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# Brain Imaging Data Structure Specification

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1.11.0

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# 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 organizing 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 organization 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 organized according to BIDS (see the [up to date list](#)).
- Databases such as [OpenNeuro.org](#) accept datasets organized 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 directory 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](https://doi.org/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](https://doi.org/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](https://doi.org/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](https://doi.org/10.1038/sdata.2018.110)

#### PET

- Norgaard, M., Matheson, G.J., Hansen, H.D., Thomas, A., Searle, G., Rizzo, G., Veronese, M., Giacomel, A., Yaqub, M., Tonietto, M., Funck, T., Gillman, A., Boniface, H., Routier, A., Dalenberg, J.R., Betthauser, T., Feingold, F., Markiewicz, C.J., Gorgolewski, K.J., Blair, R.W., Appelhoff, S., Gau, R., Salo, T., Niso, G., Pernet, C.,

Phillips, C., Oostenveld, R., Gallezot, J-D., Carson, R.E., Knudsen, G.M., Innis R.B. & Ganz M. (2021). PET-BIDS, an extension to the brain imaging data structure for positron emission tomography. *Scientific Data*, 9 (65). [doi:10.1038/s41597-022-01164-1](https://doi.org/10.1038/s41597-022-01164-1)

- 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](https://doi.org/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](https://doi.org/10.1093/gigascience/giaa104)

## Microscopy

- Bourget M.-H., Kametsky L., Ghosh S.S., Mazzamuto G., Lazari A., Markiewicz C.J., Oostenveld R., Niso G., Halchenko Y.O., Lipp I., Takerkart S., Toussaint P.-J., Khan A.R., Nilsonne G., Castelli F.M., The BIDS Maintainers and Cohen-Adad J. (2022). Microscopy-BIDS: An Extension to the Brain Imaging Data Structure for Microscopy Data. *Frontiers in Neuroscience*, 16 (871228). [doi:10.3389/fnins.2022.871228](https://doi.org/10.3389/fnins.2022.871228)

## qMRI

- Karakuzu, A., Appelhoff, S., Auer, T., Boudreau M., Feingold F., Khan A.R., Lazari A., Markiewicz C.J., Mulder M., Phillips C., Salo T., Stikov N., Whitaker K. and de Hollander G. (2022). qMRI-BIDS: An extension to the brain imaging data structure for quantitative magnetic resonance imaging data. *Scientific Data* 9, (517). [doi:10.1038/s41597-022-01571-4](https://doi.org/10.1038/s41597-022-01571-4)

## ASL

- Clement P., Castellaro M., Okell T. W., Thomas D. L., Vandemaele P., Elgayar S., Oliver-Taylor A., Kirk T., Woods J. G., Vos S. B., Kuijter J. P. A., Achten E., van Osch M. J. P., BIDS maintainers, Detre J. A., Lu H., Alsop D. C., Chappell M. A., Hernandez-Garcia L., Petr J. & Mutsaerts H. J. M. M. (2022) ASL-BIDS, the brain imaging data structure extension for arterial spin labeling. *Scientific Data* 9, (543). [doi:10.1038/s41597-022-01615-9](https://doi.org/10.1038/s41597-022-01615-9)

## NIRS

- Luke, R., Oostenveld, R., Cockx, H., Niso, G., Shader, M.J., Orihuela-Espina, F., Innes-Brown, H., Tucker, S., Boas, D., Yücel, M.A., Gau, R., Salo, T., Appelhoff, S., Markiewicz, C.J., McAlpine, D., The BIDS Maintainers, Pollonini, L. (2025) NIRS-BIDS: Brain Imaging Data Structure Extended to Near-Infrared Spectroscopy. *Scientific Data* 12, (159). [doi:10.1038/s41597-024-04136-9](https://doi.org/10.1038/s41597-024-04136-9)

## Motion

- Jeung, S., Cockx, H., Appelhoff, S., Berg, T., Gramann, K., Grothkopp, S., Warmerdam, E., Hansen, C., Oostenveld, R., BIDS Maintainers, Welzel J. (2024). Motion-BIDS: an extension to the brain imaging data structure to organize motion data for reproducible research. *Scientific Data* 11, (716). [doi:10.1038/s41597-024-03559-8](https://doi.org/10.1038/s41597-024-03559-8)

## MRS

- Bouchard, A.E., Wong, D., Bogner, W., Gau, R., Halchenko, Y.O., Lamb, D.G., Markiewicz, C.J., Mullins, P.G., Niso, G., Oeltzschner, G., BIDS Maintainers, Clarke, W.T., Wilson, M., Mikkelsen, M. (2025). MRS-BIDS, an extension to the Brain Imaging Data Structure for magnetic resonance spectroscopy. Scientific Data 12, (13841). [doi:10.1038/s41597-025-05543-2](https://doi.org/10.1038/s41597-025-05543-2)

## EMG

- (publication forthcoming)

## 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

## Language

The BIDS specification is written in American English.

## 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 [\[RFC2119\]](#).

Based on these keywords, we define three requirement levels for specifying data or metadata: REQUIRED, RECOMMENDED, and OPTIONAL. The guiding principles for when particular data is placed under a given requirement level can be loosely described as below:

- **REQUIRED:** Data cannot be interpreted without this information (or the ambiguity is unacceptably high)
- **RECOMMENDED:** Interpretation/utility would be dramatically improved with this information
- **OPTIONAL:** Users and/or tools might find it useful to have this information

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. **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.
3. **Data type** - A functional group of different types of data. Data files are contained in a directory named for the data type. 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)
- (l) **nirs** (near infrared spectroscopy)
- (m) **motion** (motion)
- (n) **mrs** (magnetic resonance spectroscopy)
- (o) **phenotype** (measurement and survey data)
- (p) **emg** (electromyography)

For files that are subject- and session- specific, the data type directory is nested inside those directories. **phenotype** data files are aggregated across subjects and sessions, and so the **phenotype/** directory is placed in the dataset root.

1. Subject - A person or animal participating in the study. Used interchangeably with term Participant.
2. 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.
3. Sample - A sample pertaining to a subject such as tissue, primary cell or cell-free sample. Sample labels MUST be unique within a subject and it is RECOMMENDED that they be unique throughout the dataset.
4. Data acquisition - A continuous uninterrupted block of time during which a brain scanning instrument or an electromyography recording device was acquiring data according to a particular scanning sequence/protocol.
5. 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.

6. 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").
7. 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, 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.
8. Template - A template (sometimes called an atlas template) is any aggregation of data across subjects. Templates MAY operationalize the notion of a common spatial frame of reference (see space) beyond individual subjects. In practical BIDS usage, templates can be recognized (via the `tpl-` entity) as standard spaces that enable analyses of data from multiple individuals.
9. Atlas - An atlas is structured neuroanatomical or neurofunctional information expressed as spatial annotations, such as anatomical landmarks, segmentations, parcellations, probabilistic maps, or feature maps, typically defined in relation to a space engendered by a specific template. Within BIDS, atlases provide standardized spatially-organized knowledge to label, localize, and interpret data features. Atlases often rely on or embed templates as their reference framework. In BIDS, templates establish the spatial coordinate frames for atlases, independently of whether or not they are considered part of specific atlases' outcomes.
10. Space - A space in BIDS is a reference coordinate system defined by neuroimaging data, which may originate from an individual participant (native space) or a standardized reference derived from multiple participants (template space).
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 (and possibly including + character(s)) 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 string that forms part of a filename, located after all entities and following a 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.

## Entities

An "entity" is an attribute that can be associated with a file, contributing to the identification of that file as a component of its filename in the form of a hyphen-separated key-value pair.

Each entity has the following attributes:

1. Name: A comprehensive name describing the context of information to be provided via the entity.
2. Key: A short string, typically a compression of the entity name, which uniquely identifies the entity when part of a filename.
3. Value type: The requisite form of the value that gets specified alongside the key whenever the entity appears in a filename. For each entity, the value is of one of two possible types:
  - (a) Index: A non-negative integer, potentially zero-padded for consistent width.
  - (b) Label: An alphanumeric (and possibly including + character(s)) string. Note that labels MUST not collide when casing is ignored (see Case collision intolerance).

The entity format is a string that prescribes how the entity appears within any given filename. For a hypothetical entity with key "key", the format can be either "key-<index>" or "key-<label>", depending on the value type of that entity.

An entity instance is the specific manifestation of an entity within the name of a specific file, based on the format of the entity but with a value that provides identifying information to the particular file in whose name it appears.

Depending on context, any one of the entity name, key, format, or a specific entity instance, may be referred to as simply an "entity".

"Subject", "session", "sample", "task", and "run" from the list of definitions above are all examples of entities. The comprehensive list of supported entities is defined in the Entities Appendix; further, whether each is OPTIONAL, REQUIRED, or MUST NOT be provided for various data files, as well as their relative ordering in a filename, are defined in the Entity Tables Appendix.

## 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 subdirectories to the existing directory 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.

It is RECOMMENDED that non-compulsory metadata fields (like `notch` in `channels.tsv` files) and/or files (like `events.tsv`) are fully omitted when they are unavailable or inapplicable, instead of specified with an `n/a` value, or included as an empty file (for example an empty `events.tsv` file with only the headers included).

## Dataset naming

BIDS does not prescribe a particular naming scheme for directories containing individual BIDS datasets. However, it is recommended to use a short descriptive name that reflects the content of the dataset, avoid spaces in the name, and use hyphens or underscores to separate words. BIDS datasets embedded within a larger BIDS dataset MAY follow some convention (see for example Storage of derived datasets).

## Filesystem structure

Data for each subject are placed in subdirectories named `"sub-<label>"`, where string `"<label>"` is substituted with the unique identification label of each subject. Additional information on each participant MAY be provided in a participants file in the root directory of the dataset.

If data for the subject were acquired across multiple sessions, then within the subject directory resides subdirectories named `"ses-<label>"`, where string `"<label>"` is substituted with a unique identification label for each session. In datasets where at least one subject has more than one session, this additional subdirectory later SHOULD be added for all subjects in the dataset. Additional information on each session MAY be provided in a sessions file within the subject directory.

Within the session subdirectory (or the subject subdirectory if no session subdirectories are present) are subdirectories named according to data type as defined above. A data type directory SHOULD NOT be defined if there are no files to be placed in that directory.

Specific structure of derived data. In the case of storing derived data (see below), template (`tpl-<label>`) directories may be found at the root of the dataset, and these may include cohort (`cohort-<label>`) subdirectories. These directories are described in Templates and atlases.

## Other top level directories

In addition to the subject directories, the root directory of a BIDS dataset MAY also contain the following directories:

- **code**: A directory in which to store any code (for example the one used to generate the derivatives from the raw data). See the Code section for more information.
- **derivatives**: Derivative data (for example preprocessed files). See the relevant section for more information.
- **phenotype**: A directory where to store participant level measurements (for example responses from multiple questionnaires) split into individual files separate from `participants.tsv`. See the relevant section for more information.
- **sourcedata**: A directory where to store data before harmonization, reconstruction, and/or file format conversion (for example, E-Prime event logs or DICOM files). See the relevant section for more information.
- **stimuli**: A directory to store any stimulus files used during an experiment. See the relevant section for more information.

## Filenames

A filename consists of a chain of entity instances and a suffix all separated by underscores, and an extension. This pattern forms filenames that are both human- and machine-readable. For instance, file `"sub-01_task-rest_eeg.edf"` contains instances of the `"subject"` and `"task"` entities, making it evident from the filename alone that it contains resting-state data from subject 01; the suffix `eeg` and extension `.edf` depend on the imaging modality and the data format, and can therefore convey further details of the file's contents.

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>`. Conversely, if the session level is omitted in the directory structure, the file name MUST begin with the string `sub-<label>`, without `ses-<label>`.

Any given entity MUST NOT appear more than once in any filename. For example, filename `"sub-01_acq-laser_acq-uneven_electrodes.tsv"` is invalid because it uses the `"acquisition"` entity twice.

In cases where an entity and a metadata field convey similar contextual information, 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` MUST 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

Filename 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.

## Dotfiles

Files and directories starting with a dot ( `.` ) are reserved for system use and no valid recognized BIDS file or directory can start with a `..`. Any file or directory starting with a `.` present in a BIDS dataset is considered hidden and not subject to BIDS validation.

## Uniqueness of data files

Data files MUST be uniquely identified by BIDS path components (entities, datatype, suffix). If multiple extensions are permissible (for example, `.nii` and `.nii.gz`), there MUST only be one such file with the same entities, datatype and suffix. This limitation does not apply to metadata files, such as JSON sidecar files or format-specific metadata files.

Note that duplicating files to make the same data available in multiple formats is not permitted. For example, if the files `sub-01_ses-01_sample-A_photo.jpg` and `sub-01_ses-01_sample-A_photo.tif` contain a representation of the same data, then the dataset MUST NOT contain both images. If the files contain different images, other entities MUST be used to distinguish the two.

## Filesystem structure & Filenames richness versus distinctness

BIDS provides a rich filesystem structure and rich filenames by using entities, but it is important to keep in mind that files also have to be readable. They have to be readable by machines, and this implies that filenames cannot be longer than 255 characters. They also have to be readable by humans, and this implies minimizing length. A useful way to think about filenames is distinctness: what is the minimal information needed to distinguish files? A simple illustration is given by using the `ses-` and `run-` entities. A T1 weighted MRI image could, in principle, be called `sub-X_ses-1_run-1_T1w.nii`. When there is only 1 session, and only 1 run, this is not needed as

`ses-` and `run-` do not increase distinctiveness. Here, it is recommended to use the shorter version `sub-X_T1w.nii`. In some cases, this principle is enforced in the BIDS validator.

## 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). Retaining the source data is especially valuable in a case when conversion fails to preserve crucial metadata unique to specific acquisition setup. 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` directory. BIDS does not prescribe a particular naming scheme for source data, but it is recommended for it to follow BIDS naming convention where possible. 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` directory or the `derivatives` directory, 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` directory.

Sharing source data may help amend errors and missing data discovered only with the reuse of the raw dataset in practice. Therefore, from an Open Science perspective, it is RECOMMENDED to share the source data whenever it is possible.

However, more stringent sharing limitations may apply to the source data than those applicable to the raw data. For example, human data almost always requires deidentification before they can be redistributed, or the subjects' consent form did not explicitly state that the source files would be shared after deidentification. Further examples in which sharing source data may not be possible include original data formats that are not redistributable as per the acquisition device's license.

As for raw data, all regulatory, ethical, and legal aspects SHOULD be carefully considered before sharing data through the `sourcedata/` directory mechanism. In the case of source data, these aspects are likely more stringent.

Templates and atlases as derived data. Templates and atlases are key neuroscientific tools to carry out group-level inferences and also employed in many atlas-based methodologies (such as atlas-based segmentation). Original templates and atlases employed as primary data to the analysis MAY be stored within the `sourcedata/atlases/` directory. Atlases and artifacts derived from atlases are considered derived data and MUST be stored as derivative datasets, as described in the next section.

## Storage of derived datasets

Derivatives can be stored/distributed in two ways:

1. Under a `derivatives/` subdirectory in the root of the source BIDS dataset directory 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 subdirectories. There are few restrictions on the directory names; it is RECOMMENDED to use the format `<pipeline-name>-<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 subdirectory name SHOULD be the `GeneratedBy.Name` field in `dataset_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/fmriprip-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 an atlas-generating pipeline, including outputs for individual subjects prior to aggregation in the `MNI152NLin2009cAsym` standard space:

```
<dataset>/derivatives/atlasgenerator/sub-0001
<dataset>/derivatives/atlasgenerator/tpl-MNI152NLin2009cAsym
```

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. Extra documentation (and relevant images) MAY be included in the `docs/` subdirectory. Logs from running the code or other commands MAY be stored under `logs/` subdirectory.

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

```
my_processed_data/
  code/
    processing_pipeline-1.0.0.img
    hpc_submitter.sh
    ...
  sourcedata/
    raw/
      sub-01/
      sub-02/
      ...
  sub-01/
  sub-02/
```

```
...
dataset_description.json
```

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-name>[-<variant>]` 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. Likewise, any template-specific derivatives SHOULD be housed within each template's directory; if cohort-specific derivatives are generated, they SHOULD be deposited under a cohort subdirectory within the corresponding template 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/` subdirectory, the contents of that directory may be a heterogeneous mix of BIDS Derivatives datasets and non-compliant derivatives.

## Study dataset

BIDS allows one to organize the data for the entire study (original source data, raw BIDS, derivatives) as a valid BIDS dataset in the following way

```
study-1/
  sourcedata/
    dicoms/
      raw/
        sub-01/
        sub-02/
        ...
        dataset_description.json
      ...
  derivatives/
    pipeline1-v1/
    pipeline2/
    ...
  dataset_description.json
  ...
```

In this example, `sourcedata/dicoms` is not nested inside `sourcedata/raw`, and only the **`sourcedata/raw`** subdirectory is a BIDS-compliant dataset among `sourcedata/` subfolders. The subdirectories of `derivatives` MAY be BIDS-compliant derivatives datasets (see Non-compliant derivatives for further discussion). The above example is a fully compliant BIDS dataset, providing a convention useful for organizing source, raw BIDS, and derived BIDS data while maintaining overall BIDS compliance. When using this convention, `dataset_description.json` MUST have `DatasetType` to be set to `"study"`. It is also RECOMMENDED to set the `SourceDatasets` field in `dataset_description.json` of each subdirectory of `derivatives` to:

```
{  
  "SourceDatasets": [ {"URL": "../..sourcedata/raw/"} ]  
}
```

## File format 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. If using compressed files, the gzip header **SHOULD** lack source filenames and timestamps. 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). Currently defined metadata fields are listed in the Glossary. Where possible, DICOM Tags are adopted directly as BIDS metadata terms and indicated with "Corresponds to DICOM Tag ID1, ID2 DICOM Tag Name.". When harmonization has been deemed necessary, this is indicated in the BIDS term description with "Based on DICOM Tag ID1, ID2 DICOM Tag Name.". Extraction of BIDS compatible metadata can be performed using [DICOM to NIfTI converters](#) such as [dcm2niix](#). 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 plain-text, tab-delimited values (TSV) files (with extension .tsv), that is, [CSV files](#) where commas are replaced by tab characters. Tabs **MUST** be true tab characters and **MUST NOT** be a series of space characters. Tabular data such as continuous physiology recordings typically containing large numbers of rows **MAY** be saved as compressed tabular files (with extension .tsv.gz), which are introduced below. Plain-text TSV and compressed TSV are not interchangeable, that is, each section of the specification prescribes which one **MUST** be used for the data type at hand. Each TSV file **MUST** start with a header line listing the names of all columns with two exceptions:

1. compressed tabular files, for which column names are defined in a sidecar metadata [JSON object](#) described below; and
2. motion recording data, which use plain-text TSV and columns are defined as described in its corresponding section of the specifications.

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`). Column names defined in the header **MUST** be separated with tabs as for the data contents. Furthermore, column names **MUST NOT** be blank (that is, an empty string) and **MUST NOT** be duplicated within a single TSV file. Missing and non-applicable values **MUST** be coded as `n/a`. String values containing tabs **MUST** be escaped using double quotes. 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:

```
tsv {linenums="1"} onset    duration    response_time    trial_type    trial_extra 200 20.0    15.8    word    240 5.0 17.34e-1    visual  
n/a
```

The TSV examples in this document (like the one above this note) are occasionally formatted with the addition of the row indices as first column. Those indices are presented for visual reference and are not part of the tabular data file's content.

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	<a href="#">string</a>	Long (unabbreviated) name of the column.
Description	RECOMMENDED	<a href="#">string</a>	Free-form natural language description. The description of the column.
Format	OPTIONAL	<a href="#">string</a>	Permitted formats for values in the described column. For a list of valid values for this field, see the Format.
Levels	RECOMMENDED	<a href="#">object</a>	For categorical variables: An object of possible values (keys) and their descriptions (values).
Units	RECOMMENDED	<a href="#">string</a>	Measurement units for the associated variable. SI units in CMIXF formatting are RECOMMENDED (see Units).
Delimiter	OPTIONAL	<a href="#">string</a>	If rows in a column may be interpreted as a lists of values, the character that separates one value from the next.
TermURL	RECOMMENDED	<a href="#">string</a>	URL pointing to a formal definition of this type of data in an ontology available on the web. For example: <a href="https://www.ncbi.nlm.nih.gov/mesh/68008297">https://www.ncbi.nlm.nih.gov/mesh/68008297</a> for "male".
HED	OPTIONAL	<a href="#">string</a> or <a href="#">object</a> of <a href="#">strings</a>	Hierarchical Event Descriptor (HED) information, see the HED for details.
Maximum	OPTIONAL	<a href="#">number</a>	Maximum value a column entry is permitted to have.
Minimum	OPTIONAL	<a href="#">number</a>	Minimum value a column entry is permitted to have.

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. In the absence of **Format**, **Units** implies the column contains numeric values, and **Levels** implies the column contains strings.

Example:

```
{
  "test": {
    "LongName": "Education level",
    "Description": "Education level, self-rated by participant",
    "Format": "integer",
    "Levels": {
      "1": "Finished primary school",
      "2": "Finished secondary school",
      "3": "Student at university",
      "4": "Has degree from university"
    }
  },
  "bmi": {
    "LongName": "Body mass index",
    "Format": "number",
    "Units": "kg/m^2",
    "Minimum": 0,
    "TermURL": "https://purl.bioontology.org/ontology/SNOMEDCT/60621009"
  }
}
```

Each level can be described with a string as in the example above, or with an object containing the fields `Description` and `TermURL` like in the example below.

```
{
  "sex": {
    "Description": "sex of the participant as reported by the participant",
    "Levels": {
      "M": {
        "Description": "Male",
        "TermURL": "https://www.ncbi.nlm.nih.gov/mesh/68008297"
      },
      "F": {
        "Description": "Female",
        "TermURL": "https://www.ncbi.nlm.nih.gov/mesh/68005260"
      }
    }
  }
}
```

## Compressed tabular files

Large tabular information, such as physiological recordings, MUST be stored with compressed tab-delineated (TSV.GZ) files when so established by the specifications. Rules for formatting plain-text tabular files apply to TSVGZ files with three exceptions:

1. The contents of TSVGZ files MUST be compressed with [gzip](#).
2. Compressed tabular files MUST NOT contain a header in the first row indicating the column names.
3. TSVGZ files MUST have an associated JSON file that defines the columns in the tabular file.

In contrast to plain-text TSV files, compressed tabular files MUST NOT include a header line. Column names MUST be provided in the JSON file with the `Columns` field. Each column MAY additionally be described with a column description, as described in Tabular files.

TSVGZ are header-less to improve compatibility with existing software (for example, FSL, or PNM), and to facilitate the support for other file formats in the future.

The above example, if stored as a TSVGZ file would have the following decompressed content:

```
tsvgz {linenums="1"} 200 20.0    15.8    word        240 5.0 17.34e-1    visual  n/a
```

## 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 events section for more information.

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



## The Inheritance Principle

In some circumstances, there can be multiple data files for which all or a subset of the relevant metadata is precisely equivalent. Where this occurs, it may be preferable to define those metadata only once, and be placed on the filesystem in such a way that those files are deemed to be applicable to each relevant data file individually, but not be erroneously associated with other data files to which the metadata contained within are not applicable. The Inheritance Principle defines a systematized set of rules to determine which metadata files to associate with which data files. Further, because multiple metadata files may apply to an individual data file, the Principle defines the order of precedence of such metadata content; this is necessary for resolution of conflicts if the same metadata field contains different values in different metadata files (though it is RECOMMENDED to avoid such overloading).

### Rules

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 "unsettling" of that field (indeed removal of existing fields is not possible).

## Examples

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
  sub-01_scans.tsv
task-rest_bold.json
scans.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-longtr\_bold.nii.gz 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).

A single scans.json, without any entity in the filename at the top level, is applicable to describe columns of the sub-01\_scans.tsv and any other \_scans.tsv potentially present in the dataset for other subjects.

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
```

Example 5: Generalization of Examples 1 and 4 for a sidecar file without entities

```
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
  bold.json
```

where `bold.json` in top directory would be applicable to all `_bold.nii.gz` regardless of any other entity in their filename.

## 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 some participants have two-digit labels) 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 entities).

## 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.10175845](https://doi.org/10.5281/zenodo.10175845). 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.ds000001.v1.0.0`. Bare DOIs such as `10.18112/openneuro.ds000001.v1.0.0` are [DEPRECATED][].

## BIDS URI

To reference files in BIDS datasets, the following URI scheme may be used:

`bids:[<dataset-name>]:<relative-path>`

The scheme component `bids` identifies a BIDS URI, which defines a `path` component of the form `<dataset-name>:<relative-path>`. The `dataset-name` component is an identifier for a BIDS dataset, and the `relative-path` component is the location of a resource within that BIDS dataset, relative to the root of that dataset. The `relative-path` MUST NOT start with a forward-slash character (`/`).

Examples:

```
bids::sub-01/fmap/sub-01_dir-AP_epi.nii.gz
bids:ds000001:sub-02/anat/sub-02_T1w.nii.gz
bids:myderivatives:sub-03/func/sub-03_task-rest_space-MNI152_bold.nii.gz
```

If no dataset name is specified, the URI is relative to the current BIDS dataset. This is made more precise in the next section.

## Resolution of BIDS URIs

In order to resolve a BIDS URI, the dataset name must be mapped to a BIDS dataset.

The special case `"` (that is, the empty string) refers to the BIDS dataset in which the BIDS URI is found. The dataset root is the nearest parent directory that contains a valid `dataset_description.json`.

All other dataset names MUST be specified in the `DatasetLinks` object in `dataset_description.json`, which maps dataset names to URIs that point to BIDS dataset locations. If the scheme is omitted from a URI in `DatasetLinks`, that path is resolved relative to the current dataset root (see `deriv1` example, below).

BIDS URIs cannot be interpreted outside a BIDS dataset, as they require a `dataset_description.json` file to resolve.

### Examples

Consider this example `dataset_description.json`:

```
{
  ...
  "DatasetLinks": {
    "deriv1": "derivatives/derivative1",
    "phantoms": "file:///data/phantoms",
    "ds000001": "doi:10.18112/openneuro.ds000001.v1.0.0"
  }
}
```

Here `deriv1` refers to a BIDS Derivatives dataset contained within the current dataset, `phantoms` refers to a BIDS dataset of phantom data stored on the local filesystem, and `ds000001` refers to a BIDS dataset that must be resolved by DOI.

Note that resolving `bids:phantoms:sub-phantom01/anat/sub-phantom01_T1w.nii.gz` is a straightforward concatenation: `file:///data/phantoms/sub-phantom01/anat/sub-phantom01_T1w.nii.gz`. However, retrieving `bids:ds000001:sub-02/anat/sub-02_T1w.nii.gz` requires first resolving the DOI, identifying the retrieval method, possibly retrieving the entire dataset, and finally constructing a URI to the desired resource.

No protocol is currently proposed to automatically resolve all possible BIDS URIs.

### Future statement

BIDS URIs are parsable as standard `[URIs]` with scheme `bids` and path `[<dataset-name>]:<relative-path>`. The authority, query and fragment components are unused. Future versions of BIDS may specify interpretations for these components, but MUST NOT change the interpretation of a previously valid BIDS URI. For example, a future version may specify an authority that would allow BIDS URIs to be resolved without reference to a local `dataset_description.json`.

## 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 the Units Appendix 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 the Units Appendix 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|+hh:mm|-hh:mm]` (year, month, day, hour (24h), minute, second, optional fractional seconds, and optional time offset). This is almost equivalent to the [RFC3339](#) "date-time" format, with the exception that UTC offsets are OPTIONAL. If no time offset is 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+01:00`.
- 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, it 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 the MEG File Formats Appendix 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 directory 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 directories 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 (and possibly including + character(s)) 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.

# Dataset description

Templates:

- `dataset_description.json`
- `README[.md|.rst|.txt]`
- `CITATION.cff`
- `CHANGES`
- `LICENSE[.md|.rst|.txt]`

## **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	<a href="#">string</a>	Name of the dataset.
BIDSVersion	REQUIRED	<a href="#">string</a>	The version of the BIDS standard that was used.
HEDVersion	RECOMMENDED	<a href="#">string</a> or <a href="#">array</a> of <a href="#">strings</a>	If HED tags are used: The version of the HED schema used to validate HED tags for study. May include a single schema or a base schema and one or more library schema.



Key name	Requirement Level	Data type	Description
DatasetLinks	OPTIONAL, but REQUIRED if DatasetLinks are used	object of strings	Used to map a given <dataset-name> from a DatasetLinks of the form bids:<dataset-name>:path/within/dataset to a local or remote location. The <dataset-name>: "" (an empty string) is a reserved keyword that MUST NOT be a key in DatasetLinks (example: bids::path/within/dataset).
DatasetType	RECOMMENDED	string	The interpretation of the dataset. For backwards compatibility, the default value is "raw". Must be one of: "raw", "derivative", "study".
License	RECOMMENDED	string	The license for the dataset. The use of license name abbreviations is RECOMMENDED for specifying a license (see License). The corresponding full license text MAY be specified in an additional LICENSE file.
Authors	OPTIONAL, but RECOMMENDED if CITATION.cff is not present	array of strings	List of individuals who contributed to the creation/curation of the dataset.
Keywords	OPTIONAL	array of strings	A list of keywords that describe the content or subject matter of the dataset. These may be used to enhance the findability of the dataset on public archives.
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.

Key name	Requirement Level	Data type	Description
ReferencesAndLinks	OPTIONAL	array of <a href="#">strings</a>	List of references to publications that contain information on the dataset. A reference may be textual or a <a href="#">ReferencesAndLinks</a> .
DatasetDOI	OPTIONAL	<a href="#">string</a>	The Digital Object Identifier of the dataset (not the corresponding paper). DOIs SHOULD be expressed as a valid <a href="#">DatasetDOI</a> ; bare DOIs such as 10.0.2.3/dfjj.10 are <a href="#">DatasetDOI</a> .
GeneratedBy	RECOMMENDED	array of <a href="#">objects</a>	Used to specify provenance of the dataset.
SourceDatasets	RECOMMENDED	array of <a href="#">objects</a>	Used to specify the locations and relevant attributes of all source datasets (BIDS or not). Valid keys in each object include "URL", "DOI" (see <a href="#">SourceDatasets</a> ), and "Version" with <a href="#">string</a> values.

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

Key name	Requirement Level	Data type	Description
Name	REQUIRED	<a href="#">string</a>	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	<a href="#">string</a>	Version of the pipeline
Description	OPTIONAL	<a href="#">string</a>	Plain-text description of the pipeline or process that generated the outputs. RECOMMENDED if Name is "Manual".
CodeURL	OPTIONAL	<a href="#">string</a>	URL where the code used to generate the dataset may be found.

Key name	Requirement Level	Data type	Description
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][uri] with string values.

Example:

```
{
  "Name": "The mother of all experiments",
  "BIDSVersion": "1.10.1",
  "DatasetType": "raw",
  "License": "CC0",
  "Authors": [
    "Paul Broca",
    "Carl Wernicke"
  ],
  "Keywords": [
    "neuroscience",
    "language",
    "brain"
  ],
  "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:10.234001/jn.2015.0001"
  ],
  "DatasetDOI": "doi:10.0.2.3/dfjj.10",
  "HEDVersion": "8.4.0",
  "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_description.json`. 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 subdirectory of the raw dataset, then the `Name` field of the first `GeneratedBy` object MUST be a substring of the derived dataset directory name. That is, in a directory `<dataset>/derivatives/<pipeline-name>[-<variant>]/`, the first `GeneratedBy` object should have a `Name` of `<pipeline-name>`.

Example:

```
{
  "Name": "fMRIPREP Outputs",
  "BIDSVersion": "1.6.0",
  "DatasetType": "derivative",
  "GeneratedBy": [
    {
      "Name": "fmriprep",
      "Version": "1.4.1",
      "Container": {
```

```
    "Type": "docker",
    "Tag": "poldracklab/fmripred: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

A REQUIRED text file, `README`, SHOULD describe the dataset in more detail. The `README` file MUST be either in ASCII or UTF-8 encoding and MAY have one of the extensions: `.md` ([Markdown](#)), `.rst` ([reStructuredText](#)), or `.txt`. A BIDS dataset MUST NOT contain more than one `README` file (with or without extension) at its root directory. BIDS does not make any recommendations with regards to the [Markdown flavor](#) and does not validate the syntax of `Markdown` and `reStructuredText`. The `README` file SHOULD be structured such that its contents can be easily understood even if the used format is not rendered. A guideline for creating a good `README` file can be found in the [bids-starter-kit](#).

## CITATION.cff

A description of the citation information for the dataset, following the [Citation File Format](#) specification. This file permits more detailed and structured descriptions than `dataset_description.json`.

For most redundant fields between `CITATION.cff` and `dataset_description.json`, the `CITATION.cff` SHOULD take precedence. To avoid inconsistency, metadata present in `CITATION.cff` SHOULD NOT be included in `dataset_description.json`, with the exception of `Name` and `DatasetDOI`, to ensure that `CITATION.cff`-unaware tools can generate references to the dataset. In particular, if `CITATION.cff` is present, the `"Authors"` field of `dataset_description.json` MUST be omitted, and the `"HowToAcknowledge"`, `"License"` and `"ReferencesAndLinks"` SHOULD be omitted in favor of the `CITATION.cff` fields `message/preferred-citation`, `license` and `references`.

## 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 and MAY have one of the extensions: `.md` ([Markdown](#)), `.rst` ([reStructuredText](#)), or `.txt`.

# Data summary files

## 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 `participant_id` entries MUST be a superset of all subject directories and all `participant_id` entries found among phenotypic and assessment data in the `phenotype/` directory.

Commonly used optional columns in `participants.tsv` files are `age`, `sex`, `handedness`, `strain`, and `strain_rrid`.

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`.

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
<code>participant_id</code>	REQUIRED	<a href="#">string</a>	A participant identifier of the form <code>sub-&lt;label&gt;</code> , matching a participant entity found in the dataset. There MUST be exactly one row for each participant. Values in <code>participant_id</code> MUST be unique. This column must appear first in the file.

Column name	Requirement Level	Data type	Description
species	RECOMMENDED	string or number	The <b>species</b> column SHOULD be a binomial species name from the <a href="#">NCBI Taxonomy</a> (for example, <b>homo sapiens</b> , <b>mus musculus</b> , <b>rattus norvegicus</b> ). For backwards compatibility, if <b>species</b> is absent, the participant is assumed to be <b>homo sapiens</b> . This column may appear anywhere in the file.
age	RECOMMENDED	number	Numeric value in years (float or integer value).For privacy purposes, participant ages should be capped at 89. Using "89+" for ages above 88 is DEPRECATED. This column may appear anywhere in the file.
sex	RECOMMENDED	string	String value indicating phenotypical sex, one of "male", "female", "other".For "male", use one of these values: <b>male</b> , <b>m</b> , <b>M</b> , <b>MALE</b> , <b>Male</b> .For "female", use one of these values: <b>female</b> , <b>f</b> , <b>F</b> , <b>FEMALE</b> , <b>Female</b> .For "other", use one of these values: <b>other</b> , <b>o</b> , <b>O</b> , <b>OTHER</b> , <b>Other</b> . This column may appear anywhere in the file.For a list of valid values for this column, see the sex.
handedness	RECOMMENDED	string	String value indicating one of "left", "right", "ambidextrous".For "left", use one of these values: <b>left</b> , <b>l</b> , <b>L</b> , <b>LEFT</b> , <b>Left</b> .For "right", use one of these values: <b>right</b> , <b>r</b> , <b>R</b> , <b>RIGHT</b> , <b>Right</b> .For "ambidextrous", use one of these values: <b>ambidextrous</b> , <b>a</b> , <b>A</b> , <b>AMBIDEXTROUS</b> , <b>Ambidextrous</b> . This column may appear anywhere in the file.For a list of valid values for this column, see the handedness.



Column name	Requirement Level	Data type	Description
strain	RECOMMENDED	string or number	For species different from <b>homo sapiens</b> , string value indicating the strain of the species, for example: C57BL/6J. This column may appear anywhere in the file.
strain_rrid	RECOMMENDED	<a href="#">string</a>	For species different from <b>homo sapiens</b> , research resource identifier ( <a href="#">RRID</a> ) of the strain of the species, for example: RRID:IMSR_JAX:000664. This column may appear anywhere in the file.
HED	OPTIONAL	<a href="#">string</a>	Hierarchical Event Descriptor (HED) tags. See the HED for details. This column may appear anywhere in the file.
Additional Columns	OPTIONAL	n/a	Additional columns are allowed.

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": "year"
  },
  "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 <code>sample-&lt;label&gt;</code> , matching a sample entity found in the dataset. The combination of <code>sample_id</code> and <code>participant_id</code> MUST be unique.

Column name	Requirement Level	Data type	Description
participant_id	REQUIRED	string	A participant identifier of the form sub- <b>&lt;label&gt;</b> , 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 <a href="#">ENCODE Biosample Type</a> . 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 or number	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- <b>&lt;label&gt;</b> entity from which a sample is derived, for example a slice of tissue (sample-02) derived from a block of tissue (sample-01).
Additional Columns	OPTIONAL	n/a	Additional columns are allowed.

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"
  }
}
```

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 recording file within one session. In general, each of these files SHOULD be described by exactly one row.

