may not capture all details. For detailed descriptions of the coordinate systems below, please see the FieldTrip webpage.

## Commonly used anatomical landmarks in MEG, EEG, and iEEG research

In the documentation below we refer to anatomical landmarks such as the Left Pre Auricular point (LPA) and the Right Pre Auricular point (RPA), or the left and right Helix-Tragus Junction (LHJ, RHJ).

These anatomical landmarks are commonly used in MEG, EEG, and iEEG research to define coordinate systems that capture digitized sensor positions.

More information can be obtained from the FieldTrip webpage.

- FAQ: LPA and RPA
- FAQ: Beyond LPA and RPA

## MEG Specific Coordinate Systems

Restricted keywords for the `<CoordSysType>CoordinateSystem` field in the `coordinatesystem.json` file for MEG datasets:

- `CTF`: ALS orientation and the origin between the ears

- `ElektaNeuromag`: RAS orientation and the origin between the ears
- `4DBti`: ALS orientation and the origin between the ears
- `KitYokogawa`: ALS orientation and the origin between the ears
- `ChietiItab`: RAS orientation and the origin between the ears
- Any keyword from the list of Standard template identifiers

In the case that MEG was recorded simultaneously with EEG, the restricted keywords for EEG specific coordinate systems can also be applied to MEG:

- `CapTrak`
- `EEGLAB`
- `EEGLAB-HJ`

## EEG Specific Coordinate Systems

Restricted keywords for the `<CoordSysType>CoordinateSystem` field in the `coordsystem.json` file for EEG datasets:

- `CapTrak`: RAS orientation and the origin approximately between LPA and RPA
- `EEGLAB`: ALS orientation and the origin exactly between LPA and RPA. For more information, see the EEGLAB wiki page.
- `EEGLAB-HJ`: ALS orientation and the origin exactly between LHJ and RHJ. For more information, see the EEGLAB wiki page.
- Any keyword from the list of Standard template identifiers

In the case that EEG was recorded simultaneously with MEG, the restricted keywords for MEG specific coordinate systems can also be applied to EEG:

- `CTF`
- `ElektaNeuromag`
- `4DBti`
- `KitYokogawa`
- `ChietiItab`

## iEEG Specific Coordinate Systems

Restricted keywords for the `<CoordSysType>CoordinateSystem` field in the `coordsystem.json` file for iEEG datasets:

- `Pixels`: If electrodes are localized in 2D space (only x and y are specified and z is n/a), then the positions in this file must correspond to the locations expressed in pixels on the photo/drawing/rendering of the electrodes on the brain. In this case, coordinates must be (row,column) pairs, with (0,0) corresponding to the upper left pixel and (N,0) corresponding to the lower left pixel.
- `ACPC`: The origin of the coordinate system is at the Anterior Commissure and the negative y-axis is passing through the Posterior Commissure. The positive z-axis is passing through a mid-hemispheric point in the superior direction. The anatomical landmarks are determined in the individual's anatomical scan and no scaling or deformations have been applied to the individual's anatomical scan. For more information, see the ACPC site on the FieldTrip toolbox wiki.
- `ScanRAS`: The origin of the coordinate system is the center of the gradient coil for the corresponding T1w image of the subject, and the x-axis increases left to right, the y-axis increases posterior to anterior and the z-axis increases inferior to superior. For more information see the Nipy Documentation. It is strongly encouraged

to align the subject's T1w to ACPC so that the `ACPC` coordinate system can be used. If the subject's T1w in the BIDS dataset is not aligned to ACPC, `ScanRAS` should be used.

- Any keyword from the list of Standard template identifiers

## Image-based Coordinate Systems

The transformation of the real world geometry to an artificial frame of reference is described in `<CoordSysType>CoordinateSystem`. Unless otherwise specified below, the origin is at the AC and the orientation of the axes is RAS. Unless specified explicitly in the sidecar file in the `<CoordSysType>CoordinateUnits` field, the units are assumed to be mm.

### Standard template identifiers

| Coordinate System | Description | Used by | Reference |
|---|---|---|---|
| ICBM452AirSpace | Reference space defined by the "average of 452 T1-weighted MRIs of normal young adult brains" with "linear transforms of the subjects into the atlas space using a 12-parameter affine transformation" | | https://www.loni.usc.edu/research/atlases |
| ICBM452Warp5Space | Reference space defined by the "average of 452 T1-weighted MRIs of normal young adult brains" "based on a 5th order polynomial transformation into the atlas space" | | https://www.loni.usc.edu/research/atlases |
| IXI549Space | Reference space defined by the average of the "549 (...) subjects from the IXI dataset" linearly transformed to ICBM MNI 452. | SPM12 | https://brain-development.org/ |
| fsaverage | The `fsaverage` is a dual template providing both volumetric and surface coordinates references. The volumetric template corresponds to a FreeSurfer variant of `MNI305` space. The `fsaverage` atlas also defines a surface reference system (formerly described as fsaverage[3\|4\|5\|6\|sym]). | Freesurfer | |

| Coordinate System | Description | Used by | Reference |
|---|---|---|---|
| fsaverageSym | The `fsaverage` is a dual template providing both volumetric and surface coordinates references. The volumetric template corresponds to a FreeSurfer variant of `MNI305` space. The `fsaverageSym` atlas also defines a symmetric surface reference system (formerly described as `fsaveragesym`). | Freesurfer | |
| fsLR | The `fsLR` is a dual template providing both volumetric and surface coordinates references. The volumetric template corresponds to `MNI152NLin6Asym`. Surface templates are given at several sampling densities: 164k (used by HCP pipelines for 3T and 7T anatomical analysis), 59k (used by HCP pipelines for 7T MRI bold and DWI analysis), 32k (used by HCP pipelines for 3T MRI bold and DWI analysis), or 4k (used by HCP pipelines for MEG analysis) fsaverage_LR surface reconstructed from the T1w image. | Freesurfer | |
| MNIColin27 | Average of 27 T1 scans of a single subject | SPM96 | https://www.bic.mni.mcgill.ca/ServicesAtlases/Colin27Highres |
| MNI152Lin | Also known as ICBM (version with linear coregistration) | SPM99 to SPM8 | https://www.bic.mni.mcgill.ca/ServicesAtlases/ICBM152Lin |
| MNI152NLin2009[a-c][Sym\|Asym] | Also known as ICBM (non-linear coregistration with 40 iterations, released in 2009). It comes in either three different flavours each in symmetric or asymmetric version. | DARTEL toolbox in SPM12b | https://www.bic.mni.mcgill.ca/ServicesAtlases/ICBM152NLin2009 |
| MNI152NLin6Sym | Also known as symmetric ICBM 6th generation (non-linear coregistration). | FSL | https://www.bic.mni.mcgill.ca/ServicesAtlases/ICBM152NLin6 |
| MNI152NLin6ASym | A variation of `MNI152NLin6Sym` built by A. Janke that is released as the MNI template of FSL. Volumetric templates included with HCP-Pipelines correspond to this template too. | HCP-Pipelines | doi:10.1016/j.neuroimage.2012.01.024 |

| Coordinate System | Description | Used by | Reference |
|---|---|---|---|
| MNI305 | Also known as avg305. | | |
| NIHPD | Pediatric templates generated from the NIHPD sample. Available for different age groups (4.5–18.5 y.o., 4.5–8.5 y.o., 7–11 y.o., 7.5–13.5 y.o., 10–14 y.o., 13–18.5 y.o. This template also comes in either -symmetric or -asymmetric flavor. | | https://www.bic.mni.mcgill.ca/ServicesAtlases/NIHPD-obj1 |
| OASIS30AntsOASISAnts | | | https://figshare.com/articles/ANTs_ANTsR_Brain_Templates/915436 |
| OASIS30Atropos | | | https://mindboggle.info/data.html |
| Talairach | Piecewise linear scaling of the brain is implemented as described in TT88. | | http://talairach.org/ |
| UNCInfant | Infant Brain Atlases from Neonates to 1- and 2-year-olds. | | https://www.nitrc.org/projects/pediatricatlas |

The following template identifiers are retained for backwards compatibility of BIDS implementations. However, their use is DEPRECATED.

| Coordinate System | Description | RECOMMENDED alternative identifier |
|---|---|---|
| fsaverage[3\|4\|5\|6\|sym] | Images were sampled to the FreeSurfer surface reconstructed from the subject’s T1w image, and registered to an fsaverage template | fsaverage[Sym] |
| UNCInfant[0\|1\|2]V[21\|22\|23] | Infant Brain Atlases from Neonates to 1- and 2-year-olds. https://www.nitrc.org/projects/pediatricatlas | UNCInfant |

## Nonstandard coordinate system identifiers

The following template identifiers are RECOMMENDED for individual- and study-specific reference spaces. In order for these spaces to be interpretable, `SpatialReference` metadata MUST be provided, as described in Common file level metadata fields.

In the case of multiple study templates, additional names may need to be defined.

| Coordinate System | Description |
|---|---|
| individual | Participant specific anatomical space (for example derived from T1w and/or T2w images). This coordinate system requires specifying an additional, participant-specific file to be fully defined. In context of surfaces this space has been referred to as `fsnative`. |
| study | Custom space defined using a group/study-specific template. This coordinate system requires specifying an additional file to be fully defined. |

## Non-template coordinate system identifiers

The `scanner` coordinate system is implicit and assumed by default if the derivative filename does not define any `space-<label>`. Please note that `space-scanner` SHOULD NOT be used, it is mentioned in this specification to make its existence explicit.

| Coordinate System | Description |
|---|---|
| scanner | The intrinsic coordinate system of the original image (the first entry of `RawSources`) after reconstruction and conversion to NIfTI or equivalent for the case of surfaces and dual volume/surface files. |

# Appendix IX: Entities

This section compiles the entities (key-value pairs) described throughout this specification, and describes each.

A general introduction to entities is given in the section on filename structure.

The ordering of entities, and whether each is OPTIONAL, REQUIRED, or MUST NOT be specified for a given file type, is specified in the Entity Table.

## sub

Full name: Subject

Format: `sub-<label>`

Definition: A person or animal participating in the study.

## ses

Full name: Session

Format: `ses-<label>`

Definition: A logical grouping of neuroimaging and behavioral data consistent across subjects. Session can (but doesn't have to) be synonymous to a visit in a longitudinal study. In general, subjects will stay in the scanner during one session. However, for example, if a subject has to leave the scanner room and then be re-positioned on the scanner bed, the set of MRI acquisitions will still be considered as a session and match sessions acquired in other subjects. Similarly, in situations where different data types are obtained over several visits (for example fMRI on one day followed by DWI the day after) those can be grouped in one session. Defining multiple sessions is appropriate when several identical or similar data acquisitions are planned and performed on all -or most- subjects, often in the case of some intervention between sessions (for example, training).

## sample

Full name: Sample

Format: `sample-<label>`

Definition: A sample pertaining to a subject such as tissue, primary cell or cell-free sample. The `sample-<label>` key/value pair is used to distinguish between different samples from the same subject. The label MUST be unique per subject and is RECOMMENDED to be unique throughout the dataset.

## task

Full name: Task

Format: `task-<label>`

Definition: Each task has a unique label that MUST only consist of letters and/or numbers (other characters, including spaces and underscores, are not allowed). Those labels MUST be consistent across subjects and sessions.

## acq

Full name: Acquisition

Format: `acq-<label>`

Definition: The `acq-<label>` key/value pair corresponds to a custom label the user MAY use to distinguish a different set of parameters used for acquiring the same modality. For example this should be used when a study includes two T1w images - one full brain low resolution and one restricted field of view but high resolution. In such case two files could have the following names: `sub-01_acq-highres_T1w.nii.gz` and `sub-01_acq-lowres_T1w.nii.gz`, however the user is free to choose any other label than `highres` and `lowres` as long as they are consistent across subjects and sessions. In case different sequences are used to record the same modality (for example, `RARE` and `FLASH` for T1w) this field can also be used to make that distinction. At what level of detail to make the distinction (for example, just between `RARE` and `FLASH`, or between `RARE`, `FLASH`, and `FLASHsubsampled`) remains at the discretion of the researcher.

## ce

Full name: Contrast Enhancing Agent

Format: `ce-<label>`

Definition: The `ce-<label>` key/value can be used to distinguish sequences using different contrast enhanced images. The label is the name of the contrast agent. The key `"ContrastBolusIngredient"` MAY also be added in the JSON file, with the same label.

## trc

Full name: Tracer

Format: `trc-<label>`

Definition: The `trc-<label>` key/value can be used to distinguish sequences using different tracers. The key `"TracerName"` MUST also be included in the associated JSON file, although the label may be different.

## stain

Full name: Stain

Format: `stain-<label>`

Definition: The `stain-<label>` key/pair values can be used to distinguish image files from the same sample using different stains or antibodies for contrast enhancement. Stains SHOULD be indicated in the `"SampleStaining"` key in the sidecar JSON file, although the label may be different. Description of antibodies SHOULD also be indicated in `"SamplePrimaryAntibodies"` and/or `"SampleSecondaryAntobodies"` as appropriate.

## rec

Full name: Reconstruction

Format: `rec-<label>`

Definition: The `rec-<label>` key/value can be used to distinguish different reconstruction algorithms (for example `MoCo` for the ones using motion correction).

## dir

Full name: Phase-Encoding Direction

Format: `dir-<label>`

Definition: The `dir-<label>` key/value can be set to an arbitrary alphanumeric label (for example, `dir-LR` or `dir-AP`) to distinguish different phase-encoding directions.

## run

Full name: Run

Format: `run-<index>`

Definition: If several scans with the same acquisition parameters are acquired in the same session, they MUST be indexed with the `run-<index>` entity: `_run-1`, `_run-2`, `_run-3`, and so on (only nonnegative integers are allowed as run labels).

If different entities apply, such as a different session indicated by `ses-<label>`, or different acquisition parameters indicated by `acq-<label>`, then `run` is not needed to distinguish the scans and MAY be omitted.

## mod

Full name: Corresponding Modality

Format: `mod-<label>`

Definition: The `mod-<label>` key/value pair corresponds to modality label for defacing masks, for example, T1w, inplaneT1, referenced by a defacemask image. For example, `sub-01_mod-T1w_defacemask.nii.gz`.

## echo

Full name: Echo

Format: `echo-<index>`

Definition: If files belonging to an entity-linked file collection are acquired at different echo times, the `_echo-<index>` key/value pair MUST be used to distinguish individual files. This entity represents the `"EchoTime"` metadata field. Please note that the `<index>` denotes the number/index (in the form of a nonnegative integer), not the `"EchoTime"` value which needs to be stored in the field `"EchoTime"` of the separate JSON file.

## flip

Full name: Flip Angle

Format: `flip-<index>`

Definition: If files belonging to an entity-linked file collection are acquired at different flip angles, the `_flip-<index>` key/value pair MUST be used to distinguish individual files. This entity represents the `"FlipAngle"` metadata field. Please note that the `<index>` denotes the number/index (in the form of a nonnegative integer), not the `"FlipAngle"` value which needs to be stored in the field `"FlipAngle"` of the separate JSON file.

## inv

Full name: Inversion Time

Format: `inv-<index>`

Definition: If files belonging to an entity-linked file collection are acquired at different inversion times, the `_inv-<index>` key/value pair MUST be used to distinguish individual files. This entity represents the `"InversionTime` metadata field. Please note that the `<index>` denotes the number/index (in the form of a nonnegative integer), not the `"InversionTime"` value which needs to be stored in the field `"InversionTime"` of the separate JSON file.

## mt

Full name: Magnetization Transfer

Format: `mt-<label>`

Allowed values: `on`, `off`

Definition: If files belonging to an entity-linked file collection are acquired at different magnetization transfer (MT) states, the `_mt-<label>` key/value pair MUST be used to distinguish individual files. This entity represents the `"MTState"` metadata field. Allowed label values for this entity are `on` and `off`, for images acquired in presence and absence of an MT pulse, respectively.

## part

Full name: Part

Format: `part-<label>`

Allowed values: `mag`, `phase`, `real`, `imag`

Definition: This entity is used to indicate which component of the complex representation of the MRI signal is represented in voxel data. The `part-<label>` key/value pair is associated with the DICOM Tag `0008, 9208`. Allowed label values for this entity are `phase`, `mag`, `real` and `imag`, which are typically used in `part-mag`/`part-phase` or `part-real`/`part-imag` pairs of files.

Phase images MAY be in radians or in arbitrary units. The sidecar JSON file MUST include the units of the `phase` image. The possible options are `"rad"` or `"arbitrary"`.

When there is only a magnitude image of a given type, the `part` key MAY be omitted.

## proc

Full name: Processed (on device)

Format: `proc-<label>`

Definition: The proc label is analogous to rec for MR and denotes a variant of a file that was a result of particular processing performed on the device.

This is useful for files produced in particular by Elekta's MaxFilter (for example, `sss`, `tsss`, `trans`, `quat` or `mc`), which some installations impose to be run on raw data because of active shielding software corrections before the MEG data can actually be exploited.

## hemi

Full name: Hemisphere

Format: `hemi-<label>`

Allowed values: `L`, `R`

Definition: The `hemi-<label>` entity indicates which hemibrain is described by the file. Allowed label values for this entity are `L` and `R`, for the left and right hemibrains, respectively.

## space

Full name: Space

Format: `space-<label>`

Definition: The space entity can be used to indicate the way in which electrode positions are interpreted (for EEG/MEG/iEEG data) or the spatial reference to which a file has been aligned (for MRI data). The space `<label>` MUST be taken from one of the modality specific lists in Appendix VIII. For example for iEEG data, the restricted keywords listed under iEEG Specific Coordinate Systems are acceptable for `<label>`.

For EEG/MEG/iEEG data, this entity can be applied to raw data, but for other data types, it is restricted to derivative data.

## split

Full name: Split

Format: `split-<index>`

Definition: In the case of long data recordings that exceed a file size of 2Gb, the .fif files are conventionally split into multiple parts. Each of these files has an internal pointer to the next file. This is important when renaming these split recordings to the BIDS convention.

Instead of a simple renaming, files should be read in and saved under their new names with dedicated tools like MNE-Python, which will ensure that not only the file names, but also the internal file pointers will be updated. It is RECOMMENDED that .fif files with multiple parts use the `split-<index>` entity to indicate each part. If there are multiple parts of a recording and the optional `scans.tsv` is provided, remember to list all files separately in `scans.tsv` and that the entries for the `acq_time` column in `scans.tsv` MUST all be identical, as described in Scans file.

## recording

Full name: Recording

Format: `recording-<label>`

Definition: More than one continuous recording file can be included (with different sampling frequencies). In such case use different labels. For example: `_recording-contrast`, `_recording-saturation`.

## chunk

Full name: Chunk

Format: `chunk-<index>`

Definition: The `chunk-<index>` key/value pair is used to distinguish between different regions, 2D images or 3D volumes files, of the same physical sample with different fields of view acquired in the same imaging experiment.

## res

Full name: Resolution

Format: `res-<label>`

Definition: Resolution of regularly sampled N-dimensional data. MUST have a corresponding `"Resolution"` metadata field to provide interpretation.

This entity is only applicable to derivative data.

## den

Full name: Density

Format: `den-<label>`

Definition: Density of non-parametric surfaces. MUST have a corresponding `Density` metadata field to provide interpretation.

This entity is only applicable to derivative data.

## label

Full name: Label

Format: `label-<label>`

Definition: Tissue-type label, following a prescribed vocabulary. Applies to binary masks and probabilistic/partial volume segmentations that describe a single tissue type.

This entity is only applicable to derivative data.

## desc

Full name: Description

Format: `desc-<label>`

Definition: When necessary to distinguish two files that do not otherwise have a distinguishing entity, the `_desc-<label>` keyword-value SHOULD be used.

This entity is only applicable to derivative data.

# Appendix X: File collections

Here, some concrete use-cases of entity-linked file collections are listed using descriptive tables, organized by modality.

The tables in this appendix catalog applications where the use of a file collection is REQUIRED.

Certain entities interlink the files in a file collection through a metadata field. Unlike other common entities (for example `run`), they require an iteration over different values of the metadata fields they represent. Please keep the following list of linking entities up-to-date with the file collections included in this appendix:

- Magnetic Resonance Imaging
  - `echo`
  - `flip`
  - `inv`
  - `mt`
  - `part`

## Magnetic Resonance Imaging

### Anatomy imaging data

Template:

```
sub-<label>/
    [ses-<label>/]
        anat/
            sub-<label>[_ses-<label>][_acq-<label>][_ce-<label>][_rec-<label>][_run-<index>]_echo-<index>[_part-<mag|phase|real|imag>]_MEGRE.json
            sub-<label>[_ses-<label>][_acq-<label>][_ce-<label>][_rec-<label>][_run-<index>]_echo-<index>[_part-<mag|phase|real|imag>]_MEGRE.nii[.gz]
            sub-<label>[_ses-<label>][_acq-<label>][_ce-<label>][_rec-<label>][_run-<index>]_echo-<index>[_part-<mag|phase|real|imag>]_MESE.json
            sub-<label>[_ses-<label>][_acq-<label>][_ce-<label>][_rec-<label>][_run-<index>]_echo-<index>[_part-<mag|phase|real|imag>]_MESE.nii[.gz]
            sub-<label>[_ses-<label>][_acq-<label>][_ce-<label>][_rec-<label>][_run-<index>][_echo-<index>]_flip-<index>[_part-<mag|phase|real|imag>]_V
            sub-<label>[_ses-<label>][_acq-<label>][_ce-<label>][_rec-<label>][_run-<index>][_echo-<index>]_flip-<index>[_part-<mag|phase|real|imag>]_V
            sub-<label>[_ses-<label>][_acq-<label>][_ce-<label>][_rec-<label>][_run-<index>]_inv-<index>[_part-<mag|phase|real|imag>]_IRT1.json
```

```
sub-<label>[_ses-<label>][_acq-<label>][_ce-<label>][_rec-<label>][_run-<index>]_inv-<index>[_part-<mag|phase|real|imag>]_IRT1.nii[.gz]
sub-<label>[_ses-<label>][_acq-<label>][_ce-<label>][_rec-<label>][_run-<index>][_echo-<index>][_flip-<index>]_inv-<index>[_part-<mag|phase
sub-<label>[_ses-<label>][_acq-<label>][_ce-<label>][_rec-<label>][_run-<index>][_echo-<index>][_flip-<index>]_inv-<index>[_part-<mag|phase
sub-<label>[_ses-<label>][_acq-<label>][_ce-<label>][_rec-<label>][_run-<index>][_echo-<index>]_flip-<index>_mt-<on|off>[_part-<mag|phase|r
sub-<label>[_ses-<label>][_acq-<label>][_ce-<label>][_rec-<label>][_run-<index>][_echo-<index>]_flip-<index>_mt-<on|off>[_part-<mag|phase|r
sub-<label>[_ses-<label>][_acq-<label>][_ce-<label>][_rec-<label>][_run-<index>][_echo-<index>]_flip-<index>_mt-<on|off>[_part-<mag|phase|r
sub-<label>[_ses-<label>][_acq-<label>][_ce-<label>][_rec-<label>][_run-<index>][_echo-<index>]_flip-<index>_mt-<on|off>[_part-<mag|phase|r
sub-<label>[_ses-<label>][_acq-<label>][_ce-<label>][_rec-<label>][_run-<index>]_mt-<on|off>[_part-<mag|phase|real|imag>]_MTR.json
sub-<label>[_ses-<label>][_acq-<label>][_ce-<label>][_rec-<label>][_run-<index>]_mt-<on|off>[_part-<mag|phase|real|imag>]_MTR.nii[.gz]
```

| Suffix | Linking entities | Application | Description |
|---|---|---|---|
| VFA | flip | Variable flip angle | The VFA method involves at least two spoiled gradient echo (SPGR) of steady-state free precession (SSFP) images acquired at different flip angles. Depending on the provided metadata fields and the sequence type, data may be eligible for DESPOT1, DESPOT2 and their variants (Deoni et al. 2005). |
| IRT1 | inv, part | Inversion recovery T1 mapping | The IRT1 method involves multiple inversion recovery spin-echo images acquired at different inversion times (Barral et al. 2010). |
| MP2RAGE | flip, inv, echo, part | Magnetization prepared two gradient echoes | The MP2RAGE method is a special protocol that collects several images at different flip angles and inversion times to create a parametric T1map by combining the magnitude and phase images (Marques et al. 2010). |
| MESE | echo | Multi-echo spin-echo | The MESE method involves multiple spin echo images acquired at different echo times and is primarily used for T2 mapping. Please note that this suffix is not intended for the logical grouping of images acquired using an Echo Planar Imaging (EPI) readout. |

| Suffix | Linking entities | Application | Description |
|---|---|---|---|
| MEGRE | echo | Multi-echo gradient-echo | Anatomical gradient echo images acquired at different echo times. Please note that this suffix is not intended for the logical grouping of images acquired using an Echo Planar Imaging (EPI) readout. |
| MTR | mt | Magnetization transfer ratio | This method is to calculate a semi-quantitative magnetization transfer ratio map. |
| MTS | flip, mt | Magnetization transfer saturation | This method is to calculate a semi-quantitative magnetization transfer saturation index map. The MTS method involves three sets of anatomical images that differ in terms of application of a magnetization transfer RF pulse (MTon or MToff) and flip angle (Helms et al. 2008). |
| MPM | flip, mt, echo, part | Multi-parametric mapping | The MPM approaches (a.k.a hMRI) involves the acquisition of highly-similar anatomical images that differ in terms of application of a magnetization transfer RF pulse (MTon or MToff), flip angle and (optionally) echo time and magnitue/phase parts (Weiskopf et al. 2013). See here for suggested MPM acquisition protocols. |

## Fieldmap data

Template:

```
sub-<label>/
    [ses-<label>/]
        fmap/
            sub-<label>[_ses-<label>][_acq-<label>][_ce-<label>][_rec-<label>][_run-<index>]_flip-<index>[_inv-<index>][_part-<mag|phase|real|imag>]_T
            sub-<label>[_ses-<label>][_acq-<label>][_ce-<label>][_rec-<label>][_run-<index>]_flip-<index>[_inv-<index>][_part-<mag|phase|real|imag>]_T
            sub-<label>[_ses-<label>][_acq-<label>][_ce-<label>][_rec-<label>][_run-<index>]_echo-<index>_flip-<index>[_inv-<index>][_part-<mag|phase|r
            sub-<label>[_ses-<label>][_acq-<label>][_ce-<label>][_rec-<label>][_run-<index>]_echo-<index>_flip-<index>[_inv-<index>][_part-<mag|phase|r
            sub-<label>[_ses-<label>][_acq-<label>][_ce-<label>][_rec-<label>][_run-<index>][_echo-<index>][_flip-<index>][_inv-<index>][_part-<mag|pha
```

```
sub-<label>[_ses-<label>][_acq-<label>][_ce-<label>][_rec-<label>][_run-<index>][_echo-<index>][_flip-<index>][_inv-<index>][_part-<mag|pha
sub-<label>[_ses-<label>][_acq-<label>][_ce-<label>][_rec-<label>][_run-<index>][_echo-<index>][_flip-<index>][_inv-<index>][_part-<mag|pha
sub-<label>[_ses-<label>][_acq-<label>][_ce-<label>][_rec-<label>][_run-<index>][_echo-<index>][_flip-<index>][_inv-<index>][_part-<mag|pha
sub-<label>[_ses-<label>][_acq-<label>][_ce-<label>][_rec-<label>][_run-<index>][_echo-<index>][_flip-<index>][_inv-<index>][_part-<mag|pha
sub-<label>[_ses-<label>][_acq-<label>][_ce-<label>][_rec-<label>][_run-<index>][_echo-<index>][_flip-<index>][_inv-<index>][_part-<mag|pha
sub-<label>[_ses-<label>][_acq-<label>][_ce-<label>][_rec-<label>][_run-<index>][_echo-<index>][_flip-<index>][_inv-<index>][_part-<mag|pha
sub-<label>[_ses-<label>][_acq-<label>][_ce-<label>][_rec-<label>][_run-<index>][_echo-<index>][_flip-<index>][_inv-<index>][_part-<mag|pha
sub-<label>[_ses-<label>][_acq-<label>][_ce-<label>][_rec-<label>][_run-<index>][_echo-<index>]_flip-<index>_inv-<index>[_part-<mag|phase|r
sub-<label>[_ses-<label>][_acq-<label>][_ce-<label>][_rec-<label>][_run-<index>][_echo-<index>]_flip-<index>_inv-<index>[_part-<mag|phase|r
```

| Suffix | Meta-data relevant entity | Application | Description |
|---|---|---|---|
| TB1DAM | flip | Double-angle B1+ mapping | The double-angle B1+ method (Insko and Bolinger 1993) is based on the calculation of the actual angles from signal ratios, collected by two acquisitions at different nominal excitation flip angles. Common sequence types for this application include spin echo and echo planar imaging. |
| TB1EPI | flip, echo | B1+ mapping with 3D EPI | This B1+ mapping method (Jiru and Klose 2006) is based on two EPI readouts to acquire spin echo (SE) and stimulated echo (STE) images at multiple flip angles in one sequence, used in the calculation of deviations from the nominal flip angle. |
| TB1AFI | Please see the qMRI appendix. | Actual Flip Angle Imaging (AFI) | This method (Yarnykh 2007) calculates a B1+ map from two images acquired at interleaved (two) TRs with identical RF pulses using a steady-state sequence. |
| TB1TFL | Please see the qMRI appendix. | Siemens `tfl_b1_map` | B1+ data acquired using `tfl_b1_map` product sequence by Siemens based on the method by Chung et al. (2010). The sequence generates one anatomical image and one scaled flip angle map. |
| TB1RFM | Please see the qMRI appendix. | Siemens `rf_map` | B1+ data acquired using `rf_map` product sequence by Siemens. |

| Suffix | Meta-data relevant entity | Application | Description |
|---|---|---|---|
| TB1SRGE | `flip`, `inv` | SA2RAGE | Saturation-prepared with 2 rapid gradient echoes (SA2RAGE) uses a ratio of two saturation recovery images with different time delays, and a simulated look-up table to estimate B1+ (Eggenschwiler et al. 2011). This sequence can also be used in conjunction with MP2RAGE T1 mapping to iteratively improve B1+ and T1 map estimation (Marques & Gruetter 2013). |
| RB1COR | Please see the qMRI appendix. | B1- field correction | Low resolution images acquired by the body coil (in the gantry of the scanner) and the head coil using identical acquisition parameters to generate a combined sensitivity map as described in Papp et al. (2016). |

# Appendix XI: Quantitative MRI

Quantitative MRI (qMRI) is a collection of methods aiming at generating parametric maps that can characterize underlying tissue properties. Unlike those of conventional MR images (for example, `T1w` or `T2w`), intensity values of quantitative maps are not represented in an arbitrary range. Instead, these maps are represented either in absolute physical units (for example, `seconds` for `T1map`), or within an application dependent range of arbitrary units (for example, myelin water fraction `MWFmap` in brain).

## Organization of qMRI data in BIDS

Unlike conventional MR images, quantitative maps are not immediate products of the image reconstruction step (from k-space data to structural images). Intensity values of qMRI maps are calculated by fitting a collection of parametrically linked images to a biophysical model or to an MRI signal representation. This processing is typically carried out in the image domain. There are two main ways to obtain a quantitative map:

1. Pre-generated qMRI maps: The qMRI maps are generated right after the reconstruction of required input images and made available to the user at the scanner console. The acquisition scenarios may include (a) vendor pipelines or (b) open-source pipelines deployed at the scanner site.
2. Post-generated qMRI maps: The qMRI maps are generated from a collection of input data after they are exported from the scanner site. This type of processing is commonly carried out using an open-source software such as hMRI toolbox, mrQ, PyQMRI, qmap, qMRLab, and QUIT.

### Inputs are file collections

The common concept of entity-linked file collections enables the description of a qMRI application by creating logical groups of input files through `suffix` and certain entities representing acquisition parameters (`echo`, `flip`, `inv`, `mt`) or file parts (`part`).

If a qMRI file collection is intended for creating structural quantitative maps (for example, `T1map`), files belonging to that collection are stored in the `anat` subfolder. Below is an example file collection for `MP2RAGE`:

```
sub-01/
   anat/
      sub-01_inv-1_part-mag_MP2RAGE.nii.gz
      sub-01_inv-1_part-phase_MP2RAGE.nii.gz
      sub-01_inv-1_MP2RAGE.json
      sub-01_inv-2_part-mag_MP2RAGE.nii.gz
```

```
        sub-01_inv-2_part-phase_MP2RAGE.nii.gz
        sub-01_inv-2_MP2RAGE.json
```

Commonly, RF fieldmaps (`B1+` and `B1-` maps) are used for the correction of structural quantitative maps. As these images do not convey substantial structural information, respective file collections of RF fieldmaps are stored in the `fmap` subfolder. Below is an example file collection for RF transmit field map `TB1EPI`:

```
sub-01/
   fmap/
      sub-01_echo-1_flip-1_TB1EPI.nii.gz
      sub-01_echo-1_flip-1_TB1EPI.json
      sub-01_echo-2_flip-1_TB1EPI.nii.gz
      sub-01_echo-2_flip-1_TB1EPI.json
      sub-01_echo-1_flip-2_TB1EPI.nii.gz
      sub-01_echo-1_flip-2_TB1EPI.json
      sub-01_echo-2_flip-2_TB1EPI.nii.gz
      sub-01_echo-2_flip-2_TB1EPI.json
```

Please visit the file collections appendix to see the list of currently supported qMRI applications.

## Quantitative maps are derivatives

Regardless of how they are obtained (pre- or post-generated), qMRI maps are stored in the `derivatives` folder. For example a `T1map` can be generated from an `MP2RAGE` file collection using either options.