For file formats that are based on several files of different extensions, or a directory of files with different extensions (multi-file file formats), only that file SHOULD be listed that would also be passed to analysis software for reading the data. For example for BrainVision data (.vhdr, .vmrk, .eeg), only the .vhdr SHOULD be listed; for EEGLAB data (.set, .fdt), only the .set file SHOULD be listed; and for CTF data (.ds), the whole .ds directory SHOULD be listed, and not the individual files in that directory.

Some neural recordings consist of multiple parts, that span several files, but that share the same extension. For example in entity-linked file collections, commonly used for qMRI, where recordings may be linked through entities such as **echo** and **part** (using .nii or .nii.gz extensions). For another example consider the case of large files in .fif format that are linked through the **split** entity (see Split files). Such recordings MUST be documented with one row per file (unlike the case of multi-file file formats described above).

Column name	Requirement Level	Data type	Description
filename	REQUIRED	string	Relative paths to files. There MUST be exactly one row for each file. Values in <b>filename</b> MUST be unique.This column must appear first in the file.

Column name	Requirement Level	Data type	Description
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 deidentification are described in acq_time. This column may appear anywhere in the file.
HED	OPTIONAL	string	Hierarchical Event Descriptor (HED) tags. See the HED for details. This column may appear anywhere in the file.
Additional Columns	OPTIONAL	n/a	Additional columns are allowed.

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 <b>ses-&lt;label&gt;</b> , matching a session found in the dataset. There MUST be exactly one row for each session. Values in <b>session_id</b> MUST be unique. This column must appear first in the file.
acq_time	OPTIONAL	string	Acquisition time refers to when the first data point of the first run was acquired. Datetime format and their deidentification are described in <b>acq_time</b> . This column may appear anywhere in the file.
pathology	RECOMMENDED	string or number	String value describing the pathology of the sample or type of control. When different from <b>healthy</b> , pathology SHOULD be specified. The pathology may be specified in either <b>samples.tsv</b> or <b>sessions.tsv</b> , depending on whether the pathology changes over time. This column may appear anywhere in the file.
HED	OPTIONAL	string	Hierarchical Event Descriptor (HED) tags. See the HED for details. This column may appear anywhere in the file.
Additional Columns	OPTIONAL	n/a	Additional columns are allowed.

```
_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
```

# 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. Filenames 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	<a href="#">object</a>	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.

Key name	Requirement Level	Data type	Description
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).



# Code

Template: `code/*`

Source code of scripts that were used to prepare the dataset MAY be stored here. Examples include deidentification 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.

# Events

The purpose of this file is to describe timing and other properties of events recorded during data acquisition. Events may include stimuli presented to the participant, participant responses that are associated with tasks, or markers of other incidents that occurred during the execution of the experiment. See the definition of Event for a more detailed explanation. A single event file MAY include any combination of stimulus, response, and other events. Events MAY overlap in time. Please keep in 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>/]
    beh/
      <matches>_events.json
      <matches>_events.tsv
    eeg/
      <matches>_events.json
      <matches>_events.tsv
    emg/
      <matches>_events.json
      <matches>_events.tsv
    func/
      <matches>_events.json
      <matches>_events.tsv
    ieeg/
      <matches>_events.json
      <matches>_events.tsv
    meg/
      <matches>_events.json
      <matches>_events.tsv
    motion/
```

```
    <matches>_events.json
    <matches>_events.tsv
mrs/
    <matches>_events.json
    <matches>_events.tsv
nirs/
    <matches>_events.json
    <matches>_events.tsv
pet/
    <matches>_events.json
    <matches>_events.tsv
```

Legend:

- `<matches>` is a placeholder to denote an arbitrary (and valid) sequence of entities and labels at the beginning of the filename (only BIDS "raw").
- `<source-entities>` is a placeholder to denote an arbitrary sequence of entities and labels at the beginning of the filename matching a source file from which the file derives (only BIDS-Derivatives).
- Filename entities or directories between square brackets (for example, `[_ses-<label>]`) are OPTIONAL.
- Some entities may only allow specific values, in which case those values are listed in `<>`, separated by `|`.
- `_<suffix>` means that there are several ( $>6$ ) valid suffixes for this filename pattern.
- `.<extension>` means that there are several ( $>6$ ) valid extensions for this file type.
- `[.gz]` means that both the unzipped and gzipped versions of the extension are valid.

Each `events.tsv` file **REQUIRES** at least one corresponding data file. Through the Inheritance Principle, a single `events.tsv` file **MAY** describe events for multiple participants, sessions, and runs. 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. A value of n/a indicates the onset time is unknown or unavailable. This column must appear first in the file.
duration	REQUIRED	number	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. This column must appear second in the file. Must be a number greater than or equal to 0.

Column name	Requirement Level	Data type	Description
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. This column may appear anywhere in the file.
response_time	OPTIONAL	number	Response time measured in seconds. A negative response time can be used to represent preemptive responses and n/a denotes a missed response. This column may appear anywhere in the file.
HED	OPTIONAL	string	Hierarchical Event Descriptor (HED) tags. See the HED for details. This column may appear anywhere in the file.
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/ directory (under the root directory of the dataset; with OPTIONAL subdirectories). 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. This column may appear anywhere in the file.

Column name	Requirement Level	Data type	Description
channel	OPTIONAL	string	Channel(s) associated with an event. If multiple channels are specified, they MUST be separated by a delimiter specified in the "Delimiter" field describing the channel column. For example, channels separated with a comma (,) require the events.json file to contain "channel": {"Delimiter": ","}. In the absence of a delimiter, tools MUST interpret any character as being part of a channel name. Note that this column only applies to data types where channels are specified, such as EEG, iEEG, MEG or NIRS. This column may appear anywhere in the file.
Additional Columns	OPTIONAL	n/a	Additional columns are allowed.

The content of `events.tsv` files SHOULD be sorted by values in the `onset` column.

An arbitrary number of additional columns can be added. Those allow describing other properties of events that could be later referenced in modeling 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.

For the precision of numeric metadata, it is RECOMMENDED that dataset curators specify numeric metadata like `onset` and `duration` with as much decimal precision as is reasonable in the context of the experiment. For example in an EEG experiment with devices operating at 1000 Hz sampling frequency, dataset curators SHOULD specify at least 3 figures after the decimal point.

For fMRI 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.

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  channel  annots
1.23   0.65    start    1.435    images/red_square.jpg  n/a  n/a
```

```
5.65    0.65    stop    1.739    images/blue_square.jpg    n/a n/a
12.1    2.35    n/a n/a n/a F,1|F,2|Cz    musc
```

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"
    }
  },
  "channel": {
    "Description": "Channel(s) associated with the event",
    "Delimiter": "|"
  },
  "annots": {
    "LongName": "Annotations",
    "Description": "Annotations associated with channels indicated in the channel column.",
    "Levels": {
      "musc": "Muscle artifact. A very common, high frequency, sharp artifact that corresponds with agitation/nervousness in a patient."
    },
    "HED": {
      "musc": "EMG-artifact"
    }
  }
}
```

In the example above:

1. Only a subset of columns are described for the sake of brevity. In a real dataset, all other columns SHOULD also be described.
2. The `channel` column contains a list of values that are separated by a delimiter (`|`), as is declared in the `Delimiter` metadata field of the `events.json` file. Thus, the channels related to the event in the third row of the example are called `F,1`, `F,2`, and `Cz`.
3. The example contains a column called `annots`. This column is not defined in BIDS, and constitutes additional, arbitrary (that is, unofficial) metadata. In the present case, it is used to describe artifacts in the data, in reference to the `channel` column. The `annots` column is making use of the powerful HED system for documenting events, see below.

Events MAY 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.

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
```

## 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` directory or by reference to a stimuli database.

### Stimuli directory

The stimulus files can be added in a `/stimuli` directory (under the root directory of the dataset; with optional subdirectories) 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` directory.

### 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](#).

```
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.
VisionCorrection	OPTIONAL	string	Equipment used to correct participant vision during an experiment. Example: "spectacles", "lenses", "none".

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).

Key name	Requirement Level	Data type	Description
ScreenDistance	RECOMMENDED	number or array of numbers or "n/a"	Distance between the participant's eye and the screen. If no screen was used, use n/a. Distance can either be expressed as a single numeric value indicating the shortest distance between the participant's eye and the screen, or a three-coordinates array indicating the X, Y, Z distances between the participant's eye and the center of the screen.
ScreenOrigin	RECOMMENDED	array of strings	Location of the spatial coordinates' origin for the visual stimuli presentation, described by a list of two keywords such as ("top", "left") if the coordinates refer to the top-left corner of the screen, or ("center", "center") if the position (0, 0) is at the center or the screen's extent.
ScreenRefreshRate	RECOMMENDED	number	Refresh rate of the screen (when used), in Hertz (equivalent to frames per second, "FPS").
ScreenResolution	RECOMMENDED	array of integers or "n/a"	Screen resolution in pixel (for example [1920, 1200] for a screen of 1920-width by 1080-height pixels), if no screen use n/a. ScreenResolution is REQUIRED when the experiment included simultaneous eye-tracking recordings with SampleCoordinateSystem matching "gaze-on-screen".
ScreenSize	RECOMMENDED	array of numbers or "n/a"	Screen size in m, excluding potential screen borders (for example [0.472, 0.295] for a screen of 47.2-width by 29.5-height cm), if no screen use n/a. ScreenSize is REQUIRED when the experiment included simultaneous eye-tracking recordings with SampleCoordinateSystem matching "gaze-on-screen".

Key name	Requirement Level	Data type	Description
SoftwareName	RECOMMENDED	string	Name of the software that was used to present the stimuli.
SoftwareRRID	RECOMMENDED	string	<a href="#">Research Resource Identifier</a> 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'.
SoftwareVersion	RECOMMENDED	string	Version of the software that was used to present the stimuli.
Code	RECOMMENDED	string	Code 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.

Some metadata of the `StimulusPresentation` object become REQUIRED with the presence of "gaze-on-screen" eye-tracking data, as identified by the `"SampleCoordinateSystem"` metadata.

The following fields pertaining to `<matches>_events.json` of tasks that were acquired with the simultaneous recording of eye-tracking escalate to REQUIRED as they are considered essential in eye-tracking data analysis:

- `StimulusPresentation.ScreenDistance`,
- `StimulusPresentation.ScreenOrigin`,
- `StimulusPresentation.ScreenResolution`,
- `StimulusPresentation.ScreenSize`.

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",
    "ScreenDistance": 1.8,
    "ScreenRefreshRate": 60,
    "ScreenResolution": [1920, 1200],
    "ScreenSize": [0.472, 0.295],
    "HeadStabilization": "none"
  },
  "VisionCorrection": "lenses"
}
```

## Continuously-sampled, stimulus-related signals

The following [BIDS-Examples](#) showcase stimulus-related signals and may be used as a reference when curating a new dataset:

- ["synthetic" example dataset](#).

Signals related to stimuli (such as parameters of a film or audio stimuli) that are evenly recorded at a constant sampling frequency **MUST** be specified using a compressed tabular file ([TSV.GZ file](#)) and a corresponding JSON file for storing metadata fields (see below).

Template:

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

```
<matches>_stim.tsv.gz
<matches>_stim.json
```

For the template directory name, <datatype> can correspond to any data recording modality.

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.

<matches>\_stim.tsv.gz files MUST NOT include a header line, as established by the common-principles. As a result, when supplying a <matches>\_stim.tsv.gz file, an accompanying <matches>\_stim.json MUST be present to indicate the column names.

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 placed in the root directory (for example, <root>/task-movie\_stim.<tsv.gz|json>) MAY be used and will apply to all <matches>\_task-movie\_<matches>\_<suffix>.<ext> files. In the following example, the two task-nback\_stim.<json|tsv.gz> apply to all the task-nback runs across the two available subjects:

```
sub-01/
  func/
    sub-01_task-nback_run-1_bold.nii.gz
    sub-01_task-nback_run-2_bold.nii.gz
sub-02/
  func/
    sub-02_task-nback_run-1_bold.nii.gz
    sub-02_task-nback_run-2_bold.nii.gz
task-nback_stim.json
task-nback_stim.tsv.gz
```

The following table specifies metadata fields for the <matches>\_stim.json file.

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). This data MAY be specified with sub-second precision using the syntax <code>s[.000000]</code> , where <code>s</code> reflects whole seconds, and <code>.000000</code> reflects OPTIONAL fractional seconds.
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 for each column.

# 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](#)) by Ben Inglis.

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

### Hardware information

Key name	Requirement Level	Data type	Description
Manufacturer	RECOMMENDED	<a href="#">string</a>	Manufacturer of the equipment that produced the measurements. Corresponds to <a href="#">DICOM Tag 0008, 0070 Manufacturer</a> .
ManufacturersModelName	RECOMMENDED	<a href="#">string</a>	Manufacturer's model name of the equipment that produced the measurements. Corresponds to <a href="#">DICOM Tag 0008, 1090 Manufacturers Model Name</a> .
DeviceSerialNumber	RECOMMENDED	<a href="#">string</a>	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 <a href="#">DICOM Tag 0018, 1000 DeviceSerialNumber</a> .

Key name	Requirement Level	Data type	Description
StationName	RECOMMENDED	string	Institution defined name of the machine that produced the measurements. Corresponds to <a href="#">DICOM Tag 0008, 1010 Station Name</a> .
SoftwareVersions	RECOMMENDED	string	Manufacturer's designation of software version of the equipment that produced the measurements. Corresponds to <a href="#">DICOM Tag 0018, 1020 Software Versions</a> .
HardcopyDeviceSoftwareVersion	HardcopyDeviceSoftwareVersion	string	Manufacturer's designation of the software of the device that created this Hardcopy Image (the printer). Corresponds to <a href="#">DICOM Tag 0018, 101A Hardcopy Device Software Version</a> .
MagneticFieldStrength	RECOMMENDED, but REQUIRED for Arterial Spin Labeling	number	Nominal field strength of MR magnet in Tesla. Corresponds to <a href="#">DICOM Tag 0018, 0087 Magnetic Field Strength</a> .
ReceiveCoilName	RECOMMENDED	string	Information describing the receiver coil. Corresponds to <a href="#">DICOM Tag 0018, 1250 Receive Coil Name</a> , 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.
NumberReceiveCoilActiveElements	OPTIONAL	integer	The number of active RF elements used by the receive coil.
GradientSetType	OPTIONAL	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	OPTIONAL	string	This is a relevant field if a non-standard transmit coil is used. Corresponds to <a href="#">DICOM Tag 0018, 9049 MR Transmit Coil Sequence</a> .
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.
NumberTransmitCoilActiveElements	OPTIONAL	integer	The number of active RF elements used by the transmit coil.
TablePosition	OPTIONAL, but RECOMMENDED if chunk entity is present	array of numbers	The table position, relative to an implementation-specific reference point, often the isocenter. Values must be an array (1x3) of three distances in millimeters in absolute coordinates (world coordinates). If an observer stands in front of the scanner looking at it, a table moving to the left, up or into the scanner (from the observer's point of view) will increase the 1st, 2nd and 3rd value in the array respectively. The origin is defined by the image affine.

#### 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.

### Institution information

Key name	Requirement Level	Data type	Description
InstitutionName	RECOMMENDED	<a href="#">string</a>	The name of the institution in charge of the equipment that produced the measurements. Corresponds to <a href="#">DICOM Tag 0008, 0080</a> InstitutionName.
InstitutionAddress	RECOMMENDED	<a href="#">string</a>	The address of the institution in charge of the equipment that produced the measurements. Corresponds to <a href="#">DICOM Tag 0008, 0081</a> InstitutionAddress.
InstitutionalDepartmentName	RECOMMENDED	<a href="#">string</a>	The department in the institution in charge of the equipment that produced the measurements. Corresponds to <a href="#">DICOM Tag 0008, 1040</a> Institutional Department Name.

### Sequence Specifics

Key name	Requirement Level	Data type	Description
PulseSequenceType	RECOMMENDED	<a href="#">string</a>	A general description of the pulse sequence used for the scan. For example, "MPRAGE", "Gradient Echo EPI", "Spin Echo EPI", "Multiband gradient echo EPI".
ScanningSequence	RECOMMENDED	<a href="#">string</a> or <a href="#">array of strings</a>	Description of the type of data acquired. Corresponds to <a href="#">DICOM Tag 0018, 0020</a> Scanning Sequence. Corresponds to <a href="#">DICOM Tag 0018, 0020</a> Scanning Sequence.
SequenceVariant	RECOMMENDED	<a href="#">string</a> or <a href="#">array of strings</a>	Variant of the ScanningSequence. Corresponds to <a href="#">DICOM Tag 0018, 0021</a> Sequence Variant.

Key name	Requirement Level	Data type	Description
ScanOptions	OPTIONAL	string or array of strings	Parameters of ScanningSequence. Corresponds to <a href="#">DICOM Tag 0018, 0022 Scan Options</a> .
SequenceName	RECOMMENDED	string	Manufacturer's designation of the sequence name. Corresponds to <a href="#">DICOM Tag 0018, 0024 Sequence Name</a> .
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 NonlinearGradientCorrection 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 <a href="#">DICOM Tag 0018, 0023 MR Acquisition Type</a> . Must be one of: "1D", "2D", "3D".
MTState	OPTIONAL, but REQUIRED if the mt entity is present	boolean	Boolean stating whether the magnetization transfer pulse is applied. Corresponds to <a href="#">DICOM Tag 0018, 9020 Magnetization Transfer</a> . Must be one of: "true", "false".
MTOffsetFrequency	OPTIONAL	number	The frequency offset of the magnetization transfer pulse with respect to the central H1 Larmor frequency in Hertz (Hz).
MTPulseBandwidth	OPTIONAL	number	The excitation bandwidth of the magnetization transfer pulse in Hertz (Hz).
MTNumberOfPulses	OPTIONAL	number	The number of magnetization transfer RF pulses applied before the readout.

Key name	Requirement Level	Data type	Description
MTPulseShape	OPTIONAL	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 "SINGGAUSS" refers to a sinc pulse with a Gaussian window. Must be one of: "HARD", "GAUSSIAN", "GAUSSHANN", "SINC", "SINCHANN", "SINGGAUSS", "FERMI".
MTPulseDuration	OPTIONAL	number	Duration of the magnetization transfer RF pulse in seconds.
NumberShots	OPTIONAL, but REQUIRED for some qMRI sequences	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 in the qMRI appendix for corresponding calculations.
SpoilingState	OPTIONAL	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	OPTIONAL	string	Specifies which spoiling method(s) are used by a spoiled sequence. Must be one of: "RF", "GRADIENT", "COMBINED".
SpoilingRFPhaseIncrement	OPTIONAL	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.

Key name	Requirement Level	Data type	Description
SpoilingGradientMoment	OPTIONAL	<a href="#">number</a>	Zeroth moment of the spoiler gradient lobe in millitesla times second per meter (mT.s/m).
SpoilingGradientDuration	OPTIONAL	<a href="#">number</a>	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.
WaterSuppression	OPTIONAL	<a href="#">boolean</a>	Boolean indicating whether water suppression was used prior to acquisition. Must be one of: "true", "false".
WaterSuppressionTechnique	OPTIONAL	<a href="#">string</a>	The name of the pulse sequence used for water suppression (for example, "CHESS", "VAPOR").
B0ShimmingTechnique	OPTIONAL	<a href="#">string</a>	The technique used to shim the B0 field (for example, "Dynamic shim updating" or "FASTMAP").
B1ShimmingTechnique	OPTIONAL	<a href="#">string</a>	The technique used to shim the B1 field (for example, "Simple phase align" or "Pre-saturated TurboFLASH").

### In- and Out-of-Plane Spatial Encoding

Key name	Requirement Level	Data type	Description
ParallelReductionFactorInPlane	OPTIONAL, but RECOMMENDED if <code>ParallelAcquisitionTechnique</code> is defined	<a href="#">number</a>	The parallel imaging (for instance, GRAPPA) factor in plane. 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 <a href="#">DICOM Tag 0018, 9069</a> <code>Parallel Reduction Factor In-plane</code> .

Key name	Requirement Level	Data type	Description
ParallelReductionFactorOutOfPlane	OPTIONAL, but RECOMMENDED if ParallelAcquisitionTechnique is defined	number	<p>The parallel imaging (for instance, GRAPPA) factor in the second phase encoding dimension of 3D sequences. Use the denominator of the fraction of k-space encoded in the second phase encoding dimension. For example, 2 means half of k-space is encoded. Will typically be 1 for 2D sequences, as each slice in a 2D acquisition is usually fully encoded.</p> <p>ParallelReductionFactorOutOfPlane should not be confused with MultibandAccelerationFactor, as they imply different methods of accelerating the acquisition. Corresponds to <a href="#">DICOM Tag 0018, 9155 Parallel Reduction Factor out-of-plane</a>.</p>
ParallelAcquisitionTechnique	OPTIONAL	string	<p>The type of parallel imaging used (for example "GRAPPA", "SENSE"). Corresponds to <a href="#">DICOM Tag 0018, 9078 Parallel Acquisition Technique</a>.</p>
PartialFourier	OPTIONAL	number	<p>The fraction of partial Fourier information collected.</p>
PartialFourierDirection	OPTIONAL, but RECOMMENDED if PartialFourier is defined	string	<p>The direction where only partial Fourier information was collected. Corresponds to <a href="#">DICOM Tag 0018, 9036 Partial Fourier Direction</a>.</p>

Key name	Requirement Level	Data type	Description
EffectiveEchoSpacing	OPTIONAL, but RECOMMENDED if corresponding fieldmap data present	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. 2Must be a number greater than 0.
MixingTime	OPTIONAL, but REQUIRED for some qMRI sequences	number	In the context of a stimulated- and spin-echo 3D EPI sequence for B1+ mapping or a stimulated-echo MRS sequence, 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.

Key name	Requirement Level	Data type	Description
PhaseEncodingDirection	RECOMMENDED, but 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).	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", "i-", "j", "j-", "k", "k-".
TotalReadoutTime	RECOMMENDED, but REQUIRED if corresponding 'field/distortion' maps acquired with opposing phase encoding directions are present (see TotalReadoutTime)	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 $\text{EffectiveEchoSpacing} * (\text{ReconMatrixPE} - 1) / 3$

2Conveniently, for Siemens data, this value is easily obtained as  $1 / (\text{BWPPPE} * \text{ReconMatrixPE})$ , 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 [Acquiring and using field maps - LCNI](#) and [TotalReadoutTime - dcm\\_qa](#).

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.	<a href="#">number</a> or <a href="#">array</a> of <a href="#">numbers</a>	The echo time (TE) for the acquisition, specified in seconds. Corresponds to <a href="#">DICOM Tag 0018, 0081 Echo Time</a> (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 EchoTime where the value of this field is iterated using the EchoTime. 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 EchoTime or variable echo time fMRI sequences.
InversionTime	OPTIONAL, but REQUIRED if <code>inv</code> entity is present	<a href="#">number</a>	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 <a href="#">DICOM Tag 0018, 0082 Inversion Time</a> (please note that the DICOM term is in milliseconds not seconds). Must be a number greater than 0.

Key name	Requirement Level	Data type	Description
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).
AcquisitionDuration	OPTIONAL	number	Duration (in seconds) of scan acquisition, including all volumes for multi-volume scans. Corresponds to <a href="#">DICOM Tag 0018, 9073 Acquisition Duration</a> . Must be a number greater than 0.

Key name	Requirement Level	Data type	Description
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	OPTIONAL	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", "i-", "j", "j-", "k", "k-".

RF & Contrast

Key name	Requirement Level	Data type	Description
FlipAngle	RECOMMENDED, but REQUIRED if LookLocker is set to <b>true</b>	<a href="#">number</a> or <a href="#">array</a> of <a href="#">numbers</a>	Flip angle (FA) for the acquisition, specified in degrees. Corresponds to: <a href="#">DICOM Tag 0018, 1314 Flip Angle</a> . 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 FlipAngle where the value of this field is iterated using the FlipAngle. 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 FlipAngle or variable flip angle fMRI sequences.
NegativeContrast	OPTIONAL	<a href="#">boolean</a>	<b>true</b> or <b>false</b> 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: " <b>true</b> ", " <b>false</b> ".

---

## Slice Acceleration

Key name	Requirement Level	Data type	Description
MultibandAccelerationFactor	OPTIONAL	<a href="#">number</a>	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/` directory 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.

## Tissue description

Key name	Requirement Level	Data type	Description
BodyPart	OPTIONAL	string	Body part of the organ / body region scanned. Corresponds to <a href="#">DICOM Tag 0018, 0015</a> Body Part Examined.

Key name	Requirement Level	Data type	Description
BodyPartDetails	OPTIONAL	<a href="#">string</a>	Additional details about body part or location (for example: "corpus callosum").
BodyPartDetailsOntology	OPTIONAL	<a href="#">string</a>	BodyPartDetailsOntology of ontology used for BodyPartDetails (for example: "https://www.ebi.ac.uk/ols/ontologies/uberon").

## Deidentification information

Describes the mechanism or method used to modify or remove metadata and/or pixel data to protect the patient or participant's identity.

Key name	Requirement Level	Data type	Description
DeidentificationMethod	OPTIONAL	<a href="#">array of strings</a>	A description of the mechanism or method used to remove the Patient's identity. Corresponds to <a href="#">DICOM Tag 0012, 0063 De-identification Method</a> . Corresponds to <a href="#">DICOM Tag 0012, 0063 De-identification Method</a> .
DeidentificationMethodCodeSequence	OPTIONAL	<a href="#">array of objects</a>	A sequence of code objects describing the mechanism or method use to remove the Patient's identity. Corresponds to <a href="#">DICOM Tag 0012, 0064 De-identification Method Code Sequence</a> . Corresponds to <a href="#">DICOM Tag 0012, 0064 De-identification Method Code Sequence</a> .

Each object in the `DeidentificationMethodCodeSequence` array includes the following RECOMMENDED keys:

Key name	Requirement Level	Data type	Description
CodeValue	RECOMMENDED	<a href="#">string</a>	An identifier that is unambiguous within the Coding Scheme denoted by Coding Scheme Designator and Coding Scheme Version. Corresponds to <a href="#">DICOM Tag 0008, 0100 Code Value</a> .



Key name	Requirement Level	Data type	Description
CodeMeaning	RECOMMENDED	string	Text that has meaning to a human and conveys the meaning of the term Corresponds to <a href="#">DICOM Tag 0008, 0104 Code Meaning</a> .
CodingSchemeDesignator	RECOMMENDED	string	The identifier of the coding scheme in which the coded entry is defined. Corresponds to <a href="#">DICOM Tag 0008, 0102 Coding Scheme Designator</a> .
CodingSchemeVersion	RECOMMENDED	string	An identifier of the version of the coding scheme if necessary to resolve ambiguity. Corresponds to <a href="#">DICOM Tag 0008, 0103 Coding Scheme Version</a> .

## Anatomy imaging data

Anatomy MRI sequences measure static, structural features of the brain.

This datatype is divided into two groups: non-parametric and parametric.

Non-parametric structural images have an arbitrary scale. For example, T1w data are T1-weighted, but the values do not correspond to actual T1 value estimates.

Parametric structural imaging, on the other hand, use a non-arbitrary scale. For example, a T1map file contains T1 value estimates, in seconds.

### Non-parametric structural MR images

Template:

```
sub-<label>/
  [ses-<label>/]
    anat/
      sub-<label>[_ses-<label>][_task-<label>][_acq-<label>][_ce-<label>][_rec-<label>][_run-<index>][_echo-<index>][_part-<mag|phase|real|imag>]
      sub-<label>[_ses-<label>][_task-<label>][_acq-<label>][_ce-<label>][_rec-<label>][_run-<index>][_echo-<index>][_part-<mag|phase|real|imag>]
      sub-<label>[_ses-<label>][_task-<label>][_acq-<label>][_ce-<label>][_rec-<label>][_run-<index>][_chunk-<index>]_UNIT1.json
      sub-<label>[_ses-<label>][_task-<label>][_acq-<label>][_ce-<label>][_rec-<label>][_run-<index>][_chunk-<index>]_UNIT1.nii.gz
```

Legend:

- **<matches>** is a placeholder to denote an arbitrary (and valid) sequence of entities and labels at the beginning of the filename (only BIDS "raw").
- **<source-entities>** is a placeholder to denote an arbitrary sequence of entities and labels at the beginning of the filename matching a source file from which the file derives (only BIDS-Derivatives).
- Filename entities or directories between square brackets (for example, `[_ses-<label>]`) are OPTIONAL.

- Some entities may only allow specific values, in which case those values are listed in `<>`, separated by `|`.
- `_<suffix>` means that there are several ( $>6$ ) valid suffixes for this filename pattern.
- `.<extension>` means that there are several ( $>6$ ) valid extensions for this file type.
- `[.gz]` means that both the unzipped and gzipped versions of the extension are valid.

Currently supported non-parametric structural MR images include the following:

Name	suffix	Description
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.
PD and T2 weighted image	PDT2	In arbitrary units (arbitrary). A two-volume 4D image, where the volumes are, respectively, PDw and T2w images acquired simultaneously. If separated into 3D volumes, the PDw and T2w suffixes SHOULD be used instead, and an acquisition entity MAY be used to distinguish the images from others with the same suffix, for example, <code>acq-PDT2_PDw.nii</code> and <code>acq-PDT2_T2w.nii</code> .
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. This contrast is achieved at short echo times and long repetition times; for gradient echo, this weighting is also possible with a short TR ( $TR \ll T1$ ) and a small flip angle.
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).

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.
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.
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 UNIT1 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.
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.

The `part-<label>` entity 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** entity MAY be omitted.

## Parametric structural MR images

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

Template:

```
sub-<label>/  
  [ses-<label>]/  
    anat/  
      sub-<label>[_ses-<label>][_task-<label>][_acq-<label>][_ce-<label>][_rec-<label>][_run-<index>][_chunk-<index>][_suffix>.json  
      sub-<label>[_ses-<label>][_task-<label>][_acq-<label>][_ce-<label>][_rec-<label>][_run-<index>][_chunk-<index>][_suffix>.nii[.gz]
```

Legend:

- **<matches>** is a placeholder to denote an arbitrary (and valid) sequence of entities and labels at the beginning of the filename (only BIDS "raw").
- **<source-entities>** is a placeholder to denote an arbitrary sequence of entities and labels at the beginning of the filename matching a source file from which the file derives (only BIDS-Derivatives).
- Filename entities or directories between square brackets (for example, `[_ses-<label>]`) are OPTIONAL.
- Some entities may only allow specific values, in which case those values are listed in `<>`, separated by `|`.
- `[_suffix>` means that there are several (>6) valid suffixes for this filename pattern.
- `[_extension>` means that there are several (>6) valid extensions for this file type.
- `[.gz]` means that both the unzipped and gzipped versions of the extension are valid.

Parametric images listed in the table below 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 example, MPM, MP2RAGE, and MTR).

Currently supported parametric maps include:

Name	suffix	Description
Quantitative susceptibility map (QSM)	Chimap	In parts per million (ppm). QSM allows for determining the underlying magnetic susceptibility of tissue (Chi) ( <a href="#">Wang &amp; Liu, 2014</a> ). Chi maps are REQUIRED to use this suffix regardless of the method used to generate them.
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).
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%.
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.
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.
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%.
Proton density image	PDmap	In arbitrary units (arbitrary). PD maps are REQUIRED to use this suffix regardless of the method used to generate them.
Longitudinal relaxation rate image	R1map	In seconds <sup>-1</sup> (1/s). R1 maps ( $R1 = 1/T1$ ) are REQUIRED to use this suffix regardless of the method used to generate them.
True transverse relaxation rate image	R2map	In seconds <sup>-1</sup> (1/s). R2 maps ( $R2 = 1/T2$ ) are REQUIRED to use this suffix regardless of the method used to generate them.
Observed transverse relaxation rate image	R2starmap	In seconds <sup>-1</sup> (1/s). R2-star maps ( $R2star = 1/T2star$ ) are REQUIRED to use this suffix regardless of the method used to generate them.

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 $\text{Amplitude}_{\text{effective}} = \text{B1-intensity} * \text{Amplitude}_{\text{ideal}}$ .
Projected baseline signal amplitude (S0) image	S0map	In arbitrary units (arbitrary). This represents a model-based estimate of signal intensity in the absence of the contrast under investigation. For a multi-echo sequence (for example, multi-echo spin echo T2 relaxometry or multi-echo fMRI), S0 maps index the baseline signal at a hypothetical echo time of zero (that is, in the absence of any T2 or T2-star 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, <a href="#">the tedana documentation</a> . S0 maps are RECOMMENDED to use this suffix if derived from an ME-fMRI dataset. For a diffusion-weighted sequence, S0 maps represent the model-based estimate of the signal intensity in the absence of any diffusion weighting; in other words, the image intensity at $b=0$ as estimated by a diffusion model fit.
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 <a href="#">this interactive book on T1 mapping</a> for further reading on T1-mapping.
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.
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.
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.

Name	suffix	Description
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 $\text{FlipAngle}_{\text{effective}} = \text{B1+intensity} * \text{FlipAngle}_{\text{nominal}}$ .

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.

Defacing masks

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>` entity corresponds to modality suffix, such as `T1w` or `inplaneT1`, referenced by the defacemask image. For example, `sub-01_mod-T1w_defacemask.nii.gz`.

Template:

```
sub-<label>/
  [ses-<label>/]
    anat/
      sub-<label>[_ses-<label>][_task-<label>][_acq-<label>][_ce-<label>][_rec-<label>][_run-<index>][_mod-<label>][_chunk-<index>]_defacemask.js
      sub-<label>[_ses-<label>][_task-<label>][_acq-<label>][_ce-<label>][_rec-<label>][_run-<index>][_mod-<label>][_chunk-<index>]_defacemask.ni
```

Legend:

- `<matches>` is a placeholder to denote an arbitrary (and valid) sequence of entities and labels at the beginning of the filename (only BIDS "raw").
- `<source-entities>` is a placeholder to denote an arbitrary sequence of entities and labels at the beginning of the filename matching a source file from which the file derives (only BIDS-Derivatives).
- Filename entities or directories between square brackets (for example, `[_ses-<label>]`) are OPTIONAL.
- Some entities may only allow specific values, in which case those values are listed in `<>`, separated by `|`.
- `_<suffix>` means that there are several (>6) valid suffixes for this filename pattern.
- `.<extension>` means that there are several (>6) valid extensions for this file type.
- `[.gz]` means that both the unzipped and gzipped versions of the extension are valid.

Task metadata for anatomical scans

The OPTIONAL `task-<label>` entity can be used in order to allow tasks during structural MR acquisitions, for example pre-described motion paradigms such as nodding, to be described.