If the map is post-generated:

```
ds-example/
   derivatives/
      qMRI-software-name/
         sub-01/
            anat/
               sub-01_T1map.nii.gz
               sub-01_T1map.json
               sub-01_UNIT1.nii.gz
               sub-01_UNIT1.json
```

If the map is pre-generated, for example, by a Siemens scanner:

```
ds-example/
   derivatives/
      Siemens/
         sub-01/
            anat/
               sub-01_T1map.nii.gz
```

```
                  sub-01_T1map.json
                  sub-01_UNIT1.nii.gz
                  sub-01_UNIT1.json
```

Note: Even though the process from which pre-generated qMRI maps are obtained (vendor pipelines) is not known, vendors generally allow exporting of the corresponding input data. It is RECOMMENDED to share them along with the vendor outputs, whenever possible for a qMRI method supported by BIDS.

### Example datasets

You can find example file collections and qMRI maps organized according to BIDS in the BIDS examples.

## Metadata requirements for qMRI data

The table of required entities for qMRI file collections are provided in the entity table. However, viability of a qMRI file collection is determined not only by the naming and organization of the input files, but also by which metadata fields are provided in accompanying json files.

### Method-specific priority levels for qMRI file collections

Anatomy imaging data

| File collection | REQUIRED metadata | OPTIONAL metadata |
|---|---|---|
| VFA | `FlipAngle`, `PulseSequenceType`, `RepetitionTimeExcitation` | `SpoilingRFPhaseIncrement` |
| IRT1 | `InversionTime` | |
| MP2RAGE* | `FlipAngle`, `InversionTime`, `RepetitionTimeExcitation`, `RepetitionTimePreperation`, `NumberShots`,`MagneticFieldStrength` | `EchoTime` |
| MESE | `EchoTime` | |
| MEGRE | `EchoTime` | |
| MTR | `MTState` | |
| MTS | `FlipAngle`, `MTState`, `RepetitionTimeExcitation` | |
| MPM | `FlipAngle`, `MTState`, `RepetitionTimeExcitation` | `EchoTime` |

* Please see MP2RAGE-specific notes for the calculation of `NumberShots` and regarding the organization of `UNIT1` image.

Explanation of the table:

- The metadata fields listed in the REQUIRED column are needed to perform a minimum viable qMRI processing for the corresponding `file collection`.

- Note that some of the metadata fields may be constant across different files in a file collection, yet still required as an input (for example, `NumberShots` in `MP2RAGE`). Such metadata fields MUST be provided in the accompanying JSON files.
- The metadata fields listed in the OPTIONAL column can be used to form different flavors of an existing file collection suffix, dispensing with the need for introducing a new suffix. See deriving the intended qMRI application from an ambiguous file collection for details.

Field maps

| File collection | REQUIRED metadata |
|---|---|
| TB1DAM | `FlipAngle` |
| TB1EPI | `EchoTime`, `FlipAngle`, `TotalReadoutTime`, `MixingTime` |
| TB1AFI | `RepetitionTime` |
| TB1TFL | |
| TB1RFM | |
| TB1SRGE* | `FlipAngle`, `InversionTime`, `RepetitionTimeExcitation`, `RepetitionTimePreperation`, `NumberShots` |
| RB1COR | |

* Please see TB1SRGE-specific notes for the calculation of `NumberShots`.

## Metadata requirements for qMRI maps

As qMRI maps are stored as derivatives, they are subjected to the metadata requirements of derived datasets.

An example `dataset_description.json` for a qMRI map derivatives folder:

```
ds-example/
   derivatives/
      qMRLab/
         dataset_description.json
         sub-01/
            anat/
               sub-01_T1map.nii.gz
               sub-01_T1map.json
               sub-01_M0map.nii.gz
               sub-01_M0map.json
```

`dataset_description.json`:

```
{
  "Name": "qMRLab Outputs",
```

```
  "BIDSVersion": "1.5.0",
  "DatasetType": "derivative",
  "GeneratedBy": [
    {
      "Name": "qMRLab",
      "Version": "2.4.1",
      "Container": {
        "Type": "docker",
        "Tag": "qmrlab/minimal:2.4.1"
        }
    },
    {
      "Name": "Manual",
      "Description": "Generated example T1map outputs"
    }
  ],
  "SourceDatasets": [
    {
      "DOI": "DOI 10.17605/OSF.IO/K4BS5",
      "URL": "https://osf.io/k4bs5/",
      "Version": "1"
    }
  ]
}
```

In addition to the metadata fields provided in the `dataset_description.json`, qMRI maps are RECOMMENDED to be accompanied by sidecar JSON files that contain further information about the quantified maps. Although this may not be the generic case for common derivative outputs, a proper interpretation of qMRI maps may critically depend on some metadata fields. For example, without the information of `MagneticFieldStrength`, white-matter T1 values in a `T1map` become elusive.

- All the acquisition parameters that are constant across the files in a file collection are RECOMMENDED to be added to the sidecar json of the qMRI maps.
- Relevant acquisition parameters that vary across files in a qMRI file collection are RECOMMENDED to be added to the sidecar json of the qMRI map in array form.
- The JSON file accompanying a qMRI map which is obtained by using open-source software is RECOMMENDED to include additional metadata fields listed in the following table:

| Key name | Requirement Level | Data type | Description |
|---|---|---|---|
| BasedOn | RECOMMENDED | string or array of strings | List of files in a file collection to generate the map. Fieldmaps are also listed, if involved in the processing. |
| EstimationReference | RECOMMENDED | string | Reference to the study/studies on which the implementation is based. |

| Key name | Requirement Level | Data type | Description |
|---|---|---|---|
| EstimationAlgorithm | RECOMMENDED | string | Type of algorithm used to perform fitting (for example, `"linear"`, `"non-linear"`, `"LM"` and such). |
| Units | RECOMMENDED | string | Measurement units for the associated file. SI units in CMIXF formatting are RECOMMENDED (see Units). |

Example:

```
sub-01_T1map.nii.gz
sub-01_T1map.json
```

sub-01_T1map.json:

```
{

<<Parameter injected by the software/pipeline>>

"BasedOn":["anat/sub-01_flip-1_VFA.nii.gz",
           "anat/sub-01_flip-2_VFA.nii.gz",
           "anat/sub-01_flip-3_VFA.nii.gz",
           "anat/sub-01_flip-4_VFA.nii.gz",
           "fmap/sub-01_TB1map.nii.gz"],
"EstimationPaper":"Deoni et. al.MRM, 2015",
"EstimationAlgorithm":"Linear",
"Units": "second",

<<Parameters that are constant across files in the (parent) file collection>>

"MagneticFieldStrength": "3",
"Manufacturer": "Siemens",
"ManufacturerModelName": "TrioTim",
"InstitutionName": "xxx",
"PulseSequenceType": "SPGR",
"PulseSequenceDetails": "Information beyond the sequence type that identifies
 specific pulse sequence used (VB version, if not standard, Siemens WIP XXX
 ersion ### sequence written by xx using a version compiled on mm/dd/yyyy/)",
"RepetitionTimeExcitation": "35",
"EchoTime": "2.86",
"SliceThickness": "5",
```

```
<<Relevant parameters that vary across the linking entity of the (parent) file collection>>

"FlipAngle": ["5","10","15","20"]

}
```

## Deriving the intended qMRI application from an ambiguous file collection

Certain file collection suffixes may refer to a generic data collection regime such as variable flip angle (VFA), rather than a more specific acquisition, for example, magnetization prepared two gradient echoes (MP2RAGE). Such generic acquisitions can serve as a basis to derive various qMRI applications by changes to the acquisition sequence (for example, readout) type or by varying additional scan parameters.

If such an inheritance relationship is applicable between an already existing file collection and a new qMRI application to be included in the specification, the inheritor qMRI method is listed in the table below instead of introducing a new file collection suffix. This approach aims at:

- preventing the list of available suffixes from over-proliferation,
- providing qMRI-focused BIDS applications with a set of meta-data driven rules to infer possible fitting options,
- keeping an inheritance track of the qMRI methods described within the specification.

| File-collection suffix | If REQUIRED metadata == Value | OPTIONAL metadata (`entity`/`fixed`) | Derived application name (NOT a suffix) |
|---|---|---|---|
| VFA | `PulseSequenceType` == `SPGR` | | DESPOT1 |
| VFA | `PulseSequenceType` == `SSFP` | `SpoilingRFPhaseIncrement` (`fixed`) | DESPOT2 |
| MP2RAGE | | `EchoTime` (`echo`) | MP2RAGE-ME |
| MPM | | `EchoTime` (`echo`) | MPM-ME |

In this table, (`entity`/`fixed`) denotes whether the OPTIONAL metadata that forms a new flavor of qMRI application for the respective suffix varies across files of a file collection (which calls for using a linking entity) or fixed. If former is the case, the entity is to be added to the files in that file collection. Note that this addition MUST be allowed by the priority levels given for that suffix in the `entity table`. If latter (`fixed`) is the case, filenames will remain the same; however, the optional metadata (third column) may define the flavor of the application (fourth column) along with the conditional value of a required metadata field (second column).

A derived qMRI application becomes available if all the optional metadata fields listed for the respective file collection suffix are provided for the data. In addition, conditional rules based on the value of a given required metadata field can be set for the description of a derived qMRI application. Note that the value of this required metadata is fixed across constituent images of a file collection and defined in Method-specific priority levels for qMRI file collections.

For example, if the optional metadata field of `PulseSequenceType` is SPGR for a collection of anatomical images listed by the `VFA` suffix, the data qualifies for `DESPOT1` T1 fitting. For the same suffix, if the `PulseSequenceType` metadata field has the value of `SSFP`, and the `SpoilingRFPhaseIncrement` is provided as a metadata field, then the dataset becomes eligible for `DESPOT2` T2 fitting application.

Please note that optional metadata fields listed in the deriving the intended qMRI application from an ambiguous file collection table are included in the optional (third) column of the priority levels table for the consistency of this appendix.

## Introducing a new qMRI file collection

If a qMRI application cannot be interpreted as a subtype of an already existing suffix of a qMRI-related file collection, we RECOMMEND adhering to the following principles to introduce a new suffix:

- All qMRI-relevant file collection suffixes are capitalized.
- Unless the pulse sequence is exclusively associated with a specific qMRI application (for example, `MP2RAGE`), sequence names are not used as suffixes.
- File collection suffixes for qMRI applications attain a clear description of the qMRI method that they relate to in the file collections appendix.
- Hyperlinks to example applications and reference method articles are encouraged whenever possible.
- If it is possible to derive a qMRI application from an already existing file collection suffix by defining a set of logical conditions over the metadata fields, the tables of the deriving the intended qMRI application from an ambiguous file collection and the anatomy data priority levels sections are extended instead of introducing a new suffix.

## Application-specific notes for qMRI file collections

### Anatomy imaging data

General notes:

- Some BIDS metadata field values are calculated based on the values of other metadata fields that are not listed as required fields. These fields include: `NumberShots`. The calculation of the values may depend on the type of the acquisition. These acquisitions include: `MP2RAGE` and `TB1SRGE`.

#### `MP2RAGE` specific notes

**`UNIT1` images** Although the `UNIT1` image is provided as an output by the acquisition sequence, it is used as an input to offline calculation of a `T1map` using a dictionary lookup approach. However, `complex` data is needed for an accurate calculation of the `UNIT1` image, which is not commonly provided by the stock sequence. Instead, the `magnitude` and `phase` images are exported. Please see the relevant discussion at qMRLab issue #255.

Therefore, the `UNIT1` image provided by the scanner is RECOMMENDED to be stored under the `anat` raw dataset directory along with the `MP2RAGE` file collection and to be used as the primary input for quantifying a `T1map`.

If an additional `UNIT1` image is calculated offline, then the output is to be stored in the `derivatives` folder with necessary provenance information.

**`NumberShots` metadata field** Note that the type of `NumberShots` field can be either a `number` or an `array of numbers`.

- If a single `number` is provided, this should correspond to the number of `SlicesPerSlab` or `ReconMatrixPE`. However, in this case, `SlicePartialFourier` or `PartialFourierPE` fraction is needed to calculate the number of partitions `before` and `after` of the k-space center to calculate a T1 map.

- If `before/after` calculation is performed during the BIDS conversion of the `MP2RAGE` data, then the value of `NumberShots` metadata field can be given as a 1X2 array, with first entry corresponding to `before` and the second to the `after`.

Formula:

If NumberShots is an array of numbers such that `"NumberShots": [before, after]`, the values of `before` and `after` are calculated as follows:

```
before = SlicesPerSlab*(SlicePartialFourier - 0.5)
after  = SlicesPerSlab/2
```

See this reference implementation.

Other metadata fields The value of the `RepetitionTimeExcitation` field is not commonly found in the DICOM files. When accessible, the value of `EchoSpacing` corresponds to this metadata. When not accessible, `2 X EchoTime` can be used as a surrogate.

Further information about other `MP2RAGE` qMRI protocol fields can be found in the qMRLab documentation.

#### `TB1SRGE` specific notes

Calculation of `before` and `after` entries for `NumberShots` metadata field of `TB1SRGE` is more involved than that of `MP2RAGE`. The formula can be found in a reference implementation, which requires information about `BaseResolution` (that is, image matrix size in PE direction), partial Fourier fraction in the PE direction, number of reference lines for parallel imaging acceleration, and the parallel imaging acceleration factor in PE direction.

### Radiofrequency (RF) field mapping

Some RF file collections call for the use of special notations that cannot be resolved by by entities that can generalize to other applications. Instead of introducing an entity that is exclusive to a single application, method developers who commonly use these file collections for the `MPM` application reached the consensus on the use of `acq` entity to distinguish individual files. These suffixes include: `TB1AFI`, `TB1TFL`, `TB1RFM`, and `RB1COR`.

#### `TB1EPI` specific notes

The `flip` and `echo` entities MUST be used to distinguish images with this suffix. The use of `flip` follows the default convention. However, this suffix defines a specific use case for the `echo` entity:

| `echo-1` | `echo-2` |
|---|---|
| Lower `EchoTime` | Higher `EchoTime` |
| Spin Echo (SE) image | Stimulated Echo (STE) image |

At each `FlipAngle`, the `TB1EPI` suffix lists two images acquired at two echo times. The first echo is a spin echo (SE) formed by the pulses alpha-2alpha. However, the second echo in this method is generated in a different fashion compared to a typical MESE acquisition. The second echo is a stimulated echo (STE) that is formed by an additional alpha pulse (that is, alpha-2alpha-alpha).

The `FlipAngle` value corresponds to the nominal flip angle value of the STE pulse. The nominal FA value of the SE pulse is twice this value.

Note that the following metadata fields MUST be defined in the accompanying JSON files:

| Field name | Definition |
|---|---|
| `TotalReadoutTime` | The effective readout length defined as `EffectiveEchoSpacing * PEReconMatrix`, with `EffectiveEchoSpacing = TrueEchoSpacing / PEacceleration` |
| `MixingTime` | Time interval between the SE and STE pulses |

To properly identify constituents of this particular method, values of the `echo` entity MUST index the images as follows:

```
sub-01/
   fmap/
      sub-01_echo-1_flip-1_TB1EPI.nii.gz # SE
      sub-01_echo-1_flip-1_TB1EPI.json
      sub-01_echo-2_flip-1_TB1EPI.nii.gz # STE
      sub-01_echo-2_flip-1_TB1EPI.json
      sub-01_echo-1_flip-2_TB1EPI.nii.gz # SE
      sub-01_echo-1_flip_2_TB1EPI.json
      sub-01_echo-2_flip-2_TB1EPI.nii.gz # STE
      sub-01_echo-2_flip-2_TB1EPI.json
```

**`TB1AFI`** specific notes

This method calculates a B1+ map from two images acquired at two interleaved excitation repetition times (TR). Note that there is no entity for the TR that can be used to label the files corresponding to the two repetition times and the definition of repetition time depends on the modality (`functional` or `anatomical`) in the specification.

Therefore, to properly identify constituents of this particular method, values of the `acq` entity SHOULD begin with either `tr1` (lower TR) or `tr2` (higher TR) and MAY be followed by freeform entries:

| First **`TR`** | Second **`TR`** | Use case |
|---|---|---|
| `_acq-tr1` | `_acq-tr2` | Single acquisition |
| `_acq-tr1Test` | `_acq-tr2Test` | Acquisition `Test` |
| `_acq-tr1Retest` | `_acq-tr2Retest` | Acquisition `Retest` |

```
sub-01/
   fmap/
      sub-01_acq-tr1_TB1AFI.nii.gz
      sub-01_acq-tr1_TB1AFI.json
      sub-01_acq-tr2_TB1AFI.nii.gz
      sub-01_acq-tr2_TB1AFI.json
```

### `TB1TFL` and `TB1RFM` specific notes

These suffixes describe two outputs generated by Siemens `tfl_b1_map` and `rf_map` product sequences, respectively. Both sequences output two images. The first image appears like an anatomical image and the second output is a scaled flip angle map.

To properly identify files of this particular file collection, values of the `acq` entity SHOULD begin with either `anat` or `famp` and MAY be followed by freeform entries:

| Anatomical (like) image | Scaled flip angle map | Use case |
|---|---|---|
| `_acq-anat` | `_acq-famp` | Single acquisition |
| `_acq-anatTest` | `_acq-fampTest` | Acquisition `Test` |
| `_acq-anatRetest` | `_acq-fampRetest` | Acquisition `Retest` |

```
sub-01/
   fmap/
      sub-01_acq-anat_TB1TFL.nii.gz
      sub-01_acq-anat_TB1TFL.json
      sub-01_acq-famp_TB1TFL.nii.gz
      sub-01_acq-famp_TB1TFL.json
```

The example above applies to the `TB1RFM` suffix as well.

### `RB1COR` specific notes

This method generates a sensitivity map by combining two low resolution images collected by two transmit coils (the body and the head coil) upon subsequent scans with identical acquisition parameters.

To properly identify constituents of this particular method, values of the `acq` entity SHOULD begin with either `body` or `head` and MAY be followed by freeform entries:

| Body coil | Head coil | Use case |
|---|---|---|
| `_acq-body` | `_acq-head` | Single acquisition |
| `_acq-bodyMTw` | `_acq-headMTw` | `MTw` for `MPM` |
| `_acq-bodyPDw` | `_acq-headPDw` | `PDw` for `MPM` |
| `_acq-bodyT1w` | `_acq-headT1w` | `T1w` for `MPM` |

```
sub-01/
   fmap/
      sub-01_acq-body_RB1COR.nii.gz # Body coil
      sub-01_acq-body_RB1COR.json
      sub-01_acq-head_RB1COR.nii.gz # Head coil
      sub-01_acq-head_RB1COR.json
```

# Appendix XI: Arterial Spin Labeling

These sections provide additional clarification for some specific topics within the BIDS specification for Arterial Spin Labeling.

## Which image is `control` and which is `label`?

The `control` and `label` images are acquired with identical acquisition parameters, except that the blood magnetization flowing into the imaging region is effectively inverted in the `label` image compared to the `control` image. In case of doubt, an easy rule of thumb is that the `deltaM=control-label` subtraction should result in a perfusion-weighted image with a positive sign. For example, in the case of FAIR this would be selective inversion (`control`) and non-selective inversion (`label`).

## `*_aslcontext.tsv`: three possible cases

The `*_aslcontext.tsv` table consists of a single column of labels identifying the `volume_type` of each volume in the corresponding `*_asl.nii[.gz]` file. See below examples of the three `*_aslcontext.tsv` cases, in order of decreasing preference.

### Case 1: `*_asl.nii[.gz]` consists of volume_types `control`, `label`

In most cases, the ASL timeseries provided by the scanner consist of a series of `control` and `label`, and optionally `m0scan` volumes. In this case, only the `control`, `label`, and optionally `m0scan` volumes should be stored in the `*_asl.nii[.gz]`, and the exact volume_type series should be specified in the `*_aslcontext.tsv`.

Example of `*_aslcontext.tsv`:

```
volume_type
control
label
control
label
m0scan
```

### Case 2: `*_asl.nii[.gz]` consists of volume_types `deltam` (scanner does not export `control` or `label` volumes)

In some cases, `control` and `label` volumes are lacking within the acquired ASL timeseries, but the intermediate `deltam` - and optionally an `m0scan` - volume is reconstructed/exported by the scanner. In this case, the `deltam` should be included in the `*_asl.nii[.gz]` and specified in the `*_aslcontext.tsv`.

Example of `*_aslcontext.tsv`:

```
volume_type
deltam
m0scan
```

### Case 3: `*_asl.nii[.gz]` consists of volume_type `cbf` (scanner does not export `control`, `label`, or `deltaM` volumes)

If `control` and `label` or intermediate ASL volumes are not reconstructed or exported, but a pre-calculated `cbf` - and optionally a `m0scan` - volume is provided by the scanner, the `cbf` should be included in the `*_asl.nii[.gz]` and specified in the `*_aslcontext.tsv`.

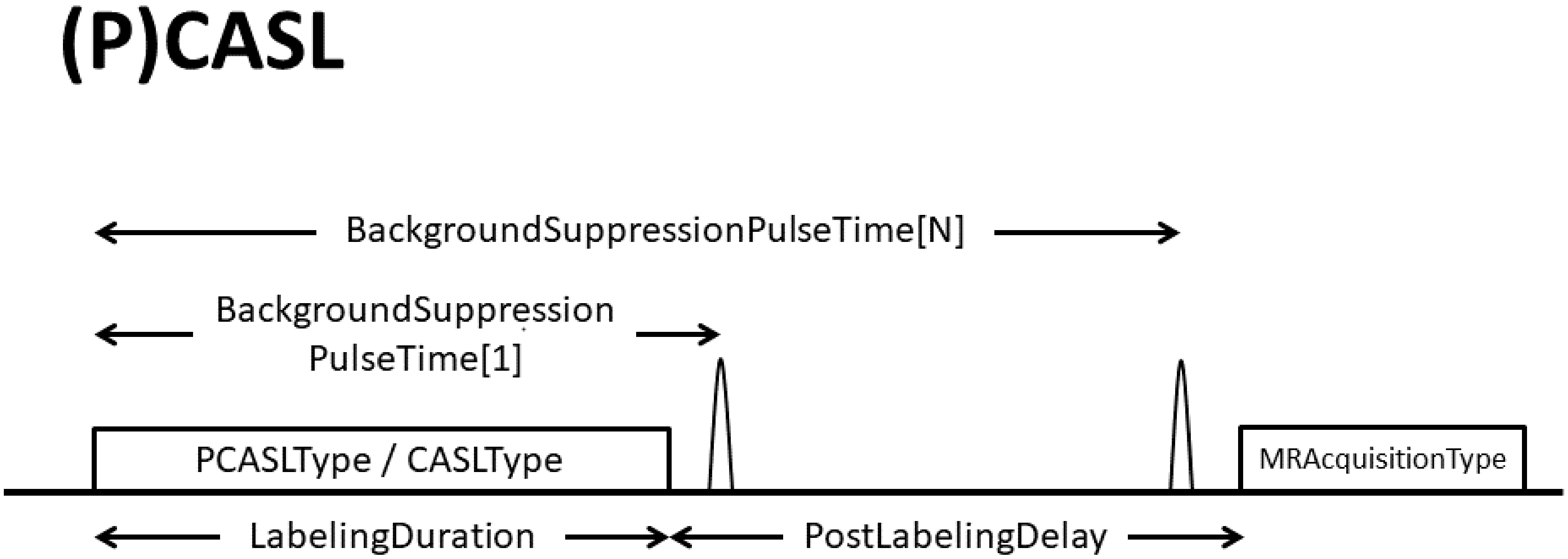
Example of `*_aslcontext.tsv`:

```
volume_type
cbf
m0scan
```

## Summary Image of the most common ASL sequences

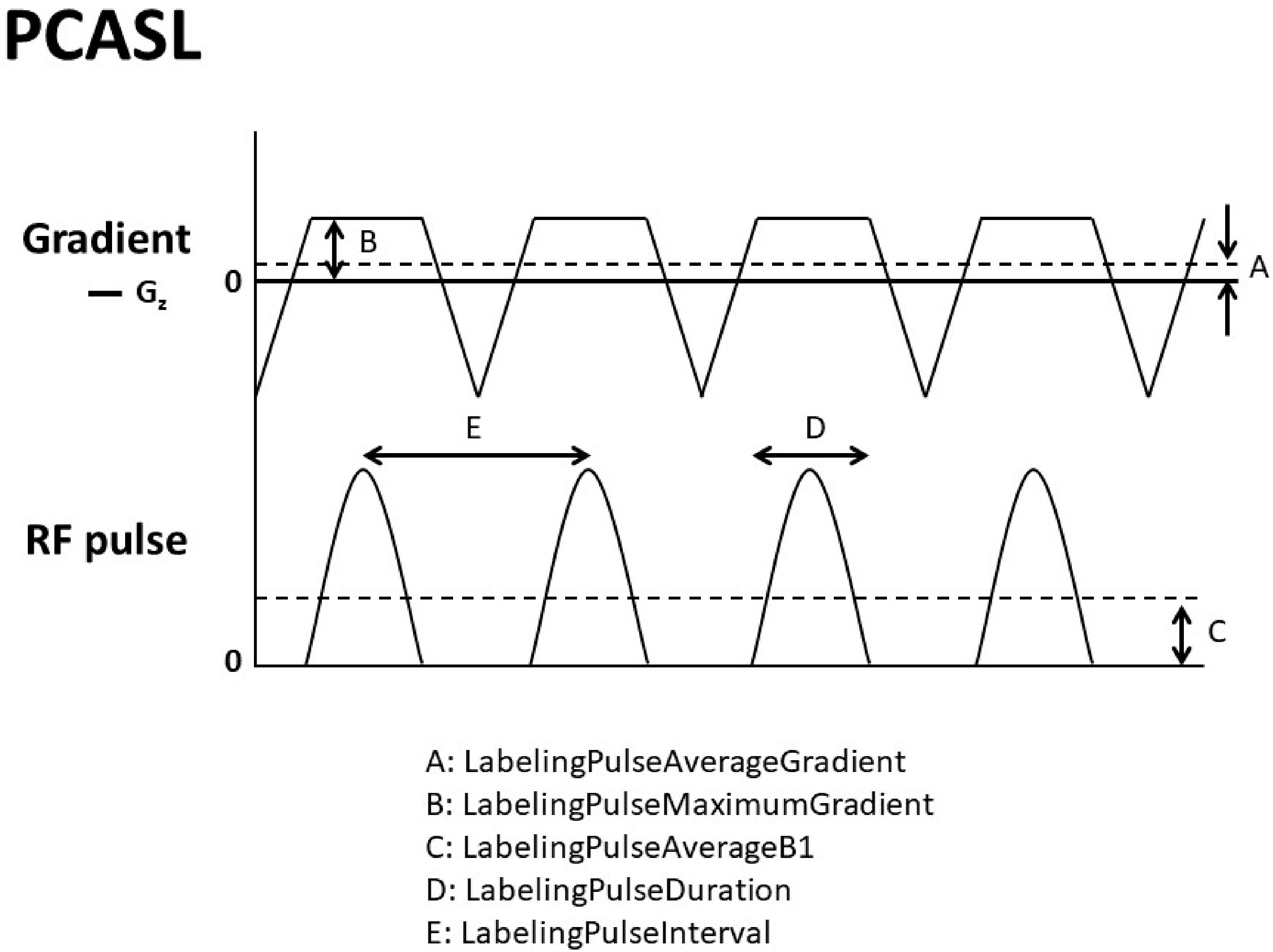
The following images illustrate the main BIDS metadata fields for three `ArterialSpinLabelingType`'s: `CASL`, `PCASL`, and `PASL`. Images are courtesy of, and adapted with permission from Y. Suzuki and OSIPI Task force 4.1: ASL lexicon milestone 1.

(P)CASL sequence



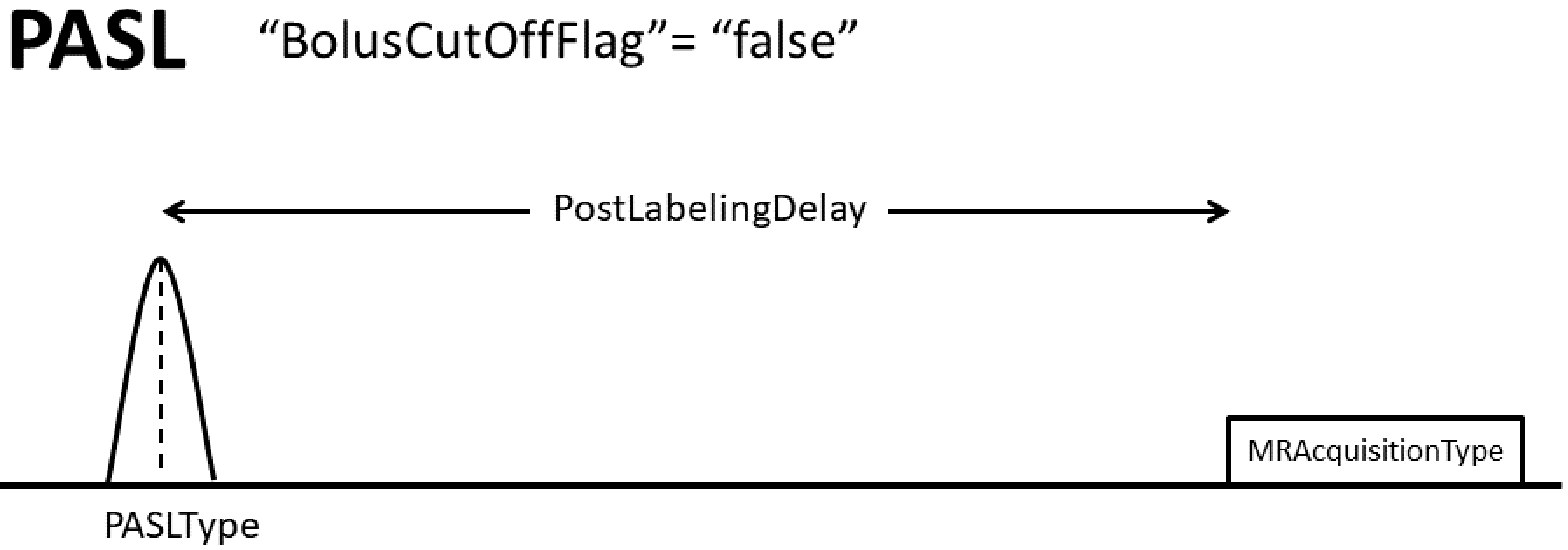
For (P)CASL, specifying the `LabelingDuration` and the `PostLabelingDelay` is required. The `LabelingDuration` is defined as the total duration of the labeling pulse train in seconds. `PostLabelingDelay` is the time in seconds after the end of the labeling until the middle of the excitation pulse applied to the imaging slab (for 3D acquisition) or first slice (for 2D acquisition). Additionally, the `BackgroundSuppressionPulseTime`'s is required in case `BackgroundSuppression` was applied. This an array of numbers containing the timing in seconds of the background suppression pulses with respect to the start of the labeling. In the case of `PCASL`, the recommended `PCASLType` field defines the type of the gradient pulses used in the `control` condition (`balanced` or `unbalanced`), whereas in case of `CASL`,the recommended `CASLType` field describes if a separate coil is used for labeling (`single-coil` or `double-coil`).

(P)CASL Labeling Pulses

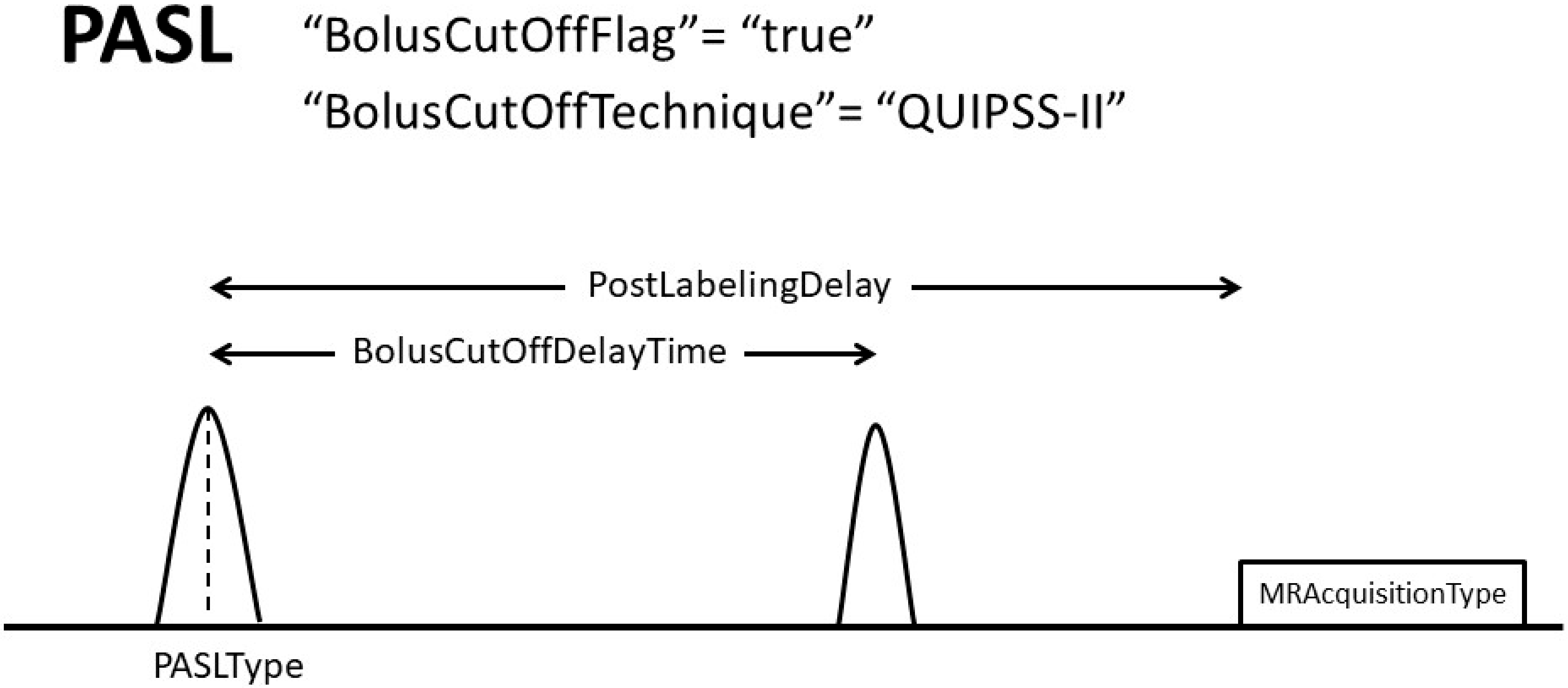


Several recommended metadata fields describe the labeling pulses of the labeling pulse train in PCASL. The `LabelingPulseAverageGradient` and the `LabelingPulseMaximumGradient` are the average labeling gradient and the maximum amplitude of the gradient switched on during the application of the labeling RF pulse(s), in milliteslas per meter. The `LabelingPulseAverageB1` is the average B1-field strength of the RF labeling pulses in microteslas. The `LabelingPulseDuration` and `LabelingPulseInterval` are the duration of, and the delay between the peaks of the individual labeling pulses in milliseconds.

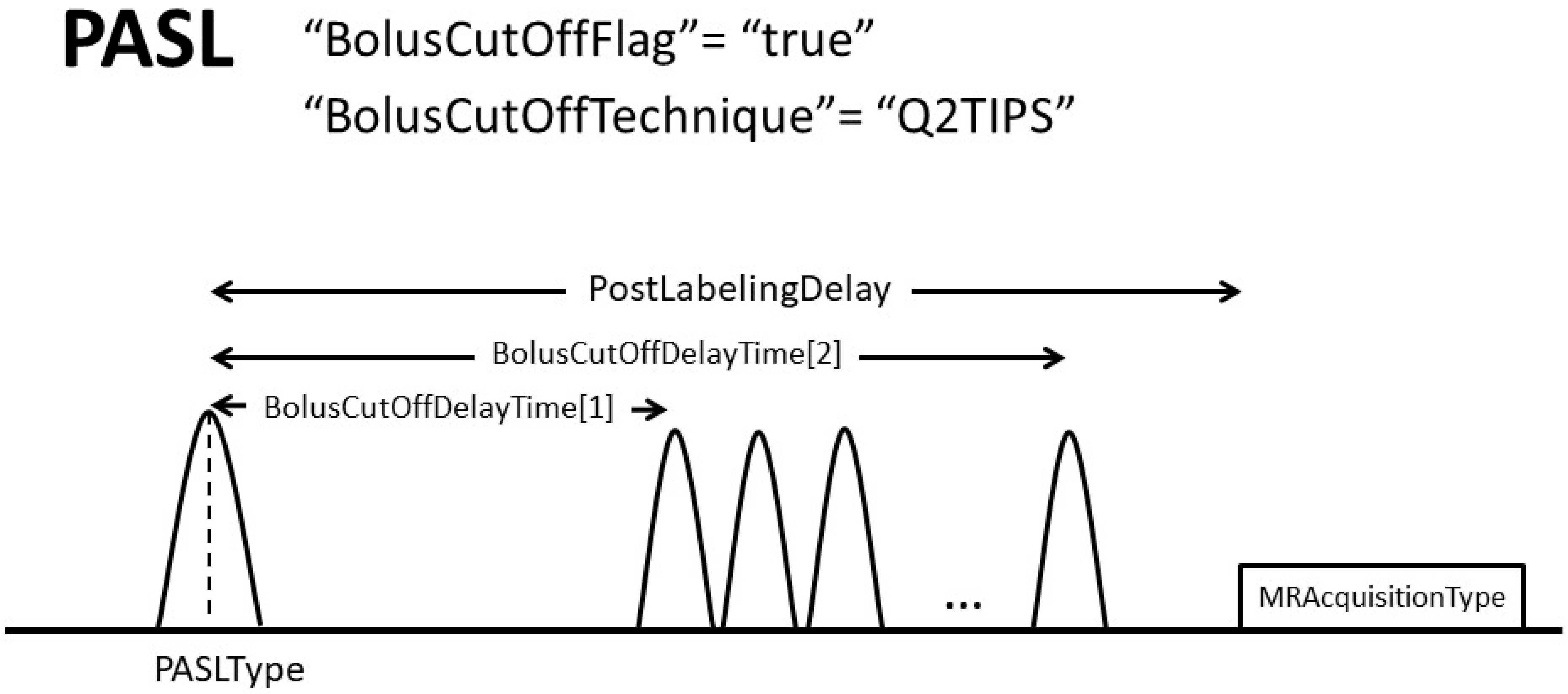
### PASL sequence



For PASL, specifying the `PostLabelingDelay` is required. `PostLabelingDelay` is the time, in seconds, from the middle of the labeling pulse until the middle of the excitation pulse applied to the imaging slab (for 3D acquisition) or first slice (for 2D acquisition). Additionally, the `BolusCutOffFlag` field is required, which is a boolean indicating if a bolus cut-off technique has been applied.



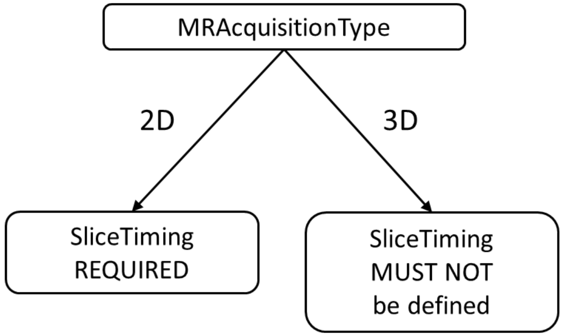
When `BolusCutOffFlag` is set true for `PASL`, two additional metadata fields are required: `BolusCutOffTechnique` and `BolusCutOffDelay`. In this example, the `BolusCutOffTechnique`, which is the name of the technique used for applying a bolus cut-off, is QUIPSS-II consisting of only one bolus cut-off pulse. The `BolusCutOffDelay` is therefore a number, representing the duration between the end of the labeling and the start of the bolus cut-off saturation pulse, in seconds.

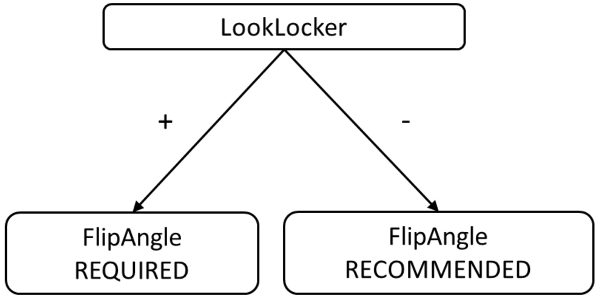


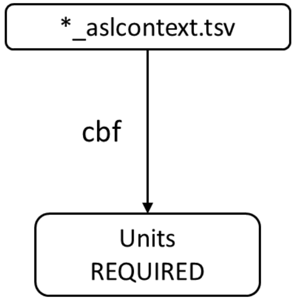
In this example, the `BolusCutOffTechnique` applied is Q2TIPS, consisting of multiple bolus cut-off pulses. In this case, only the duration of the first and last pulse should be specified in `BolusCutOffDelay`.

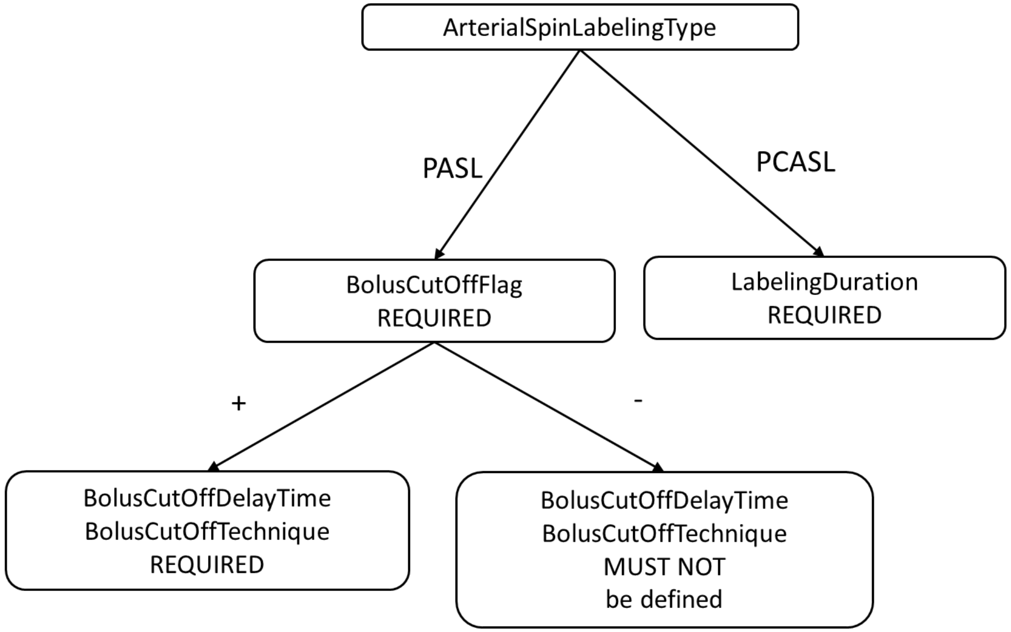
## Flowchart (based on dependency table)

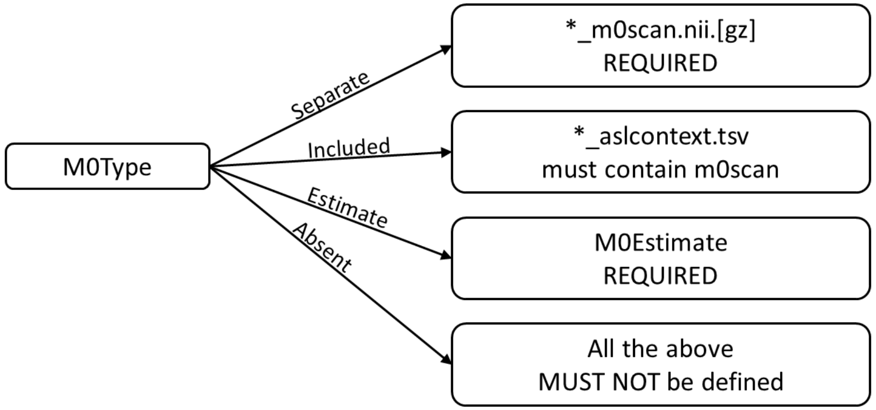
The specification includes a dependency table, describing metadata field dependencies for ASL. This flowchart is intended to further clarify that table.


MRAcquisitionType
2D
3D
SliceTiming REQUIRED
SliceTiming MUST NOT be defined


LookLocker
+
-
FlipAngle REQUIRED
FlipAngle RECOMMENDED


*_aslcontext.tsv
cbf
Units REQUIRED


ArterialSpinLabelingType
PASL
PCASL
BolusCutOffFlag REQUIRED
LabelingDuration REQUIRED
+
-
BolusCutOffDelayTime BolusCutOffTechnique REQUIRED
BolusCutOffDelayTime BolusCutOffTechnique MUST NOT be defined


M0Type
Separate
Included
Estimate
Absent
*_m0scan.nii.[gz] REQUIRED
*_aslcontext.tsv must contain m0scan
M0Estimate REQUIRED
All the above MUST NOT be defined

# Appendix XIII: Cross modality correspondence

## PET-MRI correspondence

When sharing MRI data alongside with PET data, please pay specific attention to the format the MR images are in. It is important to note whether the MR images have been unwarped in order to correct for gradient non-linearities, indicated by the `NonlinearGradientCorrection` metadata field (see Magnetic Resonance Imaging Data - Sequence Specifics). The reason for this is that the MRI needs to be corrected for nonlinear gradients in order to fit the accompanying PET scans for co-registration (Knudsen et al. 2020, doi:10.1177/0271678X20905433; Norgaard et al. 2019, doi:10.1016/j.neuroimage.2019.05.055).

# Appendix XIV: Glossary of schema objects

This section compiles the object definitions in the schema.

## 2PE (suffixes)

name: 2-photon excitation microscopy

description:

> 2-photon excitation microscopy imaging data

schema information:

```
{}
```

## Acknowledgements (metadata)

name: Acknowledgements

description:

> Text acknowledging contributions of individuals or institutions beyond those listed in Authors or Funding.

schema information:

```
{'type': 'string'}
```

## AcquisitionDuration (metadata)

name: AcquisitionDuration

description:

> Duration (in seconds) of volume acquisition. Corresponds to DICOM Tag 0018, 9073 `Acquisition Duration`. This field is mutually exclusive with `"RepetitionTime"`.

schema information:

```
{'type': 'number', 'exclusiveMinimum': 0, 'unit': 's'}
```

## AcquisitionMode (metadata)

name: AcquisitionMode

description:

> Type of acquisition of the PET data (for example, `"list mode"`).

schema information:

```
{'type': 'string'}
```

## AcquisitionVoxelSize (metadata)

name: AcquisitionVoxelSize

description:

> An array of numbers with a length of 3, in millimeters. This parameter denotes the original acquisition voxel size, excluding any inter-slice gaps and before any interpolation or resampling within reconstruction or image processing. Any point spread function effects, for example due to T2-blurring, that would decrease the effective resolution are not considered here.

schema information:

```
{'type': 'array', 'minItems': 3, 'maxItems': 3, 'items': {'type': 'number', 'exclusiveMinimum': 0, 'unit': 'mm'}}
```

## Anaesthesia (metadata)

name: Anaesthesia

description:

> Details of anaesthesia used, if any.

schema information:

```
{'type': 'string'}
```

## AnalyticalApproach (metadata)

name: AnalyticalApproach

description:

> Methodology or methodologies used to analyse the `"GeneticLevel"`. Values MUST be taken from the database of Genotypes and Phenotypes (dbGaP) under /Study/Molecular Data Type (for example, SNP Genotypes (Array) or Methylation (CpG).

schema information:

```
{'anyOf': [{'type': 'string'}, {'type': 'array', 'items': {'type': 'string'}}]}
```

## AnatomicalLandmarkCoordinateSystem (metadata)

name: AnatomicalLandmarkCoordinateSystem

description:

> Defines the coordinate system for the anatomical landmarks. See Appendix VIII for a list of restricted keywords for coordinate systems. If `"Other"`, provide definition of the coordinate system in `"AnatomicalLandmarkCoordinateSystemDescription"`.

schema information:

```
{'type': 'string', 'enum': ['CTF', 'ElektaNeuromag', '4DBti', 'KitYokogawa', 'ChietiItab', 'Other', 'CapTrak', 'EEGLAB', 'EEGLAB-HJ', 'Other', 'ICBM452
```

## AnatomicalLandmarkCoordinateSystemDescription (metadata)

name: AnatomicalLandmarkCoordinateSystemDescription

description:

> Free-form text description of the coordinate system. May also include a link to a documentation page or paper describing the system in greater detail.

schema information:

```
{'type': 'string'}
```

## AnatomicalLandmarkCoordinateUnits (metadata)

name: AnatomicalLandmarkCoordinateUnits

description:

> Units of the coordinates of `"AnatomicalLandmarkCoordinateSystem"`.

schema information:

`{'type': 'string', 'enum': ['m', 'mm', 'cm', 'n/a']}`

## AnatomicalLandmarkCoordinates sense 1 (metadata)

name: AnatomicalLandmarkCoordinates

description:

> Key:value pairs of the labels and 3-D digitized locations of anatomical landmarks, interpreted following the `"AnatomicalLandmarkCoordinateSystem"` (for example, `{"NAS": [12.7,21.3,13.9], "LPA": [5.2,11.3,9.6], "RPA": [20.2,11.3,9.1]}`. Each array MUST contain three numeric values corresponding to x, y, and z axis of the coordinate system in that exact order.

schema information:

`{'type': 'object', 'additionalProperties': {'type': 'array', 'items': {'type': 'number'}, 'minItems': 3, 'maxItems': 3}}`

## AnatomicalLandmarkCoordinates sense 2 (metadata)

name: AnatomicalLandmarkCoordinates

description:

> Key:value pairs of any number of additional anatomical landmarks and their coordinates in voxel units (where first voxel has index 0,0,0) relative to the associated anatomical MRI (for example, `{"AC": [127,119,149], "PC": [128,93,141], "IH": [131,114,206]}`, or `{"NAS": [127,213,139], "LPA": [52,113,96], "RPA": [202,113,91]}`). Each array MUST contain three numeric values corresponding to x, y, and z axis of the coordinate system in that exact order.

schema information:

`{'type': 'object', 'additionalProperties': {'type': 'array', 'items': {'type': 'number'}, 'minItems': 3, 'maxItems': 3}}`

## ArterialSpinLabelingType (metadata)

name: ArterialSpinLabelingType

description:

> The arterial spin labeling type.

schema information:

`{'type': 'string', 'enum': ['CASL', 'PCASL', 'PASL']}`

## AssociatedEmptyRoom (metadata)

name: AssociatedEmptyRoom

description:

> Relative path in BIDS folder structure to empty-room file associated with the subject's MEG recording. The path needs to use forward slashes instead of backward slashes (for example, "sub-emptyroom/ses-/meg/sub-emptyroom_ses-_task-noise_run-_meg.ds").

schema information:

```
{'anyOf': [{'type': 'array', 'items': {'type': 'string', 'format': 'dataset_relative'}}, {'type': 'string', 'format': 'dataset_relative'}]}
```

## Atlas (metadata)

name: Atlas

description:

> Which atlas (if any) was used to generate the mask.

schema information:

```
{'type': 'string'}
```

## AttenuationCorrection (metadata)

name: AttenuationCorrection

description:

> Short description of the attenuation correction method used.

schema information:

```
{'type': 'string'}
```

## AttenuationCorrectionMethodReference (metadata)

name: AttenuationCorrectionMethodReference

description:

> Reference paper for the attenuation correction method used.

schema information:

```
{'type': 'string'}
```

## Authors (metadata)

name: Authors

description:

List of individuals who contributed to the creation/curation of the dataset.

schema information:

```
{'type': 'array', 'items': {'type': 'string'}}
```

## B0FieldIdentifier (metadata)

name: B0FieldIdentifier

description:

The presence of this key states that this particular 3D or 4D image MAY be used for fieldmap estimation purposes. Each `"B0FieldIdentifier"` MUST be a unique string within one participant's tree, shared only by the images meant to be used as inputs for the estimation of a particular instance of the B0 field estimation. It is RECOMMENDED to derive this identifier from DICOM Tags, for example, DICOM tag 0018, 1030 `Protocol Name`, or DICOM tag 0018, 0024 `Sequence Name` when the former is not defined (for example, in GE devices.)

schema information:

```
{'anyOf': [{'type': 'string'}, {'type': 'array', 'items': {'type': 'string'}}]}
```

## B0FieldSource (metadata)

name: B0FieldSource

description:

At least one existing `"B0FieldIdentifier"` defined by images in the participant's tree. This field states the B0 field estimation designated by the `"B0FieldIdentifier"` that may be used to correct the dataset for distortions caused by B0 inhomogeneities. `"B0FieldSource"` and `"B0FieldIdentifier"` MAY both be present for images that are used to estimate their own B0 field, for example, in ”pepolar” acquisitions.

schema information:

```
{'anyOf': [{'type': 'string'}, {'type': 'array', 'items': {'type': 'string'}}]}
```

## BF (suffixes)

name: Bright-field microscopy

description:

Bright-field microscopy imaging data

schema information:

```
{}
```

## BIDSVersion (metadata)

name: BIDSVersion

description:

The version of the BIDS standard that was used.

schema information:

```
{'type': 'string'}
```

## BackgroundSuppression (metadata)

name: BackgroundSuppression

description:

Boolean indicating if background suppression is used.

schema information:

```
{'type': 'boolean'}
```

## BackgroundSuppressionNumberPulses (metadata)

name: BackgroundSuppressionNumberPulses

description:

The number of background suppression pulses used. Note that this excludes any effect of background suppression pulses applied before the labeling.

schema information:

```
{'type': 'number', 'minimum': 0}
```

## BackgroundSuppressionPulseTime (metadata)

name: BackgroundSuppressionPulseTime

description:

> Array of numbers containing timing, in seconds, of the background suppression pulses with respect to the start of the labeling. In case of multi-PLD with different background suppression pulse times, only the pulse time of the first PLD should be defined.

schema information:

```
{'type': 'array', 'items': {'type': 'number', 'minimum': 0, 'unit': 's'}}
```

## BasedOn (metadata)

name: BasedOn

description:

> List of files in a file collection to generate the map. Fieldmaps are also listed, if involved in the processing.

schema information:

```
{'anyOf': [{'type': 'string', 'format': 'participant_relative'}, {'type': 'array', 'items': {'type': 'string', 'format': 'participant_relative'}}]}
```

## BloodDensity (metadata)

name: BloodDensity

description:

> Measured blood density. Unit of blood density should be in `"g/mL"`.

schema information:

```
{'type': 'number', 'unit': 'g/mL'}
```

## BodyPart (metadata)

name: BodyPart

description:

> Body part of the organ / body region scanned.

schema information:

```
{'type': 'string'}
```

## BodyPartDetails (metadata)

name: BodyPartDetails

description:

> Additional details about body part or location (for example: `"corpus callosum"`).

schema information:

```
{'type': 'string'}
```

## BodyPartDetailsOntology (metadata)

name: BodyPartDetailsOntology

description:

> URI of ontology used for BodyPartDetails (for example: `"https://www.ebi.ac.uk/ols/ontologies/uberon"`).

schema information:

```
{'type': 'string', 'format': 'uri'}
```

## BolusCutOffDelayTime (metadata)

name: BolusCutOffDelayTime

description:

> Duration between the end of the labeling and the start of the bolus cut-off saturation pulse(s), in seconds. This can be a number or array of numbers, of which the values must be non-negative and monotonically increasing, depending on the number of bolus cut-off saturation pulses. For Q2TIPS, only the values for the first and last bolus cut-off saturation pulses are provided. Based on DICOM Tag 0018, 925F `ASL Bolus Cut-off Delay Time`.

schema information:

```
{'anyOf': [{'type': 'number', 'minimum': 0, 'unit': 's'}, {'type': 'array', 'items': {'type': 'number', 'unit': 's', 'minimum': 0}}]}
```

## BolusCutOffFlag (metadata)

name: BolusCutOffFlag

description:

Boolean indicating if a bolus cut-off technique is used. Corresponds to DICOM Tag 0018, 925C `ASL Bolus Cut-off Flag`.

schema information:

```
{'type': 'boolean'}
```

## BolusCutOffTechnique (metadata)

name: BolusCutOffTechnique

description:

Name of the technique used, for example `"Q2TIPS"`, `"QUIPSS"`, `"QUIPSSII"`. Corresponds to DICOM Tag 0018, 925E `ASL Bolus Cut-off Technique`.

schema information:

```
{'type': 'string'}
```

## BrainLocation (metadata)

name: BrainLocation

description:

Refers to the location in space of the `"TissueOrigin"`. Values may be an MNI coordinate, a label taken from the Allen Brain Atlas, or layer to refer to layer-specific gene expression, which can also tie up with laminar fMRI.

schema information:

```
{'type': 'string'}
```

## CARS (suffixes)

name: Coherent anti-Stokes Raman spectroscopy

description:

Coherent anti-Stokes Raman spectroscopy imaging data

schema information:

```
{}
```

## CASLType (metadata)

name: CASLType

description:

Describes if a separate coil is used for labeling.

schema information:

```
{'type': 'string', 'enum': ['single-coil', 'double-coil']}
```

## CHANGES (top_level_files)

name: CHANGES

description:

Version history of the dataset (describing changes, updates and corrections) MAY be provided in the form of a `CHANGES` text file. This file MUST follow the CPAN Changelog convention. The `CHANGES` file MUST be either in ASCII or UTF-8 encoding.

schema information:

```
{}
```

## CONF (suffixes)

name: Confocal microscopy

description:

Confocal microscopy imaging data

schema information:

```
{}
```

## CapManufacturer (metadata)

name: CapManufacturer

description:

Name of the cap manufacturer (for example, `"EasyCap"`).

schema information:

```
{'type': 'string'}
```

## CapManufacturersModelName (metadata)

name: CapManufacturersModelName

description:

> Manufacturer's designation of the EEG cap model (for example, `"actiCAP 64 Ch Standard-2"`).

schema information:

```
{'type': 'string'}
```

## CellType (metadata)

name: CellType

description:

> Describes the type of cell analyzed. Values SHOULD come from the cell ontology.

schema information:

```
{'type': 'string'}
```

## Chimap (suffixes)

name: Quantitative susceptibility map (QSM)

description:

> In parts per million (ppm). QSM allows for determining the underlying magnetic susceptibility of tissue (Chi) (Wang & Liu, 2014). Chi maps are REQUIRED to use this suffix regardless of the method used to generate them.

schema information:

```
{'unit': 'ppm'}
```

## ChunkTransformationMatrix (metadata)

name: ChunkTransformationMatrix

description:

> 3x3 or 4x4 affine transformation matrix describing spatial chunk transformation, for 2D and 3D respectively (for examples: `[[2, 0, 0], [0, 3, 0], [0, 0, 1]]` in 2D for 2x and 3x scaling along the first and second axis respectively; or `[[1, 0, 0, 0], [0, 2, 0, 0], [0, 0, 3, 0], [0, 0, 0, 1]]` in 3D for 2x and 3x scaling along the second and third axis respectively). Note that non-spatial dimensions like time and channel are not included in the transformation matrix.

schema information:

```
{'anyOf': [{'type': 'array', 'minItems': 3, 'maxItems': 3, 'items': {'type': 'array', 'minItems': 3, 'maxItems': 3, 'items': {'type': 'number'}}}, {'ty
```

## ChunkTransformationMatrixAxis (metadata)

name: ChunkTransformationMatrixAxis

description:

> Describe the axis of the ChunkTransformationMatrix (for examples: `["X", "Y"]` or `["Z", "Y", "X"]`).

schema information:

```
{'type': 'array', 'items': {'type': 'string', 'minItems': 2, 'maxItems': 3}}
```

## Code (metadata)

name: Code

description:

> URI of the code used to present the stimuli. Persistent identifiers such as DOIs are preferred. If multiple versions of code may be hosted at the same location, revision-specific URIs are recommended.

schema information:

```
{'type': 'string', 'format': 'uri'}
```

## CogAtlasID (metadata)

name: CogAtlasID

description:

> URI of the corresponding Cognitive Atlas Task term.

schema information:

```
{'type': 'string', 'format': 'uri'}
```

## CogPOID (metadata)

name: CogPOID

description:

URI of the corresponding CogPO term.

schema information:

```
{'type': 'string', 'format': 'uri'}
```

## CoilCombinationMethod (metadata)

name: CoilCombinationMethod

description:

Almost all fMRI studies using phased-array coils use root-sum-of-squares (rSOS) combination, but other methods exist. The image reconstruction is changed by the coil combination method (as for the matrix coil mode above), so anything non-standard should be reported.

schema information:

```
{'type': 'string'}
```

## Columns (metadata)

name: Columns

description:

Names of columns in file.

schema information:

```
{'type': 'array', 'items': {'type': 'string'}}
```

## ContinuousHeadLocalization (metadata)

name: ContinuousHeadLocalization

description:

`true` or `false` value indicating whether continuous head localisation was performed.

schema information:

```
{'type': 'boolean'}
```

## ContrastBolusIngredient (metadata)

name: ContrastBolusIngredient

description:

Active ingredient of agent. Corresponds to DICOM Tag 0018, 1048 `Contrast/Bolus Ingredient`.

schema information:

```
{'type': 'string', 'enum': ['IODINE', 'GADOLINIUM', 'CARBON DIOXIDE', 'BARIUM', 'XENON']}
```

## DCOffsetCorrection (metadata)

name: DCOffsetCorrection

description:

A description of the method (if any) used to correct for a DC offset. If the method used was subtracting the mean value for each channel, use ”mean”.

schema information:

```
{'type': 'string'}
```

## DF (suffixes)

name: Dark-field microscopy

description:

Dark-field microscopy imaging data

schema information:

```
{}
```

## DIC (suffixes)

name: Differential interference contrast microscopy

description:

Differential interference contrast microscopy imaging data

schema information:

```
{}
```

## DatasetDOI (metadata)

name: DatasetDOI

description:

> The Digital Object Identifier of the dataset (not the corresponding paper). DOIs SHOULD be expressed as a valid URI; bare DOIs such as `10.0.2.3/dfjj.10` are URI.

schema information:

```
{'type': 'string', 'format': 'uri'}
```

## DatasetType (metadata)

name: DatasetType

description:

> The interpretation of the dataset. For backwards compatibility, the default value is `"raw"`.

schema information:

```
{'type': 'string', 'enum': ['raw', 'derivative']}
```

## DecayCorrectionFactor (metadata)

name: DecayCorrectionFactor

description:

> Decay correction factor for each frame.

schema information:

```
{'type': 'array', 'items': {'type': 'number'}}
```

## DelayAfterTrigger (metadata)

name: DelayAfterTrigger

description:

> Duration (in seconds) from trigger delivery to scan onset. This delay is commonly caused by adjustments and loading times. This specification is entirely independent of `"NumberOfVolumesDiscardedByScanner"` or `"NumberOfVolumesDiscardedByUser"`, as the delay precedes the acquisition.

schema information:

```
{'type': 'number', 'unit': 's'}
```

## DelayTime (metadata)

name: DelayTime

description:

> User specified time (in seconds) to delay the acquisition of data for the following volume. If the field is not present it is assumed to be set to zero. Corresponds to Siemens CSA header field `lDelayTimeInTR`. This field is REQUIRED for sparse sequences using the `"RepetitionTime"` field that do not have the `"SliceTiming"` field set to allowed for accurate calculation of ”acquisition time”. This field is mutually exclusive with `"VolumeTiming"`.

schema information:

```
{'type': 'number', 'unit': 's'}
```

## Density (metadata)

name: Density

description:

> Specifies the interpretation of the density keyword. If an object is used, then the keys should be values for the `den` entity and values should be descriptions of those `den` values.

schema information:

```
{'anyOf': [{'type': 'string'}, {'type': 'object', 'additionalProperties': {'type': 'string'}}]}
```

## Derivative (metadata)

name: Derivative

description:

> Indicates that values in the corresponding column are transformations of values from other columns (for example a summary score based on a subset of items in a questionnaire).

schema information:

```
{'type': 'boolean'}
```

## Description (metadata)

name: Description

description:

Free-form natural language description.

schema information:

```
{'type': 'string'}
```

## DeviceSerialNumber (metadata)

name: DeviceSerialNumber

description:

The serial number of the equipment that produced the measurements. A pseudonym can also be used to prevent the equipment from being identifiable, so long as each pseudonym is unique within the dataset.

schema information:

```
{'type': 'string'}
```

## DewarPosition (metadata)

name: DewarPosition

description:

Position of the dewar during the MEG scan: `"upright"`, `"supine"` or `"degrees"` of angle from vertical: for example on CTF systems, `"upright=15°, supine=90°"`.

schema information:

```
{'type': 'string'}
```

## DigitizedHeadPoints (metadata)

name: DigitizedHeadPoints

description:

> `true` or `false` value indicating whether head points outlining the scalp/face surface are contained within this recording.

schema information:

```
{'type': 'boolean'}
```

## DigitizedHeadPointsCoordinateSystem (metadata)

name: DigitizedHeadPointsCoordinateSystem

description:

> Defines the coordinate system for the digitized head points. See Appendix VIII for a list of restricted keywords for coordinate systems. If `"Other"`, provide definition of the coordinate system in `"DigitizedHeadPointsCoordinateSystemDescription"`.

schema information:

```
{'type': 'string', 'enum': ['CTF', 'ElektaNeuromag', '4DBti', 'KitYokogawa', 'ChietiItab', 'Other', 'CapTrak', 'EEGLAB', 'EEGLAB-HJ', 'Other', 'ICBM452
```

## DigitizedHeadPointsCoordinateSystemDescription (metadata)

name: DigitizedHeadPointsCoordinateSystemDescription

description:

> Free-form text description of the coordinate system. May also include a link to a documentation page or paper describing the system in greater detail.

schema information:

```
{'type': 'string'}
```

## DigitizedHeadPointsCoordinateUnits (metadata)

name: DigitizedHeadPointsCoordinateUnits

description:

> Units of the coordinates of `"DigitizedHeadPointsCoordinateSystem"`.

schema information:

`{'type': 'string', 'enum': ['m', 'mm', 'cm', 'n/a']}`

## DigitizedLandmarks (metadata)

name: DigitizedLandmarks

description:

`true` or `false` value indicating whether anatomical landmark points (fiducials) are contained within this recording.

schema information:

`{'type': 'boolean'}`

## DispersionConstant (metadata)

name: DispersionConstant

description:

External dispersion time constant resulting from tubing in default unit seconds.

schema information:

`{'type': 'number', 'unit': 's'}`

## DispersionCorrected (metadata)

name: DispersionCorrected

description:

Boolean flag specifying whether the blood data have been dispersion-corrected. NOTE: not customary for manual samples, and hence should be set to `false`.

schema information:

`{'type': 'boolean'}`

## DoseCalibrationFactor (metadata)

name: DoseCalibrationFactor

description:

Multiplication factor used to transform raw data (in counts/sec) to meaningful unit (Bq/ml). Corresponds to DICOM Tag 0054, 1322 `Dose Calibration Factor`.

schema information:

`{'type': 'number'}`

## DwellTime (metadata)

name: DwellTime

description:

> Actual dwell time (in seconds) of the receiver per point in the readout direction, including any oversampling. For Siemens, this corresponds to DICOM field 0019, 1018 (in ns). This value is necessary for the optional readout distortion correction of anatomicals in the HCP Pipelines. It also usefully provides a handle on the readout bandwidth, which isn't captured in the other metadata tags. Not to be confused with `"EffectiveEchoSpacing"`, and the frequent mislabeling of echo spacing (which is spacing in the phase encoding direction) as "dwell time" (which is spacing in the readout direction).

schema information:

`{'type': 'number', 'unit': 's'}`

## ECGChannelCount (metadata)

name: ECGChannelCount

description:

> Number of ECG channels.

schema information:

`{'type': 'integer', 'minimum': 0}`

## ECOGChannelCount (metadata)

name: ECOGChannelCount

description:

> Number of ECoG channels.

schema information:

`{'type': 'integer', 'minimum': 0}`

## EEGChannelCount (metadata)

name: EEGChannelCount

description:

> Number of EEG channels recorded simultaneously (for example, `21`).

schema information:

```
{'type': 'integer', 'minimum': 0}
```

## EEGCoordinateSystem (metadata)

name: EEGCoordinateSystem

description:

> Defines the coordinate system for the EEG sensors.See Appendix VIII for a list of restricted keywords for coordinate systems. If `"Other"`, provide definition of the coordinate system in `EEGCoordinateSystemDescription`.

schema information:

```
{'type': 'string', 'enum': ['CTF', 'ElektaNeuromag', '4DBti', 'KitYokogawa', 'ChietiItab', 'Other', 'CapTrak', 'EEGLAB', 'EEGLAB-HJ', 'Other', 'ICBM452
```

## EEGCoordinateSystemDescription (metadata)

name: EEGCoordinateSystemDescription

description:

> Free-form text description of the coordinate system. May also include a link to a documentation page or paper describing the system in greater detail.

schema information:

```
{'type': 'string'}
```

## EEGCoordinateUnits (metadata)

name: EEGCoordinateUnits

description:

> Units of the coordinates of `EEGCoordinateSystem`.

schema information:

```
{'type': 'string', 'enum': ['m', 'mm', 'cm', 'n/a']}
```

## EEGGround (metadata)

name: EEGGround

description:

> Description of the location of the ground electrode (for example, `"placed on right mastoid (M2)"`).

schema information:

```
{'type': 'string'}
```

## EEGPlacementScheme (metadata)

name: EEGPlacementScheme

description:

> Placement scheme of EEG electrodes. Either the name of a standardized placement system (for example, `"10-20"`) or a list of standardized electrode names (for example, `["Cz", "Pz"]`).

schema information:

```
{'type': 'string'}
```

## EEGReference (metadata)

name: EEGReference

description:

> General description of the reference scheme used and (when applicable) of location of the reference electrode in the raw recordings (for example, `"left mastoid"`, `"Cz"`, `"CMS"`). If different channels have a different reference, this field should have a general description and the channel specific reference should be defined in the `channels.tsv` file.

schema information:

```
{'type': 'string'}
```

## EMGChannelCount (metadata)

name: EMGChannelCount

description:

Number of EMG channels.

schema information:

```
{'type': 'integer', 'minimum': 0}
```

## EOGChannelCount (metadata)

name: EOGChannelCount

description:

Number of EOG channels.

schema information:

```
{'type': 'integer', 'minimum': 0}
```

## EchoTime sense 1 (metadata)

name: EchoTime

description:

The echo time (TE) for the acquisition, specified in seconds. Corresponds to DICOM Tag 0018, 0081 `Echo Time` (please note that the DICOM term is in milliseconds not seconds). The data type number may apply to files from any MRI modality concerned with a single value for this field, or to the files in a file collection where the value of this field is iterated using the file collection. The data type array provides a value for each volume in a 4D dataset and should only be used when the volume timing is critical for interpretation of the data, such as in file collection or variable echo time fMRI sequences.

schema information:

```
{'anyOf': [{'type': 'number', 'unit': 's', 'exclusiveMinimum': 0}, {'type': 'array', 'items': {'type': 'number', 'unit': 's', 'exclusiveMinimum': 0}}]}
```

## EchoTime sense 2 (metadata)

name: EchoTime

description:

The time (in seconds) when the echo corresponding to this map was acquired.

schema information:

`{'type': 'number', 'unit': 's', 'exclusiveMinimum': 0}`

## EchoTime1 (metadata)

name: EchoTime1

description:

The time (in seconds) when the first (shorter) echo occurs.

schema information:

`{'type': 'number', 'unit': 's', 'exclusiveMinimum': 0}`

## EchoTime2 (metadata)

name: EchoTime2

description:

The time (in seconds) when the second (longer) echo occurs.

schema information:

`{'type': 'number', 'unit': 's', 'exclusiveMinimum': 0}`

## EffectiveEchoSpacing (metadata)

name: EffectiveEchoSpacing

description:

The ”effective” sampling interval, specified in seconds, between lines in the phase-encoding direction, defined based on the size of the reconstructed image in the phase direction. It is frequently, but incorrectly, referred to as ”dwell time” (see the `"DwellTime"` parameter for actual dwell time). It is required for unwarping distortions using field maps. Note that beyond just in-plane acceleration, a variety of other manipulations to the phase encoding need to be accounted for properly, including partial fourier, phase oversampling, phase resolution, phase field-of-view and interpolation.

schema information:

`{'type': 'number', 'exclusiveMinimum': 0, 'unit': 's'}`

## ElectricalStimulation (metadata)

name: ElectricalStimulation

description:

> Boolean field to specify if electrical stimulation was done during the recording (options are `true` or `false`). Parameters for event-like stimulation should be specified in the `events.tsv` file.

schema information:

```
{'type': 'boolean'}
```

## ElectricalStimulationParameters (metadata)

name: ElectricalStimulationParameters

description:

> Free form description of stimulation parameters, such as frequency or shape. Specific onsets can be specified in the events.tsv file. Specific shapes can be described here in freeform text.

schema information:

```
{'type': 'string'}
```

## ElectrodeManufacturer (metadata)

name: ElectrodeManufacturer

description:

> Can be used if all electrodes are of the same manufacturer (for example, `"AD-TECH"`, `"DIXI"`). If electrodes of different manufacturers are used, please use the corresponding table in the `_electrodes.tsv` file.

schema information:

```
{'type': 'string'}
```

## ElectrodeManufacturersModelName (metadata)

name: ElectrodeManufacturersModelName

description:

> If different electrode types are used, please use the corresponding table in the `_electrodes.tsv` file.

schema information:

`{'type': 'string'}`

## EpochLength (metadata)

name: EpochLength

description:

Duration of individual epochs in seconds (for example, `1`) in case of epoched data. If recording was continuous or discontinuous, leave out the field.

schema information:

`{'type': 'number', 'minimum': 0}`

## EstimationAlgorithm (metadata)

name: EstimationAlgorithm

description:

Type of algorithm used to perform fitting (for example, `"linear"`, `"non-linear"`, `"LM"` and such).

schema information:

`{'type': 'string'}`

## EstimationReference (metadata)

name: EstimationReference

description:

Reference to the study/studies on which the implementation is based.

schema information:

`{'type': 'string'}`

## EthicsApprovals (metadata)

name: EthicsApprovals

description:

List of ethics committee approvals of the research protocols and/or protocol identifiers.

schema information:

```
{'type': 'array', 'items': {'type': 'string'}}
```

## FLAIR (suffixes)

name: Fluid attenuated inversion recovery image

description:

In arbitrary units (arbitrary). Structural images with predominant T2 contribution (also known as T2-FLAIR), in which signal from fluids (for example, CSF) is nulled out by adjusting inversion time, coupled with notably long repetition and echo times.

schema information:

```
{'unit': 'arbitrary'}
```

## FLASH (suffixes)

name: Fast-Low-Angle-Shot image

description:

FLASH (Fast-Low-Angle-Shot) is a vendor-specific implementation for spoiled gradient echo acquisition. It is commonly used for rapid anatomical imaging and also for many different qMRI applications. When used for a single file, it does not convey any information about the image contrast. When used in a file collection, it may result in conflicts across filenames of different applications. Change: Removed from suffixes.

schema information:

```
{}
```

## FLUO (suffixes)

name: Fluorescence microscopy

description:

Fluorescence microscopy imaging data

schema information:

```
{}
```

## FiducialsCoordinateSystem (metadata)

name: FiducialsCoordinateSystem

description:

> Defines the coordinate system for the fiducials. Preferably the same as the `"EEGCoordinateSystem"`. See Appendix VIII for a list of restricted keywords for coordinate systems. If `"Other"`, provide definition of the coordinate system in `"FiducialsCoordinateSystemDescription"`.

schema information:

```
{'type': 'string', 'enum': ['CTF', 'ElektaNeuromag', '4DBti', 'KitYokogawa', 'ChietiItab', 'Other', 'CapTrak', 'EEGLAB', 'EEGLAB-HJ', 'Other', 'ICBM452
```

## FiducialsCoordinateSystemDescription (metadata)

name: FiducialsCoordinateSystemDescription

description:

> Free-form text description of the coordinate system. May also include a link to a documentation page or paper describing the system in greater detail.

schema information:

```
{'type': 'string'}
```

## FiducialsCoordinateUnits (metadata)

name: FiducialsCoordinateUnits

description:

> Units in which the coordinates that are listed in the field `"FiducialsCoordinateSystem"` are represented.

schema information:

```
{'type': 'string', 'enum': ['m', 'mm', 'cm', 'n/a']}
```

## FiducialsCoordinates (metadata)

name: FiducialsCoordinates

description:

> Key:value pairs of the labels and 3-D digitized position of anatomical landmarks, interpreted following the `"FiducialsCoordinateSystem"` (for example, `{"NAS": [12.7,21.3,13.9], "LPA": [5.2,11.3,9.6], "RPA": [20.2,11.3,9.1]}`). Each array MUST contain three numeric values corresponding to x, y, and z axis of the coordinate system in that exact order.

schema information:

```
{'type': 'object', 'additionalProperties': {'type': 'array', 'items': {'type': 'number'}, 'minItems': 3, 'maxItems': 3}}
```

## FiducialsDescription (metadata)

name: FiducialsDescription

description:

> Free-form text description of how the fiducials such as vitamin-E capsules were placed relative to anatomical landmarks, and how the position of the fiducials were measured (for example, `"both with Polhemus and with T1w MRI"`).

schema information:

```
{'type': 'string'}
```

## FlipAngle (metadata)

name: FlipAngle

description:

> Flip angle (FA) for the acquisition, specified in degrees. Corresponds to: DICOM Tag 0018, 1314 `Flip Angle`. The data type number may apply to files from any MRI modality concerned with a single value for this field, or to the files in a file collection where the value of this field is iterated using the file collection. The data type array provides a value for each volume in a 4D dataset and should only be used when the volume timing is critical for interpretation of the data, such as in file collection or variable flip angle fMRI sequences.

schema information:

```
{'anyOf': [{'type': 'number', 'unit': 'degree', 'exclusiveMinimum': 0, 'maximum': 360}, {'type': 'array', 'items': {'type': 'number', 'unit': 'degree',
```

## FrameDuration (metadata)

name: FrameDuration

description:

> Time duration of each frame in default unit seconds. This corresponds to DICOM Tag 0018, 1242 `Actual Frame Duration` converted to seconds.

schema information:

```
{'type': 'array', 'items': {'type': 'number'}, 'unit': 's'}
```

## FrameTimesStart (metadata)

name: FrameTimesStart

description:

Start times for all frames relative to `"TimeZero"` in default unit seconds.

schema information:

```
{'type': 'array', 'items': {'type': 'number'}, 'unit': 's'}
```

## Funding (metadata)

name: Funding

description:

List of sources of funding (grant numbers).

schema information:

```
{'type': 'array', 'items': {'type': 'string'}}
```

## GeneratedBy (metadata)

name: GeneratedBy

description:

Used to specify provenance of the dataset.

schema information:

```
{'type': 'array', 'minItems': 1, 'items': {'type': 'object', 'properties': {'Name': {'type': 'string'}, 'Version': {'type': 'string'}, 'Description': {
```

## GeneticLevel (metadata)

name: GeneticLevel

description:

Describes the level of analysis. Values MUST be one of `"Genetic"`, `"Genomic"`, `"Epigenomic"`, `"Transcriptomic"`, `"Metabolomic"`, or `"Proteomic"`.

schema information:

```
{'anyOf': [{'type': 'string', 'enum': ['Genetic', 'Genomic', 'Epigenomic', 'Transcriptomic', 'Metabolomic', 'Proteomic']}, {'type': 'array', 'items': {
```

## Genetics (metadata)

name: Genetics

description:

An object containing information about the genetics descriptor.

schema information:

```
{'type': 'object', 'properties': {'Database': {'name': 'Genetics.Database', 'description': '[URI](/02-common-principles.html#uniform-resource-indicator
```

## Genetics.Database (metadata)

name: Genetics.Database

description:

URI of database where the dataset is hosted.

schema information:

```
{'type': 'string', 'format': 'uri'}
```

## Genetics.Dataset (metadata)

name: Genetics.Dataset

description:

URI where data can be retrieved.

schema information:

```
{'type': 'string', 'format': 'uri'}
```

## Genetics.Descriptors (metadata)

name: Genetics.Descriptors

description:

List of relevant descriptors (for example, journal articles) for dataset using a valid URI when possible.

schema information:

```
{'anyOf': [{'type': 'string'}, {'type': 'array', 'items': {'type': 'string'}}]}
```

## GradientSetType (metadata)

name: GradientSetType

description:

> It should be possible to infer the gradient coil from the scanner model. If not, for example because of a custom upgrade or use of a gradient insert set, then the specifications of the actual gradient coil should be reported independently.

schema information:

```
{'type': 'string'}
```

## HED (columns)

name: HED

description:

> Hierarchical Event Descriptor (HED) Tag. See Appendix III for details.

schema information:

```
{'type': 'string'}
```

## HED (metadata)

name: HED

description:

> Hierarchical Event Descriptor (HED) information, see: Appendix III for details.

schema information:

```
{'anyOf': [{'type': 'string'}, {'type': 'object', 'additionalProperties': {'type': 'string'}}]}
```

## HEDVersion (metadata)

name: HEDVersion

description:

> If HED tags are used: The version of the HED schema used to validate HED tags for study.

schema information:

`{'type': 'string'}`

## Haematocrit (metadata)

name: Haematocrit

description:

> Measured haematocrit, meaning the volume of erythrocytes divided by the volume of whole blood.

schema information:

`{'type': 'number'}`

## HardcopyDeviceSoftwareVersion (metadata)

name: HardcopyDeviceSoftwareVersion

description:

> Manufacturer's designation of the software of the device that created this Hardcopy Image (the printer). Corresponds to DICOM Tag 0018, 101A `Hardcopy Device Software Version`.

schema information:

`{'type': 'string'}`

## HardwareFilters (metadata)

name: HardwareFilters

description:

> Object of temporal hardware filters applied, or `"n/a"` if the data is not available. Each key:value pair in the JSON object is a name of the filter and an object in which its parameters are defined as key:value pairs. For example, `{"Highpass RC filter": {"Half amplitude cutoff (Hz)": 0.0159, "Roll-off": "6dB/Octave"}}`.

schema information:

`{'anyOf': [{'type': 'object', 'additionalProperties': {'type': 'object'}}, {'type': 'string', 'enum': ['n/a']}]}`

## HeadCircumference (metadata)

name: HeadCircumference

description:

> Circumference of the participant's head, expressed in cm (for example, `58`).

schema information:

```
{'type': 'number', 'exclusiveMinimum': 0, 'unit': 'cm'}
```

## HeadCoilCoordinateSystem (metadata)

name: HeadCoilCoordinateSystem

description:

> Defines the coordinate system for the head coils. See Appendix VIII for a list of restricted keywords for coordinate systems. If `"Other"`, provide definition of the coordinate system in `HeadCoilCoordinateSystemDescription`.

schema information:

```
{'type': 'string', 'enum': ['CTF', 'ElektaNeuromag', '4DBti', 'KitYokogawa', 'ChietiItab', 'Other', 'CapTrak', 'EEGLAB', 'EEGLAB-HJ', 'Other', 'ICBM452
```

## HeadCoilCoordinateSystemDescription (metadata)

name: HeadCoilCoordinateSystemDescription

description:

> Free-form text description of the coordinate system. May also include a link to a documentation page or paper describing the system in greater detail.

schema information:

```
{'type': 'string'}
```

## HeadCoilCoordinateUnits (metadata)

name: HeadCoilCoordinateUnits

description:

> Units of the coordinates of `HeadCoilCoordinateSystem`.

schema information:

`{'type': 'string', 'enum': ['m', 'mm', 'cm', 'n/a']}`

## HeadCoilCoordinates (metadata)

name: HeadCoilCoordinates

description:

> Key:value pairs describing head localization coil labels and their coordinates, interpreted following the `HeadCoilCoordinateSystem` (for example, `{"NAS": [12.7,21.3,13.9], "LPA": [5.2,11.3,9.6], "RPA": [20.2,11.3,9.1]}`). Note that coils are not always placed at locations that have a known anatomical name (for example, for Elekta, Yokogawa systems); in that case generic labels can be used (for example, `{"coil1": [12.2,21.3,12.3], "coil2": [6.7,12.3,8.6], "coil3": [21.9,11.0,8.1]}`). Each array MUST contain three numeric values corresponding to x, y, and z axis of the coordinate system in that exact order.

schema information:

```
{'type': 'object', 'additionalProperties': {'type': 'array', 'items': {'type': 'number'}, 'minItems': 3, 'maxItems': 3}}
```

## HeadCoilFrequency (metadata)

name: HeadCoilFrequency

description:

> List of frequencies (in Hz) used by the head localisation coils ('HLC' in CTF systems, 'HPI' in Elekta, 'COH' in BTi/4D) that track the subject's head position in the MEG helmet (for example, `[293, 307, 314, 321]`).

schema information:

```
{'anyOf': [{'type': 'number', 'unit': 'Hz'}, {'type': 'array', 'items': {'type': 'number', 'unit': 'Hz'}}]}
```

## HowToAcknowledge (metadata)

name: HowToAcknowledge

description:

> Text containing instructions on how researchers using this dataset should acknowledge the original authors. This field can also be used to define a publication that should be cited in publications that use the dataset.

schema information:

```
{'type': 'string'}
```

## IRT1 (suffixes)

name: Inversion recovery T1 mapping

description:

The IRT1 method involves multiple inversion recovery spin-echo images acquired at different inversion times (Barral et al. 2010).

schema information:

```
{}
```

## ImageAcquisitionProtocol (metadata)

name: ImageAcquisitionProtocol

description:

Description of the image acquisition protocol or URI (for example from protocols.io).

schema information:

```
{'type': 'string'}
```

## ImageDecayCorrected (metadata)

name: ImageDecayCorrected

description:

Boolean flag specifying whether the image data have been decay-corrected.

schema information:

```
{'type': 'boolean'}
```

## ImageDecayCorrectionTime (metadata)

name: ImageDecayCorrectionTime

description:

Point in time from which the decay correction was applied with respect to `"TimeZero"` in the default unit seconds.

schema information:

```
{'type': 'number', 'unit': 's'}
```

## Immersion (metadata)

name: Immersion

description:

> Lens immersion medium. If the file format is OME-TIFF, the value MUST be consistent with the `Immersion` OME metadata field.

schema information:

```
{'type': 'string'}
```

## InfusionRadioactivity (metadata)

name: InfusionRadioactivity

description:

> Amount of radioactivity infused into the patient. This value must be less than or equal to the total injected radioactivity (`"InjectedRadioactivity"`). Units should be the same as `"InjectedRadioactivityUnits"`.

schema information:

```
{'type': 'number'}
```

## InfusionSpeed (metadata)

name: InfusionSpeed

description:

> If given, infusion speed.

schema information:

```
{'type': 'number'}
```

## InfusionSpeedUnits (metadata)

name: InfusionSpeedUnits

description:

> Unit of infusion speed (for example, `"mL/s"`).

schema information:

```
{'type': 'string', 'format': 'unit'}
```

## InfusionStart (metadata)

name: InfusionStart

description:

> Time of start of infusion with respect to `"TimeZero"` in the default unit seconds.

schema information:

```
{'type': 'number', 'unit': 's'}
```

## InjectedMass (metadata)

name: InjectedMass

description:

> Total mass of radiolabeled compound injected into subject (for example, `10`). This can be derived as the ratio of the `"InjectedRadioactivity"` and `"MolarRadioactivity"`. For those tracers in which injected mass is not available (for example FDG) can be set to **`"n/a"`**).

schema information:

```
{'anyOf': [{'type': 'number'}, {'type': 'string', 'enum': ['n/a']}]}
```

## InjectedMassPerWeight (metadata)

name: InjectedMassPerWeight

description:

> Injected mass per kilogram bodyweight.

schema information:

```
{'type': 'number'}
```

## InjectedMassPerWeightUnits (metadata)

name: InjectedMassPerWeightUnits

description:

> Unit format of the injected mass per kilogram bodyweight (for example, `"ug/kg"`).

schema information:

```
{'type': 'string', 'format': 'unit'}
```

## InjectedMassUnits (metadata)

name: InjectedMassUnits

description:

> Unit format of the mass of compound injected (for example, `"ug"` or `"umol"`). Note this is not required for an FDG acquisition, since it is not available, and SHOULD be set to `"n/a"`.

schema information:

```
{'anyOf': [{'type': 'string', 'format': 'unit'}, {'type': 'string', 'enum': ['n/a']}]}
```

## InjectedRadioactivity (metadata)

name: InjectedRadioactivity

description:

> Total amount of radioactivity injected into the patient (for example, `400`). For bolus-infusion experiments, this value should be the sum of all injected radioactivity originating from both bolus and infusion. Corresponds to DICOM Tag 0018, 1074 `Radionuclide Total Dose`.

schema information:

```
{'type': 'number'}
```

## InjectedRadioactivityUnits (metadata)

name: InjectedRadioactivityUnits

description:

> Unit format of the specified injected radioactivity (for example, `"MBq"`).

schema information:

```
{'type': 'string', 'format': 'unit'}
```

## InjectedVolume (metadata)

name: InjectedVolume

description:

Injected volume of the radiotracer in the unit `"mL"`.

schema information:

```
{'type': 'number', 'unit': 'mL'}
```

## InjectionEnd (metadata)

name: InjectionEnd

description:

Time of end of injection with respect to `"TimeZero"` in the default unit seconds.

schema information:

```
{'type': 'number', 'unit': 's'}
```

## InjectionStart (metadata)

name: InjectionStart

description:

Time of start of injection with respect to `"TimeZero"` in the default unit seconds. This corresponds to DICOM Tag 0018, 1042 `Contrast/Bolus Start Time` converted to seconds relative to `"TimeZero"`.

schema information:

```
{'type': 'number', 'unit': 's'}
```

## InstitutionAddress (metadata)

name: InstitutionAddress

description:

The address of the institution in charge of the equipment that produced the measurements.

schema information:

`{'type': 'string'}`

## InstitutionName (metadata)

name: InstitutionName

description:

The name of the institution in charge of the equipment that produced the measurements.

schema information:

`{'type': 'string'}`

## InstitutionalDepartmentName (metadata)

name: InstitutionalDepartmentName

description:

The department in the institution in charge of the equipment that produced the measurements.

schema information:

`{'type': 'string'}`

## Instructions (metadata)

name: Instructions

description:

Text of the instructions given to participants before the recording.

schema information:

`{'type': 'string'}`

## IntendedFor (metadata)

name: IntendedFor

description:

> The paths to files for which the associated file is intended to be used. Contains one or more filenames with paths relative to the participant subfolder. Paths need to use forward slashes instead of backward slashes, regardless of operating system.

schema information:

```
{'anyOf': [{'type': 'string', 'format': 'participant_relative'}, {'type': 'array', 'items': {'type': 'string', 'format': 'participant_relative'}}]}
```

## InversionTime (metadata)

name: InversionTime

description:

> The inversion time (TI) for the acquisition, specified in seconds. Inversion time is the time after the middle of inverting RF pulse to middle of excitation pulse to detect the amount of longitudinal magnetization. Corresponds to DICOM Tag 0018, 0082 `Inversion Time` (please note that the DICOM term is in milliseconds not seconds).

schema information:

```
{'type': 'number', 'unit': 's', 'exclusiveMinimum': 0}
```

## LICENSE (top_level_files)

name: LICENSE

description:

> A `LICENSE` file MAY be provided in addition to the short specification of the used license in the `dataset_description.json` `"License"` field. The `"License"` field and `LICENSE` file MUST correspond. The `LICENSE` file MUST be either in ASCII or UTF-8 encoding.

schema information:

```
{}
```

## LabelingDistance (metadata)

name: LabelingDistance

description:

> Distance from the center of the imaging slab to the center of the labeling plane (`(P)CASL`) or the leading edge of the labeling slab (`PASL`), in millimeters. If the labeling is performed inferior to the isocenter, this number should be negative. Based on DICOM macro C.8.13.5.14.

schema information:

```
{'type': 'number', 'unit': 'mm'}
```

## LabelingDuration (metadata)

name: LabelingDuration

description:

> Total duration of the labeling pulse train, in seconds, corresponding to the temporal width of the labeling bolus for `"PCASL"` or `"CASL"`. In case all control-label volumes (or deltam or CBF) have the same `LabelingDuration`, a scalar must be specified. In case the control-label volumes (or deltam or cbf) have a different `"LabelingDuration"`, an array of numbers must be specified, for which any `m0scan` in the timeseries has a `"LabelingDuration"` of zero. In case an array of numbers is provided, its length should be equal to the number of volumes specified in `*_aslcontext.tsv`. Corresponds to DICOM Tag 0018, 9258 `ASL Pulse Train Duration`.

schema information:

```
{'anyOf': [{'type': 'number', 'minimum': 0, 'unit': 's'}, {'type': 'array', 'items': {'type': 'number', 'unit': 's', 'minimum': 0}}]}
```

## LabelingEfficiency (metadata)

name: LabelingEfficiency

description:

> Labeling efficiency, specified as a number between zero and one, only if obtained externally (for example phase-contrast based).

schema information:

```
{'type': 'number', 'exclusiveMinimum': 0}
```

## LabelingLocationDescription (metadata)

name: LabelingLocationDescription

description:

> Description of the location of the labeling plane (`"CASL"` or `"PCASL"`) or the labeling slab (`"PASL"`) that cannot be captured by fields `LabelingOrientation` or `LabelingDistance`. May include a link to an anonymized screenshot of the planning of the labeling slab/plane with respect to the imaging slab or slices `*_asllabeling.jpg`. Based on DICOM macro C.8.13.5.14.

schema information:

```
{'type': 'string'}
```

## LabelingOrientation (metadata)

name: LabelingOrientation

description:

> Orientation of the labeling plane (`(P)CASL`) or slab (`PASL`). The direction cosines of a normal vector perpendicular to the ASL labeling slab or plane with respect to the patient. Corresponds to DICOM Tag 0018, 9255 `ASL Slab Orientation`.

schema information:

```
{'type': 'array', 'items': {'type': 'number'}}
```

## LabelingPulseAverageB1 (metadata)

name: LabelingPulseAverageB1

description:

> The average B1-field strength of the RF labeling pulses, in microteslas. As an alternative, `"LabelingPulseFlipAngle"` can be provided.

schema information:

```
{'type': 'number', 'exclusiveMinimum': 0, 'unit': 'uT'}
```

## LabelingPulseAverageGradient (metadata)

name: LabelingPulseAverageGradient

description:

> The average labeling gradient, in milliteslas per meter.

schema information:

```
{'type': 'number', 'exclusiveMinimum': 0, 'unit': 'mT/m'}
```

## LabelingPulseDuration (metadata)

name: LabelingPulseDuration

description:

> Duration of the individual labeling pulses, in milliseconds.

schema information:

`{'type': 'number', 'exclusiveMinimum': 0, 'unit': 'ms'}`

## LabelingPulseFlipAngle (metadata)

name: LabelingPulseFlipAngle

description:

The flip angle of a single labeling pulse, in degrees, which can be given as an alternative to `"LabelingPulseAverageB1"`.

schema information:

`{'type': 'number', 'exclusiveMinimum': 0, 'maximum': 360, 'unit': 'degree'}`

## LabelingPulseInterval (metadata)

name: LabelingPulseInterval

description:

Delay between the peaks of the individual labeling pulses, in milliseconds.

schema information:

`{'type': 'number', 'exclusiveMinimum': 0, 'unit': 'ms'}`

## LabelingPulseMaximumGradient (metadata)

name: LabelingPulseMaximumGradient

description:

The maximum amplitude of the gradient switched on during the application of the labeling RF pulse(s), in milliteslas per meter.

schema information:

`{'type': 'number', 'exclusiveMinimum': 0, 'unit': 'mT/m'}`

## LabelingSlabThickness (metadata)

name: LabelingSlabThickness

description:

Thickness of the labeling slab in millimeters. For non-selective FAIR a zero is entered. Corresponds to DICOM Tag 0018, 9254 `ASL Slab Thickness`.

schema information:

```
{'type': 'number', 'exclusiveMinimum': 0, 'unit': 'mm'}
```

## Levels (metadata)

name: Levels

description:

> For categorical variables: An object of possible values (keys) and their descriptions (values).

schema information:

```
{'type': 'object', 'additionalProperties': {'type': 'string'}}
```

## License (metadata)

name: License

description:

> The license for the dataset. The use of license name abbreviations is RECOMMENDED for specifying a license (see Appendix II). The corresponding full license text MAY be specified in an additional `LICENSE` file.

schema information:

```
{'type': 'string'}
```

## LongName (metadata)

name: LongName

description:

> Long (unabbreviated) name of the column.

schema information:

```
{'type': 'string'}
```

## LookLocker (metadata)

name: LookLocker

description:

Boolean indicating if a Look-Locker readout is used.

schema information:

```
{'type': 'boolean'}
```

## M0Estimate (metadata)

name: M0Estimate

description:

A single numerical whole-brain M0 value (referring to the M0 of blood), only if obtained externally (for example retrieved from CSF in a separate measurement).

schema information:

```
{'type': 'number', 'exclusiveMinimum': 0}
```

## M0Type (metadata)

name: M0Type

description:

Describes the presence of M0 information. `"Separate"` means that a separate `*_m0scan.nii[.gz]` is present. `"Included"` means that an m0scan volume is contained within the current `*_asl.nii[.gz]`. `"Estimate"` means that a single whole-brain M0 value is provided. `"Absent"` means that no specific M0 information is present.

schema information:

```
{'type': 'string', 'enum': ['Separate', 'Included', 'Estimate', 'Absent']}
```

## M0map (suffixes)

name: Equilibrium magnetization (M0) map

description:

In arbitrary units (arbitrary). A common quantitative MRI (qMRI) fitting variable that represents the amount of magnetization at thermal equilibrium. M0 maps are RECOMMENDED to use this suffix if generated by qMRI applications (for example, variable flip angle T1 mapping).

schema information:

```
{'unit': 'arbitrary'}
```

## MEGChannelCount (metadata)

name: MEGChannelCount

description:

Number of MEG channels (for example, `275`).

schema information:

```
{'type': 'integer', 'minimum': 0}
```

## MEGCoordinateSystem (metadata)

name: MEGCoordinateSystem

description:

Defines the coordinate system for the MEG sensors. See Appendix VIII for a list of restricted keywords for coordinate systems. If `"Other"`, provide definition of the coordinate system in `"MEGCoordinateSystemDescription"`.

schema information:

```
{'type': 'string', 'enum': ['CTF', 'ElektaNeuromag', '4DBti', 'KitYokogawa', 'ChietiItab', 'Other', 'CapTrak', 'EEGLAB', 'EEGLAB-HJ', 'Other', 'ICBM452
```

## MEGCoordinateSystemDescription (metadata)

name: MEGCoordinateSystemDescription

description:

Free-form text description of the coordinate system. May also include a link to a documentation page or paper describing the system in greater detail.

schema information:

```
{'type': 'string'}
```

## MEGCoordinateUnits (metadata)

name: MEGCoordinateUnits

description:

Units of the coordinates of `"MEGCoordinateSystem"`.

schema information:

```
{'type': 'string', 'enum': ['m', 'mm', 'cm', 'n/a']}
```

## MEGRE (suffixes)

name: Multi-echo Gradient Recalled Echo

description:

> Anatomical gradient echo images acquired at different echo times. Please note that this suffix is not intended for the logical grouping of images acquired using an Echo Planar Imaging (EPI) readout.

schema information:

```
{}
```

## MEGREFChannelCount (metadata)

name: MEGREFChannelCount

description:

> Number of MEG reference channels (for example, `23`). For systems without such channels (for example, Neuromag Vectorview), `MEGREFChannelCount` should be set to `0`.

schema information:

```
{'type': 'integer', 'minimum': 0}
```

## MESE (suffixes)

name: Multi-echo Spin Echo

description:

> The MESE method involves multiple spin echo images acquired at different echo times and is primarily used for T2 mapping. Please note that this suffix is not intended for the logical grouping of images acquired using an Echo Planar Imaging (EPI) readout.

schema information:

```
{}
```

## MP2RAGE (suffixes)

name: Magnetization Prepared Two Gradient Echoes

description:

> The MP2RAGE method is a special protocol that collects several images at different flip angles and inversion times to create a parametric T1map by combining the magnitude and phase images (Marques et al. 2010).

schema information:

```
{}
```

## MPE (suffixes)

name: Multi-photon excitation microscopy

description:

> Multi-photon excitation microscopy imaging data

schema information:

```
{}
```

## MPM (suffixes)

name: Multi-parametric Mapping

description:

> The MPM approaches (a.k.a hMRI) involves the acquisition of highly-similar anatomical images that differ in terms of application of a magnetization transfer RF pulse (MTon or MToff), flip angle and (optionally) echo time and magnitue/phase parts (Weiskopf et al. 2013). See here for suggested MPM acquisition protocols.

schema information:

```
{}
```

## MRAcquisitionType (metadata)

name: MRAcquisitionType

description:

> Type of sequence readout. Corresponds to DICOM Tag 0018, 0023 `MR Acquisition Type`.

schema information:

```
{'type': 'string', 'enum': ['2D', '3D']}
```

## MRTransmitCoilSequence (metadata)

name: MRTransmitCoilSequence

description:

This is a relevant field if a non-standard transmit coil is used. Corresponds to DICOM Tag 0018, 9049 `MR Transmit Coil Sequence`.

schema information:

```
{'type': 'string'}
```

## MTNumberOfPulses (metadata)

name: MTNumberOfPulses

description:

The number of magnetization transfer RF pulses applied before the readout.

schema information:

```
{'type': 'number'}
```

## MTOffsetFrequency (metadata)

name: MTOffsetFrequency

description:

The frequency offset of the magnetization transfer pulse with respect to the central H1 Larmor frequency in Hertz (Hz).

schema information:

```
{'type': 'number', 'unit': 'Hz'}
```

## MTPulseBandwidth (metadata)

name: MTPulseBandwidth

description:

> The excitation bandwidth of the magnetization transfer pulse in Hertz (Hz).

schema information:

```
{'type': 'number', 'unit': 'Hz'}
```

## MTPulseDuration (metadata)

name: MTPulseDuration

description:

> Duration of the magnetization transfer RF pulse in seconds.

schema information:

```
{'type': 'number', 'unit': 's'}
```

## MTPulseShape (metadata)

name: MTPulseShape

description:

> Shape of the magnetization transfer RF pulse waveform. The value `"GAUSSHANN"` refers to a Gaussian pulse with a Hanning window. The value `"SINCHANN"` refers to a sinc pulse with a Hanning window. The value `"SINCGAUSS"` refers to a sinc pulse with a Gaussian window.

schema information:

```
{'type': 'string', 'enum': ['HARD', 'GAUSSIAN', 'GAUSSHANN', 'SINC', 'SINCHANN', 'SINCGAUSS', 'FERMI']}
```

## MTR (suffixes)

name: Magnetization Transfer Ratio

description:

> This method is to calculate a semi-quantitative magnetization transfer ratio map.

schema information:

```
{}
```

## MTRmap (suffixes)

name: Magnetization transfer ratio image

description:

> In arbitrary units (arbitrary). MTR maps are REQUIRED to use this suffix regardless of the method used to generate them. MTRmap intensity values are RECOMMENDED to be represented in percentage in the range of 0-100%.

schema information:

```
{'unit': 'arbitrary', 'minValue': 0, 'maxValue': 100}
```

## MTS (suffixes)

name: Magnetization transfer saturation

description:

> This method is to calculate a semi-quantitative magnetization transfer saturation index map. The MTS method involves three sets of anatomical images that differ in terms of application of a magnetization transfer RF pulse (MTon or MToff) and flip angle (Helms et al. 2008).

schema information:

```
{}
```

## MTState (metadata)

name: MTState

description:

> Boolean stating whether the magnetization transfer pulse is applied. Corresponds to DICOM Tag 0018, 9020 `Magnetization Transfer`.

schema information:

```
{'type': 'boolean'}
```

## MTVmap (suffixes)

name: Macromolecular tissue volume (MTV) image

description:

> In arbitrary units (arbitrary). MTV maps are REQUIRED to use this suffix regardless of the method used to generate them.

schema information:

```
{'unit': 'arbitrary'}
```

## MTsat (suffixes)

name: Magnetization transfer saturation image

description:

> In arbitrary units (arbitrary). MTsat maps are REQUIRED to use this suffix regardless of the method used to generate them.

schema information:

```
{'unit': 'arbitrary'}
```

## MWFmap (suffixes)

name: Myelin water fraction image

description:

> In arbitrary units (arbitrary). MWF maps are REQUIRED to use this suffix regardless of the method used to generate them. MWF intensity values are RECOMMENDED to be represented in percentage in the range of 0-100%.

schema information:

```
{'unit': 'arbitrary', 'minValue': 0, 'maxValue': 100}
```

## MagneticFieldStrength (metadata)

name: MagneticFieldStrength

description:

> Nominal field strength of MR magnet in Tesla. Corresponds to DICOM Tag 0018, 0087 `Magnetic Field Strength`.

schema information:

```
{'type': 'number'}
```

## Magnification (metadata)

name: Magnification

description:

Lens magnification (for example: `40`). If the file format is OME-TIFF, the value MUST be consistent with the `"NominalMagnification"` OME metadata field.

schema information:

```
{'type': 'number', 'exclusiveMinimum': 0}
```

## Manual (metadata)

name: Manual

description:

Indicates if the segmentation was performed manually or via an automated process.

schema information:

```
{'type': 'boolean'}
```

## Manufacturer (metadata)

name: Manufacturer

description:

Manufacturer of the equipment that produced the measurements.

schema information:

```
{'type': 'string'}
```

## ManufacturersModelName (metadata)

name: ManufacturersModelName

description:

Manufacturer's model name of the equipment that produced the measurements.

schema information:

```
{'type': 'string'}
```

## MatrixCoilMode (metadata)

name: MatrixCoilMode

description:

> (If used) A method for reducing the number of independent channels by combining in analog the signals from multiple coil elements. There are typically different default modes when using un-accelerated or accelerated (for example, `"GRAPPA"`, `"SENSE"`) imaging.

schema information:

```
{'type': 'string'}
```

## MaxMovement (metadata)

name: MaxMovement

description:

> Maximum head movement (in mm) detected during the recording, as measured by the head localisation coils (for example, `4.8`).

schema information:

```
{'type': 'number', 'unit': 'mm'}
```

## MeasurementToolMetadata (metadata)

name: MeasurementToolMetadata

description:

> A description of the measurement tool as a whole. Contains two fields: `"Description"` and `"TermURL"`. `"Description"` is a free text description of the measurement tool. `"TermURL"` is a URL to an entity in an ontology corresponding to this tool.

schema information:

```
{'type': 'object', 'properties': {'TermURL': {'type': 'string', 'format': 'uri'}, 'Description': {'type': 'string'}}}
```

## MetaboliteAvail (metadata)

name: MetaboliteAvail

description:

> Boolean that specifies if metabolite measurements are available. If `true`, the `metabolite_parent_fraction` column MUST be present in the corresponding `*_blood.tsv` file.

schema information:

`{'type': 'boolean'}`

## MetaboliteMethod (metadata)

name: MetaboliteMethod

description:

> Method used to measure metabolites.

schema information:

`{'type': 'string'}`

## MetaboliteRecoveryCorrectionApplied (metadata)

name: MetaboliteRecoveryCorrectionApplied

description:

> Metabolite recovery correction from the HPLC, for tracers where it changes with time postinjection. If `true`, the `hplc_recovery_fractions` column MUST be present in the corresponding `*_blood.tsv` file.

schema information:

`{'type': 'boolean'}`

## MiscChannelCount (metadata)

name: MiscChannelCount

description:

> Number of miscellaneous analog channels for auxiliary signals.

schema information:

`{'type': 'integer', 'minimum': 0}`

## MixingTime (metadata)

name: MixingTime

description:

> In the context of a stimulated- and spin-echo 3D EPI sequence for B1+ mapping, corresponds to the interval between spin- and stimulated-echo pulses. In the context of a diffusion-weighted double spin-echo sequence, corresponds to the interval between two successive diffusion sensitizing gradients, specified in seconds.

schema information:

```
{'type': 'number', 'unit': 's'}
```

## ModeOfAdministration (metadata)

name: ModeOfAdministration

description:

> Mode of administration of the injection (for example, `"bolus"`, `"infusion"`, or `"bolus-infusion"`).

schema information:

```
{'type': 'string'}
```

## MolarActivity (metadata)

name: MolarActivity

description:

> Molar activity of compound injected. Corresponds to DICOM Tag 0018, 1077 `Radiopharmaceutical Specific Activity`.

schema information:

```
{'type': 'number'}
```

## MolarActivityMeasTime (metadata)

name: MolarActivityMeasTime

description:

> Time to which molar radioactivity measurement above applies in the default unit `"hh:mm:ss"`.

schema information:

```
{'type': 'string', 'pattern': '^(?:2[0-3]|[01][0-9]):[0-5][0-9]:[0-5][0-9]$'}
```

## MolarActivityUnits (metadata)

name: MolarActivityUnits

description:

Unit of the specified molar radioactivity (for example, `"GBq/umol"`).

schema information:

```
{'type': 'string', 'format': 'unit'}
```

## MultibandAccelerationFactor (metadata)

name: MultibandAccelerationFactor

description:

The multiband factor, for multiband acquisitions.

schema information:

```
{'type': 'number'}
```

## MultipartID (metadata)

name: MultipartID

description:

A unique (per participant) label tagging DWI runs that are part of a multipart scan.

schema information:

```
{'type': 'string'}
```

## NLO (suffixes)

name: Nonlinear optical microscopy

description:

Nonlinear optical microscopy imaging data

schema information:

```
{}
```

## Name (metadata)

name: Name

description:

Name of the dataset.

schema information:

```
{'type': 'string'}
```

## NegativeContrast (metadata)

name: NegativeContrast

description:

`true` or `false` value specifying whether increasing voxel intensity (within sample voxels) denotes a decreased value with respect to the contrast suffix. This is commonly the case when Cerebral Blood Volume is estimated via usage of a contrast agent in conjunction with a T2* weighted acquisition protocol.

schema information:

```
{'type': 'boolean'}
```

## NonlinearGradientCorrection (metadata)

name: NonlinearGradientCorrection

description:

Boolean stating if the image saved has been corrected for gradient nonlinearities by the scanner sequence.

schema information:

```
{'type': 'boolean'}
```

## NumberOfVolumesDiscardedByScanner (metadata)

name: NumberOfVolumesDiscardedByScanner

description:

Number of volumes ("dummy scans") discarded by the scanner (as opposed to those discarded by the user post hoc) before saving the imaging file. For example, a sequence that automatically discards the first 4 volumes before saving would have this field as 4. A sequence that does not discard dummy scans would have this set to 0. Please note that the onsets recorded in the `events.tsv` file should always refer to the beginning of the acquisition of the first volume in the corresponding imaging file - independent of the value of `"NumberOfVolumesDiscardedByScanner"` field.

schema information:

```
{'type': 'integer', 'minimum': 0}
```

## NumberOfVolumesDiscardedByUser (metadata)

name: NumberOfVolumesDiscardedByUser

description:

> Number of volumes ("dummy scans") discarded by the user before including the file in the dataset. If possible, including all of the volumes is strongly recommended. Please note that the onsets recorded in the `events.tsv` file should always refer to the beginning of the acquisition of the first volume in the corresponding imaging file - independent of the value of `"NumberOfVolumesDiscardedByUser"` field.

schema information:

```
{'type': 'integer', 'minimum': 0}
```

## NumberShots (metadata)

name: NumberShots

description:

> The number of RF excitations needed to reconstruct a slice or volume (may be referred to as partition). Please mind that this is not the same as Echo Train Length which denotes the number of k-space lines collected after excitation in a multi-echo readout. The data type array is applicable for specifying this parameter before and after the k-space center is sampled. Please see `"NumberShots"` metadata field in the qMRI appendix for corresponding calculations.

schema information:

```
{'anyOf': [{'type': 'number'}, {'type': 'array', 'items': {'type': 'number'}}]}
```

## NumericalAperture (metadata)

name: NumericalAperture

description:

> Lens numerical aperture (for example: `1.4`). If the file format is OME-TIFF, the value MUST be consistent with the `LensNA` OME metadata field.

schema information:

```
{'type': 'number', 'exclusiveMinimum': 0}
```

## OCT (suffixes)

name: Optical coherence tomography

description:

Optical coherence tomography imaging data

schema information:

```
{}
```

## OperatingSystem (metadata)

name: OperatingSystem

description:

Operating system used to run the stimuli presentation software (for formatting recommendations, see examples below this table).

schema information:

```
{'type': 'string'}
```

## OtherAcquisitionParameters (metadata)

name: OtherAcquisitionParameters

description:

Description of other relevant image acquisition parameters.

schema information:

```
{'type': 'string'}
```

## PASLType (metadata)

name: PASLType

description:

Type of the labeling pulse of the `PASL` labeling, for example `"FAIR"`, `"EPISTAR"`, or `"PICORE"`.

schema information:

`{'type': 'string'}`

## PC (suffixes)

name: Phase-contrast microscopy

description:

Phase-contrast microscopy imaging data

schema information:

`{}`

## PCASLType (metadata)

name: PCASLType

description:

The type of gradient pulses used in the `control` condition.

schema information:

`{'type': 'string', 'enum': ['balanced', 'unbalanced']}`

## PD (suffixes)

name: Proton density image

description:

Ambiguous, may refer to a parametric image or to a conventional image. Change: Replaced by `PDw` or `PDmap`.

schema information:

`{'unit': 'arbitrary'}`

## PDT2 (suffixes)

name: PD and T2 weighted image

description:

In arbitrary units (arbitrary). PDw and T2w images acquired using a dual echo FSE sequence through view sharing process (Johnson et al. 1994).

schema information:

```
{'unit': 'arbitrary'}
```

## PDT2map (suffixes)

name: Combined PD/T2 image

description:

In arbitrary units (arbitrary). Combined PD/T2 maps are REQUIRED to use this suffix regardless of the method used to generate them.

schema information:

```
{'unit': 'arbitrary'}
```

## PDmap (suffixes)

name: Proton density image

description:

In arbitrary units (arbitrary). PD maps are REQUIRED to use this suffix regardless of the method used to generate them.

schema information:

```
{'unit': 'arbitrary'}
```

## PDw (suffixes)

name: Proton density (PD) weighted image

description:

In arbitrary units (arbitrary). The contrast of these images is mainly determined by spatial variations in the spin density (1H) of the imaged specimen. In spin-echo sequences this contrast is achieved at short repetition and long echo times. In a gradient-echo acquisition, PD weighting dominates the contrast at long repetition and short echo times, and at small flip angles.

schema information:

```
{'unit': 'arbitrary'}
```

## PLI (suffixes)

name: Polarized-light microscopy

description:

Polarized-light microscopy imaging data

schema information:

```
{}
```

## ParallelAcquisitionTechnique (metadata)

name: ParallelAcquisitionTechnique

description:

The type of parallel imaging used (for example `"GRAPPA"`, `"SENSE"`). Corresponds to DICOM Tag 0018, 9078 `Parallel Acquisition Technique`.

schema information:

```
{'type': 'string'}
```

## ParallelReductionFactorInPlane (metadata)

name: ParallelReductionFactorInPlane

description:

The parallel imaging (for instance, GRAPPA) factor. Use the denominator of the fraction of k-space encoded for each slice. For example, 2 means half of k-space is encoded. Corresponds to DICOM Tag 0018, 9069 `Parallel Reduction Factor In-plane`.

schema information:

```
{'type': 'number'}
```

## PartialFourier (metadata)

name: PartialFourier

description:

The fraction of partial Fourier information collected. Corresponds to DICOM Tag 0018, 9081 `Partial Fourier`.

schema information:

`{'type': 'number'}`

## PartialFourierDirection (metadata)

name: PartialFourierDirection

description:

> The direction where only partial Fourier information was collected. Corresponds to DICOM Tag 0018, 9036 `Partial Fourier Direction`.

schema information:

`{'type': 'string'}`

## PharmaceuticalDoseAmount (metadata)

name: PharmaceuticalDoseAmount

description:

> Dose amount of pharmaceutical coadministered with tracer.

schema information:

`{'anyOf': [{'type': 'number'}, {'type': 'array', 'items': {'type': 'number'}}]}`

## PharmaceuticalDoseRegimen (metadata)

name: PharmaceuticalDoseRegimen

description:

> Details of the pharmaceutical dose regimen. Either adequate description or short-code relating to regimen documented elsewhere (for example, `"single oral bolus"`).

schema information:

`{'type': 'string'}`

## PharmaceuticalDoseTime (metadata)

name: PharmaceuticalDoseTime

description:

Time of administration of pharmaceutical dose, relative to time zero. For an infusion, this should be a vector with two elements specifying the start and end of the infusion period. For more complex dose regimens, the regimen description should be complete enough to enable unambiguous interpretation of `"PharmaceuticalDoseTime"`. Unit format of the specified pharmaceutical dose time MUST be seconds.

schema information:

```
{'anyOf': [{'type': 'number', 'unit': 's'}, {'type': 'array', 'items': {'type': 'number', 'unit': 's'}}]}
```

## PharmaceuticalDoseUnits (metadata)

name: PharmaceuticalDoseUnits

description:

Unit format relating to pharmaceutical dose (for example, `"mg"` or `"mg/kg"`).

schema information:

```
{'type': 'string', 'format': 'unit'}
```

## PharmaceuticalName (metadata)

name: PharmaceuticalName

description:

Name of pharmaceutical coadministered with tracer.

schema information:

```
{'type': 'string'}
```

## PhaseEncodingDirection (metadata)

name: PhaseEncodingDirection

description:

The letters `i`, `j`, `k` correspond to the first, second and third axis of the data in the NIFTI file. The polarity of the phase encoding is assumed to go from zero index to maximum index unless `-` sign is present (then the order is reversed - starting from the highest index instead of zero). `PhaseEncodingDirection` is defined as the direction along which phase is was modulated which may result in visible distortions. Note that this is not the same as the DICOM term `InPlanePhaseEncodingDirection` which can have `ROW` or `COL` values.

schema information:

`{'type': 'string', 'enum': ['i', 'j', 'k', 'i-', 'j-', 'k-']}`

## PixelSize (metadata)

name: PixelSize

description:

> A 2- or 3-number array of the physical size of a pixel, either `[PixelSizeX, PixelSizeY]` or `[PixelSizeX, PixelSizeY, PixelSizeZ]`, where X is the width, Y the height and Z the depth. If the file format is OME-TIFF, these values need to be consistent with `PhysicalSizeX`, `PhysicalSizeY` and `PhysicalSizeZ` OME metadata fields, after converting in `PixelSizeUnits` according to `PhysicalSizeXunit`, `PhysicalSizeYunit` and `PhysicalSizeZunit` OME fields.

schema information:

`{'type': 'array', 'minItems': 2, 'maxItems': 3, 'items': {'type': 'number', 'minimum': 0}}`

## PixelSizeUnits (metadata)

name: PixelSizeUnits

description:

> Unit format of the specified `"PixelSize"`. MUST be one of: `"mm"` (millimeter), `"um"` (micrometer) or `"nm"` (nanometer).

schema information:

`{'type': 'string', 'enum': ['mm', 'um', 'nm']}`

## PlasmaAvail (metadata)

name: PlasmaAvail

description:

> Boolean that specifies if plasma measurements are available.

schema information:

`{'type': 'boolean'}`

## PlasmaFreeFraction (metadata)

name: PlasmaFreeFraction

description:

Measured free fraction in plasma, meaning the concentration of free compound in plasma divided by total concentration of compound in plasma (Units: 0-100%).

schema information:

```
{'type': 'number', 'minimum': 0, 'maximum': 100}
```

## PlasmaFreeFractionMethod (metadata)

name: PlasmaFreeFractionMethod

description:

Method used to estimate free fraction.

schema information:

```
{'type': 'string'}
```

## PostLabelingDelay (metadata)

name: PostLabelingDelay

description:

This is the postlabeling delay (PLD) time, in seconds, after the end of the labeling (for `"CASL"` or `"PCASL"`) or middle of the labeling pulse (for `"PASL"`) until the middle of the excitation pulse applied to the imaging slab (for 3D acquisition) or first slice (for 2D acquisition). Can be a number (for a single-PLD time series) or an array of numbers (for multi-PLD and Look-Locker). In the latter case, the array of numbers contains the PLD of each volume, namely each `control` and `label`, in the acquisition order. Any image within the time-series without a PLD, for example an `m0scan`, is indicated by a zero. Based on DICOM Tags 0018, 9079 `Inversion Times` and 0018, 0082 `InversionTime`.

schema information:

```
{'anyOf': [{'type': 'number', 'exclusiveMinimum': 0, 'unit': 's'}, {'type': 'array', 'items': {'type': 'number', 'exclusiveMinimum': 0, 'unit': 's'}}]}
```

## PowerLineFrequency (metadata)

name: PowerLineFrequency

description:

Frequency (in Hz) of the power grid at the geographical location of the instrument (for example, `50` or `60`).

schema information:

```
{'anyOf': [{'type': 'number', 'exclusiveMinimum': 0, 'unit': 'Hz'}, {'type': 'string', 'enum': ['n/a']}]}
```

## PromptRate (metadata)

name: PromptRate

description:

> Prompt rate for each frame (same units as `Units`, for example, `"Bq/mL"`).

schema information:

```
{'type': 'array', 'items': {'type': 'number'}}
```

## PulseSequenceDetails (metadata)

name: PulseSequenceDetails

description:

> Information beyond pulse sequence type that identifies the specific pulse sequence used (for example, `"Standard Siemens Sequence distributed with the VB17 software"`, `"Siemens WIP ### version #.##,"` or `"Sequence written by X using a version compiled on MM/DD/YYYY"`).

schema information:

```
{'type': 'string'}
```

## PulseSequenceType (metadata)

name: PulseSequenceType

description:

> A general description of the pulse sequence used for the scan (for example, `"MPRAGE"`, `"Gradient Echo EPI"`, `"Spin Echo EPI"`, `"Multiband gradient echo EPI"`).

schema information:

```
{'type': 'string'}
```

## Purity (metadata)

name: Purity

description:

Purity of the radiolabeled compound (between 0 and 100%).

schema information:

```
{'type': 'number', 'minimum': 0, 'maximum': 100}
```

## R1map (suffixes)

name: Longitudinal relaxation rate image

description:

In seconds-1 (1/s). R1 maps (R1 = 1/T1) are REQUIRED to use this suffix regardless of the method used to generate them.

schema information:

```
{'unit': '1/s'}
```

## R2map (suffixes)

name: True transverse relaxation rate image

description:

In seconds-1 (1/s). R2 maps (R2 = 1/T2) are REQUIRED to use this suffix regardless of the method used to generate them.

schema information:

```
{'unit': '1/s'}
```

## R2starmap (suffixes)

name: Observed transverse relaxation rate image

description:

In seconds-1 (1/s). R2-star maps (R2star = 1/T2star) are REQUIRED to use this suffix regardless of the method used to generate them.

schema information:

```
{'unit': '1/s'}
```

## RB1COR (suffixes)

name: RB1COR

description:

> Low resolution images acquired by the body coil (in the gantry of the scanner) and the head coil using identical acquisition parameters to generate a combined sensitivity map as described in Papp et al. (2016).

schema information:

```
{}
```

## RB1map (suffixes)

name: RF receive sensitivity map

description:

> In arbitrary units (arbitrary). Radio frequency (RF) receive (B1-) sensitivity maps are REQUIRED to use this suffix regardless of the method used to generate them. RB1map intensity values are RECOMMENDED to be represented as percent multiplicative factors such that Amplitudeeffective = B1-intensity*Amplitudeideal.

schema information:

```
{'unit': 'arbitrary'}
```

## README (top_level_files)

name: README

description:

> In addition a free form text file (`README`) describing the dataset in more details SHOULD be provided. The `README` file MUST be either in ASCII or UTF-8 encoding.

schema information:

```
{}
```

## RandomRate (metadata)

name: RandomRate

description:

Random rate for each frame (same units as `"Units"`, for example, `"Bq/mL"`).

schema information:

```
{'type': 'array', 'items': {'type': 'number'}}
```

## RawSources (metadata)

name: RawSources

description:

A list of paths relative to dataset root pointing to the BIDS-Raw file(s) that were used in the creation of this derivative.

schema information:

```
{'type': 'array', 'items': {'type': 'string', 'format': 'dataset_relative'}}
```

## ReceiveCoilActiveElements (metadata)

name: ReceiveCoilActiveElements

description:

Information describing the active/selected elements of the receiver coil. This does not correspond to a tag in the DICOM ontology. The vendor-defined terminology for active coil elements can go in this field.

schema information:

```
{'type': 'string'}
```

## ReceiveCoilName (metadata)

name: ReceiveCoilName

description:

Information describing the receiver coil. Corresponds to DICOM Tag 0018, 1250 `Receive Coil Name`, although not all vendors populate that DICOM Tag, in which case this field can be derived from an appropriate private DICOM field.

schema information:

```
{'type': 'string'}
```

## ReconFilterSize (metadata)

name: ReconFilterSize

description:

Kernel size of post-recon filter (FWHM) in default units `"mm"`.

schema information:

```
{'anyOf': [{'type': 'number', 'unit': 'mm'}, {'type': 'array', 'items': {'type': 'number', 'unit': 'mm'}}]}
```

## ReconFilterType (metadata)

name: ReconFilterType

description:

Type of post-recon smoothing (for example, `["Shepp"]`).

schema information:

```
{'anyOf': [{'type': 'string'}, {'type': 'array', 'items': {'type': 'string'}}]}
```

## ReconMethodImplementationVersion (metadata)

name: ReconMethodImplementationVersion

description:

Identification for the software used, such as name and version.

schema information:

```
{'type': 'string'}
```

## ReconMethodName (metadata)

name: ReconMethodName

description:

Reconstruction method or algorithm (for example, `"3d-op-osem"`).

schema information:

```
{'type': 'string'}
```

## ReconMethodParameterLabels (metadata)

name: ReconMethodParameterLabels

description:

Names of reconstruction parameters (for example, `["subsets", "iterations"]`).

schema information:

```
{'type': 'array', 'items': {'type': 'string'}}
```

## ReconMethodParameterUnits (metadata)

name: ReconMethodParameterUnits

description:

Unit of reconstruction parameters (for example, `["none", "none"]`).

schema information:

```
{'type': 'array', 'items': {'type': 'string', 'format': 'unit'}}
```

## ReconMethodParameterValues (metadata)

name: ReconMethodParameterValues

description:

Values of reconstruction parameters (for example, `[21, 3]`).

schema information:

```
{'type': 'array', 'items': {'type': 'number'}}
```

## RecordingDuration (metadata)

name: RecordingDuration

description:

Length of the recording in seconds (for example, `3600`).

schema information:

```
{'type': 'number', 'unit': 's'}
```

## RecordingType (metadata)

name: RecordingType

description:

> Defines whether the recording is `"continuous"`, `"discontinuous"`, or `"epoched"`, where `"epoched"` is limited to time windows about events of interest (for example, stimulus presentations or subject responses).

schema information:

```
{'type': 'string', 'enum': ['continuous', 'epoched', 'discontinuous']}
```

## ReferencesAndLinks (metadata)

name: ReferencesAndLinks

description:

> List of references to publications that contain information on the dataset. A reference may be textual or a URI.

schema information:

```
{'items': {'type': 'string'}, 'type': 'array'}
```

## RepetitionTime (metadata)

name: RepetitionTime

description:

> The time in seconds between the beginning of an acquisition of one volume and the beginning of acquisition of the volume following it (TR). When used in the context of functional acquisitions this parameter best corresponds to DICOM Tag 0020, 0110: the "time delta between images in a dynamic of functional set of images" but may also be found in DICOM Tag 0018, 0080: "the period of time in msec between the beginning of a pulse sequence and the beginning of the succeeding (essentially identical) pulse sequence". This definition includes time between scans (when no data has been acquired) in case of sparse acquisition schemes. This value MUST be consistent with the 'pixdim[4]' field (after accounting for units stored in 'xyzt_units' field) in the NIfTI header. This field is mutually exclusive with VolumeTiming.

schema information:

```
{'type': 'number', 'exclusiveMinimum': 0, 'unit': 's'}
```

## RepetitionTimeExcitation (metadata)

name: RepetitionTimeExcitation

description:

> The interval, in seconds, between two successive excitations. [DICOM Tag 0018, 0080](http://dicomlookup.com/lookup.asp?sw=Tnumber&q=(0018,0080) best refers to this parameter. This field may be used together with the `"RepetitionTimePreparation"` for certain use cases, such as MP2RAGE. Use `RepetitionTimeExcitation` (in combination with `"RepetitionTimePreparation"` if needed) for anatomy imaging data rather than `"RepetitionTime"` as it is already defined as the amount of time that it takes to acquire a single volume in the task imaging data section.

schema information:

```
{'type': 'number', 'minimum': 0, 'unit': 's'}
```

## RepetitionTimePreparation (metadata)

name: RepetitionTimePreparation

description:

> The interval, in seconds, that it takes a preparation pulse block to re-appear at the beginning of the succeeding (essentially identical) pulse sequence block. The data type number may apply to files from any MRI modality concerned with a single value for this field. The data type array provides a value for each volume in a 4D dataset and should only be used when the volume timing is critical for interpretation of the data, such as in ASL.

schema information:

```
{'anyOf': [{'type': 'number', 'minimum': 0, 'unit': 's'}, {'type': 'array', 'items': {'type': 'number', 'minimum': 0, 'unit': 's'}}]}
```

## Resolution (metadata)

name: Resolution

description:

> Specifies the interpretation of the resolution keyword. If an object is used, then the keys should be values for the `res` entity and values should be descriptions of those `res` values.

schema information:

```
{'anyOf': [{'type': 'string'}, {'type': 'object', 'additionalProperties': {'type': 'string'}}]}
```

## S0map (suffixes)

name: Observed signal amplitude (S0) image

description:

> In arbitrary units (arbitrary). For a multi-echo (typically fMRI) sequence, S0 maps index the baseline signal before exponential (T2-star) signal decay. In other words: the exponential of the intercept for a linear decay model across log-transformed echos. For more information, please see, for example, the tedana documentation. S0 maps are RECOMMENDED to use this suffix if derived from an ME-FMRI dataset.

schema information:

```
{}
```

## SEEGChannelCount (metadata)

name: SEEGChannelCount

description:

> Number of SEEG channels.

schema information:

```
{'type': 'integer', 'minimum': 0}
```

## SEM (suffixes)

name: Scanning electron microscopy

description:

> Scanning electron microscopy imaging data

schema information:

```
{}
```

## SPIM (suffixes)

name: Selective plane illumination microscopy

description:

> Selective plane illumination microscopy imaging data

schema information:

```
{}
```

## SR (suffixes)

name: Super-resolution microscopy

description:

Super-resolution microscopy imaging data

schema information:

```
{}
```

## SampleEmbedding (metadata)

name: SampleEmbedding

description:

Description of the tissue sample embedding (for example: `"Epoxy resin"`).

schema information:

```
{'type': 'string'}
```

## SampleEnvironment (metadata)

name: SampleEnvironment

description:

Environment in which the sample was imaged. MUST be one of: `"in vivo"`, `"ex vivo"` or `"in vitro"`.

schema information:

```
{'type': 'string', 'enum': ['in vivo', 'ex vivo', 'in vitro']}
```

## SampleExtractionInstitution (metadata)

name: SampleExtractionInstitution

description:

The name of the institution in charge of the extraction of the sample, if different from the institution in charge of the equipment that produced the image.

schema information:

```
{'type': 'string'}
```

## SampleExtractionProtocol (metadata)

name: SampleExtractionProtocol

description:

Description of the sample extraction protocol or URI (for example from protocols.io).

schema information:

```
{'type': 'string'}
```

## SampleFixation (metadata)

name: SampleFixation

description:

Description of the tissue sample fixation (for example: `"4% paraformaldehyde, 2% glutaraldehyde"`).

schema information:

```
{'type': 'string'}
```

## SampleOrigin (metadata)

name: SampleOrigin

description:

Describes from which tissue the genetic information was extracted.

schema information:

```
{'type': 'string', 'enum': ['blood', 'saliva', 'brain', 'csf', 'breast milk', 'bile', 'amniotic fluid', 'other biospecimen']}
```

## SamplePrimaryAntibody (metadata)

name: SamplePrimaryAntibody

description:

Description(s) of the primary antibody used for immunostaining. Either an RRID or the name, supplier and catalogue number of a commercial antibody. For non-commercial antibodies either an RRID or the host-animal and immunogen used (for examples: `"RRID:AB_2122563"` or `"Rabbit anti-Human HTR5A Polyclonal Antibody, Invitrogen, Catalog # PA1-2453"`). MAY be an array of strings if different antibodies are used in each channel of the file.

schema information:

`{'anyOf': [{'type': 'string'}, {'type': 'array', 'items': {'type': 'string'}}]}`

## SampleSecondaryAntibody (metadata)

name: SampleSecondaryAntibody

description:

> Description(s) of the secondary antibody used for immunostaining. Either an RRID or the name, supplier and catalogue number of a commercial antibody. For non-commercial antibodies either an RRID or the host-animal and immunogen used (for examples: `"RRID:AB_228322"` or `"Goat anti-Mouse IgM Secondary Antibody, Invitrogen, Catalog # 31172"`). MAY be an array of strings if different antibodies are used in each channel of the file.

schema information:

`{'anyOf': [{'type': 'string'}, {'type': 'array', 'items': {'type': 'string'}}]}`

## SampleStaining (metadata)

name: SampleStaining

description:

> Description(s) of the tissue sample staining (for example: `"Osmium"`). MAY be an array of strings if different stains are used in each channel of the file (for example: `["LFB", "PLP"]`).

schema information:

`{'anyOf': [{'type': 'string'}, {'type': 'array', 'items': {'type': 'string'}}]}`

## SamplingFrequency (metadata)

name: SamplingFrequency

description:

> Sampling frequency (in Hz) of all the data in the recording, regardless of their type (for example, `2400`).

schema information:

`{'type': 'number', 'unit': 'Hz'}`

## ScaleFactor (metadata)

name: ScaleFactor

description:

Scale factor for each frame.

schema information:

```
{'type': 'array', 'items': {'type': 'number'}}
```

## ScanDate (metadata)

name: ScanDate

description:

Date of scan in the format `"YYYY-MM-DD[Z]"`. This field is DEPRECATED, and this metadata SHOULD be recorded in the `acq_time` column of the corresponding Scans file.

schema information:

```
{'type': 'string', 'format': 'date'}
```

## ScanOptions (metadata)

name: ScanOptions

description:

Parameters of ScanningSequence. Corresponds to DICOM Tag 0018, 0022 `Scan Options`.

schema information:

```
{'anyOf': [{'type': 'string'}, {'type': 'array', 'items': {'type': 'string'}}]}
```

## ScanStart (metadata)

name: ScanStart

description:

Time of start of scan with respect to `TimeZero` in the default unit seconds.

schema information:

```
{'type': 'number', 'unit': 's'}
```

## ScanningSequence (metadata)

name: ScanningSequence

description:

Description of the type of data acquired. Corresponds to DICOM Tag 0018, 0020 `Scanning Sequence`.

schema information:

```
{'anyOf': [{'type': 'string'}, {'type': 'array', 'items': {'type': 'string'}}]}
```

## ScatterFraction (metadata)

name: ScatterFraction

description:

Scatter fraction for each frame (Units: 0-100%).

schema information:

```
{'type': 'array', 'items': {'type': 'number', 'minimum': 0, 'maximum': 100}}
```

## SequenceName (metadata)

name: SequenceName

description:

Manufacturer's designation of the sequence name. Corresponds to DICOM Tag 0018, 0024 `Sequence Name`.