Key name	Requirement Level	Data type	Description
TaskName	RECOMMENDED if <code>task</code> entity is present	<a href="#">string</a>	Name of the task. No two tasks should have the same name. The task label included in the filename MAY be derived from this "TaskName" field by removing all non-alphanumeric or + characters (that is, all except those matching <code>[0-9a-zA-Z+]</code> ), and potentially replacing spaces with + to ease readability. For example "TaskName" "faces n-back" or "head nodding" could correspond to task labels <code>faces+n+back</code> or <code>facesnback</code> and <code>head+nodding</code> or <code>headnodding</code> , respectively.
TaskDescription	RECOMMENDED if <code>task</code> entity is present	<a href="#">string</a>	Longer description of the task.
Instructions	RECOMMENDED if <code>task</code> entity is present	<a href="#">string</a>	Text of the instructions given to participants before the recording.

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	<a href="#">string</a>	Active ingredient of agent. Corresponds to <a href="#">DICOM Tag 0018, 1048 Contrast/Bolus Ingredient</a> . Must be one of: "IODINE", "GADOLINIUM", "CARBON DIOXIDE", "BARIUM", "XENON", "UNKNOWN", "NONE".



Key name	Requirement Level	Data type	Description
RepetitionTimeExcitation	OPTIONAL	number	The interval, in seconds, between two successive excitations. <a href="#">DICOM Tag 0018, 0080</a> best refers to this parameter. This field may be used together with the "RepetitionTimePreparation" for certain use cases, such as <a href="#">MP2RAGE</a> . 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 RepetitionTimeExcitation 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 RepetitionTimePreparation.

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
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.
T2* image	T2star	Ambiguous, may refer to a parametric image or to a conventional image. Change: Replaced by T2starw or T2starmap.

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	phase. Phase information associated with magnitude information stored in BOLD contrast. This suffix should be replaced by the phase in conjunction with the <b>bold</b> suffix.

Template:

```
sub-<label>/
  [ses-<label>/]
    func/
      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>][_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>][_mod-<label>][_echo-<index>][_p
sub-<label>[_ses-<label>]_task-<label>[_acq-<label>][_ce-<label>][_rec-<label>][_dir-<label>][_run-<index>][_mod-<label>][_echo-<index>][_p
sub-<label>[_ses-<label>]_task-<label>[_acq-<label>][_ce-<label>][_rec-<label>][_dir-<label>][_run-<index>][_echo-<index>][_chunk-<index>]
sub-<label>[_ses-<label>]_task-<label>[_acq-<label>][_ce-<label>][_rec-<label>][_dir-<label>][_run-<index>][_echo-<index>][_chunk-<index>]
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>]_physioevent
sub-<label>[_ses-<label>]_task-<label>[_acq-<label>][_ce-<label>][_rec-<label>][_dir-<label>][_run-<index>][_recording-<label>]_physioevent
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

```

Legend:

- <matches> is a placeholder to denote an arbitrary (and valid) sequence of entities and labels at the beginning of the filename (only BIDS "raw").
- <source-entities> is a placeholder to denote an arbitrary sequence of entities and labels at the beginning of the filename matching a source file from which the file derives (only BIDS-Derivatives).
- Filename entities or directories between square brackets (for example, [\_ses-<label>]) are OPTIONAL.
- Some entities may only allow specific values, in which case those values are listed in <>, separated by |.
- \_<suffix> means that there are several (>6) valid suffixes for this filename pattern.
- .<extension> means that there are several (>6) valid extensions for this file type.
- [.gz] means that both the unzipped and gzipped versions of the extension are valid.

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 with the **sbref** suffix (for example, **sub-control01\_task-nback\_sbref.nii.gz**).

Multi-echo data MUST be split into one file per echo using the **echo-<index>** entity. 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>` entity.

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 mutually exclusive with VolumeTiming	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 <a href="#">DICOM Tag 0020, 0110</a> : the "time delta between images in a dynamic of functional set of images" but may also be found in <a href="#">DICOM Tag 0018, 0080</a> : "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 mutually exclusive with RepetitionTime	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 series. The list must have the same length as the series, and the values must be non-negative and monotonically increasing. This field is mutually exclusive with "RepetitionTime". This field is mutually exclusive with "DelayTime". If defined, this requires acquisition time (TA) be defined via either "SliceTiming" or "FrameAcquisitionDuration".

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 filename MAY be derived from this "TaskName" field by removing all non-alphanumeric or + characters (that is, all except those matching [0-9a-zA-Z+]), and potentially replacing spaces with + to ease readability. For example "TaskName" "faces n-back" or "head nodding" could correspond to task labels faces+n+back or facesnback and head+nodding or headnodding, respectively. 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	OPTIONAL	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 <code>events.tsv</code> file should always refer to the beginning of the acquisition of the first volume in the corresponding imaging file - independent of the value of <code>"NumberOfVolumesDiscardedByScanner"</code> field. Must be a number greater than or equal to 0.
NumberOfVolumesDiscardedByUser	OPTIONAL	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 <code>events.tsv</code> file should always refer to the beginning of the acquisition of the first volume in the corresponding imaging file - independent of the value of <code>"NumberOfVolumesDiscardedByUser"</code> field. Must be a number greater than or equal to 0.

Key name	Requirement Level	Data type	Description
DelayTime	OPTIONAL	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 <code>lDelayTimeInTR</code> . This field is REQUIRED for sparse sequences using the <code>"RepetitionTime"</code> field that do not have the <code>"SliceTiming"</code> field set to allow for accurate calculation of "acquisition time". This field is mutually exclusive with <code>"VolumeTiming"</code> .
FrameAcquisitionDuration	OPTIONAL, but REQUIRED for sequences that are described with the <code>VolumeTiming</code> field and that do not have the <code>SliceTiming</code> field set to allow for accurate calculation of "acquisition time"	number	Duration (in seconds) of volume acquisition. Corresponds to DICOM Tag 0018, 9220 <code>Frame Acquisition Duration</code> . Must be a number greater than 0.
DelayAfterTrigger	OPTIONAL	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 <code>"NumberOfVolumesDiscardedByScanner"</code> or <code>"NumberOfVolumesDiscardedByUser"</code> , as the delay precedes the acquisition.
AcquisitionDuration	AcquisitionDuration	number	Duration (in seconds) of scan acquisition, including all volumes for multi-volume scans. Corresponds to <a href="#">DICOM Tag 0018, 9073</a> <code>Acquisition Duration</code> . This field was previously used to indicate volume acquisition duration for BOLD data. The <code>FrameAcquisitionDuration</code> field should be used instead. Must be a number greater than 0.



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	FrameAcquisitionDuratic	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	<a href="#">string</a>	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	<a href="#">string</a>	Longer description of the task.
CogAtlasID	RECOMMENDED	<a href="#">string</a>	CogAtlasID of the corresponding <a href="#">Cognitive Atlas</a> Task term.
CogPOID	RECOMMENDED	<a href="#">string</a>	CogPOID of the corresponding <a href="#">CogPO</a> term.

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

Example:

```
sub-01/  
  func/  
    sub-01_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"]
}
```

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.

Additionally, the following suffixes are used for scanner-generated images:

Name	suffix	Description
Apparent diffusion coefficient (ADC)	ADC	Apparent diffusion coefficient (ADC) map
Fractional Anisotropy image	FA	Scanner-generated derivative parametric map reflecting the anisotropy of the diffusion tensor

Name	suffix	Description
Projected baseline signal amplitude (S0) image	S0map	In arbitrary units (arbitrary). This represents a model-based estimate of signal intensity in the absence of the contrast under investigation. For a multi-echo sequence (for example, multi-echo spin echo T2 relaxometry or multi-echo fMRI), S0 maps index the baseline signal at a hypothetical echo time of zero (that is, in the absence of any T2 or T2-star 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, <a href="#">the tedana documentation</a> . S0 maps are RECOMMENDED to use this suffix if derived from an ME-fMRI dataset. For a diffusion-weighted sequence, S0 maps represent the model-based estimate of the signal intensity in the absence of any diffusion weighting; in other words, the image intensity at b=0 as estimated by a diffusion model fit.
Colored Fractional Anisotropy image	colFA	Scanner-derived parametric map encoding both the anisotropy and principal direction of the diffusion tensor. Image intensity is proportional to the Fractional Anisotropy (FA) measure; image color is determined by the principal eigenvector of the diffusion tensor, where red encodes the magnitude of the left-right component of that orientation, with green and blue similarly encoding the anterior-posterior and inferior-superior components respectively.
Exponential ADC	expADC	Exponential ADC / Attenuation Coefficient / Attenuation Factor map, as the ratio of trace-weighted to non-diffusion-weighted image intensity
Trace-weighted diffusion image	trace	Trace-weighted image, as the mean intensity of diffusion-weighted images

Template:

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

```

sub-<label>[_ses-<label>][_acq-<label>][_rec-<label>][_dir-<label>][_run-<index>][_part-<mag|phase|real|imag>][_chunk-<index>]_dwi.bval
sub-<label>[_ses-<label>][_acq-<label>][_rec-<label>][_dir-<label>][_run-<index>][_part-<mag|phase|real|imag>][_chunk-<index>]_dwi.bvec
sub-<label>[_ses-<label>][_acq-<label>][_rec-<label>][_dir-<label>][_run-<index>][_part-<mag|phase|real|imag>][_chunk-<index>]_dwi.json
sub-<label>[_ses-<label>][_acq-<label>][_rec-<label>][_dir-<label>][_run-<index>][_part-<mag|phase|real|imag>][_chunk-<index>]_dwi.nii[.gz]
sub-<label>[_ses-<label>][_acq-<label>][_rec-<label>][_dir-<label>][_run-<index>][_part-<mag|phase|real|imag>][_chunk-<index>]_sbref.json
sub-<label>[_ses-<label>][_acq-<label>][_rec-<label>][_dir-<label>][_run-<index>][_part-<mag|phase|real|imag>][_chunk-<index>]_sbref.nii[.gz]
sub-<label>[_ses-<label>][_acq-<label>][_rec-<label>][_dir-<label>][_run-<index>][_chunk-<index>]_<suffix>.json
sub-<label>[_ses-<label>][_acq-<label>][_rec-<label>][_dir-<label>][_run-<index>][_chunk-<index>]_<suffix>.nii[.gz]
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>]_physioevents.json
sub-<label>[_ses-<label>][_acq-<label>][_rec-<label>][_dir-<label>][_run-<index>][_recording-<label>]_physioevents.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

```

Legend:

- `<matches>` is a placeholder to denote an arbitrary (and valid) sequence of entities and labels at the beginning of the filename (only BIDS "raw").
- `<source-entities>` is a placeholder to denote an arbitrary sequence of entities and labels at the beginning of the filename matching a source file from which the file derives (only BIDS-Derivatives).
- Filename entities or directories between square brackets (for example, `[_ses-<label>]`) are OPTIONAL.
- Some entities may only allow specific values, in which case those values are listed in `<>`, separated by `|`.
- `_<suffix>` means that there are several ( $>6$ ) valid suffixes for this filename pattern.
- `.<extension>` means that there are several ( $>6$ ) valid extensions for this file type.
- `[.gz]` means that both the unzipped and gzipped versions of the extension are valid.

The `run-<index>` entity is RECOMMENDED to encode the splits of multipart DWI scans (see below for more information on multipart DWI schemes).

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>` entity 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.

Scanner-generated derivative images, such as trace-weighted, ADC, exponentiated ADC, fractional anisotropy (FA and `colFA`), and estimated unweighted signal intensity, MAY be included using the `trace`, `ADC`, `expADC`, `FA`, `colFA` and `S0map` suffixes, respectively. If `trace`, `ADC`, `expADC`, `FA`, `colFA`, or `S0` volume filenames match a diffusion series with all applicable entities, such volumes SHOULD have been computed from that series. Otherwise, some entity, such as `acq-<label>`, SHOULD be used to indicate that the files are unrelated.

## 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. Across these three rows, each column encodes three elements of a 3-vector for the corresponding image volume; each vector **MUST** be either of unit norm, or optionally the vector `[0.0,0.0,0.0]` for non-diffusion-weighted (also called b=0 or low-b) volumes. These values are to be interpreted as cosine values with respect to the image axis orientations as defined by the corresponding NIfTI image header transformation; unless the image axes defined in the corresponding NIfTI image header form a right-handed coordinate system (that is, the 3x3 matrix of direction cosines has a positive determinant), in which case the sign of the first element of each 3-vector must be inverted for this interpretation to be valid. Note that this definition of orientations with respect to the NIfTI image axes is not equivalent to the DICOM convention, where orientations are instead defined with respect to the scanner device's coordinate system (see [Coordinate systems](#)).

The `[_]dwi.bval` file contains the b-values (in s/mm<sup>2</sup>) corresponding to the volumes in the relevant NIfTI file, with 0 designating b=0 volumes; space-delimited.

Examples of `[*]dwi.bvec` and `[*]dwi.bval` files, corresponding to a NIfTI image with 6 volumes with the first two volumes having no diffusion sensitization:

- `[*_]dwi.bvec:` Text 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
- `[_]dwi.bval:` Text 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  $\approx 160$  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	OPTIONAL	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>` entity, 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

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. Must be one of: "i", "i-", "j", "j-", "k", "k-".
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).

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>][_echo-<index>][_part-<mag|phase|real|imag>]_asl.json
      sub-<label>[_ses-<label>][_acq-<label>][_rec-<label>][_dir-<label>][_run-<index>][_echo-<index>][_part-<mag|phase|real|imag>]_asl.nii.gz
      sub-<label>[_ses-<label>][_acq-<label>][_rec-<label>][_dir-<label>][_run-<index>][_echo-<index>][_part-<mag|phase|real|imag>]_m0scan.json
      sub-<label>[_ses-<label>][_acq-<label>][_rec-<label>][_dir-<label>][_run-<index>][_echo-<index>][_part-<mag|phase|real|imag>]_m0scan.nii.gz
      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>][_run-<index>]_asllabeling.png
      sub-<label>[_ses-<label>][_acq-<label>][_rec-<label>][_run-<index>]_asllabeling.tif
      sub-<label>[_ses-<label>][_acq-<label>][_rec-<label>][_dir-<label>][_run-<index>][_mod-<label>][_echo-<index>][_part-<mag|phase|real|imag>]
      sub-<label>[_ses-<label>][_acq-<label>][_rec-<label>][_dir-<label>][_run-<index>][_mod-<label>][_echo-<index>][_part-<mag|phase|real|imag>]
      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>]_physioevents.json
      sub-<label>[_ses-<label>][_acq-<label>][_rec-<label>][_dir-<label>][_run-<index>][_recording-<label>]_physioevents.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
```

Legend:

- **<matches>** is a placeholder to denote an arbitrary (and valid) sequence of entities and labels at the beginning of the filename (only BIDS "raw").
- **<source-entities>** is a placeholder to denote an arbitrary sequence of entities and labels at the beginning of the filename matching a source file from which the file derives (only BIDS-Derivatives).
- Filename entities or directories between square brackets (for example, `[_ses-<label>]`) are **OPTIONAL**.
- Some entities may only allow specific values, in which case those values are listed in `<>`, separated by `|`.
- **\_<suffix>** means that there are several (>6) valid suffixes for this filename pattern.
- **.<extension>** means that there are several (>6) valid extensions for this file type.
- **[.gz]** means that both the unzipped and gzipped versions of the extension are valid.

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 the ASL Appendix for more information on `control` and `label`.

volume_type	Definition
<code>control</code>	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.
<code>label</code>	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.
<code>m0scan</code>	The M0 image is a calibration image, used to estimate the equilibrium magnetization of blood.
<code>deltam</code>	The deltaM image is a perfusion-weighted image, obtained by the subtraction of <code>control</code> - <code>label</code> .
<code>cbf</code>	The cerebral blood flow (CBF) image is produced by dividing the deltaM by the M0, quantified into mL/100g/min (See also <a href="https://doi.org/10.1002/mrm.25197">doi:10.1002/mrm.25197</a> ).
<code>noRF</code>	No radio frequency excitation (noRF) images are produced by disabling the radio frequency excitation, while maintaining all other parameters from the associated scan.
<code>n/a</code>	In some cases, there may be volume types that are not yet supported by BIDS, or which cannot be used by tools.

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 the ASL Appendix 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.

**\*\_asllabeling.\***

A deidentified screenshot of the planning of the labeling slab/plane with respect to the imaging slab or slices. This screenshot is based on DICOM macro C.8.13.5.14. See `LabelingLocationDescription` for more details.

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 the ASL Appendix 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".
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".

Key name	Requirement Level	Data type	Description
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.
VascularCrushing	RECOMMENDED	boolean	Boolean indicating if Vascular Crushing is used. Corresponds to <a href="#">DICOM Tag 0018, 9259</a> 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 field 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.
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 <a href="#">DICOM Tag 0018, 9255</a> ASL Slab Orientation.

Key name	Requirement Level	Data type	Description
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 <b>LabelingOrientation</b> or <b>LabelingDistance</b> . May include a link to a deidentified screenshot of the planning of the labeling slab/plane with respect to the imaging slab or slices <b>*_asllabeling.*</b> . 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".
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.
M0Estimate	OPTIONAL, but REQUIRED if M0Type is 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, but 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.

Key name	Requirement Level	Data type	Description
BackgroundSuppressionPulseTime	OPTIONAL, but 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.
VascularCrushingVENC	OPTIONAL, but 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 <a href="#">DICOM Tag 0018, 925A</a> ASL Crusher Flow Limit.

## (P)CASL-specific metadata fields

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

Key name	Requirement Level	Data type	Description
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".

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 <a href="#">DICOM Tag 0018, 9258 ASL Pulse Train Duration</a> .
LabelingPulseAverageGradient	RECOMMENDED	number	The average labeling gradient, in milliteslas per meter. Must be a number greater than 0.
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.

Key name	Requirement Level	Data type	Description
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 the ASL Appendix 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 <a href="#">DICOM Tag 0018, 925C ASL Bolus Cut-off Flag</a> . Must be one of: "true", "false".
PASLType	RECOMMENDED	string	Type of the labeling pulse of the PASL labeling, for example "FAIR", "EPISTAR", or "PICORE".
LabelingSlabThickness	RECOMMENDED	number	Thickness of the labeling slab in millimeters. For non-selective FAIR a zero is entered. Corresponds to <a href="#">DICOM Tag 0018, 9254 ASL Slab Thickness</a> . Must be a number greater than 0.

Key name	Requirement Level	Data type	Description
BolusCutOffDelayTime	OPTIONAL, but 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 <a href="#">DICOM Tag 0018, 925F</a> ASL Bolus Cut-off Delay Time.
BolusCutOffTechnique	OPTIONAL, but REQUIRED if BolusCutOffFlag is true	string	Name of the technique used, for example "Q2TIPS", "QUIPSS", "QUIPSSII". Corresponds to <a href="#">DICOM Tag 0018, 925E</a> 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	The paths to files for which the associated file is intended to be used. Contains one or more IntendedFor. Using forward-slash separated paths relative to the participant subdirectory is IntendedFor. This is used to refer to the ASL time series for which the *_m0scan.nii.gz is intended.



Key name	Requirement Level	Data type	Description
AcquisitionVoxelSize	RECOMMENDED	array of numbers	An array of numbers with a length of 3, in millimeters. This field 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 the ASL Appendix 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 inhomogeneities in the magnetic field can come in different forms. These "fieldmaps" can characterize different magnetic fields in the scanner, including the main static magnetic field (B0) and the transmit (B1+) and receive (B1-) components of the radiofrequency magnetic field (B1).

B0 fieldmaps

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
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.
Fieldmap	fieldmap	Some MR schemes such as spiral-echo imaging (SEI) sequences are able to directly provide maps of the B0 field inhomogeneity.
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 <b>phase1</b> from the <b>phase2</b> map and generate a unique <b>phasediff</b> file. For instance, this is a common output for the built-in fieldmap sequence of Siemens scanners.

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	The paths to files for which the associated file is intended to be used. Contains one or more IntendedFor. Using forward-slash separated paths relative to the participant subdirectory is IntendedFor. 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": [
    "bids::sub-01/ses-pre/func/sub-01_ses-pre_task-motor_run-1_bold.nii.gz",
    "bids::sub-01/ses-pre/func/sub-01_ses-pre_task-motor_run-2_bold.nii.gz"
  ]
}
```

Types of B0 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>][_chunk-<index>]_magnitude1.json
      sub-<label>[_ses-<label>][_acq-<label>][_run-<index>][_chunk-<index>]_magnitude1.nii[.gz]
```

```
sub-<label>[_ses-<label>][_acq-<label>][_run-<index>][_chunk-<index>]_magnitude2.json
sub-<label>[_ses-<label>][_acq-<label>][_run-<index>][_chunk-<index>]_magnitude2.nii.gz]
sub-<label>[_ses-<label>][_acq-<label>][_run-<index>][_chunk-<index>]_phasediff.json
sub-<label>[_ses-<label>][_acq-<label>][_run-<index>][_chunk-<index>]_phasediff.nii.gz]
```

Legend:

- <matches> is a placeholder to denote an arbitrary (and valid) sequence of entities and labels at the beginning of the filename (only BIDS "raw").
- <source-entities> is a placeholder to denote an arbitrary sequence of entities and labels at the beginning of the filename matching a source file from which the file derives (only BIDS-Derivatives).
- Filename entities or directories between square brackets (for example, [\_ses-<label>]) are OPTIONAL.
- Some entities may only allow specific values, in which case those values are listed in <>, separated by |.
- \_<suffix> means that there are several (>6) valid suffixes for this filename pattern.
- .<extension> means that there are several (>6) valid extensions for this file type.
- [.gz] means that both the unzipped and gzipped versions of the extension are valid.

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

Legend:

- <matches> is a placeholder to denote an arbitrary (and valid) sequence of entities and labels at the beginning of the filename (only BIDS "raw").
- <source-entities> is a placeholder to denote an arbitrary sequence of entities and labels at the beginning of the filename matching a source file from which the file derives (only BIDS-Derivatives).
- Filename entities or directories between square brackets (for example, [\_ses-<label>]) are OPTIONAL.
- Some entities may only allow specific values, in which case those values are listed in <>, separated by |.
- \_<suffix> means that there are several (>6) valid suffixes for this filename pattern.
- .<extension> means that there are several (>6) valid extensions for this file type.
- [.gz] means that both the unzipped and gzipped versions of the extension are valid.

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 sidcar JSON file to specify its corresponding EchoTime. For example, sub-<label>[\_ses-<label>][\_acq-<label>][\_run-<index>]\_phase2.json 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>][_chunk-<index>]_fieldmap.json
      sub-<label>[_ses-<label>][_acq-<label>][_run-<index>][_chunk-<index>]_fieldmap.nii.gz]
      sub-<label>[_ses-<label>][_acq-<label>][_run-<index>][_chunk-<index>]_magnitude.json
      sub-<label>[_ses-<label>][_acq-<label>][_run-<index>][_chunk-<index>]_magnitude.nii.gz]
```

Legend:

- <matches> is a placeholder to denote an arbitrary (and valid) sequence of entities and labels at the beginning of the filename (only BIDS "raw").
- <source-entities> is a placeholder to denote an arbitrary sequence of entities and labels at the beginning of the filename matching a source file from which the file derives (only BIDS-Derivatives).
- Filename entities or directories between square brackets (for example, [\_ses-<label>]) are OPTIONAL.
- Some entities may only allow specific values, in which case those values are listed in <>, separated by |.
- \_<suffix> means that there are several (>6) valid suffixes for this filename pattern.
- .<extension> means that there are several (>6) valid extensions for this file type.
- [.gz] means that both the unzipped and gzipped versions of the extension are valid.

Required fields:

Key name	Requirement Level	Data type	Description
Units	REQUIRED	string	Measurement units for the associated variable. 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": "bids::sub-01/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. Some 4D scans intended for correcting DWIs may have accompanying \*\_epi.bval and \*\_epi.bvec files. Examples of software tools using these kinds of images are FSL TOPUP and AFNI 3dqwarp.

Template:

```
sub-<label>/
  [ses-<label>/]
    fmap/
      sub-<label>[_ses-<label>][_acq-<label>][_ce-<label>][_rec-<label>][_dir-<label>][_run-<index>][_part-<mag|phase|real|imag>][_chunk-<index>]
      sub-<label>[_ses-<label>][_acq-<label>][_ce-<label>][_rec-<label>][_dir-<label>][_run-<index>][_part-<mag|phase|real|imag>][_chunk-<index>]
      sub-<label>[_ses-<label>][_acq-<label>][_ce-<label>][_rec-<label>][_dir-<label>][_run-<index>][_part-<mag|phase|real|imag>][_chunk-<index>]
      sub-<label>[_ses-<label>][_acq-<label>][_ce-<label>][_rec-<label>][_dir-<label>][_run-<index>][_part-<mag|phase|real|imag>][_chunk-<index>]
```

Legend:

- <matches> is a placeholder to denote an arbitrary (and valid) sequence of entities and labels at the beginning of the filename (only BIDS "raw").
- <source-entities> is a placeholder to denote an arbitrary sequence of entities and labels at the beginning of the filename matching a source file from which the file derives (only BIDS-Derivatives).
- Filename entities or directories between square brackets (for example, [\_ses-<label>]) are OPTIONAL.
- Some entities may only allow specific values, in which case those values are listed in <>, separated by |.
- \_<suffix> means that there are several (>6) valid suffixes for this filename pattern.
- .<extension> means that there are several (>6) valid extensions for this file type.
- [.gz] means that both the unzipped and gzipped versions of the extension are valid.

The dir-<label> entity is REQUIRED for these files. This entity MUST be used in addition to the REQUIRED PhaseEncodingDirection metadata field (see Filename 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", "i-", "j", "j-", "k", "k-".
TotalReadoutTime	OPTIONAL, but REQUIRED if other methods for calculating readout time are not present	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 $\text{EffectiveEchoSpacing} * (\text{ReconMatrixPE} - 1)$ .



Key name	Requirement Level	Data type	Description
EffectiveEchoSpacing	OPTIONAL, but REQUIRED if other methods for calculating readout time are not present	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. Must be a number greater than 0.

For example:

```
{
  "PhaseEncodingDirection": "j-",
  "TotalReadoutTime": 0.095,
  "IntendedFor": "bids::sub-01/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.

Radiofrequency (RF) field mapping

Fieldmaps may be acquired to measure the inhomogeneity in the RF (B1) field. These fieldmaps may be divided into two categories: transmit (B1+) and receive (B1-) fieldmaps.

Some B1 fieldmap acquisitions call for the use of special notations that cannot be resolved by by entities that can generalize to other applications. The acq entity is used to distinguish the individual files in these cases. These suffixes include: TB1AFI, TB1TFL, TB1RFM, and RB1COR.

## B1+ fieldmaps

Name	suffix	Description
TB1AFI	TB1AFI	This method ( <a href="#">Yarnykh 2007</a> ) calculates a B1+ map from two images acquired at interleaved (two) TRs with identical RF pulses using a steady-state sequence.
TB1DAM	TB1DAM	The double-angle B1+ method ( <a href="#">Insko and Bolinger 1993</a> ) 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	TB1EPI	This B1+ mapping method ( <a href="#">Jiru and Klose 2006</a> ) 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.
TB1RFM	TB1RFM	The result of a Siemens <code>rf_map</code> 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.
TB1SRGE	TB1SRGE	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+ ( <a href="#">Eggenschwiler et al. 2011</a> ). This sequence can also be used in conjunction with MP2RAGE T1 mapping to iteratively improve B1+ and T1 map estimation ( <a href="#">Marques &amp; Gruetter 2013</a> ).
TB1TFL	TB1TFL	The result of a Siemens <code>tf1_b1_map</code> 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.
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 $\text{FlipAngle}_{\text{effective}} = \text{B1+intensity} * \text{FlipAngle}_{\text{nominal}}$ .

Suffix	REQUIRED metadata
TB1DAM	FlipAngle
TB1EPI	EchoTime, FlipAngle, TotalReadoutTime, MixingTime
TB1AFI	RepetitionTimeExcitation
TB1TFL	
TB1RFM	
TB1SRGE*	FlipAngle, InversionTime, RepetitionTimeExcitation, RepetitionTimePreparation, NumberShots

\* Please see TB1SRGE-specific notes for the calculation of NumberShots.

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>][_c
      sub-<label>[_ses-<label>][_acq-<label>][_ce-<label>][_rec-<label>][_run-<index>]_flip-<index>[_inv-<index>][_part-<mag|phase|real|imag>][_c
      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|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>]_chunk-<index>]_TB1map.json
      sub-<label>[_ses-<label>][_acq-<label>][_ce-<label>][_rec-<label>][_run-<index>]_chunk-<index>]_TB1map.nii.gz]
```

Legend:

- **<matches>** is a placeholder to denote an arbitrary (and valid) sequence of entities and labels at the beginning of the filename (only BIDS "raw").
- **<source-entities>** is a placeholder to denote an arbitrary sequence of entities and labels at the beginning of the filename matching a source file from which the file derives (only BIDS-Derivatives).
- Filename entities or directories between square brackets (for example, `[_ses-<label>]`) are OPTIONAL.
- Some entities may only allow specific values, in which case those values are listed in `<>`, separated by `|`.
- **\_<suffix>** means that there are several ( $>6$ ) valid suffixes for this filename pattern.
- **.<extension>** means that there are several ( $>6$ ) valid extensions for this file type.
- **[.gz]** means that both the unzipped and gzipped versions of the extension are valid.

**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.

**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:

Key name	Requirement Level	Data type	Description
EchoTime	REQUIRED	<a href="#">number</a> or <a href="#">array</a> of <a href="#">numbers</a>	The echo time (TE) for the acquisition, specified in seconds. Corresponds to <a href="#">DICOM Tag 0018, 0081 Echo Time</a> (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 <b>EchoTime</b> where the value of this field is iterated using the <b>EchoTime</b> .
FlipAngle	REQUIRED	<a href="#">number</a> or <a href="#">array</a> of <a href="#">numbers</a>	Flip angle (FA) for the acquisition, specified in degrees. Corresponds to: <a href="#">DICOM Tag 0018, 1314 Flip Angle</a> . 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 <b>FlipAngle</b> where the value of this field is iterated using the <b>FlipAngle</b> .

Key name	Requirement Level	Data type	Description
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 $\text{EffectiveEchoSpacing} * (\text{ReconMatrixPE} - 1)$ .
MixingTime	REQUIRED	number	In the context of a stimulated- and spin-echo 3D EPI sequence for B1+ mapping or a stimulated-echo MRS sequence, 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.

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
<code>_acq-tr1</code>	<code>_acq-tr2</code>	Single acquisition
<code>_acq-tr1Test</code>	<code>_acq-tr2Test</code>	Acquisition Test
<code>_acq-tr1Retest</code>	<code>_acq-tr2Retest</code>	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 `tf1_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
<code>_acq-anat</code>	<code>_acq-famp</code>	Single acquisition
<code>_acq-anatTest</code>	<code>_acq-fampTest</code>	Acquisition Test
<code>_acq-anatRetest</code>	<code>_acq-fampRetest</code>	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.

B1- fieldmaps

Name	suffix	Description
RB1COR	RB1COR	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 <a href="#">Papp et al. (2016)</a> .
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 $\text{Amplitudeeffective} = \text{B1-intensity} * \text{Amplitudeideal}$ .

Template:

```
sub-<label>/
  [ses-<label>/]
    fmap/
      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>][_chunk-<index>]_RB1map.json
      sub-<label>[_ses-<label>][_acq-<label>][_ce-<label>][_rec-<label>][_run-<index>][_chunk-<index>]_RB1map.nii.gz]
```

Legend:

- <matches> is a placeholder to denote an arbitrary (and valid) sequence of entities and labels at the beginning of the filename (only BIDS "raw").
- <source-entities> is a placeholder to denote an arbitrary sequence of entities and labels at the beginning of the filename matching a source file from which the file derives (only BIDS-Derivatives).
- Filename entities or directories between square brackets (for example, [\_ses-<label>]) are OPTIONAL.
- Some entities may only allow specific values, in which case those values are listed in <>, separated by |.
- \_<suffix> means that there are several (>6) valid suffixes for this filename pattern.
- .<extension> means that there are several (>6) valid extensions for this file type.
- [.gz] means that both the unzipped and gzipped versions of the extension are valid.

**RB1COR** specific notes This method generates a receive sensitivity map by combining two low resolution images collected sequentially by two different RF coils in receive mode (the body and the head coil) with otherwise identical acquisition parameters. To correct for dynamic changes in the receive sensitivity over time due to, for example, subject motion, separate receive sensitivity maps may be acquired for each anatomical acquisition in a file collection.

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
```



# 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>]_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>][_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>][_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
```

Legend:

- `<matches>` is a placeholder to denote an arbitrary (and valid) sequence of entities and labels at the beginning of the filename (only BIDS "raw").
- `<source-entities>` is a placeholder to denote an arbitrary sequence of entities and labels at the beginning of the filename matching a source file from which the file derives (only BIDS-Derivatives).
- Filename entities or directories between square brackets (for example, `[_ses-<label>]`) are OPTIONAL.
- Some entities may only allow specific values, in which case those values are listed in `<>`, separated by `|`.
- `_<suffix>` means that there are several ( $>6$ ) valid suffixes for this filename pattern.
- `.<extension>` means that there are several ( $>6$ ) valid extensions for this file type.
- `[.gz]` means that both the unzipped and gzipped versions of the extension are valid.

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 directories which contain data files of various nature: for example, CTF's `.ds` format, or BTi/4D's data directory. 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.

The Neuromag/Elekta/Megin system may also produce datasets that require a set of `crosstalk` and `calibration` files to be used properly (see also filename templates above). Please refer to Cross-talk and fine-calibration files for more information on this detail.

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 the MEG File Formats Appendix 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 Neuromag/Elekta/MEGIN'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 (i)EEG simultaneously with MEG

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

If however (i)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, (i)EEG sensor coordinates MAY be recorded in an `electrodes.tsv` file using MEG-specific coordinate systems (see Coordinate System JSON below and the Coordinate Systems Appendix).

### Sidcar JSON (`*_meg.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.

Those fields MUST be present:

Key name	Requirement Level	Data type	Description
<code>SamplingFrequency</code>	REQUIRED	<a href="#">number</a>	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 <code>channels.tsv</code> file.
<code>PowerLineFrequency</code>	REQUIRED	<a href="#">number</a> or <code>"n/a"</code>	Frequency (in Hz) of the power grid at the geographical location of the instrument (for example, 50 or 60).
<code>DewarPosition</code>	REQUIRED	<a href="#">string</a>	Position of the dewar during the MEG scan: <code>"upright"</code> , <code>"supine"</code> or <code>"degrees"</code> of angle from vertical: for example on CTF systems, <code>"upright=15°"</code> , <code>"supine=90°"</code> .
<code>SoftwareFilters</code>	REQUIRED	<a href="#">object of objects</a> or <code>"n/a"</code>	<a href="#">Object</a> of temporal software filters applied, or <code>"n/a"</code> 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, <code>{"Anti-aliasing filter": {"half-amplitude cutoff (Hz)": 500, "Roll-off": "6dB/Octave"}}</code> ).
<code>DigitizedLandmarks</code>	REQUIRED	<a href="#">boolean</a>	<code>true</code> or <code>false</code> value indicating whether anatomical landmark points (fiducials) are contained within this recording. Must be one of: <code>"true"</code> , <code>"false"</code> .

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

Those fields 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), <b>MEGREFChannelCount</b> should be set to 0. 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.
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.

Key name	Requirement Level	Data type	Description
TriggerChannelCount	RECOMMENDED	integer	Number of channels for digital (binary TTL) triggers or analog equivalents (TTL in volt). Corresponds to the TRIG channel type. 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	OPTIONAL, but RECOMMENDED if RecordingType is "epoched"	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 localization was performed. Must be one of: "true", "false".
HeadCoilFrequency	RECOMMENDED	number or array of numbers	List of frequencies (in Hz) used by the head localization coils ('HLC' in CTF systems, 'HPI' in Neuromag/Elekta/MEGIN, '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 localization coils (for example, 4.8).

Key name	Requirement Level	Data type	Description
SubjectArtefactDescription	RECOMMENDED	string	Freeform description of the observed subject artifact 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 or string	One or more AssociatedEmptyRoom pointing to empty-room file(s) associated with the subject's MEG recording. Using forward-slash separated paths relative to the dataset root is AssociatedEmptyRoom.
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"}}.

These 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 <code>true</code> or <code>false</code> ). Parameters for event-like stimulation should be specified in the <code>events.tsv</code> file. Must be one of: "true", "false".

Key name	Requirement Level	Data type	Description
ElectricalStimulationParameters	OPTIONAL	string	Free form description of stimulation parameters, such as frequency or shape. Specific onsets can be specified in the <code>events.tsv</code> file. Specific shapes can be described here in freeform text.

## Hardware information

Key name	Requirement Level	Data type	Description
Manufacturer	RECOMMENDED	string	Manufacturer of the equipment that produced the measurements. For MEG scanners, this must be one of: "CTF", "Neuromag/Elekta/MEGIN", "BTi/4D", "KIT/Yokogawa", "ITAB", "KRISS", "Other". The use of "Elekta/Neuromag" is Manufacturer. Dataset curators SHOULD use "Neuromag/Elekta/MEGIN" instead. See the Manufacturer for preferred names.
ManufacturersModelName	RECOMMENDED	string	Manufacturer's model name of the equipment that produced the measurements. See the ManufacturersModelName for preferred names.
SoftwareVersions	RECOMMENDED	string	Manufacturer's designation of software version of the equipment that produced the measurements.
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.

## Task information

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 filename MAY be derived from this "TaskName" field by removing all non-alphanumeric or + characters (that is, all except those matching [0-9a-zA-Z+]), and potentially replacing spaces with + to ease readability. For example "TaskName" "faces n-back" or "head nodding" could correspond to task labels faces+n+back or facesnback and head+nodding or headnodding, respectively. A RECOMMENDED convention is to name resting state task using labels beginning with rest.
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	CogAtlasID of the corresponding <a href="#">Cognitive Atlas</a> Task term.
CogPOID	RECOMMENDED	string	CogPOID of the corresponding <a href="#">CogPO</a> term.

## 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.
InstitutionAddress	RECOMMENDED	string	The address of the institution in charge of the equipment that produced the measurements.



Key name	Requirement Level	Data type	Description
InstitutionalDepartmentName	RECOMMENDED	string	The department in the institution in charge of the equipment that produced the measurements.

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 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 <code>channels.tsv</code> file.

Example \*\_meg.json

```
{
  "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
```

Legend:

- `<matches>` is a placeholder to denote an arbitrary (and valid) sequence of entities and labels at the beginning of the filename (only BIDS "raw").

- `<source-entities>` is a placeholder to denote an arbitrary sequence of entities and labels at the beginning of the filename matching a source file from which the file derives (only BIDS-Derivatives).
- Filename entities or directories between square brackets (for example, `[_ses-<label>]`) are OPTIONAL.
- Some entities may only allow specific values, in which case those values are listed in `<>`, separated by `|`.
- `_<suffix>` means that there are several ( $>6$ ) valid suffixes for this filename pattern.
- `.<extension>` means that there are several ( $>6$ ) valid extensions for this file type.
- `[.gz]` means that both the unzipped and gzipped versions of the extension are valid.

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:

Column name	Requirement Level	Data type	Description
name	REQUIRED	string	Label of the channel. Values in <b>name</b> MUST be unique.This column must appear first in the file.
type	REQUIRED	string	Type of channel; MUST use the channel types listed below. Note that the type MUST be in upper-case. This column must appear second in the file.For a list of valid values for this column, see the type.
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). This column must appear third in the file.
description	OPTIONAL	string	Brief free-text description of the channel, or other information of interest. This column may appear anywhere in the file.
sampling_frequency	OPTIONAL	number	Sampling rate of the channel in Hz. This column may appear anywhere in the file.
low_cutoff	OPTIONAL	number	Frequencies used for the high-pass filter applied to the channel in Hz. If no high-pass filter applied, use n/a. This column may appear anywhere in the file.

Column name	Requirement Level	Data type	Description
high_cutoff	OPTIONAL	number	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/EMG electronics applies a low-pass filter; specify its frequency here if applicable. This column may appear anywhere in the file. Must be a number greater than or equal to 0.
notch	OPTIONAL	string	Frequencies used for the notch filter applied to the channel, in Hz. If notch filters are applied at multiple frequencies, these frequencies MAY be specified as a list, for example, [60, 120, 180]. If no notch filter was applied, use n/a. This column may appear anywhere in the file.
software_filters	OPTIONAL	string	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. This column may appear anywhere in the file.
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]. This column may appear anywhere in the file. Must be one of: "good", "bad".

Column name	Requirement Level	Data type	Description
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 the status column. This column may appear anywhere in the file.
Additional Columns	OPTIONAL	n/a	Additional columns are allowed if they are defined in the associated metadata file.

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
SEEG	Electrode channel
DBS	Electrode channel
VEOG	Vertical EOG (electrooculogram)
HEOG	Horizontal EOG
EOG	Generic EOG channel
ECG	ElectroCardioGram (heart)
EMG	ElectroMyoGram (muscle)
TRIG	Analog (TTL in Volt) or digital (binary TTL) trigger channel
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

Keyword	Description
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

Examples of free text for field description:

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

#### Example \*\_channels.tsv

```

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>][_task-<label>][_acq-<label>]_coordsystem.json

```

Legend:

- <matches> is a placeholder to denote an arbitrary (and valid) sequence of entities and labels at the beginning of the filename (only BIDS "raw").
- <source-entities> is a placeholder to denote an arbitrary sequence of entities and labels at the beginning of the filename matching a source file from which the file derives (only BIDS-Derivatives).
- Filename entities or directories between square brackets (for example, [\_ses-<label>]) are OPTIONAL.

- Some entities may only allow specific values, in which case those values are listed in <>, separated by |.
- \_<suffix> means that there are several (>6) valid suffixes for this filename pattern.
- .<extension> means that there are several (>6) valid extensions for this file type.
- [.gz] means that both the unzipped and gzipped versions of the extension are valid.

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 the MEGCoordinateSystem for a list of restricted keywords for coordinate systems. If "Other", provide definition of the coordinate system in "MEGCoordinateSystemDescription".For a list of valid values for this field, see the MEGCoordinateSystem.
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.
EEGCoordinateSystem	OPTIONAL	string	Defines the coordinate system for the EEG sensors.See the EEGCoordinateSystem for a list of restricted keywords for coordinate systems. If "Other", provide definition of the coordinate system in EEGCoordinateSystemDescription. See [Recording EEG simultaneously with MEG] (/modality-specific-files/magnetoencephalography.html#recording-ieeg-simultaneously-with-meg). Preferably the same as the MEGCoordinateSystem.For a list of valid values for this field, see the EEGCoordinateSystem.

Key name	Requirement Level	Data type	Description
EEGCoordinateUnits	OPTIONAL	string	Units of the coordinates of EEGCoordinateSystem. Must be one of: "m", "mm", "cm", "n/a".
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] (/modality-specific-files/magnetoencephalography.html#recording-ieeg-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 Neuromag/Elekta/MEGIN, 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 the HeadCoilCoordinateSystem for a list of restricted keywords for coordinate systems. If "Other", provide definition of the coordinate system in HeadCoilCoordinateSystemDescription. For a list of valid values for this field, see the HeadCoilCoordinateSystem.
HeadCoilCoordinateUnits	OPTIONAL	string	Units of the coordinates of HeadCoilCoordinateSystem. Must be one of: "m", "mm", "cm", "n/a".
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	string	Relative path to the file containing the locations of digitized head points collected during the session (for example, "sub-01_headshape.pos"). RECOMMENDED for all MEG systems, especially for CTF and BTi/4D. For Neuromag/Elekta/MEGIN, the head points will be stored in the .fif file.
DigitizedHeadPointsCoordinateSystem	OPTIONAL	string	Defines the coordinate system for the digitized head points. See the DigitizedHeadPointsCoordinateSystem for a list of restricted keywords for coordinate systems. If "Other", provide definition of the coordinate system in "DigitizedHeadPointsCoordinateSystemDescription". For a list of valid values for this field, see the DigitizedHeadPointsCoordinateSystem.

Key name	Requirement Level	Data type	Description
DigitizedHeadPointsCoordinateUnits	OPTIONAL	string	Units of the coordinates of "DigitizedHeadPointsCoordinateSystem". Must be one of: "m", "mm", "cm", "n/a".
DigitizedHeadPointsCoordinateSystemDescription	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	The paths to files for which the associated file is intended to be used. Contains one or more IntendedFor. Using forward-slash separated paths relative to the participant subdirectory is IntendedFor. 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 the AnatomicalLandmarkCoordinateSystem for a list of restricted keywords for coordinate systems. If "Other", provide definition of the coordinate system in "AnatomicalLandmarkCoordinateSystemDescription". Preferably the same as the MEGCoordinateSystem. For a list of valid values for this field, see the AnatomicalLandmarkCoordinateSystem.
AnatomicalLandmarkCoordinateUnits	OPTIONAL	string	Units of the coordinates of "AnatomicalLandmarkCoordinateSystem". Must be one of: "m", "mm", "cm", "n/a".
AnatomicalLandmarkCoordinateSystemID	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: [How are the Left and Right Pre-Auricular \(LPA and RPA\) points defined? - FieldTrip Toolbox](#)

For more information on typical coordinate systems for MEG-MRI coregistration: [How are the different head and MRI coordinate systems defined? - FieldTrip Toolbox](#) or: [Coordinate Systems - Brainstorm toolbox](#)

`*_coordsystem.json` files SHOULD NOT be duplicated for each data file, for example, across multiple tasks. The inheritance principle MUST be used to find the appropriate coordinate system description for a given data file.

Landmark photos (`*_photo.<extension>`)

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

Template:

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

Legend:

- `<matches>` is a placeholder to denote an arbitrary (and valid) sequence of entities and labels at the beginning of the filename (only BIDS "raw").
- `<source-entities>` is a placeholder to denote an arbitrary sequence of entities and labels at the beginning of the filename matching a source file from which the file derives (only BIDS-Derivatives).
- Filename entities or directories between square brackets (for example, `[_ses-<label>]`) are OPTIONAL.
- Some entities may only allow specific values, in which case those values are listed in `<>`, separated by `|`.
- `_<suffix>` means that there are several ( $>6$ ) valid suffixes for this filename pattern.
- `._<extension>` means that there are several ( $>6$ ) valid extensions for this file type.
- `[.gz]` means that both the unzipped and gzipped versions of the extension are valid.

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 `*_photo.<extension>`

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.<extension>`)

Template:

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

Legend:

- `<matches>` is a placeholder to denote an arbitrary (and valid) sequence of entities and labels at the beginning of the filename (only BIDS "raw").

- `<source-entities>` is a placeholder to denote an arbitrary sequence of entities and labels at the beginning of the filename matching a source file from which the file derives (only BIDS-Derivatives).
- Filename entities or directories between square brackets (for example, `[_ses-<label>]`) are OPTIONAL.
- Some entities may only allow specific values, in which case those values are listed in `<>`, separated by `|`.
- `_<suffix>` means that there are several (>6) valid suffixes for this filename pattern.
- `.<extension>` means that there are several (>6) valid extensions for this file type.
- `[_gz]` means that both the unzipped and gzipped versions of the extension are valid.

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 is 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 the MEG File Formats Appendix).

For 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.

It is RECOMMENDED to explicitly specify which empty-room recording should be used with which experimental run(s) or session(s). This can be done via the `AssociatedEmptyRoom` field in the `*_meg.json` sidecar files.

Empty-room recordings may be collected once per day, where a single empty-room recording may be shared between multiple subjects and/or sessions (see Example 1). Empty-room recordings may also be collected for each individual experimental session (see Example 2). In either case, the label for the `task-<label>` entity in the empty-room recording SHOULD be set to `noise`.

### Example 1

One empty-room recording per day, applying to all subjects for that day.

In the case of empty-room recordings being associated with multiple subjects and/or sessions, it is RECOMMENDED to store the empty-room recording inside a subject directory named `sub-emptyroom`. 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.

```
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
```

## Example 2

One empty-room recording per each participant's session, stored within the session directory.

In the case of empty-room recordings being collected for the individual experimental session, it is RECOMMENDED to store the empty-room recording along with that subject and session.

```
sub-control01/  
  ses-01/  
    sub-01_ses-01_scans.tsv  
    meg/  
      sub-control01_ses-01_task-rest_meg.ds  
      sub-control01_ses-01_task-rest_meg.json  
      sub-control01_ses-01_task-rest_channels.tsv  
      sub-control01_ses-01_task-noise_meg.ds  
      sub-control01_ses-01_task-noise_meg.json  
      sub-control01_ses-01_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
```

Legend:

- <matches> is a placeholder to denote an arbitrary (and valid) sequence of entities and labels at the beginning of the filename (only BIDS "raw").
- <source-entities> is a placeholder to denote an arbitrary sequence of entities and labels at the beginning of the filename matching a source file from which the file derives (only BIDS-Derivatives).
- Filename entities or directories between square brackets (for example, [\_ses-<label>]) are OPTIONAL.
- Some entities may only allow specific values, in which case those values are listed in <>, separated by |.
- \_<suffix> means that there are several (>6) valid suffixes for this filename pattern.
- .<extension> means that there are several (>6) valid extensions for this file type.



- `[.gz]` means that both the unzipped and gzipped versions of the extension are valid.

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. <code>edf+</code> files are permitted. The capital .EDF extension MUST NOT be used.
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 <a href="#">EEGLAB</a> . Each recording consists of a .set file with an OPTIONAL .fdt file.
Biosemi	.bdf	Each recording consists of a single .bdf file. <code>bdf+</code> 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.

We encourage users to provide additional metadata extracted from the manufacturer-specific data files in the sidecar JSON file.

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)

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.

Those 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 <code>channels.tsv</code> 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 <code>channels.tsv</code> 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"}}).

Those fields 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 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 channels not covered otherwise. Must be a number greater than or equal to 0.
TriggerChannelCount	RECOMMENDED	integer	Number of channels for digital (binary TTL) triggers or analog equivalents (TTL in volt). Corresponds to the TRIG channel type. 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	OPTIONAL, but RECOMMENDED if RecordingType is "epoched"	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.

Key name	Requirement Level	Data type	Description
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"}}.
SubjectArtefactDescription	RECOMMENDED	string	Freeform description of the observed subject artifact 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.

These 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 <code>true</code> or <code>false</code> ). Parameters for event-like stimulation should be specified in the <code>events.tsv</code> file. Must be one of: <code>"true"</code> , <code>"false"</code> .
ElectricalStimulationParameters	OPTIONAL	string	Free form description of stimulation parameters, such as frequency or shape. Specific onsets can be specified in the <code>events.tsv</code> file. Specific shapes can be described here in freeform text.

Hardware information

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.
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.

Task information

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 filename MAY be derived from this "TaskName" field by removing all non-alphanumeric or + characters (that is, all except those matching [0-9a-zA-Z+]), and potentially replacing spaces with + to ease readability. For example "TaskName" "faces n-back" or "head nodding" could correspond to task labels faces+n+back or facesnback and head+nodding or headnodding, respectively. A RECOMMENDED convention is to name resting state task using labels beginning with <b>rest</b> .
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	CogAtlasID of the corresponding <a href="#">Cognitive Atlas</a> Task term.
CogPOID	RECOMMENDED	string	CogPOID of the corresponding <a href="#">CogPO</a> term.

## 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.
InstitutionAddress	RECOMMENDED	string	The address of the institution in charge of the equipment that produced the measurements.

Key name	Requirement Level	Data type	Description
InstitutionalDepartmentName	RECOMMENDED	string	The department in the institution in charge of the equipment that produced the measurements.

Example \*\_eeg.json

```
{
  "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
```

Legend:

- `<matches>` is a placeholder to denote an arbitrary (and valid) sequence of entities and labels at the beginning of the filename (only BIDS "raw").
- `<source-entities>` is a placeholder to denote an arbitrary sequence of entities and labels at the beginning of the filename matching a source file from which the file derives (only BIDS-Derivatives).
- Filename entities or directories between square brackets (for example, `[_ses-<label>]`) are OPTIONAL.
- Some entities may only allow specific values, in which case those values are listed in `<>`, separated by `|`.
- `_<suffix>` means that there are several ( $>6$ ) valid suffixes for this filename pattern.
- `.<extension>` means that there are several ( $>6$ ) valid extensions for this file type.
- `[.gz]` means that both the unzipped and gzipped versions of the extension are valid.

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:

Column name	Requirement Level	Data type	Description
name	REQUIRED	string	Label of the channel. Values in <b>name</b> MUST be unique. This column must appear first in the file.



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. This column must appear second in the file. For a list of valid values for this column, see the type.
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). This column must appear third in the file.
description	OPTIONAL	string	Brief free-text description of the channel, or other information of interest. This column may appear anywhere in the file.
sampling_frequency	OPTIONAL	number	Sampling rate of the channel in Hz. This column may appear anywhere in the file.
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). This column may appear anywhere in the file.
low_cutoff	OPTIONAL	number	Frequencies used for the high-pass filter applied to the channel in Hz. If no high-pass filter applied, use n/a. This column may appear anywhere in the file.

Column name	Requirement Level	Data type	Description
high_cutoff	OPTIONAL	number	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/EMG electronics applies a low-pass filter; specify its frequency here if applicable. This column may appear anywhere in the file. Must be a number greater than or equal to 0.
notch	OPTIONAL	string	Frequencies used for the notch filter applied to the channel, in Hz. If notch filters are applied at multiple frequencies, these frequencies MAY be specified as a list, for example, [60, 120, 180]. If no notch filter was applied, use n/a. This column may appear anywhere in the file.
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]. This column may appear anywhere in the file. Must be one of: "good", "bad".
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 the status column. This column may appear anywhere in the file.
Additional Columns	OPTIONAL	n/a	Additional columns are allowed if they are defined in the associated metadata file.

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
PUPIL	Eye tracker pupil diameter
REF	Reference channel
RESP	Respiration
SYSCLOCK	System time showing elapsed time since trial started
TEMP	Temperature
TRIG	Analog (TTL in Volt) or digital (binary TTL) trigger channel
VEOG	Vertical EOG (eye)

Examples 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>][_task-<label>][_acq-<label>][_run-<index>][_space-<label>]_electrodes.json
      sub-<label>[_ses-<label>][_task-<label>][_acq-<label>][_run-<index>][_space-<label>]_electrodes.tsv
```

Legend:

- **<matches>** is a placeholder to denote an arbitrary (and valid) sequence of entities and labels at the beginning of the filename (only BIDS "raw").
- **<source-entities>** is a placeholder to denote an arbitrary sequence of entities and labels at the beginning of the filename matching a source file from which the file derives (only BIDS-Derivatives).
- Filename entities or directories between square brackets (for example, [\_ses-<label>]) are OPTIONAL.
- Some entities may only allow specific values, in which case those values are listed in <>, separated by |.
- **\_<suffix>** means that there are several (>6) valid suffixes for this filename pattern.
- **.<extension>** means that there are several (>6) valid extensions for this file type.
- **[.gz]** means that both the unzipped and gzipped versions of the extension are valid.

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.

Column name	Requirement Level	Data type	Description
name	REQUIRED	string	Name of the electrode contact point. Values in <b>name</b> MUST be unique. This column must appear first in the file.
x	REQUIRED	number	Recorded position along the x-axis. This column must appear second in the file.
y	REQUIRED	number	Recorded position along the y-axis. This column must appear third in the file.
z	REQUIRED	number	Recorded position along the z-axis. This column must appear fourth in the file.
type	RECOMMENDED	string	Type of the electrode (for example, cup, ring, clip-on, wire, needle). This column may appear anywhere in the file.

Column name	Requirement Level	Data type	Description
material	RECOMMENDED	string	Material of the electrode (for example, Tin, Ag/AgCl, Gold). This column may appear anywhere in the file.
impedance	RECOMMENDED	number	Impedance of the electrode, units MUST be in kOhm. This column may appear anywhere in the file.
Additional Columns	OPTIONAL	n/a	Additional columns are allowed if they are defined in the associated metadata file.

`*_electrodes.tsv` files SHOULD NOT be duplicated for each data file, for example, during multiple runs of a task. The inheritance principle MUST be used to find the appropriate electrode positions for a given data file. If electrodes are repositioned, it is RECOMMENDED to use multiple sessions to indicate this.

### Example `*_electrodes.tsv`

See also the corresponding `channels.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>` entity 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>][_task-<label>][_acq-<label>][_space-<label>]_coordsystem.json
```

Legend:

- `<matches>` is a placeholder to denote an arbitrary (and valid) sequence of entities and labels at the beginning of the filename (only BIDS "raw").
- `<source-entities>` is a placeholder to denote an arbitrary sequence of entities and labels at the beginning of the filename matching a source file from which the file derives (only BIDS-Derivatives).
- Filename entities or directories between square brackets (for example, `[_ses-<label>]`) are OPTIONAL.
- Some entities may only allow specific values, in which case those values are listed in `<>`, separated by `|`.
- `_<suffix>` means that there are several ( $>6$ ) valid suffixes for this filename pattern.
- `._<extension>` means that there are several ( $>6$ ) valid extensions for this file type.
- `[.gz]` means that both the unzipped and gzipped versions of the extension are valid.

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: [How are the Left and Right Pre-Auricular \(LPA and RPA\) points defined? - FieldTrip Toolbox](#)
- For more information on coordinate systems for coregistration, please visit: [How are the different head and MRI coordinate systems defined? - FieldTrip Toolbox](#)

General fields:

Key name	Requirement Level	Data type	Description
IntendedFor	OPTIONAL	string or array	The paths to files for which the associated file is intended to be used. Contains one or more IntendedFor. Using forward-slash separated paths relative to the participant subdirectory is IntendedFor. 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 the EEGCoordinateSystem for a list of restricted keywords for coordinate systems. If "Other", provide definition of the coordinate system in EEGCoordinateSystemDescription. For a list of valid values for this field, see the EEGCoordinateSystem.
EEGCoordinateUnits	REQUIRED	string	Units of the coordinates of EEGCoordinateSystem. Must be one of: "m", "mm", "cm", "n/a".
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 the FiducialsCoordinateSystem for a list of restricted keywords for coordinate systems. If "Other", provide definition of the coordinate system in "FiducialsCoordinateSystemDescription". For a list of valid values for this field, see the FiducialsCoordinateSystem.
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".
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 the AnatomicalLandmarkCoordinateSystem for a list of restricted keywords for coordinate systems. If "Other", provide definition of the coordinate system in "AnatomicalLandmarkCoordinateSystemDescription". Preferably the same as the EEGCoordinateSystem. For a list of valid values for this field, see the AnatomicalLandmarkCoordinateSystem.
AnatomicalLandmarkCoordinateUnits	RECOMMENDED	string	Units of the coordinates of "AnatomicalLandmarkCoordinateSystem". Must be one of: "m", "mm", "cm", "n/a".
AnatomicalLandmarkCoordinateSystemDescription	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]).

`*_coordsystem.json` files SHOULD NOT be duplicated for each data file, for example, across multiple tasks. The inheritance principle MUST be used to find the appropriate coordinate system description for a given data file. If electrodes are repositioned, it is RECOMMENDED to use multiple sessions to indicate this.

Example `*_coordsystem.json`

```
{
  "IntendedFor": "bids::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-axis",
  "FiducialsDescription": "Electrodes and fiducials were digitized with Polhemus, fiducials were recorded as the center of vitamin E capsules stuck on scalp"
}
```

## Landmark photos (**\*\_photo.<extension>**)

Photos of the anatomical landmarks and/or fiducials.

Template:

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

Legend:

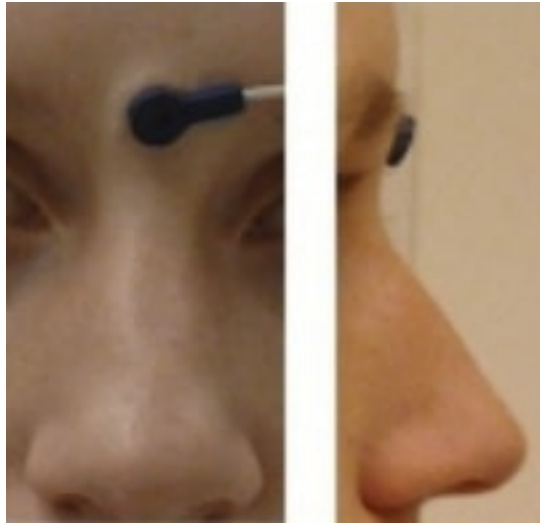
- **<matches>** is a placeholder to denote an arbitrary (and valid) sequence of entities and labels at the beginning of the filename (only BIDS "raw").
- **<source-entities>** is a placeholder to denote an arbitrary sequence of entities and labels at the beginning of the filename matching a source file from which the file derives (only BIDS-Derivatives).
- Filename entities or directories between square brackets (for example, `[_ses-<label>]`) are OPTIONAL.
- Some entities may only allow specific values, in which case those values are listed in `<>`, separated by `|`.
- **\_<suffix>** means that there are several (>6) valid suffixes for this filename pattern.
- **.<extension>** means that there are several (>6) valid extensions for this file type.
- **[.gz]** means that both the unzipped and gzipped versions of the extension are valid.

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>` 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 **\*\_photo.<extension>**

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 for 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>]_events.json
      sub-<label>[_ses-<label>]_task-<label>[_acq-<label>][_run-<index>]_events.tsv
      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>][_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
```

Legend:

- <matches> is a placeholder to denote an arbitrary (and valid) sequence of entities and labels at the beginning of the filename (only BIDS "raw").
- <source-entities> is a placeholder to denote an arbitrary sequence of entities and labels at the beginning of the filename matching a source file from which the file derives (only BIDS-Derivatives).
- Filename entities or directories between square brackets (for example, [\_ses-<label>]) are OPTIONAL.
- Some entities may only allow specific values, in which case those values are listed in <>, separated by |.
- \_<suffix> means that there are several (>6) valid suffixes for this filename pattern.
- .<extension> means that there are several (>6) valid extensions for this file type.

- `[.gz]` means that both the unzipped and gzipped versions of the extension are valid.

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. <code>edf+</code> files are permitted. The capital .EDF extension MUST NOT be used.
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 <a href="#">EEGLAB</a> . 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.

We encourage users to provide additional metadata extracted from the manufacturer-specific data files in the sidecar JSON file.

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.

Those 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).

Key name	Requirement Level	Data type	Description
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"}}).

Those fields SHOULD be present:

Key name	Requirement Level	Data type	Description
DCOffsetCorrection	DCOffsetCorrection	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 <code>_electrodes.tsv</code> file.
ElectrodeManufacturersModelName	RECOMMENDED	string	If different electrode types are used, please use the corresponding table in the <code>_electrodes.tsv</code> file.
ECOGChannelCount	RECOMMENDED	integer	Number of ECoG channels. Must be a number greater than or equal to 0.

Key name	Requirement Level	Data type	Description
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.
TriggerChannelCount	RECOMMENDED	integer	Number of channels for digital (binary TTL) triggers or analog equivalents (TTL in volt). Corresponds to the TRIG channel type. 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	OPTIONAL, but RECOMMENDED if RecordingType is "epoched"	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)").



Key name	Requirement Level	Data type	Description
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".
SubjectArtefactDescription	RECOMMENDED	string	Freeform description of the observed subject artifact 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.

These 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 <code>true</code> or <code>false</code> ). Parameters for event-like stimulation should be specified in the <code>events.tsv</code> file. Must be one of: <code>"true"</code> , <code>"false"</code> .

Key name	Requirement Level	Data type	Description
ElectricalStimulationParameters	OPTIONAL	string	Free form description of stimulation parameters, such as frequency or shape. Specific onsets can be specified in the <code>events.tsv</code> file. Specific shapes can be described here in freeform text.

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

Hardware information

Key name	Requirement Level	Data type	Description
Manufacturer	RECOMMENDED	string	Manufacturer of the equipment that produced the measurements. For example, "TDT", "Blackrock".
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.
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.

Task information

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 filename MAY be derived from this "TaskName" field by removing all non-alphanumeric or + characters (that is, all except those matching [0-9a-zA-Z+]), and potentially replacing spaces with + to ease readability. For example "TaskName" "faces n-back" or "head nodding" could correspond to task labels faces+n+back or facesnback and head+nodding or headnodding, respectively. A RECOMMENDED convention is to name resting state task using labels beginning with <b>rest</b> .
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	CogAtlasID of the corresponding <a href="#">Cognitive Atlas</a> Task term.
CogPOID	RECOMMENDED	string	CogPOID of the corresponding <a href="#">CogPO</a> term.

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**").

#### 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.

Key name	Requirement Level	Data type	Description
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 \*\_ieeg.json

```
{
  "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": "6dB0ctave"}},
  "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
}
```

## 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
```

Legend:

- <matches> is a placeholder to denote an arbitrary (and valid) sequence of entities and labels at the beginning of the filename (only BIDS "raw").
- <source-entities> is a placeholder to denote an arbitrary sequence of entities and labels at the beginning of the filename matching a source file from which the file derives (only BIDS-Derivatives).
- Filename entities or directories between square brackets (for example, [\_ses-<label>]) are OPTIONAL.
- Some entities may only allow specific values, in which case those values are listed in <>, separated by |.
- \_<suffix> means that there are several (>6) valid suffixes for this filename pattern.
- .<extension> means that there are several (>6) valid extensions for this file type.
- [.gz] means that both the unzipped and gzipped versions of the extension are valid.

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  $\geq 1000$  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:

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. Values in name MUST be unique.This column must appear first in the file.

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. This column must appear second in the file. For a list of valid values for this column, see the type.
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). This column must appear third in the file.
low_cutoff	REQUIRED	number	Frequencies used for the high-pass filter applied to the channel in Hz. If no high-pass filter applied, use n/a. This column must appear fourth in the file.
high_cutoff	REQUIRED	number	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/EMG electronics applies a low-pass filter; specify its frequency here if applicable. This column must appear fifth in the file. Must be a number greater than or equal to 0.
reference	OPTIONAL	string	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. This column may appear anywhere in the file.

Column name	Requirement Level	Data type	Description
group	OPTIONAL	string	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 <code>_electrodes.tsv</code> must match those present here. This column may appear anywhere in the file.
sampling_frequency	OPTIONAL	number	Sampling rate of the channel in Hz. This column may appear anywhere in the file.
description	OPTIONAL	string	Brief free-text description of the channel, or other information of interest. This column may appear anywhere in the file.
notch	OPTIONAL	string	Frequencies used for the notch filter applied to the channel, in Hz. If notch filters are applied at multiple frequencies, these frequencies MAY be specified as a list, for example, [60, 120, 180]. If no notch filter was applied, use n/a. This column may appear anywhere in the file.
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]. This column may appear anywhere in the file. Must be one of: "good", "bad".
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 the status column. This column may appear anywhere in the file.

Column name	Requirement Level	Data type	Description
Additional Columns	OPTIONAL	n/a	Additional columns are allowed if they are defined in the associated metadata file.

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	Analog (TTL in Volt) or digital (binary TTL) trigger channel
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

Examples of free-form text for field description:

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



### Example \*\_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

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

Template:

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

Legend:

- <matches> is a placeholder to denote an arbitrary (and valid) sequence of entities and labels at the beginning of the filename (only BIDS "raw").
- <source-entities> is a placeholder to denote an arbitrary sequence of entities and labels at the beginning of the filename matching a source file from which the file derives (only BIDS-Derivatives).
- Filename entities or directories between square brackets (for example, [\_ses-<label>]) are OPTIONAL.
- Some entities may only allow specific values, in which case those values are listed in <>, separated by |.
- \_<suffix> means that there are several (>6) valid suffixes for this filename pattern.
- .<extension> means that there are several (>6) valid extensions for this file type.
- [.gz] means that both the unzipped and gzipped versions of the extension are valid.

This REQUIRED file 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. For each \*\_electrodes.tsv file 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 the Coordinate Systems Appendix. For example for iEEG data, the restricted keywords listed under iEEG Specific Coordinate Systems are acceptable for <label>.

For examples:

- \*\_space-MNI152Lin (electrodes are coregistered and scaled to a specific MNI template)
- \*\_space-Talairach (electrodes are coregistered 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.

Column name	Requirement Level	Data type	Description
name	REQUIRED	string	Name of the electrode contact point. Values in name MUST be unique.This column must appear first in the file.
x	REQUIRED	number	Recorded position along the x-axis. This column must appear second in the file.
y	REQUIRED	number	Recorded position along the y-axis. This column must appear third in the file.
z	REQUIRED	number	Recorded position along the z-axis. If electrodes are in 2D space this should be a column of n/a values. This column must appear fourth in the file.
size	REQUIRED	number	Surface area of the electrode, units MUST be in mm^2. This column must appear fifth in the file.
material	RECOMMENDED	string	Material of the electrode (for example, Tin, Ag/AgCl, Gold). This column may appear anywhere in the file.
manufacturer	RECOMMENDED	string	The manufacturer for each electrode. Can be used if electrodes were manufactured by more than one company. This column may appear anywhere in the file.

Column name	Requirement Level	Data type	Description
group	RECOMMENDED	string	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 <code>_channels.tsv</code> . This column may appear anywhere in the file.
hemisphere	RECOMMENDED	string	The hemisphere in which the electrode is placed. This column may appear anywhere in the file. Must be one of: "L", "R".
type	OPTIONAL	string	Type of the electrode (for example, cup, ring, clip-on, wire, needle). This column may appear anywhere in the file.
impedance	OPTIONAL	number	Impedance of the electrode, units MUST be in kOhm. This column may appear anywhere in the file.
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]). This column may appear anywhere in the file.
Additional Columns	OPTIONAL	n/a	Additional columns are allowed if they are defined in the associated metadata file.

`*_electrodes.tsv` files SHOULD NOT be duplicated for each data file, for example, during multiple runs of a task. The inheritance principle MUST be used to find the appropriate electrode positions for a given data file. If electrodes are repositioned, it is RECOMMENDED to use multiple sessions to indicate this.

Example `*_electrodes.tsv`

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

Legend:

- <matches> is a placeholder to denote an arbitrary (and valid) sequence of entities and labels at the beginning of the filename (only BIDS "raw").
- <source-entities> is a placeholder to denote an arbitrary sequence of entities and labels at the beginning of the filename matching a source file from which the file derives (only BIDS-Derivatives).
- Filename entities or directories between square brackets (for example, [\_ses-<label>]) are OPTIONAL.
- Some entities may only allow specific values, in which case those values are listed in <>, separated by |.
- \_<suffix> means that there are several (>6) valid suffixes for this filename pattern.
- .<extension> means that there are several (>6) valid extensions for this file type.
- [.gz] means that both the unzipped and gzipped versions of the extension are valid.

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	<p>The paths to files for which the associated file is intended to be used. Contains one or more IntendedFor. Using forward-slash separated paths relative to the dataset root is IntendedFor. 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. For example, T1:</p> <p>'bids::sub-&lt;label&gt;/ses-&lt;label&gt;/anat/sub-01_T1w.nii.gz'</p> <p>Surface:</p> <p>'bids::derivatives/surfaces/sub-&lt;label&gt;/ses-&lt;label&gt;/sub-01_hemi-R_desc-T1w_pial.surf.gii'</p> <p>Operative photo:</p> <p>'bids::sub-&lt;label&gt;/ses-&lt;label&gt;/ieeg/sub-0001_ses-01_acq-photo1_photo.jpg'</p> <p>Talairach:</p> <p>'bids::derivatives/surfaces/sub-Talairach/sub-Talairach_hemi-R_pial.surf.gii'</p>

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 the iEEGCoordinateSystem 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 iEEGCoordinateSystem. For a list of valid values for this field, see the iEEGCoordinateSystem.
iEEGCoordinateUnits	REQUIRED	string	Units of the *_electrodes.tsv. MUST be "pixels" if iEEGCoordinateSystem is Pixels. Must be one of: "pixels", "m", "mm", "cm", "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.