schema information:

```
{'type': 'string'}
```

## SequenceVariant (metadata)

name: SequenceVariant

description:

Variant of the ScanningSequence. Corresponds to DICOM Tag 0018, 0021 `Sequence Variant`.

schema information:

```
{'anyOf': [{'type': 'string'}, {'type': 'array', 'items': {'type': 'string'}}]}
```

## SinglesRate (metadata)

name: SinglesRate

description:

> Singles rate for each frame (same units as `Units`, for example, `"Bq/mL"`).

schema information:

```
{'type': 'array', 'items': {'type': 'number'}}
```

## SkullStripped (metadata)

name: SkullStripped

description:

> Whether the volume was skull stripped (non-brain voxels set to zero) or not.

schema information:

```
{'type': 'boolean'}
```

## SliceEncodingDirection (metadata)

name: SliceEncodingDirection

description:

> The axis of the NIfTI data along which slices were acquired, and the direction in which `"SliceTiming"` is defined with respect to. `i`, `j`, `k` identifiers correspond to the first, second and third axis of the data in the NIfTI file. A `-` sign indicates that the contents of `"SliceTiming"` are defined in reverse order - that is, the first entry corresponds to the slice with the largest index, and the final entry corresponds to slice index zero. When present, the axis defined by `"SliceEncodingDirection"` needs to be consistent with the `slice_dim` field in the NIfTI header. When absent, the entries in `"SliceTiming"` must be in the order of increasing slice index as defined by the NIfTI header.

schema information:

```
{'type': 'string', 'enum': ['i', 'j', 'k', 'i-', 'j-', 'k-']}
```

## SliceThickness (metadata)

name: SliceThickness

description:

> Slice thickness of the tissue sample in the unit micrometers (`"um"`) (for example: `5`).

schema information:

```
{'type': 'number', 'unit': 'um', 'exclusiveMinimum': 0}
```

## SliceTiming (metadata)

name: SliceTiming

description:

> The time at which each slice was acquired within each volume (frame) of the acquisition. Slice timing is not slice order -- rather, it is a list of times containing the time (in seconds) of each slice acquisition in relation to the beginning of volume acquisition. The list goes through the slices along the slice axis in the slice encoding dimension (see below). Note that to ensure the proper interpretation of the `"SliceTiming"` field, it is important to check if the OPTIONAL `SliceEncodingDirection` exists. In particular, if `"SliceEncodingDirection"` is negative, the entries in `"SliceTiming"` are defined in reverse order with respect to the slice axis, such that the final entry in the `"SliceTiming"` list is the time of acquisition of slice 0. Without this parameter slice time correction will not be possible.

schema information:

```
{'type': 'array', 'items': {'type': 'number', 'minimum': 0, 'unit': 's'}}
```

## SoftwareFilters (metadata)

name: SoftwareFilters

description:

> Object of temporal software filters applied, or `"n/a"` if the data is not available. Each key:value pair in the JSON object is a name of the filter and an object in which its parameters are defined as key:value pairs (for example, `{"Anti-aliasing filter": {"half-amplitude cutoff (Hz)": 500, "Roll-off": "6dB/Octave"}}`).

schema information:

```
{'anyOf': [{'type': 'object', 'additionalProperties': {'type': 'object'}}, {'type': 'string', 'enum': ['n/a']}]}
```

## SoftwareName (metadata)

name: SoftwareName

description:

Name of the software that was used to present the stimuli.

schema information:

```
{'type': 'string'}
```

## SoftwareRRID (metadata)

name: SoftwareRRID

description:

Research Resource Identifier of the software that was used to present the stimuli. Examples: The RRID for Psychtoolbox is 'SCR_002881', and that of PsychoPy is 'SCR_006571'.

schema information:

```
{'type': 'string', 'pattern': '.+_.+'}
```

## SoftwareVersion (metadata)

name: SoftwareVersion

description:

Version of the software that was used to present the stimuli.

schema information:

```
{'type': 'string'}
```

## SoftwareVersions (metadata)

name: SoftwareVersions

description:

Manufacturer's designation of software version of the equipment that produced the measurements.

schema information:

```
{'type': 'string'}
```

## SourceDatasets (metadata)

name: SourceDatasets

description:

> Used to specify the locations and relevant attributes of all source datasets. Valid keys in each object include `"URL"`, `"DOI"` (see URI), and `"Version"` with string values.

schema information:

```
{'type': 'array', 'items': {'type': 'object', 'properties': {'URL': {'type': 'string', 'format': 'uri'}, 'DOI': {'type': 'string'}, 'Version': {'type':
```

## Sources (metadata)

name: Sources

description:

> A list of files with the paths specified relative to dataset root; these files were directly used in the creation of this derivative data file. For example, if a derivative A is used in the creation of another derivative B, which is in turn used to generate C in a chain of A->B->C, C should only list B in `"Sources"`, and B should only list A in `"Sources"`. However, in case both X and Y are directly used in the creation of Z, then Z should list X and Y in `"Sources"`, regardless of whether X was used to generate Y.

schema information:

```
{'type': 'array', 'items': {'type': 'string', 'format': 'dataset_relative'}}
```

## SpatialReference (metadata)

name: SpatialReference

description:

> For images with a single reference, the value MUST be a single string. For images with multiple references, such as surface and volume references, a JSON object MUST be used.

schema information:

```
{'anyOf': [{'type': 'string', 'enum': ['orig']}, {'type': 'string', 'format': 'uri'}, {'type': 'string', 'format': 'dataset_relative'}, {'type': 'objec
```

## SpecificRadioactivity (metadata)

name: SpecificRadioactivity

description:

> Specific activity of compound injected. Note this is not required for an FDG acquisition, since it is not available, and SHOULD be set to `"n/a"`.

schema information:

```
{'anyOf': [{'type': 'number'}, {'type': 'string', 'enum': ['n/a']}]}
```

## SpecificRadioactivityMeasTime (metadata)

name: SpecificRadioactivityMeasTime

description:

> Time to which specific radioactivity measurement above applies in the default unit `"hh:mm:ss"`.

schema information:

```
{'type': 'string', 'pattern': '^(?:2[0-3]|[01][0-9]):[0-5][0-9]:[0-5][0-9]$'}
```

## SpecificRadioactivityUnits (metadata)

name: SpecificRadioactivityUnits

description:

> Unit format of specified specific radioactivity (for example, `"Bq/g"`). Note this is not required for an FDG acquisition, since it is not available, and SHOULD be set to `"n/a"`.

schema information:

```
{'anyOf': [{'type': 'string', 'format': 'unit'}, {'type': 'string', 'enum': ['n/a']}]}
```

## SpoilingGradientDuration (metadata)

name: SpoilingGradientDuration

description:

> The duration of the spoiler gradient lobe in seconds. The duration of a trapezoidal lobe is defined as the summation of ramp-up and plateau times.

schema information:

`{'type': 'number', 'unit': 's'}`

## SpoilingGradientMoment (metadata)

name: SpoilingGradientMoment

description:

Zeroth moment of the spoiler gradient lobe in millitesla times second per meter (mT.s/m).

schema information:

`{'type': 'number', 'unit': 'mT.s/m'}`

## SpoilingRFPhaseIncrement (metadata)

name: SpoilingRFPhaseIncrement

description:

The amount of incrementation described in degrees, which is applied to the phase of the excitation pulse at each TR period for achieving RF spoiling.

schema information:

`{'type': 'number', 'unit': 'degrees'}`

## SpoilingState (metadata)

name: SpoilingState

description:

Boolean stating whether the pulse sequence uses any type of spoiling strategy to suppress residual transverse magnetization.

schema information:

`{'type': 'boolean'}`

## SpoilingType (metadata)

name: SpoilingType

description:

Specifies which spoiling method(s) are used by a spoiled sequence.

schema information:

```
{'type': 'string', 'enum': ['RF', 'GRADIENT', 'COMBINED']}
```

## StartTime (metadata)

name: StartTime

description:

Start time in seconds in relation to the start of acquisition of the first data sample in the corresponding neural dataset (negative values are allowed).

schema information:

```
{'type': 'number', 'unit': 's'}
```

## StationName (metadata)

name: StationName

description:

Institution defined name of the machine that produced the measurements.

schema information:

```
{'type': 'string'}
```

## StimulusPresentation (metadata)

name: StimulusPresentation

description:

Object containing key value pairs related to the software used to present the stimuli during the experiment, specifically: `"OperatingSystem"`, `"SoftwareName"`, `"SoftwareRRID"`, `"SoftwareVersion"` and `"Code"`. See table below for more information.

schema information:

```
{'type': 'object', 'properties': {'OperatingSystem': {'name': 'OperatingSystem', 'description': 'Operating system used to run the stimuli presentation
```

## SubjectArtefactDescription (metadata)

name: SubjectArtefactDescription

description:

> Freeform description of the observed subject artefact and its possible cause (for example, `"Vagus Nerve Stimulator"`, `"non-removable implant"`). If this field is set to `"n/a"`, it will be interpreted as absence of major source of artifacts except cardiac and blinks.

schema information:

```
{'type': 'string'}
```

## T1map (suffixes)

name: Longitudinal relaxation time image

description:

> In seconds (s). T1 maps are REQUIRED to use this suffix regardless of the method used to generate them. See this interactive book on T1 mapping for further reading on T1-mapping.

schema information:

```
{'unit': 's'}
```

## T1rho (suffixes)

name: T1 in rotating frame (T1 rho) image

description:

> In seconds (s). T1-rho maps are REQUIRED to use this suffix regardless of the method used to generate them.

schema information:

```
{'unit': 's'}
```

## T1w (suffixes)

name: T1-weighted image

description:

> In arbitrary units (arbitrary). The contrast of these images is mainly determined by spatial variations in the longitudinal relaxation time of the imaged specimen. In spin-echo sequences this contrast is achieved at relatively short repetition and echo times. To achieve this weighting in gradient-echo images, again, short repetition and echo times are selected; however, at relatively large flip angles. Another common approach to increase T1 weighting in gradient-echo images is to add an inversion preparation block to the beginning of the imaging sequence (for example, `TurboFLASH` or `MP-RAGE`).

schema information:

```
{'unit': 'arbitrary'}
```

## T2map (suffixes)

name: True transverse relaxation time image

description:

In seconds (s). T2 maps are REQUIRED to use this suffix regardless of the method used to generate them.

schema information:

```
{'unit': 's'}
```

## T2star (suffixes)

name: T2* image

description:

Ambiguous, may refer to a parametric image or to a conventional image. Change: Replaced by `T2starw` or `T2starmap`.

schema information:

```
{'anyOf': [{'unit': 'arbitrary'}, {'unit': 's'}]}
```

## T2starmap (suffixes)

name: Observed transverse relaxation time image

description:

In seconds (s). T2-star maps are REQUIRED to use this suffix regardless of the method used to generate them.

schema information:

```
{'unit': 's'}
```

## T2starw (suffixes)

name: T2star weighted image

description:

> In arbitrary units (arbitrary). The contrast of these images is mainly determined by spatial variations in the (observed) transverse relaxation time of the imaged specimen. In spin-echo sequences, this effect is negated as the excitation is followed by an inversion pulse. The contrast of gradient-echo images natively depends on T2-star effects. However, for T2-star variation to dominate the image contrast, gradient-echo acquisitions are carried out at long repetition and echo times, and at small flip angles.

schema information:

```
{'unit': 'arbitrary'}
```

## T2w (suffixes)

name: T2-weighted image

description:

> In arbitrary units (arbitrary). The contrast of these images is mainly determined by spatial variations in the (true) transverse relaxation time of the imaged specimen. In spin-echo sequences this contrast is achieved at relatively long repetition and echo times. Generally, gradient echo sequences are not the most suitable option for achieving T2 weighting, as their contrast natively depends on T2-star rather than on T2.

schema information:

```
{'unit': 'arbitrary'}
```

## TB1AFI (suffixes)

name: TB1AFI

description:

> This method (Yarnykh 2007) calculates a B1+ map from two images acquired at interleaved (two) TRs with identical RF pulses using a steady-state sequence.

schema information:

```
{}
```

## TB1DAM (suffixes)

name: TB1DAM

description:

> The double-angle B1+ method (Insko and Bolinger 1993) is based on the calculation of the actual angles from signal ratios, collected by two acquisitions at different nominal excitation flip angles. Common sequence types for this application include spin echo and echo planar imaging.

schema information:

```
{}
```

## TB1EPI (suffixes)

name: TB1EPI

description:

> This B1+ mapping method (Jiru and Klose 2006) is based on two EPI readouts to acquire spin echo (SE) and stimulated echo (STE) images at multiple flip angles in one sequence, used in the calculation of deviations from the nominal flip angle.

schema information:

```
{}
```

## TB1RFM (suffixes)

name: TB1RFM

description:

> The result of a Siemens `rf_map` product sequence. This sequence produces two images. The first image appears like an anatomical image and the second output is a scaled flip angle map.

schema information:

```
{}
```

## TB1SRGE (suffixes)

name: TB1SRGE

description:

> Saturation-prepared with 2 rapid gradient echoes (SA2RAGE) uses a ratio of two saturation recovery images with different time delays, and a simulated look-up table to estimate B1+ (Eggenschwiler et al. 2011). This sequence can also be used in conjunction with MP2RAGE T1 mapping to iteratively improve B1+ and T1 map estimation (Marques & Gruetter 2013).

schema information:

```
{}
```

## TB1TFL (suffixes)

name: TB1TFL

description:

> The result of a Siemens `tfl_b1_map` product sequence. This sequence produces two images. The first image appears like an anatomical image and the second output is a scaled flip angle map.

schema information:

```
{}
```

## TB1map (suffixes)

name: RF transmit field image

description:

> In arbitrary units (arbitrary). Radio frequency (RF) transmit (B1+) field maps are REQUIRED to use this suffix regardless of the method used to generate them. TB1map intensity values are RECOMMENDED to be represented as percent multiplicative factors such that FlipAngleeffective = B1+intensity*FlipAnglenominal .

schema information:

```
{'unit': 'arbitrary'}
```

## TEM (suffixes)

name: Transmission electron microscopy

description:

> Transmission electron microscopy imaging data

schema information:

```
{}
```

## TaskDescription (metadata)

name: TaskDescription

description:

> Longer description of the task.

schema information:

`{'type': 'string'}`

## TaskName (metadata)

name: TaskName

description:

> Name of the task. No two tasks should have the same name. The task label included in the file name is derived from this `"TaskName"` field by removing all non-alphanumeric (`[a-zA-Z0-9]`) characters. For example `"TaskName"` `"faces n-back"` will correspond to task label `facesnback`.

schema information:

`{'type': 'string'}`

## TermURL (metadata)

name: TermURL

description:

> URL pointing to a formal definition of this type of data in an ontology available on the web.

schema information:

`{'type': 'string'}`

## TimeZero (metadata)

name: TimeZero

description:

> Time zero to which all scan and/or blood measurements have been adjusted to, in the unit ”hh:mm:ss”. This should be equal to `"InjectionStart"` or `"ScanStart"`.

schema information:

`{'type': 'string', 'pattern': '^(?:2[0-3]|[01][0-9]):[0-5][0-9]:[0-5][0-9]$'}`

## TissueDeformationScaling (metadata)

name: TissueDeformationScaling

description:

> Estimated deformation of the tissue, given as a percentage of the original tissue size (for examples: for a shrinkage of 3%, the value is `97`; and for an expansion of 100%, the value is `200`).

schema information:

```
{'type': 'number', 'exclusiveMinimum': 0}
```

## TissueOrigin (metadata)

name: TissueOrigin

description:

> Describes the type of tissue analyzed for `"SampleOrigin"` `brain`.

schema information:

```
{'type': 'string', 'enum': ['gray matter', 'white matter', 'csf', 'meninges', 'macrovascular', 'microvascular']}
```

## TotalAcquiredPairs (metadata)

name: TotalAcquiredPairs

description:

> The total number of acquired `control-label` pairs. A single pair consists of a single `control` and a single `label` image.

schema information:

```
{'type': 'number', 'exclusiveMinimum': 0}
```

## TotalReadoutTime (metadata)

name: TotalReadoutTime

description:

> This is actually the "effective" total readout time, defined as the readout duration, specified in seconds, that would have generated data with the given level of distortion. It is NOT the actual, physical duration of the readout train. If `"EffectiveEchoSpacing"` has been properly computed, it is just `EffectiveEchoSpacing * (ReconMatrixPE - 1)`.

schema information:

`{'type': 'number', 'unit': 's'}`

## TracerMolecularWeight (metadata)

name: TracerMolecularWeight

description:

Accurate molecular weight of the tracer used.

schema information:

`{'type': 'number'}`

## TracerMolecularWeightUnits (metadata)

name: TracerMolecularWeightUnits

description:

Unit of the molecular weights measurement (for example, `"g/mol"`).

schema information:

`{'type': 'string', 'format': 'unit'}`

## TracerName (metadata)

name: TracerName

description:

Name of the tracer compound used (for example, `"CIMBI-36"`)

schema information:

`{'type': 'string'}`

## TracerRadLex (metadata)

name: TracerRadLex

description:

ID of the tracer compound from the RadLex Ontology.

schema information:

```
{'type': 'string'}
```

## TracerRadionuclide (metadata)

name: TracerRadionuclide

description:

Radioisotope labelling tracer (for example, `"C11"`).

schema information:

```
{'type': 'string'}
```

## TracerSNOMED (metadata)

name: TracerSNOMED

description:

ID of the tracer compound from the SNOMED Ontology (subclass of Radioactive isotope).

schema information:

```
{'type': 'string'}
```

## TriggerChannelCount (metadata)

name: TriggerChannelCount

description:

Number of channels for digital (TTL bit level) triggers.

schema information:

```
{'type': 'integer', 'minimum': 0}
```

## TubingLength (metadata)

name: TubingLength

description:

The length of the blood tubing, from the subject to the detector in meters.

schema information:

```
{'type': 'number', 'unit': 'm'}
```

## TubingType (metadata)

name: TubingType

description:

Description of the type of tubing used, ideally including the material and (internal) diameter.

schema information:

```
{'type': 'string'}
```

## Type (metadata)

name: Type

description:

Short identifier of the mask. The value `"Brain"` refers to a brain mask. The value `"Lesion"` refers to a lesion mask. The value `"Face"` refers to a face mask. The value `"ROI"` refers to a region of interest mask.

schema information:

```
{'type': 'string', 'enum': ['Brain', 'Lesion', 'Face', 'ROI']}
```

## UNIT1 (suffixes)

name: Homogeneous (flat) T1-weighted MP2RAGE image

description:

In arbitrary units (arbitrary). UNIT1 images are REQUIRED to use this suffix regardless of the method used to generate them. Note that although this image is T1-weighted, regions without MR signal will contain white salt-and-pepper noise that most segmentation algorithms will fail on. Therefore, it is important to dissociate it from `T1w`. Please see `MP2RAGE` specific notes in the qMRI appendix for further information.

schema information:

```
{}
```

## Units (metadata)

name: Units

description:

Measurement units for the associated file. SI units in CMIXF formatting are RECOMMENDED (see Units).

schema information:

```
{'type': 'string', 'format': 'unit'}
```

## VFA (suffixes)

name: Variable flip angle

description:

The VFA method involves at least two spoiled gradient echo (SPGR) of steady-state free precession (SSFP) images acquired at different flip angles. Depending on the provided metadata fields and the sequence type, data may be eligible for DESPOT1, DESPOT2 and their variants (Deoni et al. 2005).

schema information:

```
{}
```

## VascularCrushing (metadata)

name: VascularCrushing

description:

Boolean indicating if Vascular Crushing is used. Corresponds to DICOM Tag 0018, 9259 `ASL Crusher Flag`.

schema information:

```
{'type': 'boolean'}
```

## VascularCrushingVENC (metadata)

name: VascularCrushingVENC

description:

> The crusher gradient strength, in centimeters per second. Specify either one number for the total time-series, or provide an array of numbers, for example when using QUASAR, using the value zero to identify volumes for which `VascularCrushing` was turned off. Corresponds to DICOM Tag 0018, 925A `ASL Crusher Flow Limit`.

schema information:

```
{'anyOf': [{'type': 'number', 'unit': 'cm/s'}, {'type': 'array', 'items': {'type': 'number', 'unit': 'cm/s'}}]}
```

## VolumeTiming (metadata)

name: VolumeTiming

description:

> The time at which each volume was acquired during the acquisition. It is described using a list of times referring to the onset of each volume in the BOLD series. The list must have the same length as the BOLD series, and the values must be non-negative and monotonically increasing. This field is mutually exclusive with `"RepetitionTime"` and `"DelayTime"`. If defined, this requires acquisition time (TA) be defined via either `"SliceTiming"` or `"AcquisitionDuration"` be defined.

schema information:

```
{'type': 'array', 'minItems': 1, 'items': {'type': 'number', 'unit': 's'}}
```

## WholeBloodAvail (metadata)

name: WholeBloodAvail

description:

> Boolean that specifies if whole blood measurements are available. If `true`, the `whole_blood_radioactivity` column MUST be present in the corresponding `*_blood.tsv` file.

schema information:

```
{'type': 'boolean'}
```

## WithdrawalRate (metadata)

name: WithdrawalRate

description:

> The rate at which the blood was withdrawn from the subject. The unit of the specified withdrawal rate should be in `"mL/s"`.

schema information:

`{'type': 'number', 'unit': 'mL/s'}`

## abbreviation (columns)

name: abbreviation

description:

> The unique label abbreviation

schema information:

`{'type': 'string'}`

## acq_time sense 1 (columns)

name: acq_time

description:

> Acquisition time refers to when the first data point in each run was acquired. Furthermore, if this header is provided, the acquisition times of all files from the same recording MUST be identical. Datetime format and their anonymization are described in Units.

schema information:

`{'type': 'string', 'format': 'datetime'}`

## acq_time sense 2 (columns)

name: acq_time

description:

> Acquisition time refers to when the first data point of the first run was acquired. Datetime format and their anonymization are described in Units.

schema information:

`{'type': 'string', 'format': 'datetime'}`

## acquisition (entities)

name: Acquisition

description:

> The `acq-<label>` key/value pair corresponds to a custom label the user MAY use to distinguish a different set of parameters used for acquiring the same modality. For example this should be used when a study includes two T1w images - one full brain low resolution and one restricted field of view but high resolution. In such case two files could have the following names: `sub-01_acq-highres_T1w.nii.gz` and `sub-01_acq-lowres_T1w.nii.gz`, however the user is free to choose any other label than `highres` and `lowres` as long as they are consistent across subjects and sessions. In case different sequences are used to record the same modality (for example, `RARE` and `FLASH` for T1w) this field can also be used to make that distinction. At what level of detail to make the distinction (for example, just between `RARE` and `FLASH`, or between `RARE`, `FLASH`, and `FLASHsubsampled`) remains at the discretion of the researcher.

schema information:

```
{'entity': 'acq', 'type': 'string', 'format': 'label'}
```

## age (columns)

name: age

description:

> Numeric value in years (float or integer value).

schema information:

```
{'type': 'number', 'unit': 'year'}
```

## anat (datatypes)

name: Anatomical Magnetic Resonance Imaging

description:

> Magnetic resonance imaging sequences designed to characterize static, anatomical features.

schema information:

```
{}
```

## angio (suffixes)

name: Angiogram

description:

> Magnetic resonance angiography sequences focus on enhancing the contrast of blood vessels (generally arteries, but sometimes veins) against other tissue types.

schema information:

```
{}
```

## asl (suffixes)

name: Arterial Spin Labeling

description:

> The complete ASL time series stored as a 4D NIfTI file in the original acquisition order, with possible volume types including: control, label, m0scan, deltam, cbf.

schema information:

```
{}
```

## aslcontext (suffixes)

name: Arterial Spin Labeling Context

description:

> A TSV file defining the image types for volumes in an associated ASL file.

schema information:

```
{}
```

## asllabeling (suffixes)

name: ASL Labeling Screenshot

description:

> An anonymized screenshot of the planning of the labeling slab/plane with respect to the imaging slab or slices `*_asllabeling.jpg`. Based on DICOM macro C.8.13.5.14.

schema information:

```
{}
```

## beh (datatypes)

name: Behavioral Data

description:

Behavioral data.

schema information:

```
{}
```

## beh (modalities)

name: Behavioral experiments

description:

Behavioral data acquired without accompanying neuroimaging data.

schema information:

```
{}
```

## beh (suffixes)

name: Behavioral recording

description:

Behavioral recordings from tasks. These files are similar to events files, but do not include the `"onset"` and `"duration"` columns that are mandatory for events files.

schema information:

```
{}
```

## blood (suffixes)

name: Blood recording data

description:

Blood measurements of radioactivity stored in tabular files and located in the `pet/` directory along with the corresponding PET data.

schema information:

```
{}
```

## bold (suffixes)

name: Blood-Oxygen-Level Dependent image

description:

Blood-Oxygen-Level Dependent contrast (specialized T2* weighting)

schema information:

```
{}
```

## cardiac (columns)

name: cardiac

description:

continuous pulse measurement

schema information:

```
{'type': 'number'}
```

## cbv (suffixes)

name: Cerebral blood volume image

description:

Cerebral Blood Volume contrast (specialized T2* weighting or difference between T1 weighted images)

schema information:

```
{}
```

## ceagent (entities)

name: Contrast Enhancing Agent

description:

> The `ce-<label>` key/value can be used to distinguish sequences using different contrast enhanced images. The label is the name of the contrast agent. The key `"ContrastBolusIngredient"` MAY also be added in the JSON file, with the same label.

schema information:

```
{'entity': 'ce', 'type': 'string', 'format': 'label'}
```

## channels (suffixes)

name: Channels File

description:

> Channel information.

schema information:

```
{}
```

## chunk (entities)

name: Chunk

description:

> The `chunk-<index>` key/value pair is used to distinguish between different regions, 2D images or 3D volumes files, of the same physical sample with different fields of view acquired in the same imaging experiment.

schema information:

```
{'entity': 'chunk', 'type': 'string', 'format': 'index'}
```

## code (associated_data)

name: Code

description:

> A folder in which to store any code used to generate the derivatives from the source data.

schema information:

```
{}
```

## color (columns)

name: color

description:

Hexadecimal. Label color for visualization.

schema information:

```
{'type': 'string', 'unit': 'hexadecimal'}
```

## coordsystem (suffixes)

name: Coordinate System File

description:

A JSON document specifying the coordinate system(s) used for the MEG, EEG, head localization coils, and anatomical landmarks.

schema information:

```
{}
```

## dataset_description (top_level_files)

name: Dataset Description

description:

The file `dataset_description.json` is a JSON file describing the dataset.

schema information:

```
{}
```

## defacemask (suffixes)

name: Defacing Mask

description:

A binary mask that was used to remove facial features from an anatomical MRI image.

schema information:

```
{}
```

## density (entities)

name: Density

description:

> Density of non-parametric surfaces. MUST have a corresponding `Density` metadata field to provide interpretation.This entity is only applicable to derivative data.

schema information:

```
{'entity': 'den', 'type': 'string', 'format': 'label'}
```

## derivatives (associated_data)

name: Derivative data

description:

> Derivative data

schema information:

```
{}
```

## derived_from (columns)

name: derived_from

description:

> `sample-<label>` key/value pair from which a sample is derived, for example a slice of tissue (`sample-02`) derived from a block of tissue (`sample-01`).

schema information:

```
{'type': 'string', 'pattern': '^sample-[0-9a-zA-Z]+$'}
```

## description (columns)

name: description

description:

> Brief free-text description of the channel, or other information of interest.

schema information:

```
{'type': 'string'}
```

## description (entities)

name: Description

description:

> When necessary to distinguish two files that do not otherwise have a distinguishing entity, the `_desc-<label>` keyword-value SHOULD be used.This entity is only applicable to derivative data.

schema information:

```
{'entity': 'desc', 'type': 'string', 'format': 'label'}
```

## dimension (columns)

name: dimension

description:

> Size of the group (grid/strip/probe) that this electrode belongs to. Must be of form `[AxB]` with the smallest dimension first (for example, `[1x8]`).

schema information:

```
{'type': 'string'}
```

## direction (entities)

name: Phase-Encoding Direction

description:

> The `dir-<label>` key/value can be set to an arbitrary alphanumeric label (for example, `dir-LR` or `dir-AP`) to distinguish different phase-encoding directions.

schema information:

```
{'entity': 'dir', 'type': 'string', 'format': 'label'}
```

## duration (columns)

name: duration

description:

> Duration of the event (measured from onset) in seconds. Must always be either zero or positive (or `n/a` if unavailable). A ”duration” value of zero implies that the delta function or event is so short as to be effectively modeled as an impulse.

schema information:

```
{'anyOf': [{'type': 'number', 'unit': 's', 'minimum': 0}, {'type': 'string', 'enum': ['n/a']}]}
```

## dwi (datatypes)

name: Diffusion-Weighted Imaging

description:

> Diffusion-weighted imaging (DWI).

schema information:

```
{}
```

## dwi (suffixes)

name: Diffusion-weighted image

description:

> Diffusion-weighted imaging contrast (specialized T2 weighting).

schema information:

```
{}
```

## echo (entities)

name: Echo

description:

> If files belonging to an entity-linked file collection are acquired at different echo times, the `_echo-<index>` key/value pair MUST be used to distinguish individual files. This entity represents the `"EchoTime"` metadata field. Please note that the `<index>` denotes the number/index (in the form of a nonnegative integer), not the `"EchoTime"` value which needs to be stored in the field `"EchoTime"` of the separate JSON file.

schema information:

```
{'entity': 'echo', 'type': 'string', 'format': 'index'}
```

## eeg (datatypes)

name: Electroencephalography

description:

Electroencephalography

schema information:

```
{}
```

## eeg (modalities)

name: Electroencephalography

description:

Data acquired with EEG.

schema information:

```
{}
```

## eeg (suffixes)

name: Electroencephalography

description:

Electroencephalography recording data.

schema information:

```
{}
```

## electrodes (suffixes)

name: Electrodes

description:

File that gives the location of (i)EEG electrodes.

schema information:

```
{}
```

## epi (suffixes)

name: EPI

description:

> The phase-encoding polarity (PEpolar) technique combines two or more Spin Echo EPI scans with different phase encoding directions to estimate the underlying inhomogeneity/deformation map.

schema information:

```
{}
```

## events (suffixes)

name: Events

description:

> Event timing information from a behavioral task.

schema information:

```
{}
```

## fieldmap (suffixes)

name: Fieldmap

description:

> Some MR schemes such as spiral-echo imaging (SEI) sequences are able to directly provide maps of the B0 field inhomogeneity.

schema information:

```
{}
```

## filename (columns)

name: filename

description:

> Relative paths to files.

schema information:

```
{'type': 'string', 'format': 'participant_relative'}
```

## flip (entities)

name: Flip Angle

description:

> If files belonging to an entity-linked file collection are acquired at different flip angles, the `_flip-<index>` key/value pair MUST be used to distinguish individual files. This entity represents the `"FlipAngle"` metadata field. Please note that the `<index>` denotes the number/index (in the form of a nonnegative integer), not the `"FlipAngle"` value which needs to be stored in the field `"FlipAngle"` of the separate JSON file.

schema information:

```
{'entity': 'flip', 'type': 'string', 'format': 'index'}
```

## fmap (datatypes)

name: Field maps

description:

> MRI scans for estimating B0 inhomogeneity-induced distortions.

schema information:

```
{}
```

## func (datatypes)

name: Task-Based Magnetic Resonance Imaging

description:

> Task (including resting state) imaging data

schema information:

```
{}
```

## genetic_info (top_level_files)

name: Genetic Information

description:

> The `genetic_info.json` file describes the genetic information available in the `participants.tsv` file and/or the genetic database described in `dataset_description.json`. Datasets containing the `Genetics` field in `dataset_description.json` or the `genetic_id` column in `participants.tsv` MUST include this file.

schema information:

```
{}
```

## group (columns)

name: group

description:

> Which group of channels (grid/strip/seeg/depth) this channel belongs to. This is relevant because one group has one cable-bundle and noise can be shared. This can be a name or number.

schema information:

```
{'anyOf': [{'type': 'string'}, {'type': 'number'}]}
```

## handedness (columns)

name: handedness

description:

> String value indicating one of ”left”, ”right”, ”ambidextrous”.For ”left”, use one of these values: `left`, `l`, `L`, `LEFT`, `Left`.For ”right”, use one of these values: `right`, `r`, `R`, `RIGHT`, `Right`.For ”ambidextrous”, use one of these values: `ambidextrous`, `a`, `A`, `AMBIDEXTROUS`, `Ambidextrous`.

schema information:

```
{'type': 'string', 'enum': ['left', 'l', 'L', 'LEFT', 'Left', 'right', 'r', 'R', 'RIGHT', 'Right', 'ambidextrous', 'a', 'A', 'AMBIDEXTROUS', 'Ambidextr
```

## headshape (suffixes)

name: Headshape File

description:

> The 3-D locations of points that describe the head shape and/or electrode locations can be digitized and stored in separate files.

schema information:

`{}`

## hemisphere (columns)

name: hemisphere

description:

> The hemisphere in which the electrode is placed.

schema information:

`{'type': 'string', 'enum': ['L', 'R']}`

## hemisphere (entities)

name: Hemisphere

description:

> The `hemi-<label>` entity indicates which hemibrain is described by the file. Allowed label values for this entity are `L` and `R`, for the left and right hemibrains, respectively.

schema information:

`{'entity': 'hemi', 'type': 'string', 'format': 'label', 'enum': ['L', 'R']}`

## high_cutoff (columns)

name: high_cutoff

description:

> Frequencies used for the low-pass filter applied to the channel in Hz. If no low-pass filter applied, use `n/a`. Note that hardware anti-aliasing in A/D conversion of all MEG/EEG electronics applies a low-pass filter; specify its frequency here if applicable.

schema information:

`{'anyOf': [{'type': 'number', 'unit': 'Hz', 'minimum': 0}, {'type': 'string', 'enum': ['n/a']}]}`

## hplc_recovery_fractions (columns)

name: hplc_recovery_fractions

description:

HPLC recovery fractions (the fraction of activity that gets loaded onto the HPLC).