\*\_coordsystem.json files SHOULD NOT be duplicated for each data file, for example, across multiple tasks. The inheritance principle MUST be used to find the appropriate coordinate system description for a given data file. If electrodes are repositioned, it is RECOMMENDED to use multiple sessions to indicate this.

## 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 the BIDS Coordinate Systems Appendix 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 `*_coordsystem.json`

```
{
  "IntendedFor": "bids::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.<extension>`)

Template:

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

Legend:

- `<matches>` is a placeholder to denote an arbitrary (and valid) sequence of entities and labels at the beginning of the filename (only BIDS "raw").
- `<source-entities>` is a placeholder to denote an arbitrary sequence of entities and labels at the beginning of the filename matching a source file from which the file derives (only BIDS-Derivatives).
- Filename entities or directories between square brackets (for example, `[_ses-<label>]`) are OPTIONAL.
- Some entities may only allow specific values, in which case those values are listed in `<>`, separated by `|`.
- `_<suffix>` means that there are several ( $>6$ ) valid suffixes for this filename pattern.
- `._<extension>` means that there are several ( $>6$ ) valid extensions for this file type.
- `[_gz]` means that both the unzipped and gzipped versions of the extension are valid.

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

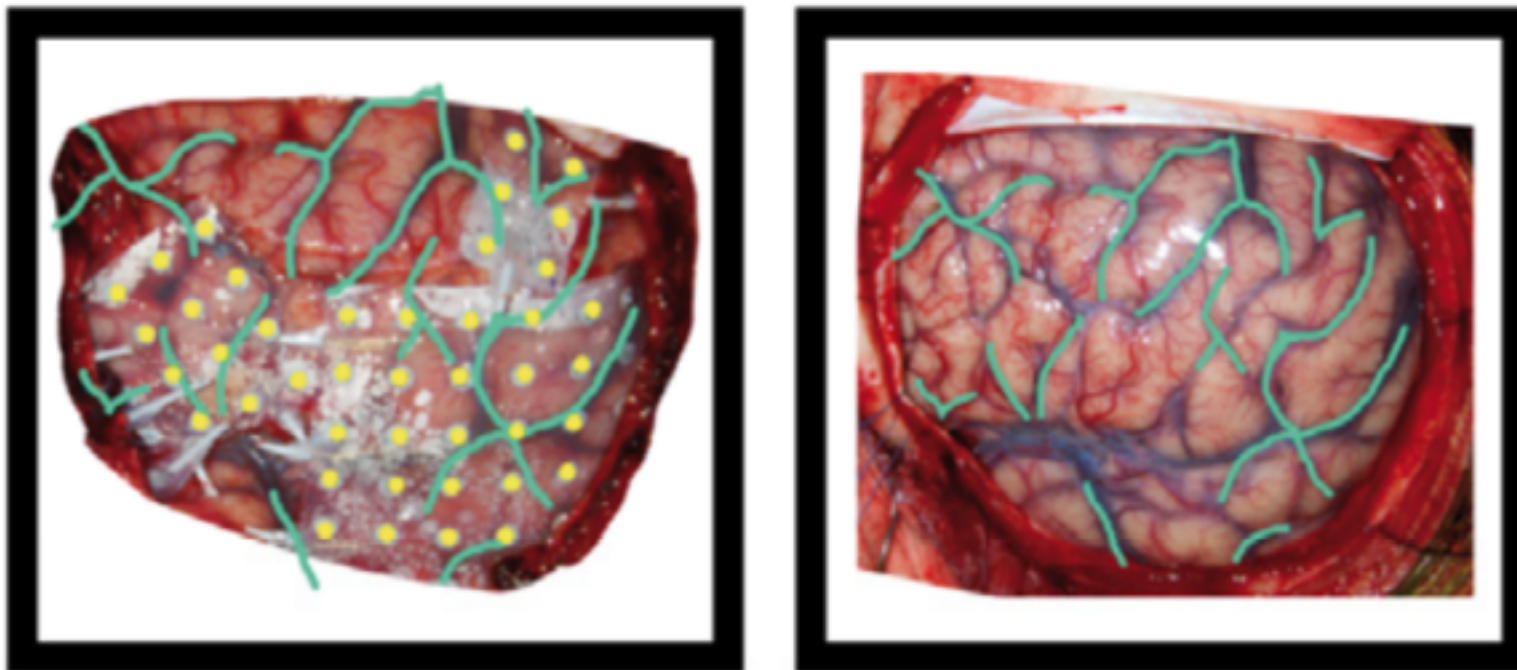
The `ses-<label>` entity may be used to specify when the photo was taken.

### Example `*_photo.<extension>`

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

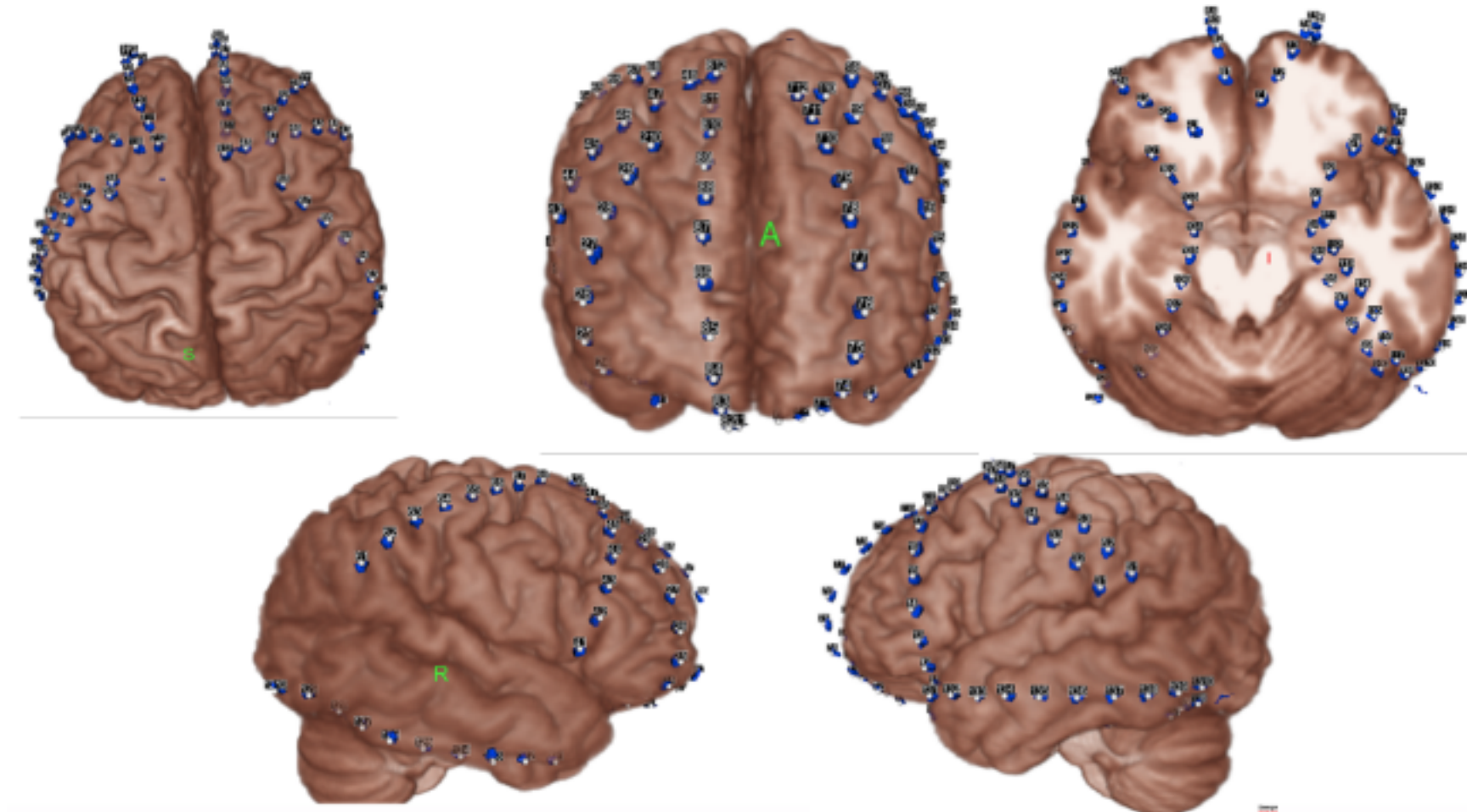




Below is an example of a volume rendering of the cortical surface with a superimposed subdural electrode implantation. This map is often provided by the EEG technician and provided to the epileptologists (for example, see Burneo JG et al.

1. [doi:10.1016/j.clineuro.2014.03.020](https://doi.org/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 directory in the `/stimuli/` directory. For example: `/stimuli/electrical_stimulation_functions/biphasic.tsv`

Example **\*\_events.tsv**

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

# Physiological 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](#)

## General specifications

Continuous (that is, regularly sampled over time at a fixed frequency) physiological recordings such as cardiac and respiratory signals, and asynchronous events corresponding to those signals MAY be specified using compressed tabular files ([TSV.GZ file](#)). TSV.GZ files MUST be accompanied by a JSON file with the same name as their corresponding tabular file but with a `.json` extension.

Template:

```
sub-<label>/
  [ses-<label>/]
    anat/
      <matches>[_recording-<label>]_physio.json
      <matches>[_recording-<label>]_physio.tsv.gz
      <matches>[_recording-<label>]_physioevents.json
      <matches>[_recording-<label>]_physioevents.tsv.gz
    beh/
      <matches>[_recording-<label>]_physio.json
      <matches>[_recording-<label>]_physio.tsv.gz
      <matches>[_recording-<label>]_physioevents.json
      <matches>[_recording-<label>]_physioevents.tsv.gz
    dwi/
      <matches>[_recording-<label>]_physio.json
      <matches>[_recording-<label>]_physio.tsv.gz
      <matches>[_recording-<label>]_physioevents.json
```

```
<matches>[_recording-<label>]_physioevents.tsv.gz
eeg/
  <matches>[_recording-<label>]_physio.json
  <matches>[_recording-<label>]_physio.tsv.gz
  <matches>[_recording-<label>]_physioevents.json
  <matches>[_recording-<label>]_physioevents.tsv.gz
func/
  <matches>[_recording-<label>]_physio.json
  <matches>[_recording-<label>]_physio.tsv.gz
  <matches>[_recording-<label>]_physioevents.json
  <matches>[_recording-<label>]_physioevents.tsv.gz
ieeg/
  <matches>[_recording-<label>]_physio.json
  <matches>[_recording-<label>]_physio.tsv.gz
  <matches>[_recording-<label>]_physioevents.json
  <matches>[_recording-<label>]_physioevents.tsv.gz
meg/
  <matches>[_recording-<label>]_physio.json
  <matches>[_recording-<label>]_physio.tsv.gz
  <matches>[_recording-<label>]_physioevents.json
  <matches>[_recording-<label>]_physioevents.tsv.gz
motion/
  <matches>[_recording-<label>]_physio.json
  <matches>[_recording-<label>]_physio.tsv.gz
  <matches>[_recording-<label>]_physioevents.json
  <matches>[_recording-<label>]_physioevents.tsv.gz
nirs/
  <matches>[_recording-<label>]_physio.json
  <matches>[_recording-<label>]_physio.tsv.gz
  <matches>[_recording-<label>]_physioevents.json
  <matches>[_recording-<label>]_physioevents.tsv.gz
perf/
  <matches>[_recording-<label>]_physio.json
  <matches>[_recording-<label>]_physio.tsv.gz
  <matches>[_recording-<label>]_physioevents.json
  <matches>[_recording-<label>]_physioevents.tsv.gz
pet/
  <matches>[_recording-<label>]_physio.json
  <matches>[_recording-<label>]_physio.tsv.gz
  <matches>[_recording-<label>]_physioevents.json
```

`<matches>[_recording-<label>]_physioevents.tsv.gz`

Legend:

- `<matches>` is a placeholder to denote an arbitrary (and valid) sequence of entities and labels at the beginning of the filename (only BIDS "raw").
- `<source-entities>` is a placeholder to denote an arbitrary sequence of entities and labels at the beginning of the filename matching a source file from which the file derives (only BIDS-Derivatives).
- Filename entities or directories between square brackets (for example, `[_ses-<label>]`) are OPTIONAL.
- Some entities may only allow specific values, in which case those values are listed in `<>`, separated by `|`.
- `_<suffix>` means that there are several ( $>6$ ) valid suffixes for this filename pattern.
- `.<extension>` means that there are several ( $>6$ ) valid extensions for this file type.
- `[_gz]` means that both the unzipped and gzipped versions of the extension are valid.

The `recording-<label>` entity is OPTIONAL, and is described in Continuous physiological recordings, below.

Columns of TSV.GZ files MUST be defined in the corresponding JSON sidecar and the tabular content MUST NOT include a header line.

As a consequence, when supplying a `<matches>_<physio|physioevents>.tsv.gz` file, an accompanying `<matches>_<physio|physioevents>.json` MUST be supplied as well.

For multi-echo data, a single `_physio.<tsv.gz|json>` file without the `echo-<index>` entity applies to all echos of a particular run. For example:

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

This specification section first describes the organization of continuous physiological recordings, and then events corresponding to the physiological recordings. Finally, the remainder of the document describes specific types of continuous recordings such as eye-tracking.

## Continuous physiological recordings

Continuous physiological recordings, such as pulse monitoring, electrocardiogram, respiratory movement measured with a respiration belt, gas concentration, or eye-tracking, MUST use `_physio.<tsv.gz|json>` pairs.

### Storing different recordings

The `recording-<label>` entity MAY be used to distinguish between several recording files. Recordings with different metadata such as sampling frequencies or recording device MUST be stored in separate files with different `recording-<label>` entities. For example, given a BOLD acquisition of a breath-holding task (`task-bht`) for which pulse and respiratory movement were sampled at different frequencies, recordings are separated as follows:

```
sub-01/
  func/
    sub-01_task-bht_bold.nii.gz
    sub-01_task-bht_recording-cardiac_physio.json
    sub-01_task-bht_recording-cardiac_physio.tsv.gz
    sub-01_task-bht_recording-respiratory_physio.json
    sub-01_task-bht_recording-respiratory_physio.tsv.gz
```

Metadata fields for `<matches>_physio.json` files. General metadata fields include `SamplingFrequency`, `StartTime`, `Columns`, and `Manufacturer`, in addition to individual column descriptions. Each individual column in the TSV file MAY be documented as its own field in the JSON file (identical to the practice in other TSV+JSON file pairs).

Recordings with different key metadata MUST be split into separate files.

When key metadata such as sampling frequencies, manufacturers varies between recordings, tabular data MUST be split into separate files. In such cases, the `recording-<label>` entity MUST be used to distinguish these files.

Metadata sidecar files (`<matches>_physio.json`) MAY define the field `PhysioType` to indicate a specific type of recording. The default value of `PhysioType` is `"generic"`, and MUST be assumed if the `PhysioType` metadata is not defined. Specific recording types (that is, when `PhysioType` takes a valid value other than `"generic"`) have separate prescriptions for columns in the TSV.GZ files and corresponding metadata specifications.

Using specific recording types is RECOMMENDED when available in the specification.

The allowed physiological recording types encoded by `PhysioType` and their corresponding metadata specifications are described in subsection `Specific physiological signal types` below, and its subsections:

- eye-tracking ([subsection Eye-tracking](#)).

The following table specifies metadata fields for `"generic"` recordings:

Key name	Requirement Level	Data type	Description
SamplingFrequency	REQUIRED	<a href="#">number</a>	Sampling frequency (in Hz) of all the data in the recording, regardless of their type (for example, 2400).
StartTime	REQUIRED	<a href="#">number</a>	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). This data MAY be specified with sub-second precision using the syntax <code>s[.000000]</code> , where <code>s</code> reflects whole seconds, and <code>.000000</code> reflects OPTIONAL fractional seconds.
Columns	REQUIRED	<a href="#">array of strings</a>	Names of columns in file.

Key name	Requirement Level	Data type	Description
PhysioType	RECOMMENDED	string	Defines the specific type of physiological recording. For backwards compatibility, the default value is "generic".Must be one of: "generic", "eyetrack".

Hardware information. Details about the hardware MAY be stored with the following metadata fields.

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

Additional metadata may be included as in any TSV file to specify, for example, the units of the recorded time series.

Column naming recommendations for "generic" recordings. 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
Additional Columns	OPTIONAL	n/a	Additional columns are allowed.

Please note that the specification of columns such as cardiac, respiratory, and trigger above follow the general specifications for tabular files:



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	For categorical variables: An object of possible values (keys) and their descriptions (values).
Units	RECOMMENDED	string	Measurement units for the associated variable. SI units in CMIXF formatting are RECOMMENDED (see Units).
Delimiter	OPTIONAL	string	If rows in a column may be interpreted as a lists of values, the character that separates one value from the next.
TermURL	RECOMMENDED	string	URL pointing to a formal definition of this type of data in an ontology available on the web. For example: <a href="https://www.ncbi.nlm.nih.gov/mesh/68008297">https://www.ncbi.nlm.nih.gov/mesh/68008297</a> for "male".
HED	OPTIONAL	string or object of strings	Hierarchical Event Descriptor (HED) information, see the HED for details.

Examples. Let’s encode cardiac and respiratory recordings, as well as a trigger signal, the three of them sampled at 100.0 Hz by the same device during a behavioral task:

```
sub-01/  
  func/  
    sub-01_task-nback_physio.json  
    sub-01_task-nback_physio.tsv.gz
```

In this example, the contents of `sub-01_task-nback_physio.tsv.gz` after decompression are:

```
tsvgz {linenums="1"} 34  110 0 44  112 0 23  100 1
```

and the header-less TSV.GZ contents are described with the following metadata `sub-01_task-nback_physio.json` where the `Columns` field defines the names corresponding to the three columns above:

```
{  
  "Columns": ["cardiac", "respiratory", "trigger"],  
  "Manufacturer": "Brain Research Equipment ltd.",  
  "PhysioType": "generic",  
  "SamplingFrequency": 100.0,
```

```
"StartTime": -22.345,
"cardiac": {
  "Description": "continuous pulse measurement",
  "Units": "mV"
},
"respiratory": {
  "Description": "continuous measurements by respiration belt",
  "Units": "mV"
},
"trigger": {
  "Description": "continuous measurement of the scanner trigger signal",
  "Units": "V"
}
}
```

The example shows the three REQUIRED metadata entries `Columns`, `SamplingFrequency`, and `StartTime`. Columns are further described following the specifications for tabular files, indicating `Description` and `Units` fields. Other fields, such as `TermURL`, `LongName`, MAY be included.

Because a missing `PhysioType` is assumed to be "generic", the following sidecar is equivalent:

```
{
  "Columns": ["cardiac", "respiratory", "trigger"],
  "Manufacturer": "Brain Research Equipment ltd.",
  "SamplingFrequency": 100.0,
  "StartTime": -22.345,
  "cardiac": {
    "Description": "continuous pulse measurement",
    "Units": "mV"
  },
  "respiratory": {
    "Description": "continuous measurements by respiration belt",
    "Units": "mV"
  },
  "trigger": {
    "Description": "continuous measurement of the scanner trigger signal",
    "Units": "V"
  }
}
```

If the "cardiac" and "respiratory" signals above were acquired at different sampling frequencies, then the recordings MUST be separated into two files disambiguated by the recording-`<label>` entity:

sub-01/

```
func/  
  sub-01_task-nback_recording-cardiac_physio.json  
  sub-01_task-nback_recording-cardiac_physio.tsv.gz  
  sub-01_task-nback_recording-respiratory_physio.json  
  sub-01_task-nback_recording-respiratory_physio.tsv.gz
```

Physiology ”events”

Discontinuous data associated with continuous recordings stored in <matches>\_physio.tsv.gz files MAY be specified following the summary template pattern above. Physiology ”events” files <matches>\_recording-<label>\_physioevents.tsv.gz MUST follow specific column specifications:

Column name	Requirement Level	Data type	Description
onset	REQUIRED	number	Onset of the event relative to the timeline defined by the corresponding physiological recording file. Typically, it will correspond to a timestamp issued by the recording device. This column must appear first in the file.
duration	RECOMMENDED	number	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. This column may appear anywhere in the file. Must be a number greater than or equal to 0.
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. This column may appear anywhere in the file.

Column name	Requirement Level	Data type	Description
message	OPTIONAL	string	Brief free-text description of a message (for example in a log generated by a device), or other information of interest. This column may appear anywhere in the file.
Additional Columns	OPTIONAL	n/a	Additional columns are allowed.

The following table specifies metadata fields for the <matches>[\_recording-<label>]\_physioevents.json file.

Key name	Requirement Level	Data type	Description
Columns	REQUIRED	array of strings	Names of columns in file.
Description	RECOMMENDED	string	Free-form natural language description.
OnsetSource	REQUIRED	string	An existing column name in an corresponding recoding data TSV file that indexes or is correspondent to the "onset" column of the present TSV file. For example, "timestamp" column.

The REQUIRED OnsetSource metadata specifies the interpretation of the values of the onset column. If OnsetSource is the name of a column in the associated <matches>[\_recording-<label>]\_physio.tsv.gz file, the values have the same interpretation as values in the named column.

For example, considering the following structure:

```
sub-01/
  func/
    sub-01_task-nback_physio.json
    sub-01_task-nback_physio.tsv.gz
    sub-01_task-nback_physioevents.json
    sub-01_task-nback_physioevents.tsv.gz
```

The decompressed contents of sub-01\_task-nback\_physio.tsv.gz are:

```
{.text noheader="1" linenums="1"} 13894432329 10.1 13894432330 10.0 13894432331      9.5 13894432332      9.2 13894432333      9.0 13894432334
10.2 13894432335 10.3 13894432336 10.1
```

And sub-01\_task-nback\_physio.json defines timestamp column:

```
{
  "SamplingFrequency": 100.0,
  "StartTime": -22.345,
```

```
    "Columns": ["timestamp", "cardiac"],
    "cardiac": {
      "Description": "continuous pulse measurement",
      "Units": "mV"
    },
    "timestamp": {
      "Description": "a continuously increasing identifier of the sampling time registered by the device",
      "Units": "ms",
      "Origin": "System startup"
    }
  }
}
```

The decompressed contents of the corresponding `sub-01_task-nback_physioevents.tsv.gz` are:

```
{.text noheader="1" linenums="1"} 13894432325 Ready 13894432331 Synchronous recalibration triggered 13894432334 External message received:
new block
```

To indicate that the first column (onset) is to be interpreted as a timestamp, the `OnsetSource` MUST be set to "timestamp" in `sub-01_task-nback_physioevents.json`:

```
{
  "Columns": ["onset", "message"],
  "Description": "Messages logged by the measurement device",
  "OnsetSource": "timestamp"
}
```

If there is no appropriate source column in `<matches>[_recording-<label>]_physio.tsv.gz`, `OnsetSource` MAY be set to "n/a". In this case, the values of `onset` MUST be interpreted as row indices into the `physio` file, with the first row having index zero (0). Negative onsets are possible, and such events are interpreted as occurring prior to the start of the recording, at the same sampling rate.

For example, the above `sub-01_task-nback_physioevents.tsv.gz` could be equivalently written:

```
{.text noheader="1"} -3 Ready 3 Synchronous recalibration triggered 6 External message received: new block
```

To indicate that the first column (onset) is to be interpreted as an index, the `OnsetSource` is set to "n/a" in `sub-01_task-nback_physioevents.json`:

```
{
  "Columns": ["onset", "message"],
  "Description": "Messages logged by the measurement device",
  "OnsetSource": "n/a"
}
```

## Specific physiological signal types

### Eye-tracking

[Example datasets](#) with eye-tracking data have been formatted using this specification and can be used for practical guidance when curating a new dataset:

- Combined fMRI and eye-tracking data in a resting-state task, measured with an Eyelink (SR research). Human participant kept their gaze steady at the screen center.

### BIDS dataset

- Combined behavioral and eye-tracking data, measured with and Eyelink (SR Research). Human participants freely viewed as set of natural images. Published paper: <https://doi.org/10.1523/ENEURO.0287-23.2023>

### BIDS dataset

Setting `PhysioType` to the keyword "eyetrack" specifies that the physiological recordings in the `<matches>_physio.tsv.gz` have been acquired with an eye-tracker. In the following, eye-tracker refers to the apparatus allowing the recording of gaze position, and, optionally, pupil size.

Eye-tracking data MUST be stored following the general specifications for "generic" physiological recordings. However, it is REQUIRED that recordings corresponding to each eye (and/or cyclopean or averaged signals for binocular eye-trackers providing a third recording) are split into files with different `recording-<label>`. Therefore, the use of `recording-<label>` is REQUIRED with eye-tracking data. The values "eye1", "eye2", and "eye3" are RECOMMENDED as the respective labels for the `recording-<label>` entity.

The correspondence of labels and the recorded eye MUST be encoded by the MANDATORY `RecordedEye` metadata.

The `recording-<label>` entity MAY take other values such as "left", "cyclopean", or "right" corresponding to the `RecordedEye` metadata. However, it is RECOMMENDED that metadata is not encoded in the file names to avoid conflicts between filenames and metadata. For example, if `recording-<label>` takes the value "left" but the corresponding sidecar JSON file contains a definition of `RecordedEye` being "right".

Eye-tracking files `<matches>_recording-<label>_physio.tsv.gz` MUST follow specific column prescriptions:

Column name	Requirement Level	Data type	Description
timestamp	REQUIRED	<a href="#">number</a>	Timestamp issued by the eye-tracker indexing the continuous recordings corresponding to the sampled eye. This column must appear first in the file.
x_coordinate	REQUIRED	<a href="#">number</a>	Gaze position x-coordinate of the recorded eye, in the coordinate units specified in the corresponding metadata sidecar. This column must appear second in the file.

Column name	Requirement Level	Data type	Description
y_coordinate	REQUIRED	number	Gaze position y-coordinate of the recorded eye, in the coordinate units specified in the corresponding metadata sidecar. This column must appear third in the file.
pupil_size	OPTIONAL	number	Pupil size, as area or diameter, of the recorded eye, in the units specified in the corresponding metadata sidecar. It is RECOMMENDED to indicate the particular type of pupil size that is being recorded in the <b>Description</b> field of this column. It is RECOMMENDED to specify the <b>Units</b> field corresponding to this column. This column may appear anywhere in the file.
Additional Columns	OPTIONAL	n/a	Additional columns are allowed.

Please note that the specification of columns such as `timestamp`, `x_coordinate`, `y_coordinate`, and `pupil_size` follow the general specifications for tabular files and MAY define metadata fields such as `LongName`, `Description`, `Levels`, or `TermURL`. However, in the case of eye-tracking, the metadata entry `Units`, becomes REQUIRED for the columns `x_coordinate` and `y_coordinate`:

Key name	Requirement Level	Data type	Description
Units	REQUIRED	string	Measurement units for the associated variable. SI units in CMIXF formatting are RECOMMENDED (see Units).

The following table specifies metadata fields for the `<matches>_recording-<label>_physio.json` file:

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).

Key name	Requirement Level	Data type	Description
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). This data MAY be specified with sub-second precision using the syntax <code>s[.000000]</code> , where <code>s</code> reflects whole seconds, and <code>.000000</code> reflects OPTIONAL fractional seconds.
Columns	REQUIRED	array of strings	Names of columns in file.
DeviceSerialNumber	OPTIONAL	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.
Manufacturer	OPTIONAL	string	Manufacturer of the equipment that produced the measurements.
ManufacturersModelName	OPTIONAL	string	Manufacturer's model name of the equipment that produced the measurements.
SoftwareVersions	OPTIONAL	string	Manufacturer's designation of software version of the equipment that produced the measurements.
PhysioType	REQUIRED	string	Defines the specific type of physiological recording. For backwards compatibility, the default value is "generic". Must be one of: "generic", "eyetrack".
RecordedEye	REQUIRED	string	Indicates the eye being tracked, for example, "left" or "right". It SHOULD be set to "cyclopean" for recordings combining both eyes as potentially generated by binocular eye-trackers. Must be one of: "left", "right", "cyclopean".



Key name	Requirement Level	Data type	Description
SampleCoordinateSystem	REQUIRED	string	Coordinate system of the gaze position recordings. Generally eye-trackers are set to use "gaze-on-screen" coordinate system, but you may use "eye-in-head" or "gaze-in-world". If none of the three default options properly describe the coordinate system, the "custom" keyword MUST be employed and the coordinate system MUST be described using additional metadata entries. Must be one of: "gaze-on-screen", "eye-in-head", "gaze-in-world", "custom".
AverageCalibrationError	OPTIONAL	number	Average calibration error in degrees of visual angle.
CalibrationCount	OPTIONAL	integer	The number of calibrations corresponding to this run. Must be a number greater than or equal to 0.
CalibrationPosition	OPTIONAL	array of arrays	A list of [x, y] coordinates in the CalibrationUnit. For example, using 5 positions calibration presented on an HD screen, it could be [ [960, 50], [960, 540], [960, 1030], [50, 540], [187
CalibrationType	OPTIONAL	string	The type of the calibration procedure executed last. For example the "H3" for horizontal calibration with 3 positions or "HV9" for horizontal and vertical calibration with 9 positions, or one point calibration.
CalibrationUnit	OPTIONAL	string	Unit of "CalibrationPosition". Must be one of: "pixel", "mm", "cm".

Key name	Requirement Level	Data type	Description
EyeTrackerDistance	OPTIONAL	number or array of numbers	Distance (in meters) between the eye-tracker and the participant eye(s). Distance can either be expressed as a single numeric value indicating the shortest distance between the participant's eye and the eye-tracker's camera, or a three-coordinates array indicating the X, Y, Z distances between the participant's eye and the eye-tracker's camera.
EyeTrackingMethod	OPTIONAL	string	Method used to track gaze or pupil position: "P-CR" for video based eye-tracking using pupil and corneal reflection; "DPI" for Dual-Purkinje Imaging system, "SSC" for scleral search coils; "EOG" for electro-oculogram; "Limbus" for trackers estimating limbus borders between the iris and sclera; or other.
MaximalCalibrationError	OPTIONAL	number	Maximal calibration error in degrees of visual angle.
PupilFitMethod	OPTIONAL	string	The method employed for fitting the pupil, for example "centre-of-mass" or "ellipse". If "centre-of-mass" or "ellipse" method is used, it is RECOMMENDED to use these exact labels.
RawDataFilters	OPTIONAL	string	Filter settings applied to eye-movement raw data.

Comprehensively documenting the calibration metadata is RECOMMENDED.

Eye-tracking files `<matches>_recording-<label>_physio.tsv.gz` MAY be annotated with a corresponding `<matches>_recording-<label>_physioevents.tsv.gz` file. The `<matches>_recording-<label>_physioevents.tsv.gz` file MAY be employed to record discontinuous model parameters generated by the eye-tracker, for example, those derived from the saccade and blinks model some eye-trackers produce.

For eye-tracking recordings where "SampleCoordinateSystem" is set to "gaze-on-screen", the following fields pertaining to `<matches>_events.json` escalate to REQUIRED as they are considered essential in eye-tracking data analysis:

- `StimulusPresentation.ScreenDistance`,

- StimulusPresentation.ScreenOrigin,
- StimulusPresentation.ScreenResolution,
- StimulusPresentation.ScreenSize.

Examples. The recordings produced by a monocular eye-tracker during a visual search task may display the following structure:

```
sub-01/  
  func/  
    sub-01_task-visualSearch_bold.json  
    sub-01_task-visualSearch_bold.nii.gz  
    sub-01_task-visualSearch_events.json  
    sub-01_task-visualSearch_events.tsv  
    sub-01_task-visualSearch_recording-eye1_physio.json  
    sub-01_task-visualSearch_recording-eye1_physio.tsv.gz  
    sub-01_task-visualSearch_recording-eye1_physioevents.json  
    sub-01_task-visualSearch_recording-eye1_physioevents.tsv.gz
```

The above example is extended to a binocular eye-tracker producing three signals (left and right eyes, plus a cyclopean recording), as follows:

```
sub-01/  
  func/  
    sub-01_task-visualSearch_bold.json  
    sub-01_task-visualSearch_bold.nii.gz  
    sub-01_task-visualSearch_events.json  
    sub-01_task-visualSearch_events.tsv  
    sub-01_task-visualSearch_recording-eye1_physio.json  
    sub-01_task-visualSearch_recording-eye1_physio.tsv.gz  
    sub-01_task-visualSearch_recording-eye1_physioevents.json  
    sub-01_task-visualSearch_recording-eye1_physioevents.tsv.gz  
    sub-01_task-visualSearch_recording-eye2_physio.json  
    sub-01_task-visualSearch_recording-eye2_physio.tsv.gz  
    sub-01_task-visualSearch_recording-eye2_physioevents.json  
    sub-01_task-visualSearch_recording-eye2_physioevents.tsv.gz  
    sub-01_task-visualSearch_recording-eye3_physio.json  
    sub-01_task-visualSearch_recording-eye3_physio.tsv.gz  
    sub-01_task-visualSearch_recording-eye3_physioevents.json  
    sub-01_task-visualSearch_recording-eye3_physioevents.tsv.gz
```

Given the above example file structures, a corresponding sub-01\_task-visualSearch\_recording-eye1\_physio.json sidecar could read:

```
{  
  "DeviceSerialNumber": "17535483",  
  "Columns": ["timestamp", "x_coordinate", "y_coordinate", "pupil_size"],
```

```
"Manufacturer": "SR-Research",
"ManufacturersModelName": "EYELINK II CL v4.56 Aug 18 2010",
"PhysioType": "eyetrack",
"RecordedEye": "right",
"SampleCoordinateSystem": "gaze-on-screen",
"SamplingFrequency": 1000,
"SoftwareVersions": "SREB1.10.1630 WIN32 LID:F2AE011 Mod:2017.04.21 15:19 CEST",
"timestamp": {
  "Description": "a continuously increasing identifier of the sampling time registered by the device",
  "Units": "ms",
  "Origin": "System startup"
},
"x_coordinate": {
  "LongName": "Gaze position (x)",
  "Description": "Gaze position x-coordinate of the recorded eye, in the coordinate units specified in the corresponding metadata sidecar.",
  "Units": "pixel"
},
"y_coordinate": {
  "LongName": "Gaze position (y)",
  "Description": "Gaze position y-coordinate of the recorded eye, in the coordinate units specified in the corresponding metadata sidecar.",
  "Units": "pixel"
},
"pupil_size": {
  "Description": "Pupil area of the recorded eye as calculated by the eye-tracker in arbitrary units (see EyeLink's documentation for conversion)",
  "Units": "arbitrary"
}
}
```

Content of sub-01\_task-VisualSearch\_events.json:

```
{
  "TaskName": "Visual Search",
  "InstitutionName": "Stanford University",
  "InstitutionAddress": "450 Serra Mall, Stanford, CA 94305-2004, USA",
  "StimulusPresentation": {
    "ScreenDistance": 0.6,
    "ScreenOrigin": ["top", "left"],
    "ScreenRefreshRate": 60,
    "ScreenResolution": [1024, 768],
    "ScreenSize": [0.386, 0.29]
  }
}
```