schema information:

```
{'type': 'number', 'unit': 'arbitrary'}
```

## iEEGCoordinateProcessingDescription (metadata)

name: iEEGCoordinateProcessingDescription

description:

Has any post-processing (such as projection) been done on the electrode positions (for example, `"surface_projection"`, `"none"`).

schema information:

```
{'type': 'string'}
```

## iEEGCoordinateProcessingReference (metadata)

name: iEEGCoordinateProcessingReference

description:

A reference to a paper that defines in more detail the method used to localize the electrodes and to post-process the electrode positions.

schema information:

```
{'type': 'string'}
```

## iEEGCoordinateSystem (metadata)

name: iEEGCoordinateSystem

description:

Defines the coordinate system for the iEEG sensors. See Appendix VIII for a list of restricted keywords for coordinate systems. If `"Other"`, provide definition of the coordinate system in `iEEGCoordinateSystemDescription`. If positions correspond to pixel indices in a 2D image (of either a volume-rendering, surface-rendering, operative photo, or operative drawing), this MUST be `"Pixels"`. For more information, see the section on Appendix VIII.

schema information:

```
{'type': 'string', 'enum': ['Pixels', 'ACPC', 'Other', 'ICBM452AirSpace', 'ICBM452Warp5Space', 'IXI549Space', 'fsaverage', 'fsaverageSym', 'fsLR', 'MNI
```

## iEEGCoordinateSystemDescription (metadata)

name: iEEGCoordinateSystemDescription

description:

Free-form text description of the coordinate system. May also include a link to a documentation page or paper describing the system in greater detail.

schema information:

```
{'type': 'string'}
```

## iEEGCoordinateUnits (metadata)

name: iEEGCoordinateUnits

description:

Units of the `*_electrodes.tsv`. MUST be `"pixels"` if `iEEGCoordinateSystem` is `Pixels`.

schema information:

```
{'type': 'string', 'enum': ['m', 'mm', 'cm', 'pixels', 'n/a']}
```

## iEEGElectrodeGroups (metadata)

name: iEEGElectrodeGroups

description:

Field to describe the way electrodes are grouped into strips, grids or depth probes. For example, `"grid1: 10x8 grid on left temporal pole, strip2: 1x8 electrode strip on xxx"`.

schema information:

```
{'type': 'string'}
```

## iEEGGround (metadata)

name: iEEGGround

description:

Description of the location of the ground electrode (`"placed on right mastoid (M2)"`).

schema information:

```
{'type': 'string'}
```

## iEEGPlacementScheme (metadata)

name: iEEGPlacementScheme

description:

> Freeform description of the placement of the iEEG electrodes. Left/right/bilateral/depth/surface (for example, `"left frontal grid and bilateral hippocampal depth"` or `"surface strip and STN depth"` or `"clinical indication bitemporal, bilateral temporal strips and left grid"`).

schema information:

```
{'type': 'string'}
```

## iEEGReference (metadata)

name: iEEGReference

description:

> General description of the reference scheme used and (when applicable) of location of the reference electrode in the raw recordings (for example, `"left mastoid"`, `"bipolar"`, `"T01"` for electrode with name T01, `"intracranial electrode on top of a grid, not included with data"`, `"upside down electrode"`). If different channels have a different reference, this field should have a general description and the channel specific reference should be defined in the `channels.tsv` file.

schema information:

```
{'type': 'string'}
```

## ieeg (datatypes)

name: Intracranial electroencephalography

description:

> Intracranial electroencephalography (iEEG) or electrocorticography (ECoG) data

schema information:

```
{}
```

## ieeg (modalities)

name: Intracranial Electroencephalography

description:

Data acquired with iEEG.

schema information:

```
{}
```

## ieeg (suffixes)

name: Intracranial Electroencephalography

description:

Intracranial electroencephalography recording data.

schema information:

```
{}
```

## impedance (columns)

name: impedance

description:

Impedance of the electrode, units MUST be in `kOhm`.

schema information:

```
{'type': 'number', 'unit': 'kOhm'}
```

## index (columns)

name: index

description:

The label integer index.

schema information:

```
{'type': 'integer'}
```

# inplaneT1 (suffixes)

name: Inplane T1

description:

> In arbitrary units (arbitrary). T1 weighted structural image matched to a functional (task) image.

schema information:

```
{'unit': 'arbitrary'}
```

# inplaneT2 (suffixes)

name: Inplane T2

description:

> In arbitrary units (arbitrary). T2 weighted structural image matched to a functional (task) image.

schema information:

```
{'unit': 'arbitrary'}
```

# inversion (entities)

name: Inversion Time

description:

> If files belonging to an entity-linked file collection are acquired at different inversion times, the `_inv-<index>` key/value pair MUST be used to distinguish individual files. This entity represents the `"InversionTime` metadata field. Please note that the `<index>` denotes the number/index (in the form of a nonnegative integer), not the `"InversionTime"` value which needs to be stored in the field `"InversionTime"` of the separate JSON file.

schema information:

```
{'entity': 'inv', 'type': 'string', 'format': 'index'}
```

# label (entities)

name: Label

description:

> Tissue-type label, following a prescribed vocabulary. Applies to binary masks and probabilistic/partial volume segmentations that describe a single tissue type.This entity is only applicable to derivative data.

schema information:

`{'entity': 'label', 'type': 'string', 'format': 'label'}`

## low_cutoff (columns)

name: low_cutoff

description:

> Frequencies used for the high-pass filter applied to the channel in Hz. If no high-pass filter applied, use `n/a`.

schema information:

`{'anyOf': [{'type': 'number', 'unit': 'Hz'}, {'type': 'string', 'enum': ['n/a']}]}`

## m0scan (suffixes)

name: M0 image

description:

> The M0 image is a calibration image, used to estimate the equilibrium magnetization of blood.

schema information:

`{}`

## magnitude (suffixes)

name: Magnitude

description:

> Field-mapping MR schemes such as gradient-recalled echo (GRE) generate a Magnitude image to be used for anatomical reference. Requires the existence of Phase, Phase-difference or Fieldmap maps.

schema information:

`{}`

## magnitude1 (suffixes)

name: Magnitude

description:

Magnitude map generated by GRE or similar schemes, associated with the first echo in the sequence.

schema information:

```
{}
```

## magnitude2 (suffixes)

name: Magnitude

description:

Magnitude map generated by GRE or similar schemes, associated with the second echo in the sequence.

schema information:

```
{}
```

## manufacturer (columns)

name: manufacturer

description:

The manufacturer for each electrode. Can be used if electrodes were manufactured by more than one company.

schema information:

```
{'type': 'string'}
```

## mapping (columns)

name: mapping

description:

Corresponding integer label in the standard BIDS label lookup.

schema information:

```
{'type': 'integer'}
```

## markers (suffixes)

name: MEG Sensor Coil Positions

description:

> Another manufacturer-specific detail pertains to the KIT/Yokogawa/Ricoh system, which saves the MEG sensor coil positions in a separate file with two possible filename extensions (`.sqd`, `.mrk`). For these files, the `markers` suffix MUST be used. For example: `sub-01_task-nback_markers.sqd`

schema information:

```
{}
```

## material (columns)

name: material

description:

> Material of the electrode (for example, `Tin`, `Ag/AgCl`, `Gold`).

schema information:

```
{'type': 'string'}
```

## meg (datatypes)

name: Magnetoencephalography

description:

> Magnetoencephalography

schema information:

```
{}
```

## meg (modalities)

name: Magnetoencephalography

description:

> Data acquired with an MEG scanner.

schema information:

```
{}
```

## meg (suffixes)

name: Magnetoencephalography

description:

> Unprocessed MEG data stored in the native file format of the MEG instrument with which the data was collected.

schema information:

```
{}
```

## metabolite_parent_fraction (columns)

name: metabolite_parent_fraction

description:

> Parent fraction of the radiotracer (0-1).

schema information:

```
{'type': 'number', 'minimum': 0, 'maximum': 1}
```

## metabolite_polar_fraction (columns)

name: metabolite_polar_fraction

description:

> Polar metabolite fraction of the radiotracer (0-1).

schema information:

```
{'type': 'number', 'minimum': 0, 'maximum': 1}
```

## micr (datatypes)

name: Microscopy

description:

> Microscopy

schema information:

```
{}
```

## micr (modalities)

name: Microscopy

description:

> Data acquired with a microscope.

schema information:

```
{}
```

## modality (entities)

name: Corresponding Modality

description:

> The `mod-<label>` key/value pair corresponds to modality label for defacing masks, for example, T1w, inplaneT1, referenced by a defacemask image. For example, `sub-01_mod-T1w_defacemask.nii.gz`.

schema information:

```
{'entity': 'mod', 'type': 'string', 'format': 'label'}
```

## mri (modalities)

name: Magnetic Resonance Imaging

description:

> Data acquired with an MRI scanner.

schema information:

```
{}
```

## mtransfer (entities)

name: Magnetization Transfer

description:

> If files belonging to an entity-linked file collection are acquired at different magnetization transfer (MT) states, the `_mt-<label>` key/value pair MUST be used to distinguish individual files. This entity represents the `"MTState"` metadata field. Allowed label values for this entity are `on` and `off`, for images acquired in presence and absence of an MT pulse, respectively.

schema information:

```
{'entity': 'mt', 'type': 'string', 'enum': ['on', 'off']}
```

## name sense 1 (columns)

name: name

description:

> Label of the channel.

schema information:

```
{'type': 'string'}
```

## name sense 2 (columns)

name: name

description:

> Name of the electrode contact point.

schema information:

```
{'type': 'string'}
```

## name sense 3 (columns)

name: name

description:

> The unique label name.

schema information:

```
{'type': 'string'}
```

## notch (columns)

name: notch

description:

Frequencies used for the notch filter applied to the channel, in Hz. If no notch filter applied, use `n/a`.

schema information:

`{'anyOf': [{'type': 'number', 'unit': 'Hz'}, {'type': 'string', 'enum': ['n/a']}]}`

## onset (columns)

name: onset

description:

Onset (in seconds) of the event, measured from the beginning of the acquisition of the first data point stored in the corresponding task data file. Negative onsets are allowed, to account for events that occur prior to the first stored data point. For example, in case there is an in-scanner training phase that begins before the scanning sequence has started events from this sequence should have negative onset time counting down to the beginning of the acquisition of the first volume.If any data points have been discarded before forming the data file (for example, ”dummy volumes” in BOLD fMRI), a time of 0 corresponds to the first stored data point and not the first acquired data point.

schema information:

`{'type': 'number', 'unit': 's'}`

## part (entities)

name: Part

description:

This entity is used to indicate which component of the complex representation of the MRI signal is represented in voxel data. The `part-<label>` key/value pair is associated with the DICOM Tag `0008, 9208`. Allowed label values for this entity are `phase`, `mag`, `real` and `imag`, which are typically used in `part-mag`/`part-phase` or `part-real`/`part-imag` pairs of files.Phase images MAY be in radians or in arbitrary units. The sidecar JSON file MUST include the units of the `phase` image. The possible options are `"rad"` or `"arbitrary"`.When there is only a magnitude image of a given type, the `part` key MAY be omitted.

schema information:

`{'entity': 'part', 'type': 'string', 'enum': ['mag', 'phase', 'real', 'imag']}`

## participant_id (columns)

name: participant_id

description:

A participant identifier of the form `sub-<label>`, matching a participant entity found in the dataset.

schema information:

```
{'type': 'string', 'pattern': '^sub-[0-9a-zA-Z]+$'}
```

## participants (top_level_files)

name: Participant Information

description:

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.Commonly used optional columns in `participant.tsv` files are `age`, `sex`, and `handedness`. We RECOMMEND to make use of these columns, and in case that you do use them, we RECOMMEND to use the following values for them:- `age`: numeric value in years (float or integer value)- `sex`: string value indicating phenotypical sex, one of ”male”, ”female”, ”other” - for ”male”, use one of these values: `male`, `m`, `M`, `MALE`, `Male` - for ”female”, use one of these values: `female`, `f`, `F`, `FEMALE`, `Female` - for ”other”, use one of these values: `other`, `o`, `O`, `OTHER`, `Other`- `handedness`: string value indicating one of ”left”, ”right”, ”ambidextrous” - for ”left”, use one of these values: `left`, `l`, `L`, `LEFT`, `Left` - for ”right”, use one of these values: `right`, `r`, `R`, `RIGHT`, `Right` - for ”ambidextrous”, use one of these values: `ambidextrous`, `a`, `A`, `AMBIDEXTROUS`, `Ambidextrous`Throughout BIDS you can indicate missing values with `n/a` (for ”not available”).

schema information:

```
{}
```

## pathology (columns)

name: pathology

description:

String value describing the pathology of the sample or type of control. When different from `healthy`, pathology SHOULD be specified. The pathology may be specified in either `samples.tsv` or `sessions.tsv`, depending on whether the pathology changes over time.

schema information:

```
{'type': 'string'}
```

## perf (datatypes)

name: Perfusion imaging

description:

Blood perfusion imaging data, including arterial spin labeling (ASL)

schema information:

```
{}
```

## pet (datatypes)

name: Positron Emission Tomography

description:

Positron emission tomography data

schema information:

```
{}
```

## pet (modalities)

name: Positron Emission Tomography

description:

Data acquired with PET.

schema information:

```
{}
```

## pet (suffixes)

name: Positron Emission Tomography

description:

PET imaging data SHOULD be stored in 4D (or 3D, if only one volume was acquired) NIfTI files with the `_pet` suffix. Volumes MUST be stored in chronological order (the order they were acquired in).

schema information:

```
{}
```

## phase (suffixes)

name: Phase image

description:

> DEPRECATED. Phase information associated with magnitude information stored in BOLD contrast. This suffix should be replaced by the `part-phase` in conjunction with the `bold` suffix.

schema information:

```
{'anyOf': [{'unit': 'arbitrary'}, {'unit': 'rad'}]}
```

## phase1 (suffixes)

name: Phase

description:

> Phase map generated by GRE or similar schemes, associated with the first echo in the sequence.

schema information:

```
{}
```

## phase2 (suffixes)

name: Phase

description:

> Phase map generated by GRE or similar schemes, associated with the second echo in the sequence.

schema information:

```
{}
```

## phasediff (suffixes)

name: Phase-difference

description:

> Some scanners subtract the `phase1` from the `phase2` map and generate a unique `phasediff` file. For instance, this is a common output for the built-in fieldmap sequence of Siemens scanners.

schema information:

```
{}
```

## photo (suffixes)

name: Photo File

description:

> Photos of the anatomical landmarks, head localization coils or tissue sample.

schema information:

```
{}
```

## physio (suffixes)

name: Physiological recording

description:

> Physiological recordings such as cardiac and respiratory signals.

schema information:

```
{}
```

## plasma_radioactivity (columns)

name: plasma_radioactivity

description:

> Radioactivity in plasma, in unit of plasma radioactivity (for example, `kBq/mL`).

schema information:

```
{'type': 'number'}
```

## processing (entities)

name: Processed (on device)

description:

> The proc label is analogous to rec for MR and denotes a variant of a file that was a result of particular processing performed on the device.This is useful for files produced in particular by Elekta's MaxFilter (for example, `sss`, `tsss`, `trans`, `quat` or `mc`), which some installations impose to be run on raw data because of active shielding software corrections before the MEG data can actually be exploited.

schema information:

```
{'entity': 'proc', 'type': 'string', 'format': 'label'}
```

## reconstruction (entities)

name: Reconstruction

description:

> The `rec-<label>` key/value can be used to distinguish different reconstruction algorithms (for example `MoCo` for the ones using motion correction).

schema information:

```
{'entity': 'rec', 'type': 'string', 'format': 'label'}
```

## recording (entities)

name: Recording

description:

> More than one continuous recording file can be included (with different sampling frequencies). In such case use different labels. For example: `_recording-contrast`, `_recording-saturation`.

schema information:

```
{'entity': 'recording', 'type': 'string', 'format': 'label'}
```

## reference sense 1 (columns)

name: reference

description:

Name of the reference electrode(s). This column is not needed when it is common to all channels. In that case the reference electrode(s) can be specified in `*_eeg.json` as `EEGReference`).

schema information:

```
{'type': 'string'}
```

## reference sense 2 (columns)

name: reference

description:

Specification of the reference (for example, `mastoid`, `ElectrodeName01`, `intracranial`, `CAR`, `other`, `n/a`). If the channel is not an electrode channel (for example, a microphone channel) use `n/a`.

schema information:

```
{'anyOf': [{'type': 'string'}, {'type': 'string', 'enum': ['n/a']}]}
```

## resolution (entities)

name: Resolution

description:

Resolution of regularly sampled N-dimensional data. MUST have a corresponding `"Resolution"` metadata field to provide interpretation.This entity is only applicable to derivative data.

schema information:

```
{'entity': 'res', 'type': 'string', 'format': 'label'}
```

## respiratory (columns)

name: respiratory

description:

continuous breathing measurement

schema information:

```
{'type': 'number'}
```

## response_time (columns)

name: response_time

description:

Response time measured in seconds. A negative response time can be used to represent preemptive responses and `n/a` denotes a missed response.

schema information:

```
{'anyOf': [{'type': 'number', 'unit': 's'}, {'type': 'string', 'enum': ['n/a']}]}
```

## run (entities)

name: Run

description:

If several scans with the same acquisition parameters are acquired in the same session, they MUST be indexed with the `run-<index>` entity: `_run-1`, `_run-2`, `_run-3`, and so on (only nonnegative integers are allowed as run labels).If different entities apply, such as a different session indicated by `run-<index>`, or different acquisition parameters indicated by `run-<index>`, then `run` is not needed to distinguish the scans and MAY be omitted.

schema information:

```
{'entity': 'run', 'type': 'string', 'format': 'index'}
```

## sample (columns)

name: sample

description:

Onset of the event according to the sampling scheme of the recorded modality (that is, referring to the raw data file that the `events.tsv` file accompanies).

schema information:

```
{'type': 'integer'}
```

## sample (entities)

name: Sample

description:

A sample pertaining to a subject such as tissue, primary cell or cell-free sample. The `sample-<label>` key/value pair is used to distinguish between different samples from the same subject. The label MUST be unique per subject and is RECOMMENDED to be unique throughout the dataset.

schema information:

```
{'entity': 'sample', 'type': 'string', 'format': 'label'}
```

## sample_id (columns)

name: sample_id

description:

A sample identifier of the form `sample-<label>`, matching a sample entity found in the dataset.

schema information:

```
{'type': 'string', 'pattern': '^sample-[0-9a-zA-Z]+$'}
```

## sample_type (columns)

name: sample_type

description:

Biosample type defined by ENCODE Biosample Type.

schema information:

```
{'type': 'string', 'enum': ['cell line', 'in vitro differentiated cells', 'primary cell', 'cell-free sample', 'cloning host', 'tissue', 'whole organism
```

## samples (top_level_files)

name: Sample Information

description:

The purpose of this file is to describe properties of samples, indicated by the `sample` entity. This file is REQUIRED if `sample-<label>` is present in any file name within the dataset. If this file exists, it MUST contain the three following columns:- `sample_id`: MUST consist of `sample-<label>` values identifying one row for each sample- `participant_id`: MUST consist of `sub-<label>`- `sample_type`: MUST consist of sample type values, either `cell line`, `in vitro differentiated cells`, `primary cell`, `cell-free sample`, `cloning host`, `tissue`, `whole organisms`, `organoid` or `technical sample` from ENCODE Biosample TypeOther optional columns MAY be used to describe the samples. Each sample MUST be described by one and only one row.Commonly used optional columns in `samples.tsv` files are `pathology` and `derived_from`. We RECOMMEND to make use of these columns, and in case that you do use them, we RECOMMEND to use the following values for them:- `pathology`: string value describing the pathology of the sample or type of control. When different from `healthy`, pathology SHOULD be specified in `samples.tsv`. The pathology MAY instead be specified in Sessions files in case it changes over time.- `derived_from`: `sample-<label>` key/value pair from which a sample is derived from, for example a slice of tissue (`sample-02`) derived from a block of tissue (`sample-01`)

schema information:

```
{}
```

## sampling_frequency (columns)

name: sampling_frequency

description:

> Sampling rate of the channel in Hz.

schema information:

```
{'type': 'number', 'unit': 'Hz'}
```

## sbref (suffixes)

name: Single-band reference image

description:

> Single-band reference for one or more multi-band `dwi` images.

schema information:

```
{}
```

## session (entities)

name: Session

description:

> A logical grouping of neuroimaging and behavioral data consistent across subjects. Session can (but doesn't have to) be synonymous to a visit in a longitudinal study. In general, subjects will stay in the scanner during one session. However, for example, if a subject has to leave the scanner room and then be re-positioned on the scanner bed, the set of MRI acquisitions will still be considered as a session and match sessions acquired in other subjects. Similarly, in situations where different data types are obtained over several visits (for example fMRI on one day followed by DWI the day after) those can be grouped in one session. Defining multiple sessions is appropriate when several identical or similar data acquisitions are planned and performed on all -or most- subjects, often in the case of some intervention between sessions (for example, training).

schema information:

```
{'entity': 'ses', 'type': 'string', 'format': 'label'}
```

## session_id (columns)

name: session_id

description:

A session identifier of the form `ses-<label>`, matching a session found in the dataset.

schema information:

```
{'type': 'string', 'pattern': '^ses-[0-9a-zA-Z]+$'}
```

## sex (columns)

name: sex

description:

String value indicating phenotypical sex, one of ”male”, ”female”, ”other”.For ”male”, use one of these values: `male`, `m`, `M`, `MALE`, `Male`.For ”female”, use one of these values: `female`, `f`, `F`, `FEMALE`, `Female`.For ”other”, use one of these values: `other`, `o`, `O`, `OTHER`, `Other`.

schema information:

```
{'type': 'string', 'enum': ['male', 'm', 'M', 'MALE', 'Male', 'female', 'f', 'F', 'FEMALE', 'Female', 'other', 'o', 'O', 'OTHER', 'Other', 'n/a']}
```

## size (columns)

name: size

description:

Surface area of the electrode, units MUST be in `mm^2`.

schema information:

```
{'type': 'number', 'unit': 'mm2'}
```

## software_filters (columns)

name: software_filters

description:

List of temporal and/or spatial software filters applied (for example, `SSS`, `SpatialCompensation`). Note that parameters should be defined in the general MEG sidecar .json file. Indicate `n/a` in the absence of software filters applied.

schema information:

```
{'anyOf': [{'type': 'string'}, {'type': 'string', 'enum': ['n/a']}]}
```

## sourcedata (associated_data)

name: Source data

description:

> Data before harmonization, reconstruction, and/or file format conversion (for example, E-Prime event logs or DICOM files).

schema information:

```
{}
```

## space (entities)

name: Space

description:

> The space entity can be used to indicate the way in which electrode positions are interpreted (for EEG/MEG/iEEG data) or the spatial reference to which a file has been aligned (for MRI data). The space `<label>` MUST be taken from one of the modality specific lists in Appendix VIII. For example for iEEG data, the restricted keywords listed under Appendix VIII are acceptable for `<label>`.For EEG/MEG/iEEG data, this entity can be applied to raw data, but for other data types, it is restricted to derivative data.

schema information:

```
{'entity': 'space', 'type': 'string', 'format': 'label'}
```

## species (columns)

name: species

description:

> The `species` column SHOULD be a binomial species name from the NCBI Taxonomy (for example, `homo sapiens`, `mus musculus`, `rattus norvegicus`). For backwards compatibility, if `species` is absent, the participant is assumed to be `homo sapiens`.

schema information:

```
{'type': 'string'}
```

# split (entities)

name: Split

description:

> In the case of long data recordings that exceed a file size of 2Gb, the .fif files are conventionally split into multiple parts. Each of these files has an internal pointer to the next file. This is important when renaming these split recordings to the BIDS convention.Instead of a simple renaming, files should be read in and saved under their new names with dedicated tools like MNE-Python, which will ensure that not only the file names, but also the internal file pointers will be updated. It is RECOMMENDED that .fif files with multiple parts use the `split-<index>` entity to indicate each part. If there are multiple parts of a recording and the optional `scans.tsv` is provided, remember to list all files separately in `scans.tsv` and that the entries for the `acq_time` column in `scans.tsv` MUST all be identical, as described in Scans file.

schema information:

```
{'entity': 'split', 'type': 'string', 'format': 'index'}
```

# stain (entities)

name: Stain

description:

> The `stain-<label>` key/pair values can be used to distinguish image files from the same sample using different stains or antibodies for contrast enhancement. Stains SHOULD be indicated in the `"SampleStaining"` key in the sidecar JSON file, although the label may be different. Description of antibodies SHOULD also be indicated in `"SamplePrimaryAntibodies"` and/or `"SampleSecondaryAntobodies"` as appropriate.

schema information:

```
{'entity': 'stain', 'type': 'string', 'format': 'label'}
```

# status (columns)

name: status

description:

> Data quality observed on the channel. A channel is considered `bad` if its data quality is compromised by excessive noise. If quality is unknown, then a value of `n/a` may be used. Description of noise type SHOULD be provided in `[status_description]`.

schema information:

```
{'type': 'string', 'enum': ['good', 'bad', 'n/a']}
```

## status_description (columns)

name: status_description

description:

Freeform text description of noise or artifact affecting data quality on the channel. It is meant to explain why the channel was declared bad in `[status]`.

schema information:

```
{'type': 'string'}
```

## stim (suffixes)

name: Continuous recording

description:

Continuous measures, such as parameters of a film or audio stimulus.

schema information:

```
{}
```

## stim_file (columns)

name: stim_file

description:

Represents the location of the stimulus file (such as an image, video, or audio file) presented at the given onset time. There are no restrictions on the file formats of the stimuli files, but they should be stored in the `/stimuli` folder (under the root folder of the dataset; with optional subfolders). The values under the `stim_file` column correspond to a path relative to `/stimuli`. For example `images/cat03.jpg` will be translated to `/stimuli/images/cat03.jpg`.

schema information:

```
{'type': 'string', 'format': 'stimuli_relative'}
```

## stimuli (associated_data)

name: Stimulus files

description:

> The stimulus files can be added in a `/stimuli` folder (under the root folder of the dataset; with optional subfolders) AND using a stim_file column in *_events.tsv mentioning which stimulus file was used for a given event.There are no restrictions on the file formats of the stimuli files, but they should be stored in the `/stimuli` folder.

schema information:

```
{}
```

## strain (columns)

name: strain

description:

> For species different from `homo sapiens`, string value indicating the strain of the species, for example: `C57BL/6J`.

schema information:

```
{'type': 'string'}
```

## strain_rrid (columns)

name: strain_rrid

description:

> For species different from `homo sapiens`, research resource identifier (RRID) of the strain of the species, for example: `RRID:IMSR_JAX:000664`.

schema information:

```
{'type': 'string', 'format': 'rrid'}
```

## subject (entities)

name: Subject

description:

> A person or animal participating in the study.

schema information:

```
{'entity': 'sub', 'type': 'string', 'format': 'label'}
```

## task (entities)

name: Task

description:

> Each task has a unique label that MUST only consist of letters and/or numbers (other characters, including spaces and underscores, are not allowed). Those labels MUST be consistent across subjects and sessions.

schema information:

```
{'entity': 'task', 'type': 'string', 'format': 'label'}
```

## time (columns)

name: time

description:

> Time, in seconds, relative to `TimeZero` defined by the `*_pet.json`. For example, 5.

schema information:

```
{'type': 'number', 'unit': 's'}
```

## tracer (entities)

name: Tracer

description:

> The `trc-<label>` key/value can be used to distinguish sequences using different tracers. The key `"TracerName"` MUST also be included in the associated JSON file, although the label may be different.

schema information:

```
{'entity': 'trc', 'type': 'string', 'format': 'label'}
```

## trial_type (columns)

name: trial_type

description:

> Primary categorisation of each trial to identify them as instances of the experimental conditions. For example: for a response inhibition task, it could take on values `go` and `no-go` to refer to response initiation and response inhibition experimental conditions.

schema information:

```
{'type': 'string'}
```

## trigger (columns)

name: trigger

description:

continuous measurement of the scanner trigger signal

schema information:

```
{'type': 'number'}
```

## type sense 1 (columns)

name: type

description:

Type of channel; MUST use the channel types listed below. Note that the type MUST be in upper-case.

schema information:

```
{'type': 'string', 'enum': ['MEGMAG', 'MEGGRADAXIAL', 'MEGGRADPLANAR', 'MEGREFMAG', 'MEGREFGRADAXIAL', 'MEGREFGRADPLANAR', 'MEGOTHER', 'EEG', 'ECOG', '
```

## type sense 2 (columns)

name: type

description:

Type of the electrode (for example, cup, ring, clip-on, wire, needle).

schema information:

```
{'type': 'string'}
```

## uCT (suffixes)

name: Micro-CT

description:

Micro-CT imaging data

schema information:

```
{}
```

# units (columns)

name: units

description:

Physical unit of the value represented in this channel, for example, `V` for Volt, or `fT/cm` for femto Tesla per centimeter (see Units).

schema information:

```
{'type': 'string', 'format': 'unit'}
```

# value (columns)

name: value

description:

Marker value associated with the event (for example, the value of a TTL trigger that was recorded at the onset of the event).

schema information:

```
{'anyOf': [{'type': 'number'}, {'type': 'string'}]}
```

# volume_type (columns)

name: volume_type

description:

The `*_aslcontext.tsv` table consists of a single column of labels identifying the `volume_type` of each volume in the corresponding `*_asl.nii[.gz]` file.

schema information:

```
{'type': 'string', 'enum': ['control', 'label', 'm0scan', 'deltam', 'cbf']}
```

## whole_blood_radioactivity (columns)

name: whole_blood_radioactivity

description:

Radioactivity in whole blood samples, in unit of radioactivity measurements in whole blood samples (for example, `kBq/mL`).

schema information:

```
{'type': 'number'}
```

## x (columns)

name: x

description:

Recorded position along the x-axis.

schema information:

```
{'type': 'number'}
```

## y (columns)

name: y

description:

Recorded position along the y-axis.

schema information:

```
{'type': 'number'}
```

## z (columns)

name: z

description:

Recorded position along the z-axis.

schema information:

```
{'anyOf': [{'type': 'number'}, {'type': 'string', 'enum': ['n/a']}]}
```

# Changelog

## v1.7.0 (2022-02-15)

- BF: Use wikipedia for TIFF URL, adobe's page is 404ing now #1007 (yarikoptic)
- [FIX] update highlighting of examples, JSON keys and values, and TSV headers or values in the schema #998 (Remi-Gau)
- [SCHEMA, FIX] Remove mentions of auxdatatypes #996 (tsalo)
- [MISC] minor wording and consistency improvements for channels.tsv in EEG, MEG, iEEG #993 (sappelhoff)
- [FIX] typo: extra sentence in anat section #991 (Remi-Gau)
- [FIX] Optionally support echo entity for VFA suffix #989 (TheChymera)
- [FIX] update definition acq_time for sessions.tsv #986 (Remi-Gau)
- [FIX] add microscopy to modalities in schema #984 (Remi-Gau)
- [INFRA] Fix linkchecker #982 (sappelhoff)
- [DOC] update steering group composition #976 (Remi-Gau)
- customize footer on html spec #975 (sappelhoff)
- [FIX] Update HED appendix to comply with current HED version #970 (VisLab)
- ENH: Update B0Field metadata to accommodate single-blip fieldmaps #968 (effigies)
- [FIX] harmonize 'file name' into 'filename' #962 (yarikoptic)
- [FIX] Reword front page #958 (arokem)
- [MAINT] Update links to starter kit website #957 (effigies)
- [FIX] Entity table: Clarify meaning of empty cells #955 (Lestropie)
- [MISC] Add Eric Earl as a Maintainer #953 (ericearl)
- [FIX] Spelling errors in appendices #951 (Lestropie)
- [FIX] Broken hyperlink in entity list file #949 (Lestropie)
- [FIX] Rewrite inheritance principle #946 (Lestropie)
- [INFRA] fix "CircleCI redirector" GH-action: remove the 2nd (sanity) check #944 (yarikoptic)
- [FIX] Typo: ECG_headshape #942 (Moo-Marc)
- [FIX] description: dwi is specialized T2 weighting, not T2* #939 (sappelhoff)
- [FIX] relax unrealistically strict requirements with ieeg channels.tsv 'name' column #938 (sappelhoff)
- [INFRA] expand submenus on landing page automatically #937 (sappelhoff)

- [FIX] Add links from derivatives section to entity list #936 (sappelhoff)
- [FIX] Remove repeated words #934 (DimitriPapadopoulos)
- [INFRA/FIX] Use string concatenation in table macro #933 (effigies)
- [INFRA] Run linkchecker in stock docker image #932 (effigies)
- [INFRA] add (optional) pre-commit config file #929 (sappelhoff)
- [FIX] Clarify that EDF/BDF files MUST have lower case extensions in BIDS #927 (adam2392)
- [ENH] Generate glossary page from schema #923 (tsalo)
- [ENH] Render valid value restrictions in tables based on object definitions in schema #921 (tsalo)
- [ENH] add `hemi` entity to schema #917 (Remi-Gau)
- [INFRA] PDF version of spec: fix handling of internal links #915 (sappelhoff)
- [ENH] update and reformat table for template in coordinate system page #903 (Remi-Gau)
- [ENH] add details for content of `\*\_beh.json` #902 (Remi-Gau)
- [SCHEMA] Add MeasurementToolMetadata and Derivative metadata fields #899 (tsalo)
- [SCHEMA] Add new MEG files and fix entity tables #898 (tsalo)
- [FIX] small typo in json example #897 (Remi-Gau)
- [INFRA] tiny speedup of building PDF by moving `re.compile\(\)` outside of a loop #896 (DimitriPapadopoulos)
- [INFRA] Document *.webm video files as binary #895 (DimitriPapadopoulos)
- [SCHEMA] add physio to schema or EEG, MEG, iEEG, PET, ASL, DWI #894 (Remi-Gau)
- [SCHEMA] Reorganize schema code into a package #892 (tsalo)
- [FIX] Clarify shifting dates RECOMMENDED, add example EDF #891 (sappelhoff)
- [INFRA] fix draft rendering css on mobile or when browser window is narrow #889 (sappelhoff)
- [MISC] Add an animated BIDS logo #886 (adswa)
- [SCHEMA] Consolidate schema files by term type #883 (tsalo)
- [ENH] BEP031: Microscopy #881 (mariehbourget)
- [INFRA] jQuery 3.4.1 → 3.6.0 #875 (DimitriPapadopoulos)
- [INFRA] Add ”codespell” tool to CI checks to catch typos sooner #873 (DimitriPapadopoulos)
- [INFRA] Several style fixes (Flake8) for Python code in the repo #872 (DimitriPapadopoulos)
- [FIX] Make subheadings consistent in 06-longitudinal-and-multi-site-studies.md #870 (guiomar)
- [DOC] add Anthony as maintainer #868 (Remi-Gau)
- [MISC] add ”forward slash” requirement for paths to common principles #867 (sappelhoff)
- [ENH] Add ”ScanRAS” as an accepted coordinate frame for ieeg #866 (alexrockhill)
- [INFRA] Add .lgtm.yml file for better usage of LGTM CI tool #865 (DimitriPapadopoulos)
- [FIX] update physio bids name in longitudinal study page examples #863 (Remi-Gau)
- [INFRA] Enforce consistent line endings via .gitattributes #861 (DimitriPapadopoulos)
- [INFRA] dos2unix #859 (DimitriPapadopoulos)
- [FIX] Clarify case collision intolerance as a file naming principle #858 (yarikoptic)
- [INFRA] LGTM recommendation: Unused local variable #853 (DimitriPapadopoulos)
- [INFRA] LGTM warning: Variable defined multiple times #851 (DimitriPapadopoulos)
- [FIX] Typos found by codespell #848 (DimitriPapadopoulos)
- [ENH] Add links to example datasets for each modality #845 (Remi-Gau)

- [INFRA] Add basic documentation on how to use metadata table macros #840 (Remi-Gau)
- [ENH] make "Institutional department name" available for all datatypes #839 (Remi-Gau)
- [INFRA] use macro to render examples in a "tree" like fashion #837 (Remi-Gau)
- [FIX] Add angio suffix to the non-parametric aMRI suffix table #835 (tsalo)
- [FIX] Remove last hardcoded suffix table #833 (tsalo)
- [MISC] make explicit that EDF+ (and for EEG: BDF+) are included in iEEG / EEG format requirements #831 (sappelhoff)
- [SCHEMA] Add TSV column files #827 (tsalo)
- [ENH] add metadata to PET calibration factor: "DoseCalibrationFactor" #825 (CPernet)
- [FIX] correct file location of scans.tsv file in example #824 (ghisvail)
- [FIX] Add missing closing parenthesis in 02-common-principle.md #822 (sebastientourbier)
- [MISC] update available datatypes in specification #819 (sappelhoff)
- [FIX] document required column order MEG, EEG, iEEG, PET, and fix typo iEEG #818 (sappelhoff)
- [ENH] BEP031 - New columns to participants.tsv file #816 (mariehbourget)
- [MISC] make table headers bold #815 (Remi-Gau)
- [FIX] What is a composite instance? Change to measurement for non MRI modalities? #813 (rob-luke)
- [ENH] BEP031 - New entity: sample and samples.tsv file #812 (mariehbourget)
- [ENH] Add device and acquisition metadata for physio files #806 (Remi-Gau)
- [MISC] Move section on sessions.tsv file: longitudinal files -> modality agnostic files #805 (Remi-Gau)
- [ENH] Make explicit that "task" metadata applies to "beh" modality #804 (Remi-Gau)
- [MISC] Make MRI-centric language more general in Events #801 (sappelhoff)
- [ENH] clarify that entities MUST be unique #800 (sappelhoff)
- [MISC] deprecate DCOffsetCorrection field from ieeg.json: Use SoftwareFilters field instead #799 (sappelhoff)
- [FIX] Deprecate ScanDate (PET) in favor of AcquisitionTime in scans.tsv files #798 (mnoergaard)
- [MISC] add IETF standard link for json #797 (sappelhoff)
- [INFRA] In PDF, color every other row in table in light gray fill #794 (sappelhoff)
- [MISC] add link to guide on how to write a good README #793 (sappelhoff)
- [SCHEMA] Apply schema rules to entity values #792 (tsalo)
- [INFRA] fix md ci and update ci badges #791 (sappelhoff)
- [SCHEMA] Use macro for filename templates in file collections appendix #787 (tsalo)
- [FIX] consistently refer to DICOM Tags throughout the specification #786 (Hboni)
- [FIX] Amend note about *b*-vecs on DWI specs #782 (oesteban)
- [INFRA] add CI to find trailing whitespace #780 (sappelhoff)
- [MISC] Add info on HED key to common principles #777 (sappelhoff)
- [ENH] add EEGLAB as valid coordinate system for EEG #775 (sappelhoff)
- [SCHEMA] Add metadata term files #774 (tsalo)
- [SCHEMA] Add suffix term files #772 (tsalo)
- [ENH] Allow encoding the fieldmapping intent of the protocol #622 (oesteban)
- [FIX] Correct iEEG example that contained double suffixes #463 (yarikoptic)
- [ENH] introduce GeneratedBy to "core" BIDS #440 (yarikoptic)

## v1.6.0 (2021-04-22)

- [FIX] Typos discovered by codespell #784 (yarikoptic)
- [FIX] Rename ”Unit” metadata to ”Units” for consistency with existing fields #773 (effigies)
- [FIX] typo in pet: institution -> institutional #771 (sappelhoff)
- [INFRA] install git in linkchecker job #767 (sappelhoff)
- [INFRA] Fix CircleCI workflows #764 (sappelhoff)
- [INFRA] do not run remark on auto CHANGES #755 (sappelhoff)
- [FIX] Mix up (typo) between ficiduals and landmarks in EEG spec #754 (rob-luke)
- [INFRA] updating remark, CIs, contributor docs #745 (sappelhoff)
- [FIX] schema for i/eeg coordsys+elecs: sub-ses-acq-space are allowed entities #743 (sappelhoff)
- [DOC] move schema documentation into the schema folder #740 (Remi-Gau)
- [MISC] standardize string examples format in tables #739 (Remi-Gau)
- [MISC] Clarify participant_id in participants.tsv file if it exists #738 (adam2392)
- [FIX] split MEG files should be listed separately in scans.tsv #735 (eort)
- [FIX] 1) Clarify appropriate labels for space entity, 2) Clarify channels+electrodes do not have to match #734 (sappelhoff)
- [MISC] refactor stimuli mentioning sections in the events page #697 (Remi-Gau)
- [ENH] Bep 009: Positron Emission Tomography #633 (melanieganz)

## v1.5.0 (2021-02-23)

- [MISC] Updated TotalAcquiredVolumes into TotalAcquiredPairs #742 (effigies)
- [SCHEMA] Update qMRI fieldmap schema #728 (effigies)
- [FIX] Add deprecated anatomical MRI suffixes back into schema #725 (tsalo)
- [FIX] Correct schema irregularities for func datatype #724 (tsalo)
- [FIX] Make flip optional for MP2RAGE #722 (tsalo)
- [FIX] Correct entity names in YAML files #720 (tsalo)
- [ENH] Clarify run indexing information for MRI acquisitions #719 (effigies)
- [ENH] Harmonize CoordinateSystem details for MRI, MEG, EEG, iEEG #717 (sappelhoff)
- [SCHEMA] Update entity YAML keys #714 (effigies)
- [MISC] Added full names for some contributors in .mailmap file #705 (yarikoptic)
- [INFRA] Migrate md and yml checks from travis to GH actions #693 (sappelhoff)
- [INFRA] Move part entity to before recording entity #692 (tsalo)
- [ENH] BEP001 - qMRI maps and some additional metadata #690 (agahkarakuzu)
- [ENH] BEP001 - Entity-linked file collections #688 (effigies)
- [ENH] BEP001 - New entities: inv & mt #681 (agahkarakuzu)
- [DOC] add contributing guidelines to add figures in the specs #679 (Remi-Gau)
- [MISC] use RFC 2119 language in legend of the ”volume timing” table #678 (Remi-Gau)
- [FIX] Add OPTIONAL acq entity to channels.tsv, events.tsv to match electrophysiological acquisitions #677 (sappelhoff)
- [MISC] Update all links to use HTTPS whenever possible. #676 (gllmflndn)

- [INFRA] Relax line length limit for linting YAML files #673 (effigies)
- [ENH] BEP001 - New entity: flip #672 (agahkarakuzu)
- [ENH] BEP001 - RepetitionTimeExcitation and RepetitionTimePreparation #671 (agahkarakuzu)
- [ENH] Bep 005: Arterial Spin Labeling #669 (sappelhoff)
- [FIX] Added white space after table #660 (robertoostenveld)
- [MISC] add remi as maintainer #657 (Remi-Gau)
- [MISC] update Contributing with info on how to respond to reviews #655 (Remi-Gau)
- [FIX] add paragraph on MEG specific "markers" suffix in MEG spec #653 (sappelhoff)
- [FIX] Rewrite the MRI/fieldmaps subsection for consistency with the rest of specs #651 (oesteban)
- [FIX] Fixing template string on electrodes for eeg and ieeg. #650 (adam2392)
- [ENH] Update genetics-BIDS citation #646 (effigies)
- [SCHEMA] Add derivatives entities to the schema #645 (tsalo)
- [MISC] add brief note that TSV example in the spec may currently use either tab or space characters #643 (yarikoptic)
- [ENH] Add "multipart DWI" acquisitions and refactor DWI specifications #624 (oesteban)
- [SCHEMA] Render schema elements in text #610 (tsalo)
- [ENH] Add part entity for complex-valued data #424 (tsalo)

## v1.4.1 (2020-10-13)

- [INFRA] minor robustness enhancements to pdf build shell script #642 (yarikoptic)
- [FIX] consistent CoordinateSystem fields for ephys #641 (sappelhoff)
- [INFRA] set up github action to detect latin phrases #636 (Remi-Gau)
- [ENH] Add a definition for "deprecation" #634 (sappelhoff)
- [MISC] consolidate BIDS citations in introduction #630 (sappelhoff)
- [FIX] URI "definition" and recommendation #629 (Remi-Gau)
- [FIX] change remaining latin expressions (etc and i.e.) #628 (Remi-Gau)
- [FIX] replace "e.g.," by "for example" #626 (Remi-Gau)
- [FIX] arrays of 3D coordinates MUST supply numeric values in x, y, z order #623 (sappelhoff)
- [FIX] Accidentally swapped Neuromag/Elekta/MEGIN cross-talk & fine-calibration filename extensions #621 (hoechenberger)
- [FIX] improve HED documentation #619 (VisLab)
- [INFRA] Move MRI section headings up a level #618 (tsalo)
- [INFRA] SCHEMA: Declare entities by concept names, add entity field for filename components #616 (effigies)
- [FIX] Change wrong text references from *CoordinateSystemUnits to *CoordinateUnits #614 (sappelhoff)
- [ENH] Describe arbitrary units in Common Principles #606 (tsalo)
- [FIX] Clarify data types and requirement levels for all JSON files #605 (sappelhoff)
- [INFRA] downgrade github-changelog-generator to 1.14.3 due to issue with 1.15.2 #600 (sappelhoff)
- [FIX] tighter rules for sharing MEG cross-talk and fine-calibration .fif files #598 (sappelhoff)
- [MISC] Add tsalo as a BIDS maintainer #597 (tsalo)
- [FIX] clarify definition of events in common principles #595 (sappelhoff)
- [INFRA] use --release-branch option in github-changelog-generator #594 (sappelhoff)

- [ENH] Define "modality" and clarify "data type" #592 (effigies)
- [FIX] Adjust index definition to be nonnegative integer #590 (nicholst)
- [MISC] fix links, make json object links consistent, fix pandoc rendering #587 (sappelhoff)
- [FIX] Fix link in Common principles #583 (tsalo)
- [ENH] Specify how to share cross-talk and fine-calibration for Neuromag/Elekta/MEGIN data #581 (sappelhoff)
- [ENH] Specify echo and run indices are nonnegative integers in schema #578 (tsalo)
- [ENH] add optional presentation software name, version, OS, and code to events.json #573 (Remi-Gau)
- [ENH] added PPG as an accepted channel type for EEG, MEG and iEEG #570 (robertoostenveld)
- [INFRA] Move entity definitions to a separate page #568 (tsalo)
- [INFRA] enable pandoc emojis for the pdf build #562 (sappelhoff)
- [INFRA] Auto adjust table fences before PDF conversion #560 (sebastientourbier)
- [ENH] Support run and acq entities in behavior-only data #556 (tsalo)
- [FIX] Clarify requirement levels for TSV metadata fields #555 (sappelhoff)
- [FIX] Reorganize rec, ce entities, _defacemask #550 (emdupre)
- [FIX] Clarify Upper-casing of Channels.tsv Channel Type #548 (adam2392)
- [ENH] Extend date time information to include optional UTC syntax, warn about FIF requirements #546 (sappelhoff)
- [FIX] clarify that <physio|stim>.json is REQUIRED #542 (sappelhoff)
- [FIX] Replace all non-breaking spaces with vanilla spaces #536 (nicholst)
- [FIX] Clarify indices are nonnegative integers. #535 (nicholst)
- [FIX] Clarify use of session entity in filenames #532 (Moo-Marc)
- [ENH] Add the ability of users to specify an explicit HED.xml schema for validation. #527 (VisLab)
- [FIX] clarify that scans.json is allowed and recommended #523 (sappelhoff)
- [INFRA] add copyright holder to license. #521 (sappelhoff)
- [FIX] clarify XXXCoord* in the coordinate systems appendix #520 (sappelhoff)
- [ENH] Update `beh/` specification to contrast with any neural recordings #515 (effigies)
- [Fix] 'segmentation' spelling in 05-derivatives/03-imaging.md #514 (rwblair)
- [FIX] restructure and clarify *_physio/*_stim section #513 (sappelhoff)
- [FIX] clarify file formats in EEG, iEEG #511 (sappelhoff)
- [Fix] Add links and release dates to pre GH changelog, fix formatting #509 (sappelhoff)
- [FIX] Clarify that `acq\_time` in `scans.json` refers to first data point acquired #506 (tsalo)
- [INFRA] make circle artifact link a GH action, point to pdf #505 (sappelhoff)
- [FIX] Typos in DECISION-MAKING file #504 (tsalo)
- [ENH] Add `Commenting on a PR` to CONTRIBUTING.md #490 (franklin-feingold)
- [FIX] clarify MEG empty-room recording naming conventions #480 (sappelhoff)
- [INFRA] Convert entity table to yaml #475 (tsalo)
- [FIX] Recommend SI units formatting to adhere to CMIXF-12 #411 (sappelhoff)

## v1.4.0 (2020-06-11)

- [FIX] Clarify language on unsetting a key/value pair #495 (nicholst)

- [ENH] optionally allow LICENSE file #483 (sappelhoff)
- [INFRA] linkchecker - ignore github pull and tree URLs #477 (yarikoptic)
- [ENH] Allow fractional seconds in scans file datetimes #470 (tsalo)
- [MISC] Maintainers - `Scope` responsibility #467 (franklin-feingold)
- [FIX] Align tables in MRI section #465 (sappelhoff)
- [FIX] Drop `\_part-` reference from example, introduce `\_split-` entity #460 (sappelhoff)
- [FIX] clarify participants tsv+json with examples and recommendations #459 (sappelhoff)
- [FIX] Remove BESA from list of restricted keywords of EEG coordsystems #457 (sappelhoff)
- [INFRA] add steps for release protocol (PDF upload) #455 (sappelhoff)
- [FIX] Add reference to PDF on front page of specification #452 (nicholst)
- [INFRA] Add conditional for link-checking releases #451 (franklin-feingold)
- [FIX] unordered list formatting in BEP018 #449 (sappelhoff)
- [FIX] fix inconsistencies for task label between sections #446 (Remi-Gau)
- [FIX] update DECISION-MAKING.md document with new governance #441 (sappelhoff)
- [ENH] BEP 003: Common Derivatives #265 (effigies)
- [ENH] Add Glossary of terms/abbreviations used in the specification #152 (yarikoptic)

## v1.3.0 (2020-04-14)

- [INFRA] add zenodo badge to README #447 (sappelhoff)
- [MISC] Added contributors from VisLab #444 (VisLab)
- [FIX] Clarify snake_case+CamelCase in TSV+JSON #442 (sappelhoff)
- [FIX] Eliminate web/online-specific language #437 (nicholst)
- [INFRA] ensure build_docs_pdf CircleCI job runs last #436 (sappelhoff)
- [INFRA] Add issue templates for GitHub #434 (sappelhoff)
- [INFRA] Get latest PDF build from CircleCI artifacts #433 (sappelhoff)
- [INFRA] Update release protocol #432 (franklin-feingold)
- [INFRA] add support for building PDF versions of the spec #431 (Arshitha)
- [ENH] Explicitly mention bids-validator and update link #428 (sappelhoff)
- [INFRA] use new bids-maintenance GitHub account to take over automatic work #426 (sappelhoff)
- [FIX] Unify section titles and table-of-contents entries #422 (nicholst)
- [INFRA] add # before heading in CHANGES #419 (sappelhoff)
- [INFRA] fix heading of auto changelog to be a markdown header #417 (sappelhoff)
- [ENH] Add OPTIONAL EthicsApprovals field to dataset description #412 (effigies)
- [ENH] BEP 018 - Genetic Information #395 (effigies)

## v1.2.2 (2020-02-12)

- [FIX] improve wording on data dictionaries #410 (sappelhoff)

- [MISC] update contributions by CPernet #409 (CPernet)
- [MISC] Add Sébastien Tourbier to contributors #394 (sebastientourbier)
- [FIX] consistent units description between EEG/MEG/iEEG. Clarify (derived) SI units + prefixes #391 (sappelhoff)
- [MISC] moved list of extension proposals to the main BIDS website #389 (robertoostenveld)
- [FIX] Typos and clarifications #386 (apjanke)
- [INFRA] Add watermark to drafts #383 (effigies)
- [MISC] Teon Brooks retiring moderator duties for BEP021 #381 (teonbrooks)
- [FIX] clarify that string is expected for HowToAcknowledge field in dataset_description.json #380 (sappelhoff)
- [MISC] Typo and style #378 (TheChymera)
- [FIX] divide readme into 3 parts #374 (sappelhoff)
- [FIX] Refer to BIDS consistently, instead of ”<Modality>-BIDS” #366 (sappelhoff)
- [FIX] Change recommended anonymization date from 1900 to 1925 #363 (alexrockhill)
- [FIX] Minor fixups of inconsistencies while going through a PDF version #362 (yarikoptic)
- [FIX] clarify that filters should be specified as object of objects #348 (sappelhoff)
- [FIX] Clarify channels.tsv is RECOMMENDED consistently across ephys #347 (sappelhoff)
- [FIX] Typo fix (contract -> contrast) in events documentation #346 (snastase)
- [MISC] rm TOC.md - seems no longer pertinent/used #341 (yarikoptic)
- [MISC] Move the PR template to a separate folder and improve contents #338 (jhlegarreta)
- [INFRA] Find npm requirements file in Circle #336 (franklin-feingold)
- [ENH] Clarify phenotypic and assessment data in new section #331 (sappelhoff)
- [MISC] add information about continuous integration checks to PR template #330 (sappelhoff)
- [FIX] Fix `Common principles` `Key/value files` section level #328 (jhlegarreta)
- [INFRA] Set the maximum heading length lint check to `false` #325 (jhlegarreta)
- [FIX] Number explicitly all cases in MRI field map section headers #323 (jhlegarreta)
- [FIX] Add SoftwareFilters to EEG sidecar example #322 (Remi-Gau)
- [MISC] Fixing Travis errors with Remark #320 (franklin-feingold)
- [INFRA] Link to doc builds in CI checks #315 (jasmainak)
- [MISC] Add BEP027 - BIDS Execution to BEP list #314 (effigies)
- [FIX] Add CBV and phase to Entity table #312 (tsalo)
- [FIX] Normalization of template-generated standard spaces #306 (oesteban)
- [ENH] Release protocol notes #304 (franklin-feingold)
- [INFRA] Adding contributor appendix sentence to PR template #299 (franklin-feingold)
- [ENH] Added discontinuous datatype for EEG and iEEG #286 (wouterpotters)
- [FIX] Clarify paragraph about custom data types #264 (effigies)

## v1.2.1 (2019-08-14)

- [FIX] repair link in anatomical MRI table #297 (sappelhoff)
- [ENH] Clarify requirements in Release Protocol #294 (franklin-feingold)
- [INFRA+FIX] Use linkchecker (from a dedicated docker image) to check all URLs #293 (yarikoptic)

- [ENH] Adding Contributors and updating contributions #284 (franklin-feingold)
- [MISC] update Code of Conduct contact #281 (franklin-feingold)
- [ENH] Update contributing guide and README to make discussion forums easy to find #279 (emdupre)
- [ENH] Starter Kit dropdown menu #278 (franklin-feingold)
- [ENH] BEP Update #277 (franklin-feingold)
- [INFRA] Update pipenv #274 (sappelhoff)
- [INFRA] Transpose the entity table and link to text anchors describing each entity #272 (sappelhoff)
- [ENH] Add Twitter badge to README and link to website to landing page #268 (franklin-feingold)
- [ENH] adding release guidelines #267 (franklin-feingold)
- [FIX] Common principles: Fix filename in inheritance principle #261 (Lestropie)
- [MISC] update modality references #258 (sappelhoff)
- [INFRA] adding logo to RTD #256 (franklin-feingold)
- [INFRA] add footer, replacing mkdocs/material advert with Github link #250 (sappelhoff)
- [MISC] rename logo files, add a README of where they come from, fix favicon #249 (sappelhoff)
- [MISC] updating MEG doc links, manufacturer names, and adding a missing MEG example #248 (sappelhoff)
- [ENH] Add favicon to RTD #246 (franklin-feingold)
- [MISC] Update Authors in BEP025 #241 (josator2)
- [MISC] Document BEPs that are not active anymore, but have not been merged #240 (sappelhoff)
- [FIX] remove ManufacturersAmplifierModelName (again) #236 (robertoostenveld)
- [INFRA] Update release protocol #235 (effigies)
- [INFRA] Enable version panel for quickly finding previous versions #232 (effigies)
- [FIX] Clarify Appendix II: The list of licenses only lists examples #222 (sappelhoff)
- [FIX] Trivial column header fix #220 (nicholst)
- [INFRA] Add clarification on merge methods to DECISION_MAKING #217 (sappelhoff)
- [INFRA] Enable permalink urls to appear at (sub)section headings #214 (yarikoptic)
- [INFRA] bump up mkdocs-materials version #211 (sappelhoff)
- [MISC] Fix github username for @chrisgorgo #204 (chrisgorgo)
- [FIX] clarify example 3 in common principles (inheritance) #202 (sappelhoff)
- [MISC] Expand entity table for MEG/EEG/iEEG specific files #198 (sappelhoff)
- [FIX] make iEEG ToC more consistent with MEG and EEG #191 (robertoostenveld)
- [FIX] Clarify use of acq and task parameters in EEG, MEG, and iEEG #188 (sappelhoff)
- [FIX] clarify use of tools for CTF data renaming #187 (sappelhoff)
- [MISC] Add bep006 and bep010 to completed beps and fix links #186 (sappelhoff)
- [FIX] change file for definition of electrical stimulation labels from _electrodes.json to _events.json #185 (ezemikulan)
- [ENH] relax ieeg channel name requirements of letters and numbers only #182 (sappelhoff)
- [FIX] make MEG section headings and ToC consistent to the EEG and iEEG specs #181 (robertoostenveld)
- [FIX] make section headings and ToC consistent between meg and eeg specs #180 (robertoostenveld)
- [MISC] Spelling fixes #179 (DimitriPapadopoulos)
- [ENH] Alternative folder organization for raw, derived, and source data #178 (chrisgorgo)
- [INFRA] Adding instructions for naming PRs #177 (chrisgorgo)

- [MISC] Introducing Stefan Appelhoff as the first Maintainer #176 (chrisgorgo)
- [FIX] Clarify name of ”BrainVision” format #175 (JegouA)
- [FIX] Fixes spelling of continuous #171 (emdupre)
- [FIX] Clarify continuous recording metadata fields #167 (effigies)
- [FIX] changed reference of `dcm2nii` to `dcm2niix` #166 (DimitriPapadopoulos)
- [FIX] Removing a leftover file #162 (chrisgorgo)
- [FIX] Specify marker filenames for KIT data (MEG) #62 (monkeyman192)
- [FIX] Remove father-level for meg filetypes other than BTi/4D data #19 (teonbrooks)

## v1.2.0 (2019-03-04)

- [MISC] Adding Dimitri Papadopoulos Orfanos to the list of contributors #157 (DimitriPapadopoulos)
- [FIX] use ”specification” not ”protocol” to refer to BIDS #156 (yarikoptic)
- [FIX] Fix example misalignment #155 (DimitriPapadopoulos)
- [INFRA] Update Pipfile.lock #144 (franklin-feingold)
- [ENH] clarify decimal sep and numerical notation convention #143 (sappelhoff)
- [ENH] clarify encoding of README, CHANGES, TSV, and JSON files #140 (sappelhoff)
- [MISC] Update site_name and release protocol #137 (franklin-feingold)
- [FIX] Example for IntendedFor was missing session indicator in the filename #129 (yarikoptic)
- [ENH] Add ”_phase” suffix to func datatype for functional phase data #128 (tsalo)
- [MISC] Update to Release_Protocol.md #126 (franklin-feingold)
- [MISC] Update tag naming convention #123 (chrisgorgo)
- [ENH] Merge bep006 and bep010 #108 (sappelhoff)
- [MISC] Adding formal decision-making rules #104 (chrisgorgo)
- [FIX] number of small corrections to the specification #98 (robertoostenveld)

## v1.1.2 (2019-01-10)

- [MISC] Update 01-contributors.md #120 (oesteban)
- [ENH] Global fields in data dictionaries #117 (chrisgorgo)
- [MISC] Propose BEP026 MER #116 (greydongilmore)
- [FIX] Remove duplicate entries in MEG table #113 (franklin-feingold)
- [MISC] Propose BEP025 MIDS #110 (josator2)
- [FIX] repair links #106 (sappelhoff)
- [INFRA] Autogenerate CHANGES.md #103 (franklin-feingold)
- [MISC] Added contributor information #100 (jgrethe)
- [ENH] First(?) good practice recommendation. No excessive overrides in Inheritance principle #99 (yarikoptic)
- [MISC] adding extensions page #97 (choldgraf)
- [FIX] fix some urls (as detected to be broken/inconsistent) #95 (yarikoptic)

- [MISC] Change BEP numbers to include MRS #94 (Hboni)
- [FIX] harmonize and thus shorten templates etc #93 (yarikoptic)
- [MISC] put links and some text into README #91 (sappelhoff)
- [MISC] Add extension proposal in 01-introduction.md #88 (Hboni)
- [FIX] additional table to recap 'volume acquisition timing' #87 (Remi-Gau)
- [FIX] Small typo in "scanning sequence" DICOM Tag #84 (Remi-Gau)
- [MISC] Update 01-contributors.md #83 (teonbrooks)
- [ENH] Added CBV contrast #82 (TheChymera)
- [MISC] Add CC-BY 4.0 license #81 (KirstieJane)
- [INFRA] Fix Travis break #80 (franklin-feingold)
- [ENH] allow _dir for other EPI (func, dwi) sequences #78 (yarikoptic)
- [MISC] Added appendix to mkdocs and added some internal links #77 (franklin-feingold)
- [MISC] added JC Houde as contributor. #76 (jchoude)
- [MISC] Updated my contributions #75 (nicholst)
- [FIX] update HED appendix #74 (sappelhoff)
- [FIX] unicode: replace greek mu and omega by micro and ohm signs #73 (sappelhoff)
- [MISC] Update 01-contributors.md #72 (francopestilli)
- [ENH] add ce-<label> for fmri data #70 (dasturge)
- [INFRA] pin pip version #68 (chrisgorgo)
- [MISC] Fix link in index #46 (chrisgorgo)
- [MISC] edit contributing guide #44 (Park-Patrick)
- [INFRA] Mkdocs configuration and RTD setup #42 (choldgraf)
- [MISC] Move definitions, compulsory, and raw/derivatives sections to principles #40 (chrisgorgo)
- [MISC] Remove duplicate section #39 (chrisgorgo)
- [INFRA] mkdocs rendering #36 (chrisgorgo)
- [MISC] Style consistency #35 (chrisgorgo)
- [MISC] Renaming files to conform with style guide #34 (chrisgorgo)
- [INFRA] enable travis cache #32 (chrisgorgo)
- [MISC] corrected link that is shown for CC0 #31 (robertoostenveld)
- [INFRA] added linter integration via travis #30 (chrisgorgo)
- [MISC] Cleanup #29 (chrisgorgo)
- [MISC] split intro, commons, mr, and meg into folder from specification.md #28 (teonbrooks)
- [MISC] Add some bids starter kit contributors #27 (KirstieJane)
- [MISC] Embedded footnotes into text #25 (franklin-feingold)
- [MISC] Making HED Strategy Guide link prettier #24 (fake-filo)
- [MISC] more cleanup #21 (chrisgorgo)
- [MISC] formatted MEG (8.4) #17 (franklin-feingold)
- [MISC] small fixes #16 (chrisgorgo)
- [MISC] Add meg img #14 (sappelhoff)
- [MISC] Cleaning up the specification #13 (chrisgorgo)

- [MISC] Adding code of conduct #6 (chrisgorgo)
- [INFRA] Renaming the main document #1 (chrisgorgo)

## 1.1.1 (2018-06-06)

- Improved the MEG landmark coordinates description.
- Replaced `ManufacturersCapModelName` in `meg.json` with `CapManufacturer` and `CapManufacturersModelName`.
- Remove `EEGSamplingFrequency` and `ManufacturersAmplifierModelName` from the `meg.json.`
- Improved the behavioral data description.

## 1.1.0 (2018-04-19)

- Added support for MEG data (merged BEP008).
- Added `SequenceName` field.
- Added support for describing events with Hierarchical Event Descriptors: 4.3 Task events.
- Added `VolumeTiming` and `AcquisitionDuration` fields: 4.1 Task (including resting state) imaging data.
- Added `DwellTime` field.

## 1.0.2 (2017-07-18)

- Added support for high resolution (anatomical) T2star images: 4.1 Anatomy imaging data.
- Added support for multiple defacing masks: 4.1 Anatomy imaging data.
- Added optional key and metadata field for contrast enhanced structural scans: 4.1 Anatomy imaging data.
- Added `DelayTime` field: 4.1 Task (including resting state) imaging data.
- Added support for multi echo BOLD data: 4.1 Task (including resting state) imaging data.

## 1.0.1 (2017-03-13)

- Added `InstitutionName` field: 4.1 Task (including resting state) imaging data.
- Added `InstitutionAddress` field: 4.1 Task (including resting state) imaging data.
- Added `DeviceSerialNumber` field: 4.1 Task (including resting state) imaging data.
- Added `NumberOfVolumesDiscardedByUser` and `NumberOfVolumesDiscardedByScanner` field: 4.1 Task (including resting state) imaging data.
- Added `TotalReadoutTime to` functional images metadata list: 4.1 Task (including resting state) imaging data.

## 1.0.1-rc1

- Added T1 Rho maps: 4.1 Anatomy imaging data.

- Added support for phenotypic information split into multiple files: 3.2 Participant key file.
- Added recommendations for multi site datasets.
- Added `SoftwareVersions`.
- Added `run-<run_index>` to the phase encoding maps. Improved the description.
- Added `InversionTime` metadata key.
- Clarification on the source vs raw language.
- Added `trial_type` column to the event files.
- Added missing `sub-<participant_label>` in behavioral data filenames.
- Added ability to store stimuli files.
- Clarified the language describing allowed subject labels.
- Added quantitative proton density maps.

## 1.0.0 (2016-06-23)

- Added ability to specify fieldmaps acquired with multiple parameter sets.
- Added ability to have multiple runs of the same fieldmap.
- Added FLASH anatomical images.

## 1.0.0-rc4

- Replaced links to neurolex with explicit DICOM Tags.
- Added sourcedata.
- Added data dictionaries.
- Be more explicit about contents of JSON files for structural (anatomical) scans.

## 1.0.0-rc3

- Renamed `PhaseEncodingDirection` values from ”x”, ”y”, ”z” to ”i”, ”j”, ”k” to avoid confusion with FSL parameters.
- Renamed `SliceEncodingDirection` values from ”x”, ”y”, ”z” to ”i”, ”j”, ”k”.

## 1.0.0-rc2

- Removed the requirement that TSV files cannot include more than two consecutive spaces.
- Refactor of the definitions sections (copied from the manuscript).
- Make support for uncompressed `.nii` files more explicit.
- Added `BIDSVersion` to `dataset.json`.
- Remove the statement that `SliceEncodingDirection` is necessary for slice time correction.

- Change dicom converter recommendation from dcmstack to dcm2nii and dicm2nii following interactions with the community (see https://github.com/moloney/dcmstack/issues/39 and https://github.com/neurolabusc/dcm2niix/issues/4).
- Added section on behavioral experiments with no accompanying MRI acquisition.
- Add `_magnitude.nii[.gz]` image for GE type fieldmaps.
- Replaced EchoTimeDifference with EchoTime1 and EchoTime2 (SPM toolbox requires this input).
- Added support for single band reference image for DWI.
- Added DatasetDOI field in the dataset description.
- Added description of more metadata fields relevant to DWI fieldmap correction.
- PhaseEncodingDirection is now expressed in ”x”, ”y” etc. instead of ”PA” ”RL” for DWI scans (so it’s the same as BOLD scans).
- Added `rec-<label>` flag to BOLD files to distinguish between different reconstruction algorithms (analogous to anatomical scans).
- Added recommendation to use `_physio` suffix for continuous recordings of motion parameters obtained by the scanner side reconstruction algorithms.

## 1.0.0-rc1

- Initial release

* This Change Log was automatically generated by github_changelog_generator