```
}
```

Example eye-tracking recording. Given the above sub-01\_task-visualSearch\_recording-eye1\_physio.json metadata specification, the decompressed content of the sub-01\_task-visualSearch\_recording-eye1\_physio.tsv.gz can be:

7186799	416.29	267.39	4612.0
7186800	416.29	268.10	4623.0
7186801	416.20	269.00	4623.0
7186802	415.89	269.60	4613.0
7186803	415.70	269.20	4603.0
7186804	415.60	266.79	4591.0
7186805	415.79	264.60	4589.0
7186806	416.10	263.89	4587.0
7186807	416.29	265.20	4587.0
7186808	416.39	266.50	4588.0
7186809	416.50	266.79	4594.0
7186810	416.50	267.20	4599.0
7186811	416.10	268.00	4609.0
7186812	415.70	268.29	4612.0
7186813	416.00	268.60	4605.0

Example sub-01\_task-visualSearch\_recording-eye1\_physioevents.tsv.gz corresponding to the above eye-tracking recording, after decompressing:

7184392	n/a	n/a	n/a	"NO Reply is disabled for function eyelink_cal_result"
7184392	n/a	n/a	n/a	"RECCFG CR 1000 2 0 R"
7184392	n/a	n/a	n/a	"ELCLCFG TOWER"
7186771	n/a	n/a	n/a	"First task trigger"
7186806	72	fixation	0	n/a
7186879	231	saccade	1	n/a
7187111	6186	fixation	0	n/a
7193298	216	saccade	1	n/a
7193515	1286	fixation	0	n/a
7194802	24	saccade	0	n/a
7194827	2403	fixation	0	n/a
7197231	17	saccade	0	n/a
7197249	1640	fixation	0	n/a
7198890	6	saccade	0	n/a
7198897	1105	fixation	0	n/a
7200003	233	saccade	1	n/a
7200237	184	fixation	0	n/a
7200422	15	saccade	0	n/a
7200438	264	fixation	0	n/a

where the first three rows are logged by the eye-tracker and the fourth row shows a message asynchronously received by the eye-tracker. The remainder of the rows contain a subset of parameters registered by the device, derived from applying a model to identify saccades and blinks. The corresponding sub-01\_task-visualSearch\_recording-eye1\_physi sidcar would read:

```
{
  "Columns": ["onset", "duration", "trial_type", "blink", "message"],
  "Description": "Messages logged by the measurement device",
  "OnsetSource": "timestamp",
  "blink": {
    "Description": "Gives status of the eye.",
    "Levels": {
      "0": "Indicates if the eye was open.",
      "1": "Indicates if the eye was closed."
    }
  },
  "message": {
    "Description": "String messages logged by the eye-tracker."
  },
  "trial_type": {
    "Description": "Event type as identified by the eye-tracker's model.",
    "Levels": {
      "fixation": "Indicates a fixation.",
      "saccade": "Indicates a saccade."
    }
  }
}
```

# Behavioral experiments (with no neural recordings)

Datasets containing behavioral data can be found in the [BIDS examples repository](#) and can be used as helpful guidance when curating new datasets.

Template:

```
sub-<label>/
  [ses-<label>]/
    beh/
      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
      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>]_physioevents.json
      sub-<label>[_ses-<label>]_task-<label>[_acq-<label>][_run-<index>][_recording-<label>]_physioevents.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
```

Legend:

- **<matches>** is a placeholder to denote an arbitrary (and valid) sequence of entities and labels at the beginning of the filename (only BIDS "raw").
- **<source-entities>** is a placeholder to denote an arbitrary sequence of entities and labels at the beginning of the filename matching a source file from which the file derives (only BIDS-Derivatives).
- Filename entities or directories between square brackets (for example, `[_ses-<label>]`) are OPTIONAL.
- Some entities may only allow specific values, in which case those values are listed in `<>`, separated by `|`.
- **\_<suffix>** means that there are several (>6) valid suffixes for this filename pattern.
- **.<extension>** means that there are several (>6) valid extensions for this file type.
- **[.gz]** means that both the unzipped and gzipped versions of the extension are valid.

In addition to logs from behavioral experiments performed alongside imaging data acquisitions, one MAY also include data from experiments performed with no neural recordings. The results of those experiments MAY be stored in the `beh` directory 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 MAY be included, but MUST be labeled `_beh.tsv` rather than `_events.tsv`.

The following OPTIONAL columns are pre-defined for behavioral data files:

Column name	Requirement Level	Data type	Description
<code>trial_type</code>	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 <code>go</code> and <code>no-go</code> to refer to response initiation and response inhibition experimental conditions.
<code>response_time</code>	OPTIONAL	number	Response time measured in seconds. A negative response time can be used to represent preemptive responses and <code>n/a</code> denotes a missed response.
<code>HED</code>	OPTIONAL	string	Hierarchical Event Descriptor (HED) tags. See the HED for details.
<code>stim_file</code>	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 <code>/stimuli/</code> directory (under the root directory of the dataset; with OPTIONAL subdirectories). The values under the <code>stim_file</code> column correspond to a path relative to <code>/stimuli</code> . For example <code>images/cat03.jpg</code> will be translated to <code>/stimuli/images/cat03.jpg</code> .
Additional Columns	OPTIONAL	n/a	Additional columns are allowed.

Sidecar JSON (`*_beh.json`)

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` directory (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 directory.

### Task information

Key name	Requirement Level	Data type	Description
TaskName	RECOMMENDED	<a href="#">string</a>	Name of the task. No two tasks should have the same name. The task label included in the filename MAY be derived from this "TaskName" field by removing all non-alphanumeric or + characters (that is, all except those matching <code>[0-9a-zA-Z+]</code> ), and potentially replacing spaces with + to ease readability. For example "TaskName" "faces n-back" or "head nodding" could correspond to task labels <code>faces+n+back</code> or <code>facesnback</code> and <code>head+nodding</code> or <code>headnodding</code> , respectively.
Instructions	RECOMMENDED	<a href="#">string</a>	Text of the instructions given to participants before the recording.
TaskDescription	RECOMMENDED	<a href="#">string</a>	Longer description of the task.
CogAtlasID	RECOMMENDED	<a href="#">string</a>	CogAtlasID of the corresponding <a href="#">Cognitive Atlas</a> Task term.
CogPOID	RECOMMENDED	<a href="#">string</a>	CogPOID of the corresponding <a href="#">CogPO</a> term.

### Institution information

Key name	Requirement Level	Data type	Description
InstitutionName	RECOMMENDED	<a href="#">string</a>	The name of the institution in charge of the equipment that produced the measurements.
InstitutionAddress	RECOMMENDED	<a href="#">string</a>	The address of the institution in charge of the equipment that produced the measurements.

Key name	Requirement Level	Data type	Description
InstitutionalDepartmentName	RECOMMENDED	string	The department in the institution in charge of the equipment that produced the measurements.

Example `_beh.tsv`

```
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 for 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

If information on associated genetic data is supplied as part of a BIDS dataset, these "genetic descriptors" are encoded as an additional, REQUIRED entry in the `dataset_description.json` file.

Datasets linked to a genetic database entry include the following REQUIRED and OPTIONAL keys in the `Genetics` sub-object of `dataset_description.json`:

Key name	Requirement Level	Data type	Description
Dataset	REQUIRED	<a href="#">string</a>	Dataset where data can be retrieved.
Database	OPTIONAL	<a href="#">string</a>	Database of database where the dataset is hosted.
Descriptors	OPTIONAL	<a href="#">string</a> or <a href="#">array</a> of <a href="#">strings</a>	List of relevant descriptors (for example, journal articles) for dataset using a valid Descriptors 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 following fields are defined for `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.

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". For more information on these levels, see <a href="#">Multi-omics approaches to disease</a> by Hasin et al. 2017.
AnalyticalApproach	OPTIONAL	string or array of strings	Methodology or methodologies used to analyze the "GeneticLevel". Values MUST be taken from the <a href="#">database of Genotypes and Phenotypes (dbGaP)</a> 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 <a href="#">Allen Brain Atlas</a> , 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 <a href="#">cell ontology</a> .

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".

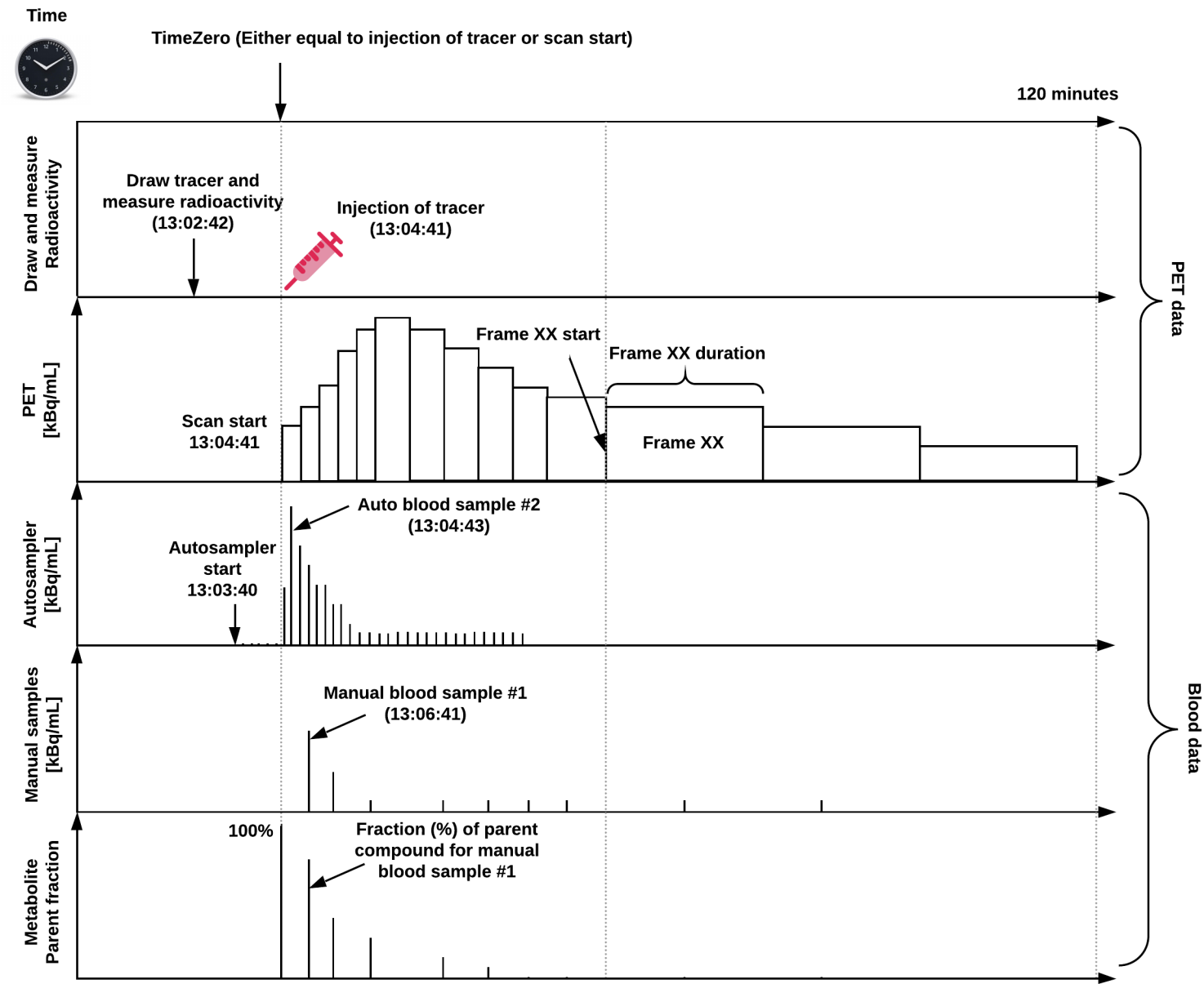




Figure 1: Overview of a common PET experiment, including blood measurements, and defined on a common time scale. Note, "time zero" is often defined as time of injection or scan start, but if a pharmaceutical challenge is carried out during the scan, this time point may also be chosen as time zero. The 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>]_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>]_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>][_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
```

Legend:

- `<matches>` is a placeholder to denote an arbitrary (and valid) sequence of entities and labels at the beginning of the filename (only BIDS "raw").
- `<source-entities>` is a placeholder to denote an arbitrary sequence of entities and labels at the beginning of the filename matching a source file from which the file derives (only BIDS-Derivatives).
- Filename entities or directories between square brackets (for example, `[_ses-<label>]`) are OPTIONAL.
- Some entities may only allow specific values, in which case those values are listed in `<>`, separated by `|`.
- `_<suffix>` means that there are several ( $>6$ ) valid suffixes for this filename pattern.
- `.<extension>` means that there are several ( $>6$ ) valid extensions for this file type.
- `[.gz]` means that both the unzipped and gzipped versions of the extension are valid.

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 `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](https://doi.org/10.1177/0271678X20905433), which we divide into several categories:

Radiochemistry

Key name	Requirement Level	Data type	Description
TracerName	REQUIRED	string	Name of the tracer compound used (for example, "CIMBI-36") Corresponds to DICOM Tags (0008,0105) Mapping Resource and (0008,0122) Mapping Resource Name.
TracerRadionuclide	REQUIRED	string	Radioisotope labeling tracer (for example, "C11"). Corresponds to DICOM Tags (0008,0104) CodeValue and (0008,0104) CodeMeaning.

Key name	Requirement Level	Data type	Description
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 <a href="#">DICOM Tag 0018, 1074 Radionuclide Total Dose</a> .
InjectedRadioactivityUnits	REQUIRED	string	Unit format of the specified injected radioactivity (for example, "MBq").
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.

Key name	Requirement Level	Data type	Description
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").
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 <a href="#">DICOM Tag 0018, 1077 Radiopharmaceutical Specific Activity</a> .
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").

Key name	Requirement Level	Data type	Description
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. For pharmaceutical co-administered with tracer. Corresponds to <a href="#">DICOM Tag 0018, 0034 Intervention Drug Name</a> .
PharmaceuticalDoseAmount	RECOMMENDED	number or array of numbers	Dose amount of administered pharmaceutical. For pharmaceutical co-administered with tracer. Corresponds to <a href="#">DICOM Tag 0018, 0028 Intervention Drug Dose</a> .
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").

Key name	Requirement Level	Data type	Description
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. Corresponds to a combination of DICOM Tags 0018, 0027 Intervention Drug Stop Time and 0018, 0035 Intervention Drug Start Time.
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.
InjectionStart	REQUIRED	number	Time of start of injection with respect to "TimeZero" in the default unit seconds. This corresponds to DICOM Tag 0018, 1072 Contrast/Bolus Start Time converted to seconds relative to "TimeZero". Corresponds to DICOM Tag 0018, 1072 Radiopharmaceutical Start Time.

Key name	Requirement Level	Data type	Description
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 <a href="#">DICOM Tag 0018, 1242 Actual Frame Duration</a> converted to seconds.
InjectionEnd	RECOMMENDED	number	Time of end of injection with respect to "TimeZero" in the default unit seconds. Corresponds to <a href="#">DICOM Tag 0018, 1073 Radiopharmaceutical Stop Time</a> converted to seconds relative to TimeZero.
ScanDate	ScanDate	string	Date of scan in the format "YYYY-MM-DD[Z] ". This field is DEPRECATED, and this metadata SHOULD be recorded in the <code>acq_time</code> column of the corresponding ScanDate. Corresponds to <a href="#">DICOM Tag 0008, 0022 Acquisition Date</a> .

We refer to the common principles for the standards for describing dates and timestamps, including possibilities for deidentification (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.

Key name	Requirement Level	Data type	Description
ReconMethodName	REQUIRED	string	Reconstruction method or algorithm (for example, "3d-op-osem"). This partly matches the <a href="#">DICOM Tag 0054, 1103 Reconstruction Method</a> .
ReconMethodParameterLabels	REQUIRED	array of strings	Names of reconstruction parameters (for example, ["subsets", "iterations"]). This partly matches the <a href="#">DICOM Tag 0054, 1103 Reconstruction Method</a> .
ReconMethodParameterUnits	RECOMMENDED, but REQUIRED if ReconMethodParameterLabels does not contain "none"	array of strings	Unit of reconstruction parameters (for example, ["none", "none"]). This partly matches the <a href="#">DICOM Tag 0054, 1103 Reconstruction Method</a> .
ReconMethodParameterValues	RECOMMENDED, but REQUIRED if ReconMethodParameterLabels does not contain "none"	array of numbers	Values of reconstruction parameters (for example, [21, 3]). This partly matches the <a href="#">DICOM Tag 0054, 1103 Reconstruction Method</a> .
ReconFilterType	REQUIRED	string or array of strings	Type of post-recon smoothing (for example, ["Shepp"]). This partly matches the <a href="#">DICOM Tag 0018, 1210 Convolution Kernel</a> .
ReconFilterSize	RECOMMENDED, but REQUIRED if ReconFilterType is not "none"	number or array of numbers	Kernel size of post-recon filter (FWHM) in default units "mm". This partly matches the <a href="#">DICOM Tag 0018, 1210 Convolution Kernel</a> .
AttenuationCorrection	REQUIRED	string	Short description of the attenuation correction method used. This corresponds to <a href="#">DICOM Tag 0054, 1101 Attenuation Correction Method</a> .
ReconMethodImplementationVersion	RECOMMENDED	string	Identification for the software used, such as name and version.
AttenuationCorrectionMethodReference	RECOMMENDED	string	Reference paper for the attenuation correction method used.



Key name	Requirement Level	Data type	Description
ScaleFactor	RECOMMENDED	array of numbers	Scale factor for each frame. This field MUST be defined if the imaging data (.nii.gz) are scaled. If this field is not defined, then it is assumed that the scaling factor is 1. Defining this field when the scaling factor is 1 is RECOMMENDED, for the sake of clarity.
ScatterFraction	RECOMMENDED	array of numbers	Scatter fraction for each frame (Units: 0-100%). Corresponds to DICOM Tag 0054, 1323 Scatter Fraction Factor.
DecayCorrectionFactor	RECOMMENDED	array of numbers	Decay correction factor for each frame. Corresponds to DICOM Tag 0054, 1321 Decay Factor.
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. 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").
SinglesRate	RECOMMENDED	array of numbers	Singles 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").

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

Hardware information

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.

Key name	Requirement Level	Data type	Description
ManufacturersModelName	REQUIRED	<a href="#">string</a>	Manufacturer's model name of the equipment that produced the measurements. Corresponds to <a href="#">DICOM Tag 0008, 1090 Manufacturers Model Name</a> .
Units	REQUIRED	<a href="#">string</a>	Measurement units for the associated variable. SI units in CMIXF formatting are RECOMMENDED (see Units). SI unit for radioactivity (Becquerel) should be used (for example, "Bq/mL"). Corresponds to <a href="#">DICOM Tag 0054, 1001 Units</a> .
BodyPart	RECOMMENDED	<a href="#">string</a>	Body part of the organ / body region scanned. Corresponds to <a href="#">DICOM Tag 0018, 0015 Body Part Examined</a> .

## Institution information

Key name	Requirement Level	Data type	Description
InstitutionName	RECOMMENDED	<a href="#">string</a>	The name of the institution in charge of the equipment that produced the measurements. Corresponds to <a href="#">DICOM Tag 0008, 0080 InstitutionName</a> .
InstitutionAddress	RECOMMENDED	<a href="#">string</a>	The address of the institution in charge of the equipment that produced the measurements. Corresponds to <a href="#">DICOM Tag 0008, 0081 InstitutionAddress</a> .
InstitutionalDepartmentName	RECOMMENDED	<a href="#">string</a>	The department in the institution in charge of the equipment that produced the measurements. Corresponds to <a href="#">DICOM Tag 0008, 1040 Institutional Department Name</a> .

## Tissue description

Key name	Requirement Level	Data type	Description
BodyPart	OPTIONAL	string	Body part of the organ / body region scanned. Corresponds to <a href="#">DICOM Tag 0018, 0015</a> Body Part Examined.
BodyPartDetails	OPTIONAL	string	Additional details about body part or location (for example: "corpus callosum").
BodyPartDetailsOntology	OPTIONAL	string	BodyPartDetailsOntology of ontology used for BodyPartDetails (for example: "https://www.ebi.ac.uk/ols/ontologies/uberon").

#### Deidentification information

Describes the mechanism or method used to modify or remove metadata and/or pixel data to protect the patient or participant's identity.

Key name	Requirement Level	Data type	Description
DeidentificationMethod	OPTIONAL	array of strings	A description of the mechanism or method used to remove the Patient's identity. Corresponds to <a href="#">DICOM Tag 0012, 0063</a> De-identification Method. Corresponds to <a href="#">DICOM Tag 0012, 0063</a> De-identification Method.
DeidentificationMethodCodeSequence	OPTIONAL	array of objects	A sequence of code objects describing the mechanism or method use to remove the Patient's identity. Corresponds to <a href="#">DICOM Tag 0012, 0064</a> De-identification Method Code Sequence. Corresponds to <a href="#">DICOM Tag 0012, 0064</a> De-identification Method Code Sequence.

Each object in the `DeidentificationMethodCodeSequence` array includes the following RECOMMENDED keys:

Key name	Requirement Level	Data type	Description
CodeValue	RECOMMENDED	string	An identifier that is unambiguous within the Coding Scheme denoted by Coding Scheme Designator and Coding Scheme Version. Corresponds to <a href="#">DICOM Tag 0008, 0100 Code Value</a> .
CodeMeaning	RECOMMENDED	string	Text that has meaning to a human and conveys the meaning of the term Corresponds to <a href="#">DICOM Tag 0008, 0104 Code Meaning</a> .
CodingSchemeDesignator	RECOMMENDED	string	The identifier of the coding scheme in which the coded entry is defined. Corresponds to <a href="#">DICOM Tag 0008, 0102 Coding Scheme Designator</a> .
CodingSchemeVersion	RECOMMENDED	string	An identifier of the version of the coding scheme if necessary to resolve ambiguity. Corresponds to <a href="#">DICOM Tag 0008, 0103 Coding Scheme Version</a> .

Task

If the OPTIONAL `task-<label>` is used, the following metadata SHOULD be used.

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 filename MAY be derived from this "TaskName" field by removing all non-alphanumeric or + characters (that is, all except those matching [0-9a-zA-Z+]), and potentially replacing spaces with + to ease readability. For example "TaskName" "faces n-back" or "head nodding" could correspond to task labels faces+n+back or facesnback and head+nodding or headnodding, respectively. If used to denote resting scans, a RECOMMENDED convention is to use labels beginning with rest.
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.
CogAtlasID	RECOMMENDED	string	CogAtlasID of the corresponding <a href="#">Cognitive Atlas</a> Task term.
CogPOID	RECOMMENDED	string	CogPOID of the corresponding <a href="#">CogPO</a> term.

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, 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](https://doi.org/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
```

Legend:

- <matches> is a placeholder to denote an arbitrary (and valid) sequence of entities and labels at the beginning of the filename (only BIDS "raw").
- <source-entities> is a placeholder to denote an arbitrary sequence of entities and labels at the beginning of the filename matching a source file from which the file derives (only BIDS-Derivatives).
- Filename entities or directories between square brackets (for example, [\_ses-<label>]) are OPTIONAL.
- Some entities may only allow specific values, in which case those values are listed in <>, separated by |.
- \_<suffix> means that there are several (>6) valid suffixes for this filename pattern.
- .<extension> means that there are several (>6) valid extensions for this file type.
- [.gz] means that both the unzipped and gzipped versions of the extension are valid.

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 REQUIRED `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 the sampling method is unknown, then recording SHOULD be set as `manual`. 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](https://doi.org/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	<a href="#">boolean</a>	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 <code>true</code> , the <code>metabolite_parent_fraction</code> column MUST be present in the corresponding <code>*_blood.tsv</code> file. Must be one of: <code>"true"</code> , <code>"false"</code> .
WholeBloodAvail	REQUIRED	boolean	Boolean that specifies if whole blood measurements are available. If <code>true</code> , the <code>whole_blood_radioactivity</code> column MUST be present in the corresponding <code>*_blood.tsv</code> file. Must be one of: <code>"true"</code> , <code>"false"</code> .
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 <code>false</code> . Must be one of: <code>"true"</code> , <code>"false"</code> .
WithdrawalRate	RECOMMENDED	number	The rate at which the blood was withdrawn from the subject. The unit of the specified withdrawal rate should be in <code>"mL/s"</code> .
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 <code>"g/mL"</code> .

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 <code>hplc_recovery_fractions</code> column MUST be present in the corresponding <code>*_blood.tsv</code> 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 <code>TimeZero</code> defined by the <code>*_pet.json</code> . For example, 5. This column must appear first in the file.
plasma_radioactivity	OPTIONAL, but REQUIRED if PlasmaAvail is true	number	Radioactivity in plasma, in unit of plasma radioactivity (for example, <code>kBq/mL</code> ). This column may appear anywhere in the file.
metabolite_parent_fraction	OPTIONAL, but REQUIRED if MetaboliteAvail is true	number	Parent fraction of the radiotracer (0-1). This column may appear anywhere in the file. Must be a number greater than or equal to 0 and less than or equal to 1.

Column name	Requirement Level	Data type	Description
metabolite_polar_fraction	OPTIONAL, but RECOMMENDED if MetaboliteAvail is true	number	Polar metabolite fraction of the radiotracer (0-1). This column may appear anywhere in the file. Must be a number greater than or equal to 0 and less than or equal to 1.
hplc_recovery_fractions	OPTIONAL, but REQUIRED if MetaboliteRecoveryCorrectionApplied is true	number	HPLC recovery fractions (the fraction of activity that gets loaded onto the HPLC). This column may appear anywhere in the file.
whole_blood_radioactivity	OPTIONAL, but REQUIRED if WholeBloodAvail is true	number	Radioactivity in whole blood samples, in unit of radioactivity measurements in whole blood samples (for example, kBq/mL). This column may appear anywhere in the file.
Additional Columns	OPTIONAL	n/a	Additional columns are allowed.

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
```

Legend:

- <matches> is a placeholder to denote an arbitrary (and valid) sequence of entities and labels at the beginning of the filename (only BIDS "raw").
- <source-entities> is a placeholder to denote an arbitrary sequence of entities and labels at the beginning of the filename matching a source file from which the file derives (only BIDS-Derivatives).
- Filename entities or directories between square brackets (for example, [\_ses-<label>]) are OPTIONAL.
- Some entities may only allow specific values, in which case those values are listed in <>, separated by |.
- \_<suffix> means that there are several (>6) valid suffixes for this filename pattern.
- .<extension> means that there are several (>6) valid extensions for this file type.
- [.gz] means that both the unzipped and gzipped versions of the extension are valid.

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. Further, OME-ZARR (sometimes referred to as OME-NGFF or NGFF) has been developed to provide improved access and storage for large data via chunked and compressed N-dimensional arrays.

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.btif` for [BigTIFF](#) files)
- [OME-ZARR/NGFF](#) (`.ome.zarr` directories)

Modality suffixes

Microscopy data currently support the following imaging modalities:

Name	suffix	Description
2-photon excitation microscopy	2PE	2-photon excitation microscopy imaging data
Bright-field microscopy	BF	Bright-field microscopy imaging data
Coherent anti-Stokes Raman spectroscopy	CARS	Coherent anti-Stokes Raman spectroscopy imaging data
Confocal microscopy	CONF	Confocal microscopy imaging data
Differential interference contrast microscopy	DIC	Differential interference contrast microscopy imaging data
Dark-field microscopy	DF	Dark-field microscopy imaging data
Fluorescence microscopy	FLUO	Fluorescence microscopy imaging data
Multi-photon excitation microscopy	MPE	Multi-photon excitation microscopy imaging data
Nonlinear optical microscopy	NLO	Nonlinear optical microscopy imaging data
Optical coherence tomography	OCT	Optical coherence tomography imaging data
Phase-contrast microscopy	PC	Phase-contrast microscopy imaging data
Polarized-light microscopy	PLI	Polarized-light microscopy imaging data
Scanning electron microscopy	SEM	Scanning electron microscopy imaging data

Name	suffix	Description
Selective plane illumination microscopy	SPIM	Selective plane illumination microscopy imaging data
Super-resolution microscopy	SR	Super-resolution microscopy imaging data
Transmission electron microscopy	TEM	Transmission electron microscopy imaging data
X-ray Phase-Contrast Tomography	XPCT	X-ray phase-contrast tomography imaging data
Micro-CT	uCT	Micro-CT 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
```

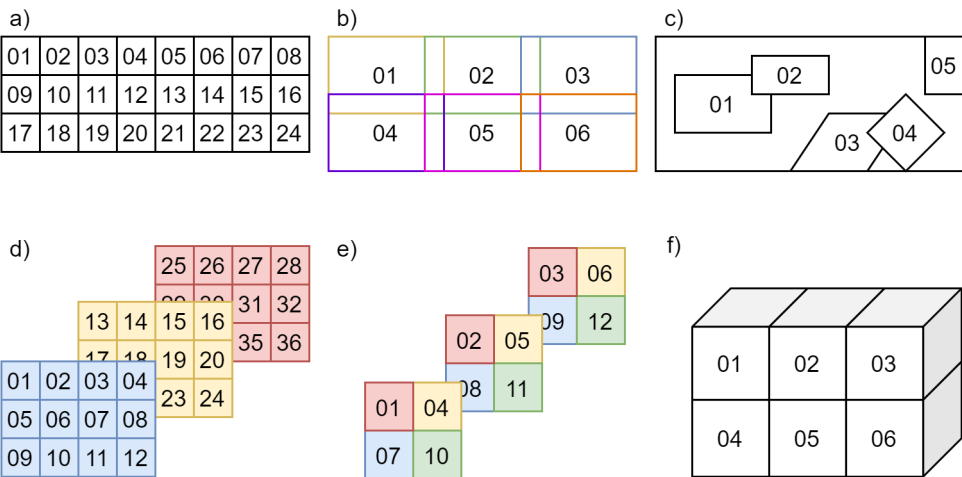
In this example, the entity stain is used to distinguish images with different stains in separate files from the same sample. In the case where a single file contains different staining in each channel, the `stain-<label>` is omitted.

Stains SHOULD be indicated in the "SampleStaining" key in the sidcar JSON file, although the label may be different. Description of antibodies SHOULD also be indicated in "SamplePrimaryAntibodies" and/or "SampleSecondaryAntibodies" 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` directory 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.



## Image Acquisition

Key name	Requirement Level	Data type	Description
PixelSize	REQUIRED	array of <a href="#">numbers</a>	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.
PixelSizeUnits	REQUIRED	<a href="#">string</a>	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	<a href="#">string</a>	Lens immersion medium. If the file format is OME-TIFF, the value MUST be consistent with the Immersion OME metadata field.
NumericalAperture	OPTIONAL	<a href="#">number</a>	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	<a href="#">number</a>	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	<a href="#">string</a>	Description of the image acquisition protocol or ImageAcquisitionProtocol (for example from <a href="#">protocols.io</a> ).

Key name	Requirement Level	Data type	Description
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 <a href="#">DICOM Body Part Examined</a> (for example "BRAIN").
BodyPartDetails	RECOMMENDED	string	Additional details about body part or location (for example: "corpus callosum").
BodyPartDetailsOntology	OPTIONAL	string	BodyPartDetailsOntology 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"]).

Key name	Requirement Level	Data type	Description
SamplePrimaryAntibody	RECOMMENDED	<a href="#">string</a> or <a href="#">array of strings</a>	Description(s) of the primary antibody used for immunostaining. Either an <a href="#">RRID</a> or the name, supplier and catalog number of a commercial antibody. For non-commercial antibodies either an <a href="#">RRID</a> 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.
SampleSecondaryAntibody	RECOMMENDED	<a href="#">string</a> or <a href="#">array of strings</a>	Description(s) of the secondary antibody used for immunostaining. Either an <a href="#">RRID</a> or the name, supplier and catalog number of a commercial antibody. For non-commercial antibodies either an <a href="#">RRID</a> 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	<a href="#">number</a>	Slice thickness of the tissue sample in the unit micrometers ("um") (for example: 5).Must be a number greater than 0.
TissueDeformationScaling	OPTIONAL	<a href="#">number</a>	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	<a href="#">string</a>	Description of the sample extraction protocol or SampleExtractionProtocol (for example from <a href="#">protocols.io</a> ).

Key name	Requirement Level	Data type	Description
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 <code>chunk-&lt;index&gt;</code> is used in filenames	array of arrays	3x3 or 4x4 affine transformation matrix describing spatial chunk transformation, for 2D and 3D respectively (for examples: <code>[[2, 0, 0], [0, 3, 0], [0, 0, 1]]</code> in 2D for 2x and 3x scaling along the first and second axis respectively; or <code>[[1, 0, 0, 0], [0, 2, 0, 0], [0, 0, 3, 0], [0, 0, 0, 1]]</code> 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 <code>ChunkTransformationMatrix</code> is present	array of strings	Describe the axis of the <code>ChunkTransformationMatrix</code> (for examples: <code>["X", "Y"]</code> or <code>["Z", "Y", "X"]</code> ).

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

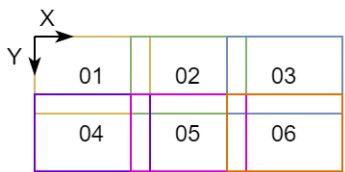


Figure 2: Example figure for chunks transformations.

In this example, there is no scaling and `chunk-01` is at the origin. `chunk-05` is translated by 5  $\mu\text{m}$  along  $X+$  and by 3  $\mu\text{m}$  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"]
}
```

Hardware information

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.

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.
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 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://rrid.site/data/source/nlx\_154697-1/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>
      sub-<label>[_ses-<label>]_sample-<label>[_acq-<label>]_photo.json
```

Legend:

- <matches> is a placeholder to denote an arbitrary (and valid) sequence of entities and labels at the beginning of the filename (only BIDS "raw").
- <source-entities> is a placeholder to denote an arbitrary sequence of entities and labels at the beginning of the filename matching a source file from which the file derives (only BIDS-Derivatives).
- Filename entities or directories between square brackets (for example, [\_ses-<label>]) are OPTIONAL.
- Some entities may only allow specific values, in which case those values are listed in <>, separated by |.
- \_<suffix> means that there are several (>6) valid suffixes for this filename pattern.
- .<extension> means that there are several (>6) valid extensions for this file type.
- [.gz] means that both the unzipped and gzipped versions of the extension are valid.

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/
  ses-01/
    micr/
      sub-01_ses-01_sample-01_acq-1_photo.jpg
      sub-01_ses_01_sample-01_acq-2_photo.jpg
```

Photo data MAY be accompanied by a JSON file containing the following fields. The IntendedFor field is used to link the photo to specific image(s) it was acquired for.

Key name	Requirement Level	Data type	Description
PhotoDescription	OPTIONAL	string	Description of the photo.
IntendedFor	OPTIONAL	string or array	The paths to files for which the associated file is intended to be used. Contains one or more IntendedFor. Using forward-slash separated paths relative to the participant subdirectory is IntendedFor. This field is OPTIONAL, in case the photos do not correspond to any particular images, it does not have to be filled.



For example: sub-01\_ses-01\_sample-01\_acq-1\_photo.json

```
{
  "PhotoDescription": "After clearing",
  "IntendedFor": [
    "ses-01/micr/sub-01_ses-01_sample-01_run-1_chunk-01_SPIM.ome.tif",
    "ses-01/micr/sub-01_ses-01_sample-01_run-1_chunk-02_SPIM.ome.tif",
    "ses-01/micr/sub-01_ses-01_sample-01_run-1_chunk-03_SPIM.ome.tif",
    "ses-01/micr/sub-01_ses-01_sample-01_run-1_chunk-04_SPIM.ome.tif"
  ]
}
```

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

sub-01\_sample-01\_photo.jpg



# Near-Infrared Spectroscopy

Support for Near-Infrared Spectroscopy (NIRS) 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 NIRS datasets](#) have been formatted using this specification and can be used for practical guidance when curating a new dataset.

## NIRS recording data

Template:

```
sub-<label>/
  [ses-<label>/]
    nirs/
      sub-<label>[_ses-<label>]_task-<label>[_acq-<label>][_run-<index>]_channels.json
      sub-<label>[_ses-<label>]_task-<label>[_acq-<label>][_run-<index>]_channels.tsv
      sub-<label>[_ses-<label>][_task-<label>][_acq-<label>]_coordsystem.json
      sub-<label>[_ses-<label>][_acq-<label>]_optodes.json
      sub-<label>[_ses-<label>][_acq-<label>]_optodes.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
      sub-<label>[_ses-<label>]_task-<label>[_acq-<label>][_run-<index>]_nirs.json
      sub-<label>[_ses-<label>]_task-<label>[_acq-<label>][_run-<index>]_nirs.snirf
      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
```

Legend:

- `<matches>` is a placeholder to denote an arbitrary (and valid) sequence of entities and labels at the beginning of the filename (only BIDS "raw").

- `<source-entities>` is a placeholder to denote an arbitrary sequence of entities and labels at the beginning of the filename matching a source file from which the file derives (only BIDS-Derivatives).
- Filename entities or directories between square brackets (for example, `[_ses-<label>]`) are OPTIONAL.
- Some entities may only allow specific values, in which case those values are listed in `<>`, separated by `|`.
- `_<suffix>` means that there are several ( $>6$ ) valid suffixes for this filename pattern.
- `._<extension>` means that there are several ( $>6$ ) valid extensions for this file type.
- `[.gz]` means that both the unzipped and gzipped versions of the extension are valid.

Only the Shared Near Infrared Spectroscopy Format ([SNIRF](#)) file specification is supported in BIDS. The SNIRF specification supports one or more NIRS datasets to be stored in a single `.snirf` file. However, to be BIDS compatible, each SNIRF file MUST contain only a single run. A limited set of fields from the SNIRF specification are replicated in the BIDS specification. This redundancy allows the data to be easily parsed by humans and machines that do not have a SNIRF reader at hand, which improves findability and tooling development.

## Terminology

For proper documentation of NIRS recording metadata, it is important to understand the difference between a Source, Detector, and Channel as these are defined differently to other modalities, such as EEG. The following definitions apply in this document:

- Source - A light emitting device, sometimes called a transmitter.
- Detector - A photoelectric transducer, sometimes called a receiver.
- Optode - Refers to either a source or detector.
- Channel - A paired coupling of a source and a detector with one specific wavelength of light. It is common for a single Source-Detector pair to result in two or more channels with different wavelengths.

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

It is common within the NIRS community for researchers to build their own caps and optode holders to position their sources and detectors, or for optodes to be directly attached to the scalp with adhesive. To facilitate description of the wide variety of possible configurations, several fields are RECOMMENDED within the `*_nirs.json` file. Additionally, in certain situations, reserved keywords MUST be used. When custom modifications are made to a commercially available cap or a custom cap is used, then the reserved keyword `custom` MUST be used for the `CapManufacturersModelName` field. When a custom-made cap is used, that is, no (modified) commercially available cap, the reserved keyword `custom` MUST be used in the `CapManufacturer` field. If no cap is used, the reserved keyword `none` MUST be used in the `CapManufacturer` and `CapManufacturersModelName` field. The use of `NIRSPlacementScheme` is RECOMMENDED when no cap or a customized cap is used, and describes the positioning of the optodes. This field may also contain a reference to a file providing a graphical depiction of the cap, for example a PDF file, a photo, or a bitmap drawing. If the referred file is not specified in BIDS, it MAY be placed in the `/sourcedata` directory. To clarify the usage and interaction of these fields, the following examples are provided:

- If a commercial cap such as EasyCap actiCAP 64 Ch Standard-2 was used: 

```
JSON { "CapManufacturer": "EasyCap", "CapManufacturersModelName": "actiCAP 64 Ch Standard-2", "NIRSPlacementScheme": "10-20" }
```
- If an Artinis Medical Systems cap with custom positions, as may be done by cutting custom holes in the cap, was used: 

```
JSON { "CapManufacturer": "Artinis Medical Systems", "CapManufacturersModelName": "headcap with print, size L, it was modified by adding holes for the" }
```

optodes according to the NIRSPlacementScheme and optode\_layout.pdf", "NIRSPlacementScheme": "see optode\_layout.pdf: 2 groups over the left and right dlPFC, 2 groups over the left and right PPC, 1 group over the left M1 and PMC" }

- If a completely custom cap was knitted: JSON { "CapManufacturer": "custom", "CapManufacturersModelName": "custom knitted cap with holes for optodes according to the NIRSPlacementScheme and optode\_knitted\_layout.jpg", "NIRSPlacementScheme": "see optode\_knitted\_layout.jpg: 2 groups over the left and right dlPFC, 2 groups over the left and right PPC." }
- If no cap was used and optodes were taped to the scalp at positions Cz, C1 and C2: JSON { "CapManufacturer": "none", "CapManufacturersModelName": "none", "NIRSPlacementScheme": ["Cz", "C1", "C2"] } In these cases additional information regarding channels and optodes SHOULD be placed in \*\_channels.tsv and \*\_optodes.tsv files.

Closely spaced or short-separation source-detector pairs are often included in NIRS measurements to obtain a measure of systemic, rather than neural, activity. These source-detector pairs are referred to as short channels. There is variation in how manufacturers implement these short channels, some use specialized sources or detectors, and the placement mechanisms vary. It is beyond the scope of the BIDS specification to define what constitutes a short channel, and detailed characteristics of channels may be stored within the SNIRF file (for example, in the `sourcePower` field). However, to improve searchability and ease of access for users, it is useful to know if short channels were included in the NIRS measurements; the presence of short channels is stored in the field `ShortChannelCount`. If the field `ShortChannelCount` is populated, then the optional column `short_channel` may be used in `*_channels.tsv` to describe which channels were specified as short.

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.

Specific NIRS fields that are REQUIRED or may be REQUIRED depending on other metadata values:

Key name	Requirement Level	Data type	Description
SamplingFrequency	REQUIRED	number or "n/a"	Sampling frequency (in Hz) of all the data in the recording, regardless of their type (for example, 2400). Sampling frequency (in Hz) of all the data in the recording, regardless of their type (for example, 12). If individual channels have different sampling rates, then the field here MUST be specified as n/a and the values MUST be specified in the <code>sampling_frequency</code> column in <code>channels.tsv</code> .)
NIRSChannelCount	REQUIRED	integer	Total number of NIRS channels, including short channels. Corresponds to the number of rows in <code>channels.tsv</code> with any NIRS type. Must be a number greater than or equal to 0.

Key name	Requirement Level	Data type	Description
NIRSSourceOptodeCount	REQUIRED	integer	Number of NIRS sources. Corresponds to the number of rows in <code>optodes.tsv</code> with type "source". Must be a number greater than or equal to 1.
NIRSDetectorOptodeCount	REQUIRED	integer	Number of NIRS detectors. Corresponds to the number of rows in <code>optodes.tsv</code> with type "detector". Must be a number greater than or equal to 1.
ACCELChannelCount	OPTIONAL, but REQUIRED if any channel type is ACCEL	integer	Number of acceleration channels. Must be a number greater than or equal to 0.
GYROChannelCount	OPTIONAL, but REQUIRED if any channel type is GYRO	integer	Number of gyrometer channels. Must be a number greater than or equal to 0.
MAGNChannelCount	OPTIONAL, but REQUIRED if any channel type is MAGN	integer	Number of magnetometer channels. Must be a number greater than or equal to 0.

Specific NIRS fields that SHOULD be present:

Key name	Requirement Level	Data type	Description
CapManufacturer	RECOMMENDED	string	Name of the cap manufacturer (for example, "EasyCap"). If no cap was used, such as with optodes that are directly taped to the scalp, then the string <code>none</code> MUST be used and the <code>NIRSPlacementScheme</code> field MAY be used to specify the optode placement.
CapManufacturersModelName	RECOMMENDED	string	Manufacturer's designation of the cap model (for example, "actiCAP 64 Ch Standard-2"). If there is no official model number then a description may be provided (for example, <code>Headband with print (S-M)</code> ). If a cap from a manufacturer was modified, then the field MUST be set to <code>custom</code> . If no cap was used, then the <code>CapManufacturer</code> field MUST be <code>none</code> and this field MUST be <code>n/a.</code> ")

Key name	Requirement Level	Data type	Description
SourceType	RECOMMENDED	string	Type of source. Preferably a specific model/part number is supplied. This is a freeform description, but the following keywords are suggested: "LED", "LASER", "VCSEL". If individual channels have different SourceType, then the field here should be specified as "mixed" and this column should be included in <code>optodes.tsv</code> .
DetectorType	RECOMMENDED	string	Type of detector. This is a free form description with the following suggested terms: "SiPD", "APD". Preferably a specific model/part number is supplied. If individual channels have different DetectorType, then the field here should be specified as "mixed" and this column should be included in <code>optodes.tsv</code> .
ShortChannelCount	RECOMMENDED	integer	The number of short channels. 0 indicates no short channels. Must be a number greater than or equal to 0.
NIRSPlacementScheme	RECOMMENDED	string or array of strings	Placement scheme of NIRS optodes. Either the name of a standardized placement system (for example, "10-20") or an array of standardized position names (for example, ["Cz", "Pz"]). This field should only be used if a cap was not used. If a standard cap was used, then it should be specified in <code>CapManufacturer</code> and <code>CapManufacturersModelName</code> and this field should be set to "n/a"

Generic information

Key name	Requirement Level	Data type	Description
RecordingDuration	RECOMMENDED	number	Length of the recording in seconds (for example, 3600).
HeadCircumference	RECOMMENDED	number	Circumference of the participant's head, expressed in cm (for example, 58). Must be a number greater than 0.
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"}}.
SubjectArtefactDescription	RECOMMENDED	string	Freeform description of the observed subject artifact 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.

## Hardware information

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.

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.
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.

Task information

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 filename MAY be derived from this "TaskName" field by removing all non-alphanumeric or + characters (that is, all except those matching [0-9a-zA-Z+]), and potentially replacing spaces with + to ease readability. For example "TaskName" "faces n-back" or "head nodding" could correspond to task labels faces+n+back or facesnback and head+nodding or headnodding, respectively.
TaskDescription	RECOMMENDED	string	Longer description of the task.
Instructions	RECOMMENDED	string	Text of the instructions given to participants before the recording.
CogAtlasID	RECOMMENDED	string	CogAtlasID of the corresponding <a href="#">Cognitive Atlas</a> Task term.
CogPOID	RECOMMENDED	string	CogPOID of the corresponding <a href="#">CogPO</a> term.

Example \*\_nirs.json

```
{
  "TaskName": "visual",
  "InstitutionName": "Macquarie University. Australian Hearing Hub",
  "InstitutionAddress": "6 University Ave, Macquarie University NSW 2109 Australia",
  "Manufacturer": "NIRx",
  "ManufacturersModelName": "NIRScout",
  "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",
  "SamplingFrequency": 3.7,
  "NIRSChannelCount": 56,
  "NIRSSourceOptodeCount": 16,
  "NIRSDetectorOptodeCount": 16,
  "ACCELChannelCount": 0,
  "SoftwareFilters": "n/a",
  "RecordingDuration": 233.639,
```

```
"HardwareFilters": {"Highpass RC filter": {"Half amplitude cutoff (Hz)": 0.0159, "Roll-off": "6dB0ctave"}},
"CapManufacturer": "NIRx",
"CapManufacturersModelName": "Headband with print (S-M)",
"NIRSPlacementScheme": "n/a"
}
```

Channels description (\*\_channels.tsv)

Template:

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

Legend:

- <matches> is a placeholder to denote an arbitrary (and valid) sequence of entities and labels at the beginning of the filename (only BIDS "raw").
- <source-entities> is a placeholder to denote an arbitrary sequence of entities and labels at the beginning of the filename matching a source file from which the file derives (only BIDS-Derivatives).
- Filename entities or directories between square brackets (for example, [\_ses-<label>]) are OPTIONAL.
- Some entities may only allow specific values, in which case those values are listed in <>, separated by |.
- \_<suffix> means that there are several (>6) valid suffixes for this filename pattern.
- .<extension> means that there are several (>6) valid extensions for this file type.
- [.gz] means that both the unzipped and gzipped versions of the extension are valid.

This file is RECOMMENDED as it provides easily searchable information across BIDS datasets. Channels are a pairing of source and detector optodes with a specific wavelength of light. Unlike in other modalities, not all pairings of optodes correspond to meaningful data and not all pairs have to be recorded or represented in the data. Note that the source and detector names used in the channel specifications are specified in the \*\_optodes.tsv file below. If a \*\_channels.tsv file is specified, an \*\_optodes.tsv file MUST be specified as well. The required columns in the \*\_channels.tsv file MUST be ordered as listed below.

The BIDS specification supports several types of NIRS devices which output raw data in different forms. The type of measurement is specified in the type column. For example, when measurements are taken with a continuous wave (CW) device that saves the data as optical density, the type should be NIRSCWOPTICALDENSITY and the units should be unitless, this is equivalent to SNIRF data type dOD.

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

Column name	Requirement Level	Data type	Description
name	REQUIRED	string	Label of the channel. This column must appear first in the file.

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. This column must appear second in the file. For a list of valid values for this column, see the type.
source	REQUIRED	string	Name of the source as specified in the *_optodes.tsv file. n/a for channels that do not contain fNIRS signals (for example, acceleration). This column must appear third in the file.
detector	REQUIRED	string	Name of the detector as specified in the *_optodes.tsv file. n/a for channels that do not contain NIRS signals (for example, acceleration). This column must appear fourth in the file.
wavelength_nominal	REQUIRED	number	Specified wavelength of light in nm. n/a for channels that do not contain raw NIRS signals (for example, acceleration). This field is equivalent to /nirs(i)/probe/wavelengths in the SNIRF specification. This column must appear fifth in the file.
units	REQUIRED	string	Physical unit of the value represented in this channel, specified according to the SI unit symbol and possibly prefix symbol, or as a derived SI unit (for example, V, or unitless for changes in optical densities). For guidelines about units see the units and units pages. This column must appear sixth in the file.
sampling_frequency	OPTIONAL, but REQUIRED if SamplingFrequency is n/a in _nirs.json	number	Sampling rate of the channel in Hz. This column may appear anywhere in the file.

Column name	Requirement Level	Data type	Description
component	OPTIONAL, but REQUIRED if type is ACCEL, GYRO or MAGN	string	Description of the spatial axis or label of quaternion component associated with the channel. For example, x,y,z for position channels, or quat_x, quat_y, quat_z, quat_w for quaternion orientation channels. This column may appear anywhere in the file. Must be one of: "x", "y", "z", "quat_x", "quat_y", "quat_z", "quat_w".
wavelength_actual	OPTIONAL	number	Measured wavelength of light in nm. n/a for channels that do not contain raw NIRS signals (acceleration). This field is equivalent to <code>measurementList.wavelengthActual</code> in the SNIRF specification. This column may appear anywhere in the file.
low_cutoff	OPTIONAL	number	Frequencies used for the high-pass filter applied to the channel in Hz. If no high-pass filter applied, use n/a. This column may appear anywhere in the file.
high_cutoff	OPTIONAL	number	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/EMG electronics applies a low-pass filter; specify its frequency here if applicable. This column may appear anywhere in the file. Must be a number greater than or equal to 0.
description	OPTIONAL	string	Brief free-text description of the channel, or other information of interest. This column may appear anywhere in the file.

Column name	Requirement Level	Data type	Description
wavelength_emission_actual	OPTIONAL	number	Measured emission wavelength of light in nm. n/a for channels that do not contain raw NIRS signals (acceleration). This field is equivalent to <code>measurementList.wavelengthEmissionActual</code> in the SNIRF specification. This column may appear anywhere in the file.
short_channel	OPTIONAL	boolean	Is the channel designated as short. The total number of channels listed as short channels SHOULD be stored in <code>ShortChannelCount</code> in <code>*_nirs.json</code> . This column may appear anywhere in the file. Must be one of: "true", "false".
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 <code>[status_description]</code> . This column may appear anywhere in the file. Must be one of: "good", "bad".
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 the <code>status</code> column. This column may appear anywhere in the file.
Additional Columns	OPTIONAL	n/a	Additional columns are allowed if they are defined in the associated metadata file.

### Restricted keyword list for the channel types

All NIRS channels types MUST correspond to a [valid SNIRF data type](#). Additional channels that are recorded simultaneously with the NIRS device and stored in the same data file SHOULD be included as well. However, additional channels that are simultaneously recorded with a different device SHOULD be stored according to their appropriate modality specification. For example, motion data that was simultaneously recorded with a different device should be specified according to the Motion and

not according to the NIRS data type. Whereas, if the motion data was acquired in with the NIRS device itself, it should be included here with the NIRS data. Any of the channel types defined in other BIDS specification MAY be used here as well such as **ACCEL** or **MAGN**. As several of these data types are commonly acquired using NIRS devices they are included as an example at the base of the table. Note that upper-case is **REQUIRED**.

Keyword	Description
NIRSCWAMPLITUDE	Continuous wave amplitude measurements. Equivalent to dataType 001 in SNIRF.
NIRSCWFLUORESCENSEAMPLITUDE	Continuous wave fluorescence amplitude measurements. Equivalent to dataType 051 in SNIRF.
NIRSCWOPTICALDENSITY	Continuous wave change in optical density measurements. Equivalent to dataTypeLabel dOD in SNIRF.
NIRSCWHBO	Continuous wave oxygenated hemoglobin (oxyhemoglobin) concentration measurements. Equivalent to dataTypeLabel HbO in SNIRF.
NIRSCWHBR	Continuous wave deoxygenated hemoglobin (deoxyhemoglobin) concentration measurements. Equivalent to dataTypeLabel HbR in SNIRF.
NIRSCWMUA	Continuous wave optical absorption measurements. Equivalent to dataTypeLabel mua in SNIRF.
ACCEL	Accelerometer channel, one channel for each spatial axis. An extra column <b>component</b> for the axis MUST be added to the *_channels.tsv file (x, y or z).
GYRO	Gyrometer channel, one channel for each spatial axis. An extra column <b>component</b> for the axis MUST be added to the *_channels.tsv file (x, y or z).
MAGN	Magnetometer channel, one channel for each spatial axis. An extra column <b>component</b> for the axis MUST be added to the *_channels.tsv file (x, y or z).
MISC	Miscellaneous

Example \*\_channels.tsv

name	type	source	detector	wavelength_nominal	units
S1-D1	NIRSCWAMPLITUDE	A1	Fz	760	V
S1-D1	NIRSCWAMPLITUDE	A1	Fz	850	V
S1-D2	NIRSCWAMPLITUDE	A1	Cz	760	V
S2-D1	NIRSCWAMPLITUDE	A2	Fz	760	V
S3-D4	NIRSCWAMPLITUDE	VisS2	VisD4	760	V

Optode description (\*\_optodes.tsv)

Template:

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

```
nirs/  
  sub-<label>[_ses-<label>][_acq-<label>]_optodes.json  
  sub-<label>[_ses-<label>][_acq-<label>]_optodes.tsv
```

Legend:

- <matches> is a placeholder to denote an arbitrary (and valid) sequence of entities and labels at the beginning of the filename (only BIDS "raw").
- <source-entities> is a placeholder to denote an arbitrary sequence of entities and labels at the beginning of the filename matching a source file from which the file derives (only BIDS-Derivatives).
- Filename entities or directories between square brackets (for example, [\_ses-<label>]) are OPTIONAL.
- Some entities may only allow specific values, in which case those values are listed in <>, separated by |.
- \_<suffix> means that there are several (>6) valid suffixes for this filename pattern.
- .<extension> means that there are several (>6) valid extensions for this file type.
- [.gz] means that both the unzipped and gzipped versions of the extension are valid.

File that provides the location and type of optodes. Note that coordinates MUST be expressed in Cartesian coordinates according to the NIRSCoordinateSystem and NIRSCoordinateSystemUnits fields in \*\_coordsystem.json. If an \*\_optodes.tsv file is specified, a \*\_coordsystem.json file MUST be specified as well. The order of the required columns in the \*\_optodes.tsv file MUST be as listed below.

The x, y, and z positions are for measured locations, for example, with a polhemus digitizer. If you also have idealized positions, where you wish the optodes to be placed, these can be listed in the template values (for example for "template positions" computed on a sphere). SNIRF contains arrays for both the 3D and 2D locations of data. In BIDS the \*\_optodes.tsv file MUST contain the 3D locations. Only in case 3D positions are unavailable the 2D locations should be used, setting the z field to an n/a value.

The columns of the optodes description table stored in \*\_optodes.tsv are:

Column name	Requirement Level	Data type	Description
name	REQUIRED	string	Name of the optode, must be unique. This column must appear first in the file.
type	REQUIRED	string	The type of the optode. This column must appear second in the file. Must be one of: "source", "detector".
x	REQUIRED	number	Recorded position along the x-axis. "n/a" if not available. This column must appear third in the file.
y	REQUIRED	number	Recorded position along the y-axis. "n/a" if not available. This column must appear fourth in the file.
z	REQUIRED	number	Recorded position along the z-axis. "n/a" if not available. This column must appear fifth in the file.



Column name	Requirement Level	Data type	Description
template_x	OPTIONAL, but REQUIRED if x is n/a	number	Assumed or ideal position along the x axis. This column may appear anywhere in the file.
template_y	OPTIONAL, but REQUIRED if y is n/a	number	Assumed or ideal position along the y axis. This column may appear anywhere in the file.
template_z	OPTIONAL, but REQUIRED if z is n/a	number	Assumed or ideal position along the z axis. This column may appear anywhere in the file.
description	OPTIONAL	string	Free-form text description of the optode, or other information of interest. This column may appear anywhere in the file.
detector_type	OPTIONAL	string	The type of detector. Only to be used if the field <code>DetectorType</code> in <code>*_nirs.json</code> is set to <code>mixed</code> . This column may appear anywhere in the file.
source_type	OPTIONAL	string	The type of source. Only to be used if the field <code>SourceType</code> in <code>*_nirs.json</code> is set to <code>mixed</code> . This column may appear anywhere in the file.
Additional Columns	OPTIONAL	n/a	Additional columns are allowed if they are defined in the associated metadata file.

Example `*_optodes.tsv`

```
name    type    x    y    z    template_x  template_y  template_z
A1  source -0.0707 0.0000 -0.0707 -0.07    0.00    0.07
Fz  detector    0.0000 0.0714 0.0699 0.0 0.07    0.07
S1  source -0.2707 0.0200 -0.1707 -0.03    0.02    -0.2
D2  detector    0.0022 0.1214 0.0299 0.0 0.12    0.03
VisS2 source -0.1707 0.1200 -0.3707 -0.1    0.1    -0.4
VisD4 detector    0.0322 0.2214 0.2299 0.02    0.22    0.23
```

Coordinate System JSON (`*_coordsystem.json`)

Template:

```
sub-<label>/
  [ses-<label>/]
    nirs/
      sub-<label>[_ses-<label>][_task-<label>][_acq-<label>]_coordsystem.json
```

Legend:

- <matches> is a placeholder to denote an arbitrary (and valid) sequence of entities and labels at the beginning of the filename (only BIDS "raw").
- <source-entities> is a placeholder to denote an arbitrary sequence of entities and labels at the beginning of the filename matching a source file from which the file derives (only BIDS-Derivatives).
- Filename entities or directories between square brackets (for example, [\_ses-<label>]) are OPTIONAL.
- Some entities may only allow specific values, in which case those values are listed in <>, separated by |.
- \_<suffix> means that there are several (>6) valid suffixes for this filename pattern.
- .<extension> means that there are several (>6) valid extensions for this file type.
- [.gz] means that both the unzipped and gzipped versions of the extension are valid.

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 optodes and landmarks is expressed. Fiducials are objects with a well-defined location used to facilitate the localization of sensors and co-registration, anatomical landmarks are locations on a research subject such as the nasion (for a detailed definition see coordinate system appendix). The \*\_coordsystem.json is REQUIRED if the optional \*\_optodes.tsv is present. If a corresponding anatomical MRI is available, the locations of anatomical landmarks in that scan should also be stored in the \*\_T1w.json file which goes alongside the NIRS data.

Not all NIRS systems provide 3D coordinate information or digitization capabilities. In this case, only x and y are specified and z is "n/a".

General fields:

Key name	Requirement Level	Data type	Description
IntendedFor	OPTIONAL	string or array	The paths to files for which the associated file is intended to be used. Contains one or more IntendedFor. Using forward-slash separated paths relative to the participant subdirectory is IntendedFor. This identifies the MRI or CT scan associated with the optodes, landmarks, and fiducials.

Fields relating to the NIRS optode positions:

Key name	Requirement Level	Data type	Description
NIRSCoordinateSystem	REQUIRED	string	Defines the coordinate system in which the optode positions are expressed. See NIRSCoordinateSystem for a list of restricted keywords for coordinate systems. If "Other", a definition of the coordinate system MUST be provided in NIRSCoordinateSystemDescription. For a list of valid values for this field, see the NIRSCoordinateSystem.
NIRSCoordinateUnits	REQUIRED	string	Units of the coordinates of NIRSCoordinateSystem. Must be one of: "m", "mm", "cm", "n/a".
NIRSCoordinateProcessingDescription	RECOMMENDED	string	Has any post-processing (such as projection) been done on the optode positions (for example, "surface_projection", "n/a").
NIRSCoordinateSystemDescription	RECOMMENDED, but REQUIRED if NIRSCoordinateSystem 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 NIRS 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").

Key name	Requirement Level	Data type	Description
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.
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".
FiducialsCoordinateSystem	RECOMMENDED	string	Defines the coordinate system for the fiducials. Preferably the same as the "EEGCoordinateSystem". See the FiducialsCoordinateSystem for a list of restricted keywords for coordinate systems. If "Other", provide definition of the coordinate system in "FiducialsCoordinateSystemDescription".For a list of valid values for this field, see the FiducialsCoordinateSystem.
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 landmarks measured during an NIRS 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.
AnatomicalLandmarkCoordinateSystem	RECOMMENDED	string	Defines the coordinate system for the anatomical landmarks. See the AnatomicalLandmarkCoordinateSystem for a list of restricted keywords for coordinate systems. If "Other", provide definition of the coordinate system in "AnatomicalLandmarkCoordinateSystemDescription". a list of valid values for this field, see the AnatomicalLandmarkCoordinateSystem.
AnatomicalLandmarkCoordinateUnits	RECOMMENDED	string	Units of the coordinates of "AnatomicalLandmarkCoordinateSystem".Must be one of: "m", "mm", "cm", "n/a".
AnatomicalLandmarkCoordinateSystemDescription	RECOMMENDED, but REQUIRED if NIRSCoordinateSystem 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.

\*\_coordsystem.json files SHOULD NOT be duplicated for each data file, for example, across multiple tasks. The inheritance principle MUST be used to find the appropriate coordinate system description for a given data file. If optodes are repositioned, it is RECOMMENDED to use multiple sessions to indicate this.

Example \*\_coordsystem.json

```
{
  "NIRSCoordinateSystem": "Other",
  "NIRSCoordinateUnits": "mm",
  "NIRSCoordinateSystemDescription": "RAS orientation: Origin halfway between LPA and RPA, positive x-axis towards RPA, positive y-axis orthogonal to x"
```

```
"FiducialsDescription": "Optodes and fiducials were digitized with Polhemus, fiducials were recorded as the center of vitamin E capsules stucked on t
}
```

# Motion

For information on how to cite this extension when referencing it in the context of the academic literature, please read [Citing BIDS](#).

Motion datasets formatted using this specification are available on the [BIDS examples repository](#) and can be used as helpful guidance when curating new datasets.

## Motion recording data

Template:

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

Legend:

- <matches> is a placeholder to denote an arbitrary (and valid) sequence of entities and labels at the beginning of the filename (only BIDS "raw").
- <source-entities> is a placeholder to denote an arbitrary sequence of entities and labels at the beginning of the filename matching a source file from which the file derives (only BIDS-Derivatives).
- Filename entities or directories between square brackets (for example, [\_ses-<label>]) are OPTIONAL.
- Some entities may only allow specific values, in which case those values are listed in <>, separated by |.
- \_<suffix> means that there are several (>6) valid suffixes for this filename pattern.
- .<extension> means that there are several (>6) valid extensions for this file type.
- [.gz] means that both the unzipped and gzipped versions of the extension are valid.

A wide variety of motion capture systems are used in human research, resulting in different proprietary data formats.

This BIDS extension deals with common outputs from motion capture systems such as positions, orientations, or their time derivatives.

The extension is not limited to motion data in physical space but also encompasses simulated movement in virtual space, as far as these are comparable to movements in physical space. Other dynamic objects than human body parts whose motion is tracked may as well be included as tracked objects. This specification does not include raw camera footages (from camera-based or optical motion capture recordings), but includes the positions or orientations computed using such data.

In this specification, positions (and their time derivatives) are represented as Cartesian coordinates along up to three spatial axes, and orientations (and their time derivatives) are represented as Euler angles. However, to cover recordings from computer graphics applications (for example, virtual 3D motion or immersive virtual reality recording in physical space), orientations are also allowed to be represented as [quaternions](#).

In this case, the quaternion channels can be distinguished from channels containing Euler angles based on the entries in columns `component` and `units` in the `*_channels.tsv` file. See subsection on `Channels description` for further details.

Motion data from one tracking system **MUST** be stored in a single `*_motion.tsv` file. A tracking system is defined as a group of motion channels that share hardware properties (the recording device) and software properties (the recording duration and number of samples). For example, if the position time series of multiple optical markers is processed via one recording unit, this **MAY** be defined as a single tracking system. Note that it is not uncommon to have multiple tracking systems to record at the same time.

Each tracking system **MUST** have its own `*_tracksys-<label>_motion.tsv` file, where `<label>` is a user-defined keyword to be used to identify each file belonging to a tracking system. This is especially helpful when more than one tracking system is used. Data from different tracking systems **MUST** be stored in different `*_tracksys-<label>_motion.tsv` files, each of which is accompanied by `*_tracksys-<label>_motion.json` and `*_tracksys-<label>_channels.tsv` files. Between `tracksys-<label>` entity and `*_motion.tsv`, `*_motion.json`, or `*_channels.tsv` suffixes, optional `acq-<label>` or `acq-<label>` entity **MAY** be inserted.

One column in the `*_tracksys-<label>_motion.tsv` file represents one data channel. Motion files **MUST NOT** have a header row; the ordering of columns is given by the order of rows in the associated `*_channels.tsv` file. The number of columns in `_motion.tsv` files **MUST** equal the number of rows in the associated `_channels.tsv` file. All relevant metadata about a tracking systems is stored in accompanying sidecar `*_tracksys-<label>_motion.json` file.

When multiple tracking systems are used to record motion or motion capture is used alongside the recording of other BIDS modalities and recordings should be interpreted together, it is advised to provide a possibility to synchronize recordings. The preferred way to do so is to use the acquisition time of the first data point of recordings and to store this information in the `acq_time` column of the `*_scans.tsv` file. Note that the BIDS date time format allows optional fractional seconds, which **SHOULD** be used to maximize the precision of the synchronization. Only if the precision of the synchronization is not high enough, the `*_events.tsv` file **SHOULD** be used to synchronize recordings. In this file, the start- and stop time of the recording of a system are specified in relation to a system to synchronize with. If more than two systems are to be synchronized, it is up to the user to identify the "main" system.

In case a tracking system provides time information with every recorded sample, these time information **MAY** be stored in form of latencies to recording onset (first sample) in the `*_motion.tsv` file. If a system has uneven sampling rate behavior, the `LATENCY` channel can be used to share these information.

To store events alongside motion data when there are multiple tracking systems simultaneously in use, it is **RECOMMENDED** to designate a tracking system to the events file. Such an events filename **SHOULD** include the `tracksys` key and looks like `sub-<label>[_ses-<label>]_task-<label>[_tracksys-<label>][_acq-<label>][_run-<index>]_e`. Event latencies can then be related to motion samples of multiple tracking systems also by using `acq_time` column entries in the `*_scans.tsv`. The same principle applies when the events file is saved alongside a simultaneously recorded non-motion data (for example EEG).



Sidecar JSON (\*\_motion.json)

Task information

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 filename MAY be derived from this "TaskName" field by removing all non-alphanumeric or + characters (that is, all except those matching [0-9a-zA-Z+]), and potentially replacing spaces with + to ease readability. For example "TaskName" "faces n-back" or "head nodding" could correspond to task labels faces+n+back or facesnback and head+nodding or headnodding, respectively. Task names for motion datasets usually contain information about the specific motion task (for example, "walking").
TaskDescription	RECOMMENDED	string	Longer description of the task.
Instructions	RECOMMENDED	string	Text of the instructions given to participants before the recording.

Hardware information

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.
Manufacturer	RECOMMENDED	string	Manufacturer of the equipment that produced the measurements.

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.

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.
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.

Motion specific fields

Motion specific 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). This field refers to the nominal sampling frequency. For motion data one can use "SamplingFrequencyEffective" if nominal and effective differ. The sampling frequency of data channels that deviate from the main (nominal) sampling frequency SHOULD be specified in the "_tracksys-<label>_channels.tsv" file.

Motion specific fields SHOULD be present:

Key name	Requirement Level	Data type	Description
ACCELChannelCount	RECOMMENDED	integer	Number of acceleration channels. Must be a number greater than or equal to 0.
ANGACCELChannelCount	RECOMMENDED	integer	Number of angular acceleration channels. Must be a number greater than or equal to 0.
GYROChannelCount	RECOMMENDED	integer	Number of gyrometer channels. Must be a number greater than or equal to 0.
JNTANGChannelCount	RECOMMENDED	integer	Number of joint angle channels. Must be a number greater than or equal to 0.
LATENCYChannelCount	RECOMMENDED	integer	Number of Latency channels. Must be a number greater than or equal to 0.
MAGNChannelCount	RECOMMENDED	integer	Number of magnetometer channels. Must be a number greater than or equal to 0.
MISCChannelCount	RECOMMENDED	integer	Number of miscellaneous channels not covered otherwise. Must be a number greater than or equal to 0.

Key name	Requirement Level	Data type	Description
MissingValues	RECOMMENDED	string	Describes how missing values are represented in the given recording system (for example a tracking system in motion), can take values such as, "NaN", "0".
MotionChannelCount	RECOMMENDED	integer	Number of motion channels (for example, 275). Must be a number greater than or equal to 0.
ORNTChannelCount	RECOMMENDED	integer	Number of orientation channels. Must be a number greater than or equal to 0.
POSChannelCount	RECOMMENDED	integer	Number of position channels. Must be a number greater than or equal to 0.
SamplingFrequencyEffective	RECOMMENDED	number	Effective sampling frequency (in Hz) of all the data in the recording, regardless of their type (for example, 2400) which can be determined if timestamps per sample are provided. If not available, the field takes value n/a.
SubjectArtefactDescription	RECOMMENDED	string	Freeform description of the observed subject artifact 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.
TrackedPointsCount	RECOMMENDED	number	Number of different tracked points tracked in a motion tracking system.
TrackingSystemName	OPTIONAL	string	A human-readable name of the tracking system to complement "tracksys" label of the corresponding *_motion.tsv filename.
VELChannelCount	RECOMMENDED	integer	Number of linear velocity channels. Must be a number greater than or equal to 0.

Example \*\_tracksys-<label>\_motion.json

```
{
  "SamplingFrequency": 60,
  "SamplingFrequencyEffective": 60.00197437,
  "TaskName": "BIDS Motion fictive example",
  "TrackingSystemName": "IMU Right Hand",
  "TaskDescription": "walking and talking",
  "InstitutionAddress": "Fictive address",
  "InstitutionName": "Fictive Institution",
  "MotionChannelCount": 18,
  "RecordingDuration": 4667.641106,
  "SubjectArtefactDescription": "n/a",
  "TrackedPointsCount": 2,
  "ACCELChannelCount": 6,
  "GYROChannelCount": 6,
  "MAGNChannelCount": 6,
  "Manufacturer": "BWSensing",
  "ManufacturersModelName": "BW-IMU600"
}
```

In this example, the \*\_motion.json contains data from one tracking system consisting of two [inertial measurement units \(imu\)](#). If there are additional tracking systems (for example [optical motion capture](#)), data from these MUST be stored as separate files like \*\_tracksys-omcA\_motion.tsv and \*\_tracksys-omcB\_motion.tsv. All specified tracking systems MAY share tracked\_point defined in \*\_channels.tsv, when tracking devices are placed on the same object or body part.

Note that the onsets of the recordings SHOULD be stored in the study key file (scans.tsv). Here, date-time information MUST be expressed as indicated in Units. The scans.tsv file contains the filename and the acquisition time of a recording, which MAY be used to synchronize multiple recordings.

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

Template:

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

Legend:

- <matches> is a placeholder to denote an arbitrary (and valid) sequence of entities and labels at the beginning of the filename (only BIDS "raw").
- <source-entities> is a placeholder to denote an arbitrary sequence of entities and labels at the beginning of the filename matching a source file from which the file derives (only BIDS-Derivatives).

- Filename entities or directories between square brackets (for example, [\_ses-<label>]) are OPTIONAL.
- Some entities may only allow specific values, in which case those values are listed in <>, separated by |.
- \_<suffix> means that there are several (>6) valid suffixes for this filename pattern.
- .<extension> means that there are several (>6) valid extensions for this file type.
- [.gz] means that both the unzipped and gzipped versions of the extension are valid.

This file is REQUIRED as it makes it easy to browse or query over larger collections of datasets. The REQUIRED columns are channel name, component, type, tracked\_point and units. Any number of additional columns MAY be added to provide additional information about the channels. The \*\_tracksys-<label>\_channels.tsv file SHOULD give additional information about individual recorded channel, some of which may not be found summarized in \*\_motion.json. To store information about reference frames for a channel, the reference\_frame column SHOULD be used (see Reference frame description (\*\_channels.json)).

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

Column name	Requirement Level	Data type	Description
name	REQUIRED	string	Label of the channel. This column must appear first in the file.
component	REQUIRED	string	Description of the spatial axis or label of quaternion component associated with the channel. For example, x,y,z for position channels, or quat_x, quat_y, quat_z, quat_w for quaternion orientation channels. This column must appear second in the file. Must be one of: "x", "y", "z", "quat_x", "quat_y", "quat_z", "quat_w".
type	REQUIRED	string	Type of channel; MUST use the channel types listed below. Note that the type MUST be in upper-case. This column must appear third in the file. For a list of valid values for this column, see the type.
tracked_point	REQUIRED	string	Label of the point that is being tracked, for example, label of a tracker or a marker (for example, "LeftFoot", "RightWrist"). This column must appear fourth in the file.

Column name	Requirement Level	Data type	Description
units	REQUIRED	<a href="#">string</a>	Physical or virtual unit of the value represented in this channel, for example, "rad" or "deg" for angular quantities or "m" for position data. If motion data is recorded in a virtual space and deviate from standard SI units, the unit used MUST be specified in the sidecar *_motion.json file (for example "vm" for virtual meters). "rad" is used for Euler angles and "n/a" for quaternions. For guidelines about units see the units and units pages. This column must appear fifth in the file.
placement	RECOMMENDED	<a href="#">string</a>	Placement of the tracked point on the body (for example, participant, avatar centroid, torso, left arm). It can refer to an external vocabulary for describing body parts. This column may appear anywhere in the file.
reference_frame	RECOMMENDED	<a href="#">string</a>	Specification of a reference frame in which the motion data are to be interpreted. The description of the levels in *_channels.json SHOULD use <code>RotationRule</code> , <code>RotationOrder</code> , and <code>SpatialAxes</code> , and MAY use <code>Description</code> for the specification. This column may appear anywhere in the file.
description	OPTIONAL	<a href="#">string</a>	Brief free-text description of the channel, or other information of interest. This column may appear anywhere in the file.
sampling_frequency	OPTIONAL	<a href="#">number</a>	Sampling rate of the channel in Hz. This column may appear anywhere in the file.

Column name	Requirement Level	Data type	Description
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]. This column may appear anywhere in the file. Must be one of: "good", "bad".
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 the status column. This column may appear anywhere in the file.
Additional Columns	OPTIONAL	n/a	Additional columns are allowed if they are defined in the associated metadata file.

### Restricted keyword list for channel component

Restricted keyword list for column **component**. When using quaternions to represent orientations, the axial components that corresponds to the three spatial axes MUST be specified as "quat\_x", "quat\_y", "quat\_z", and the non-axial component as "quat\_w".

Keyword	Description
x	Position along the X-axis, or rotation about the X-axis among the Euler angles that represent the orientation, or magnetic field strength along the X-axis.
y	Position along the Y-axis or rotation about the Y-axis among the Euler angles that represent the orientation, or magnetic field strength along the Y-axis.
z	Position along the Z-axis or rotation about the Z-axis among the Euler angles that represent the orientation, or magnetic field strength along the Z-axis.
quat_x	Quaternion component associated with the X-axis.
quat_y	Quaternion component associated with the Y-axis.
quat_z	Quaternion component associated with the Z-axis.
quat_w	Non-axial quaternion component.
n/a	Channels that have no corresponding spatial axis.



## Restricted keyword list for channel type

Restricted keyword list for column `type` in alphabetic order. Note that upper-case is REQUIRED:

Keyword	Description
ACCEL	Accelerometer channel, one channel for each spatial axis. Column component for the axis MUST be added to the <code>*_channels.tsv</code> file (x, y, or z).
ANGACCEL	Angular acceleration channel, one channel for each spatial axis. Column component for the axis MUST be added to the <code>*_channels.tsv</code> file (x, y, or z).
GYRO	Gyrometer channel, one channel for each spatial axis. Column component for the axis MUST be added to the <code>*_channels.tsv</code> file (x, y, or z).
JNTANG	Joint angle channel between two fixed axis belonging to two bodyparts. Angle SHOULD be defined between proximal and distal bodypart in deg.
LATENCY	Latency of samples in seconds from recording onset (see <code>acq_time</code> column of the respective <code>*_scans.tsv</code> file). MUST be in form of <code>s[.000000]</code> , where <code>s</code> reflects whole seconds, and <code>.000000</code> reflects OPTIONAL fractional seconds.
MAGN	Magnetic field strength, one channel for each spatial axis. Column component for the axis MUST be added to the <code>*_channels.tsv</code> file (x, y or z).
MISC	Miscellaneous channels.
ORNT	Orientation channel, one channel for each spatial axis or quaternion component. Column component for the axis or quaternion label MUST be added to the <code>*_channels.tsv</code> file (x, y, z, <code>quat_x</code> , <code>quat_y</code> , <code>quat_z</code> , or <code>quat_w</code> ).
POS	Position in space, one channel for each spatial axis. Column component for the axis MUST be added to the <code>*_channels.tsv</code> file (x, y or z).
VEL	Velocity, one channel for each spatial axis. Column component for the axis MUST be added to the <code>*_channels.tsv</code> file (x, y or z).

Example `*_channels.tsv`

name	component	type	tracked_point	units	reference_frame
t1_acc_x	x	ACCEL	LeftFoot	m/s <sup>2</sup>	global
t1_acc_y	y	ACCEL	LeftFoot	m/s <sup>2</sup>	global
t1_acc_z	z	ACCEL	LeftFoot	m/s <sup>2</sup>	global
t1_gyro_x	x	GYRO	LeftFoot	rad/s	global
t1_gyro_y	y	GYRO	LeftFoot	rad/s	global
t1_gyro_z	z	GYRO	LeftFoot	rad/s	global
...					
t2_acc_x	x	ACCEL	RightWrist	m/s <sup>2</sup>	global
t2_acc_y	y	ACCEL	RightWrist	m/s <sup>2</sup>	global
t2_acc_z	z	ACCEL	RightWrist	m/s <sup>2</sup>	global

t2_gyro_x	x	GYRO	RightWrist	rad/s	global
t2_gyro_y	y	GYRO	RightWrist	rad/s	global
t2_gyro_z	z	GYRO	RightWrist	rad/s	global

Reference frame description (\*\_channels.json)

A reference frame specifies the origin and orientation of the spatial axes with respect to which motion data is to be interpreted. In case the information is available, sharing this can immensely boost the usability of shared data. The description of the `reference_frame` column SHOULD use the "Levels" field to describe the named field using [objects](#) with following fields.

Key name	Requirement Level	Data type	Description
RotationOrder	RECOMMENDED	<a href="#">string</a>	The sequence in which the extrinsic rotations are applied around the three axes. One of "XYZ", "XZY", "YXZ", "YZX", "ZXY", or "ZYX".
RotationRule	RECOMMENDED	<a href="#">string</a>	The direction of rotation around each axis. One of "left-hand" or "right-hand".
SpatialAxes	RECOMMENDED	<a href="#">string</a>	The coordinate system in which the motion data are to be interpreted. A sequence of characters from the set {'A', 'P', 'L', 'R', 'S', 'I', '_'} indicating the direction of each axis. For example "ARS" indicates positive values in the X, Y, Z axes are respectively anterior, right, and superior of the origin, while "PLI" indicates positive values are posterior, left, and inferior of the origin. The "_" character may be used for unused axes.
Description	OPTIONAL, but RECOMMENDED if no other keys are present	<a href="#">string</a>	A description of the <code>reference_frame</code>

Example of \*\_channels.json

```
{
  "reference_frame": {
    "Levels": {
      "global": {
```

```
    "SpatialAxes": "ALS",
    "RotationOrder": "ZXY",
    "RotationRule": "right-hand"
  },
  "local": {
    "Description": "Joint angles are described following [...]"
  }
}
}
```

# Magnetic Resonance Spectroscopy

Support for Magnetic Resonance Spectroscopy (MRS) 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 MRS datasets](#) have been formatted using this specification and can be used for practical guidance when curating a new dataset.

## MRS data

Template:

```
sub-<label>/
  [ses-<label>/]
    mrs/
      sub-<label>[_ses-<label>][_task-<label>][_acq-<label>][_nuc-<label>][_voi-<label>][_rec-<label>][_run-<index>]_events.json
      sub-<label>[_ses-<label>][_task-<label>][_acq-<label>][_nuc-<label>][_voi-<label>][_rec-<label>][_run-<index>]_events.tsv
      sub-<label>[_ses-<label>][_task-<label>][_acq-<label>][_nuc-<label>][_voi-<label>][_rec-<label>][_run-<index>][_echo-<index>][_inv-<index>]
      sub-<label>[_ses-<label>][_task-<label>][_acq-<label>][_nuc-<label>][_voi-<label>][_rec-<label>][_run-<index>][_echo-<index>][_inv-<index>]
      sub-<label>[_ses-<label>][_task-<label>][_acq-<label>][_nuc-<label>][_voi-<label>][_rec-<label>][_run-<index>][_echo-<index>][_inv-<index>]
      sub-<label>[_ses-<label>][_task-<label>][_acq-<label>][_nuc-<label>][_voi-<label>][_rec-<label>][_run-<index>][_echo-<index>][_inv-<index>]
      sub-<label>[_ses-<label>][_task-<label>][_acq-<label>][_nuc-<label>][_voi-<label>][_rec-<label>][_run-<index>][_echo-<index>][_inv-<index>]
      sub-<label>[_ses-<label>][_task-<label>][_acq-<label>][_nuc-<label>][_voi-<label>][_rec-<label>][_run-<index>][_echo-<index>][_inv-<index>]
      sub-<label>[_ses-<label>][_task-<label>][_acq-<label>][_nuc-<label>][_voi-<label>][_rec-<label>][_run-<index>][_echo-<index>][_inv-<index>]
      sub-<label>[_ses-<label>][_task-<label>][_acq-<label>][_nuc-<label>][_voi-<label>][_rec-<label>][_run-<index>][_echo-<index>][_inv-<index>]
```

Legend:

- **<matches>** is a placeholder to denote an arbitrary (and valid) sequence of entities and labels at the beginning of the filename (only BIDS "raw").
- **<source-entities>** is a placeholder to denote an arbitrary sequence of entities and labels at the beginning of the filename matching a source file from which the file derives (only BIDS-Derivatives).
- Filename entities or directories between square brackets (for example, `[_ses-<label>]`) are OPTIONAL.
- Some entities may only allow specific values, in which case those values are listed in `<>`, separated by `|`.

- `<suffix>` means that there are several (>6) valid suffixes for this filename pattern.
- `<extension>` means that there are several (>6) valid extensions for this file type.
- `[.gz]` means that both the unzipped and gzipped versions of the extension are valid.

MRS is a spectroscopic technique based on the phenomenon of nuclear magnetic resonance that allows for the noninvasive detection and quantification of molecules in biochemical samples, such as brain tissue. It can be conducted in humans using conventional MRI systems.

Due to the diversity in manufacturers’ MRS data file formats, source data MUST be converted into the [NIfTI-MRS format \(\\*.nii.gz\)](#) ([doi:10.1002/mrm.29418](#)). This format is based on the NIfTI framework and is designed to accommodate the nuances of raw MRS data. All necessary information to parse this `*.nii.gz` file (for example, spectrometer frequency, echo time, repetition time, and so on) are stored in a JSON header extension. Conversion of proprietary MRS file formats to NIfTI-MRS and extraction of some (but not all) BIDS-compliant metadata can be performed using [spec2nii](#). Note that the “rawness” of data stored in the NIfTI-MRS file will depend on the format of the source data. It is RECOMMENDED that users export their source data from the scanner in an appropriately raw format prior to conversion.

For MRSI data, “raw” signifies spatially reconstructed data (that is, data in image space rather than (k,t)-space), given the complexity and diversity of sampling approaches. Note that NIfTI-MRS is not designed to store data that has not been spatially reconstructed.

Regarding source data, each manufacturer has its own file format (sometimes multiple formats) for exporting MRS data from the MRI scanner console for offline processing. GE exports a P-file (\*.7) that stores unprocessed, un-coil-combined data with metadata embedded in a proprietary data header. Philips has multiple export formats, the most common being the SDAT/SPAR format. The `*.sdatt` file contains either each coil-combined transient stored separately or all transients summed into a signal average. The `*.spar` file is a plaintext file describing acquisition parameters. It is also possible to export raw data as `*.data/*`.list or DICOM files. Siemens scanners allow data export in four formats:

1. a proprietary DICOM-structured file known as IMA (\*.ima);
2. a conventional DICOM MR Spectroscopy Storage format (\*.dcm);
3. RDA (\*.rda), a proprietary file format with a text-formatted header followed by the binary data points;
4. TWIX (\*.dat), a proprietary file format designed for storing unreconstructed, unprocessed MRS data from each individual coil element.

The IMA, DICOM MRS, and RDA formats are typically used to export reconstructed and processed data; however, the sequence designer may choose to also allow the export of un-averaged transients or data from individual coil elements. Bruker data are exported as two binary files: one file stores each transient separately, while the other stores the sum of the transients. A separate plaintext file stores the sequence name, voxel position, voxel orientation, and other metadata. All of these files are considered source data and, if present, MUST be stored in the `sourcedata` directory.

Single-voxel spectroscopy and MRS imaging

Name	suffix	Description
Single-voxel spectroscopy	svs	MRS acquisitions where the detected MR signal is spatially localized to a single volume.
Magnetic resonance spectroscopic imaging	mrsi	MRS acquisitions where additional imaging gradients are used to detect the MR signal from 1, 2, or 3 spatial dimensions.
Unlocalized spectroscopy	unloc	MRS acquisitions run without localization. This includes signals detected using coil sensitivity only.

Name	suffix	Description
Concentration or calibration reference	mrsref	An MRS acquisition collected to serve as a concentration reference for absolute quantification or as a calibration reference for preprocessing (for example, eddy-current correction).

A major distinction between MRS acquisitions is whether the acquisition technique probes spectral information from a single volume (single-voxel spectroscopy, SVS) or encodes this information along 1, 2, or 3 spatial dimensions resulting in multiple sub-volumes (MRS imaging, MRSI). To avoid confusion, the suffixes `svs` and `mrsi` MUST be used to distinguish the two techniques. For cases where localization is not used, the suffix `unloc` MUST be used.

Furthermore, it is common to acquire an additional MRS dataset that may serve as a reference for scaling metabolite signal levels (for example, to obtain concentrations) and/or for preprocessing steps (such as eddy-current correction, RF coil combination, phasing, and frequency calibration). This could be either an external reference (for example, a phantom or a synthetic signal) or, more typically, an internal tissue water reference. For such datasets, the suffix `mrsref` MUST be used. Should multiple references exist for a given dataset, the user MAY use the `acq-<label>` entity to distinguish the files. For example, `sub-01_acq-conc_mrsref.nii.gz` and `sub-01_acq-ecc_mrsref.nii.gz` could be used to name two references to be used for concentration scaling and eddy-current correction, respectively.

MRS sequences

Given the large variety of MRS sequences, there will be times when providing sufficient detail of acquisition parameters in filenames is helpful or necessary to distinguish datasets in a given study.

Here we present a set of labels that can be used when using the `acq-<label>` entity in the filename. These are based on the most commonly used in vivo MRS sequences/techniques, and are OPTIONAL to use. Users are free to choose any label they wish as long as they are consistent across participants and sessions and use only legal label characters. If used, the chosen label SHOULD also be described in the `PulseSequenceType` field in the sidecar JSON file.

Name	label	Description
PRESS	press	A double spin-echo sequence that achieves spatial localization by employing three slice-selective RF pulses: 90°–180°–180°–acq.
STEAM	steam	A stimulated-echo sequence that uses three 90° slice-selective pulses for spatial localization.
LASER	laser	LASER uses three pairs of slice-selective 180° adiabatic full-passage (AFP) refocusing pulses for localization. These are preceded by a non-slice-selective adiabatic half-passage (AHP) excitation pulse.

Name	label	Description
sLASER	slaser	sLASER is a modification of LASER where the AHP and first pair of AFP pulses are replaced with a non-adiabatic slice-selective 90° excitation pulse, typically employed to reduce the minimum TE.
SPECIAL	special	SPECIAL is a two-shot experiment. In the first shot, a pre-excitation slice-selective 180° AFP inversion pulse precedes a spin-echo acquisition with slice selection (90°–180°–acq). In the second shot, the adiabatic pulse is not applied. The 3D localized signal is derived by subtracting the two shots.
MEGA	mega	MEGA is a spectral editing technique that applies narrowband frequency-selective 180° pulses to refocus J-coupled spins at a specific frequency without affecting the spins of metabolites with resonances beyond the frequency range. Applying these pulses in alternating scans (for example, edit ON and edit OFF) and then subtracting the ON/OFF pairs results in a J-difference-edited spectrum that removes the unedited signals, leaving only those signals that were affected by the editing pulses.
HERMES	hermes	HERMES is an extension of MEGA editing whereby the two-step experiment becomes a four-step experiment. This permits multiple metabolites to be edited in a multiplexed manner. By employing Hadamard combination of the four edited sub-spectra, HERMES can reveal several metabolites unambiguously.
HERCULES	hercules	HERCULES is a different flavor of HERMES that targets more metabolites using the same four-step experiment.
Multiple quantum coherence (MQC) editing	mqc	MQC editing targets J-coupled resonances by selecting desired coherence pathways using MQ gradients and frequency-selective RF pulses.
Localized correlation spectroscopy (L-COSY)	lcosy	L-COSY is a 2D MRS technique whereby one of the interpulse durations is changed sequentially. A 2D Fourier transform produces a 2D spectrum that displays singlets on the diagonal and J-coupled metabolites on the off-diagonal, with the offsets equal to the J-coupling constants.

Name	label	Description
J-resolved spectroscopy	j	Another 2D technique, where in a J-resolved acquisition, a series of transients are collected at different TEs. A 2D Fourier transform is applied to generate a 2D spectrum where one dimension characterizes both chemical shift and J-coupling and the other only J-coupling.
Diffusion-weighted (DW) spectroscopy	dw	The diffusion of intracellular metabolites can be characterized using DW spectroscopy. In such acquisitions, the strength of gradients in a conventional MRS sequence is modulated to sensitize the metabolite signals to diffusion.
FID spectroscopy	fid	FID spectroscopy is a pulse-acquire acquisition where an excitation pulse is followed by direct acquisition of the FID. This approach is most often used in MRSI (that is, FID-MRSI) when combined with slice- or slab-selection.
Metabolite-cycled (MC) spectroscopy	mc	MC spectroscopy involves the use of asymmetric adiabatic inversion of the upfield and downfield parts of the MR spectrum, allowing for simultaneous acquisition of water and metabolite spectra.
Spin-echo spectroscopy	spinecho	An MRS experiment whereby the MR signal is detected using a spin-echo acquisition: 90°–180°–acq.

Each <label> in the table above MAY be combined with another to better describe the acquisition used. For example, `megaspecial`, `jpress`, `dwslicer`, `mcdwsteam`, and so on.

The OPTIONAL `nuc-<label>` entity can be used to distinguish acquisitions tuned to detect different nuclei. The label is the name of the nucleus or nuclei, which corresponds to DICOM Tag 0018, 9100. For example, `nuc-1H`, `nuc-31P`, `nuc-1H13C`. If used, the field `ResonantNucleus` MUST also be included in the corresponding sidecar JSON file, using the same label.

Similarly, the OPTIONAL `voi-<label>` entity can be used to distinguish between acquisitions localized to different regions (that is, acquisitions with different VOI). The label SHOULD be the name of the body region or part scanned. If used, the fields `BodyPart` and `BodyPartDetails` MUST also be included in the corresponding sidecar JSON file. `BodyPartDetailsOntology` is OPTIONAL to also include.

## Sidecar JSON

MRS data files MUST be described by metadata fields, stored in sidecar JSON files (\*.json).



## Common metadata fields

Metadata described in the following sections are shared with other MR modalities that SHOULD or MAY be present in the sidecar JSON files.

### Scanner hardware

Key name	Requirement Level	Data type	Description
Manufacturer	RECOMMENDED	<a href="#">string</a>	Manufacturer of the equipment that produced the measurements.
ManufacturersModelName	RECOMMENDED	<a href="#">string</a>	Manufacturer's model name of the equipment that produced the measurements.
DeviceSerialNumber	RECOMMENDED	<a href="#">string</a>	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	<a href="#">string</a>	Institution defined name of the machine that produced the measurements.
SoftwareVersions	RECOMMENDED	<a href="#">string</a>	Manufacturer's designation of software version of the equipment that produced the measurements.
MagneticFieldStrength	RECOMMENDED	<a href="#">number</a>	Nominal field strength of MR magnet in Tesla. Corresponds to <a href="#">DICOM Tag 0018, 0087 Magnetic Field Strength</a> .
ReceiveCoilName	RECOMMENDED	<a href="#">string</a>	Information describing the receiver coil. Corresponds to <a href="#">DICOM Tag 0018, 1250 Receive Coil Name</a> , although not all vendors populate that DICOM Tag, in which case this field can be derived from an appropriate private DICOM field.
ReceiveCoilActiveElements	RECOMMENDED	<a href="#">string</a>	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.
NumberReceiveCoilActiveElements	OPTIONAL	<a href="#">integer</a>	The number of active RF elements used by the receive coil.

Key name	Requirement Level	Data type	Description
NumberTransmitCoilActiveElements	OPTIONAL	integer	The number of active RF elements used by the transmit coil.

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.
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.

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, "sLASER", "MEGA-PRESS", "EPSI", "Metabolite-cycled MRSI".
ScanningSequence	RECOMMENDED	string	Description of the type of data acquired. Must be one of: "SVS", "MRSI", "Unlocalized MRS".
SequenceName	RECOMMENDED	string	Manufacturer's designation of the sequence name. Corresponds to <a href="#">DICOM Tag 0018, 0024 Sequence Name</a> .

Key name	Requirement Level	Data type	Description
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").
WaterSuppression	RECOMMENDED	boolean	Boolean indicating whether water suppression was used prior to acquisition. Must be one of: "true", "false".
WaterSuppressionTechnique	OPTIONAL	string	The name of the pulse sequence used for water suppression (for example, "CHESS", "VAPOR").
OuterVolumeSuppression	OPTIONAL	boolean	Boolean indicating whether outer-volume suppression was used prior to acquisition. Must be one of: "true", "false".
B0ShimmingTechnique	OPTIONAL	string	The technique used to shim the B0 field (for example, "Dynamic shim updating" or "FASTMAP").
B1ShimmingTechnique	OPTIONAL	string	The technique used to shim the B1 field (for example, "Simple phase align" or "Pre-saturated TurboFLASH").

## Tissue description

Key name	Requirement Level	Data type	Description
BodyPart	OPTIONAL, but REQUIRED if voi entity is present	string	Body part of the organ / body region scanned. Corresponds to <a href="#">DICOM Tag 0018, 0015</a> Body Part Examined.
BodyPartDetails	OPTIONAL, but REQUIRED if voi entity is present	string	Additional details about body part or location (for example: "corpus callosum").

Key name	Requirement Level	Data type	Description
BodyPartDetailsOntology	OPTIONAL	<a href="#">string</a>	BodyPartDetailsOntology of ontology used for BodyPartDetails (for example: " <a href="https://www.ebi.ac.uk/ols/ontologies/uberon">https://www.ebi.ac.uk/ols/ontologies/uberon</a> ").

## MRS-relevant fields

Metadata fields that MUST be present:

Key name	Requirement Level	Data type	Description
ResonantNucleus	REQUIRED	<a href="#">string</a> or <a href="#">array</a> of <a href="#">strings</a>	The isotope of interest of an MR experiment (for example, "1H", "13C", "31P"). For multi-nuclei experiments such as 1H-[13C] MR, an array can be used: ["1H", "13C"]. Corresponds to <a href="#">DICOM Tag 0018, 9100 Resonant Nucleus</a> .
SpectrometerFrequency	REQUIRED	<a href="#">number</a> or <a href="#">array</a> of <a href="#">numbers</a>	The frequency of the spectrometer, specified in MHz. For example, this could be 127.764 for a 3T scanner tuned to the resonant frequency of 1H. For multi-nuclei experiments such as 1H-[13C] MR at 3T, an array can be used: [127.731, 32.125].
SpectralWidth	REQUIRED	<a href="#">number</a>	The spectral bandwidth of the MR signal that is sampled, specified in Hz. Corresponds to <a href="#">DICOM Tag 0018, 9052 Spectral Width</a> .
EchoTime	REQUIRED	<a href="#">number</a> or <a href="#">array</a> of <a href="#">numbers</a>	The echo time (TE) for the acquisition, specified in seconds. Corresponds to <a href="#">DICOM Tag 0018, 0081 Echo Time</a> (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 EchoTime where the value of this field is iterated using the EchoTime.

Metadata fields that SHOULD be present:

Key name	Requirement Level	Data type	Description
NumberOfSpectralPoints	RECOMMENDED	<a href="#">integer</a>	The number of complex data points in each recorded transient of the detected time-domain MR signal, equivalent to the number of points in a single spectrum.
MixingTime	RECOMMENDED	<a href="#">number</a>	In the context of a stimulated- and spin-echo 3D EPI sequence for B1+ mapping or a stimulated-echo MRS sequence, 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.
FlipAngle	RECOMMENDED	<a href="#">number</a> or <a href="#">array of numbers</a>	Flip angle (FA) for the acquisition, specified in degrees. Corresponds to: <a href="#">DICOM Tag 0018, 1314 Flip Angle</a> . 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 FlipAngle where the value of this field is iterated using the FlipAngle.
AcquisitionVoxelSize	RECOMMENDED	<a href="#">array of numbers</a>	An array of numbers with a length of 3, in millimeters. This field 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.

Key name	Requirement Level	Data type	Description
ReferenceSignal	RECOMMENDED	string or array of strings	The path(s) to the MRS reference file(s), if present, to which the associated MRS data file corresponds. Contains one or more ReferenceSignal.
RepetitionTime	RECOMMENDED mutually exclusive with VolumeTiming	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 <a href="#">DICOM Tag 0020, 0110</a> : the "time delta between images in a dynamic of functional set of images" but may also be found in <a href="#">DICOM Tag 0018, 0080</a> : "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	RECOMMENDED mutually exclusive with RepetitionTime	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 series. The list must have the same length as the series, and the values must be non-negative and monotonically increasing. This field is mutually exclusive with "RepetitionTime".

Key name	Requirement Level	Data type	Description
NumberOfTransients	RECOMMENDED for SVS and unlocalized acquisitions	integer	The number of single applications of the pulse sequence recorded during an MRS acquisition.
MRAcquisitionType	RECOMMENDED for MRSI	string	Type of sequence readout. Corresponds to <a href="#">DICOM Tag 0018, 0023 MR Acquisition Type</a> . Must be one of: "1D", "2D", "3D".
MatrixSize	RECOMMENDED for MRSI	array of integers	An array of integers with a length of 3 denoting the matrix size of the acquisition slab. This should be specified as, for example, [32, 32, 1] for a 2D acquisition or [32, 1, 1] for a 1D acquisition.
VolumeAffineMatrix	RECOMMENDED for MRSI	array of arrays	A 4-by-4 matrix using identical conventions and coordinate system to the {qs}form NIfTI affine matrix to define the orientation, position, and size of an additional VOI. This VOI defines a spatial region in addition to the primary method of localization (encoded in the NIfTI header {qs}form). Typically not defined for data stored with a single spatial voxel or FID-MRSI. For example: [[30, 0, 0, -30], [0, 30, -2.27, -72.67], [0, 2.27, 29.91, 5.47], [0, 0, 0, 1]].
EncodingTechnique	RECOMMENDED for MRSI	string	The encoding technique used during readout. For example, "Cartesian", "EPSI", "Spiral", or "Density-weighted concentric ring trajectory".

Key name	Requirement Level	Data type	Description
InversionTime	RECOMMENDED if <code>inv</code> entity is present	<a href="#">number</a>	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 <a href="#">DICOM Tag 0018, 0082 Inversion Time</a> (please note that the DICOM term is in milliseconds not seconds). Must be a number greater than 0.
AnatomicalImage	RECOMMENDED if anatomical MRI data are present	<a href="#">string</a> or <a href="#">array of strings</a>	The path(s) to the anatomical MR image file(s), if present, to which the associated MRS data file corresponds. Contains one or more <code>AnatomicalImage</code> .

Metadata fields that MAY be present:

Key name	Requirement Level	Data type	Description
ChemicalShiftOffset	OPTIONAL	<a href="#">number</a>	The chemical shift at the center of <code>SpectralWidth</code> corresponding to 0 Hz, specified in ppm (for example, 4.65).
ChemicalShiftReference	OPTIONAL	<a href="#">number</a>	The chemical shift at the transmitter frequency, specified in ppm (for example, 2.68). Corresponds to <a href="#">DICOM Tag 0018, 9053 Chemical Shift Reference</a> .
EditTarget	OPTIONAL	<a href="#">string</a> or <a href="#">array of strings</a>	If spectral editing was applied, this describes the metabolites that were selectively targeted (for example, "GABA" or "Lac"). If multiple metabolites were targeted (for example, in a HERMES acquisition), an array can be used: ["GABA", "GSH"].



Key name	Requirement Level	Data type	Description
EditPulse	OPTIONAL	object of objects	If spectral editing was applied, this details the editing parameters. For example: {"ON": {"FrequencyOffset": 1.9, "PulseDuration": 16}, "OFF": {"FrequencyOffset": 7.5, "PulseDuration": 16}}.
EditCondition	OPTIONAL	string or array of strings	If spectral editing was applied, this lists the application order of "EditPulse". For example, ["ON", "OFF"] for a MEGA-edited experiment or ["A", "B", "C", "D"] for a HERMES-edited experiment.
EchoAcquisition	OPTIONAL	string	How the detected echo was acquired when the analog-to-digital converter was turned on. For example, "Half echo", "Full echo".
ParallelReductionFactorInPlane	OPTIONAL	number	The parallel imaging (for instance, GRAPPA) factor in plane. 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 <a href="#">DICOM Tag 0018, 9069 Parallel Reduction Factor In-plane</a> .
ParallelAcquisitionTechnique	OPTIONAL	string	The type of parallel imaging used (for example "GRAPPA", "SENSE"). Corresponds to <a href="#">DICOM Tag 0018, 9078 Parallel Acquisition Technique</a> .
MultibandAccelerationFactor	OPTIONAL	number	The multiband factor, for multiband acquisitions.
PulseSequenceTiming	OPTIONAL	array of numbers	The time when each RF pulse of the pulse sequence was played out relative to the beginning of the pulse sequence (that is, the top of the excitation RF pulse), specified in seconds.

Key name	Requirement Level	Data type	Description
PulseSequencePulses	OPTIONAL	array of strings	The list of pulses used in the pulse sequence. If this field is specified, the array size MUST equal the array size of "PulseSequenceTiming". The strings MAY be of the format <pulse_name>_R<time-bandwidth_product>. For example, a sLASER sequence may be described as such: ["P10_R6", "HS4_R25", "HS4_R25", "HS4_R25", "HS4_R25"].
ReceiveGain	OPTIONAL	number or array of numbers	The gain of the receive coil.

Example \*\_svs.json

```
{
  "InstitutionName": "Weill Cornell Medicine",
  "InstitutionAddress": "1300 York Avenue, New York, NY 10065, USA",
  "Manufacturer": "GE",
  "ManufacturersModelName": "Discovery MR750",
  "MagneticFieldStrength": 3,
  "PulseSequenceType": "PRESS",
  "ResonantNucleus": "1H",
  "SpectrometerFrequency": 127.771,
  "SpectralWidth": 2000,
  "EchoTime": 0.035,
  "NumberOfSpectralPoints": 2048,
  "NumberOfTransients": 64,
  "RepetitionTime": 2,
  "AcquisitionVoxelSize": [40, 20, 30],
  "BodyPart": "BRAIN",
  "BodyPartDetails": "Anterior cingulate cortex",
  "ReferenceSignal": "bids::sub-01/mrs/sub-01_acq-press_mrsref.nii.gz",
  "AnatomicalImage": "bids::sub-01/anat/sub-01_T1w.nii.gz"
}
```

Combining MRS with anatomical MRI

For combining MRS data with anatomical MRI data, see MRS-MRI correspondence in the Appendix.

# Electromyography

Support for Electromyography (EMG) 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.

Electromyography datasets formatted according to this specification are available on the [BIDS examples repository](#) and can be emulated when curating new datasets.

## EMG data

Template:

```
sub-<label>/
  [ses-<label>]/
    emg/
      sub-<label>[_ses-<label>]_task-<label>[_acq-<label>][_run-<index>][_recording-<label>]_emg.bdf
      sub-<label>[_ses-<label>]_task-<label>[_acq-<label>][_run-<index>][_recording-<label>]_emg.edf
      sub-<label>[_ses-<label>]_task-<label>[_acq-<label>][_run-<index>][_recording-<label>]_emg.json
      sub-<label>[_ses-<label>]_task-<label>[_acq-<label>][_run-<index>][_recording-<label>]_events.json
      sub-<label>[_ses-<label>]_task-<label>[_acq-<label>][_run-<index>][_recording-<label>]_events.tsv
```

Legend:

- <matches> is a placeholder to denote an arbitrary (and valid) sequence of entities and labels at the beginning of the filename (only BIDS "raw").
- <source-entities> is a placeholder to denote an arbitrary sequence of entities and labels at the beginning of the filename matching a source file from which the file derives (only BIDS-Derivatives).
- Filename entities or directories between square brackets (for example, [\_ses-<label>]) are OPTIONAL.
- Some entities may only allow specific values, in which case those values are listed in <>, separated by |.
- \_<suffix> means that there are several (>6) valid suffixes for this filename pattern.
- .<extension> means that there are several (>6) valid extensions for this file type.
- [.gz] means that both the unzipped and gzipped versions of the extension are valid.

EMG device manufacturers use a variety of formats for storing raw data, and there is no single standard that all researchers agree on. For BIDS, EMG data MUST be stored in one of the following formats:

Format	Extension(s)	Description
Biosemi data format	.bdf	Each recording consists of a single .bdf file. <b>bdf+</b> files are permitted. The capital .BDF extension MUST NOT be used.
European data format	.edf	Each recording consists of a single .edf file. <b>edf+</b> files are permitted. The capital .EDF extension MUST NOT be used.

EDF, EDF+, BDF, and BDF+ are all open data formats with broad support in various programming languages for reading and writing the files. BDF and BDF+ formats store data samples using 3 bytes instead of 2 bytes as in EDF and EDF+ formats, allowing for greater resolution. EDF+/BDF+ accommodate more header metadata than EDF/BDF, and support storing event or annotation information in the file. Thus it is RECOMMENDED to use the BDF+ data format.

The `recording-<label>` entity MAY be used to indicate simultaneous acquisition of data from multiple EMG devices, in cases where the devices store data in separate data files. If separate devices are being used with separate sampling rates, start times, or other acquisition parameters, the `recording-<label>` entity MUST be used to distinguish between them. The synchronization of data from multiple devices SHOULD be described in the Scans (`scans.tsv`) file, using the `acq_time` entity.

In cases where the allowed formats do not encode all relevant metadata present in the device manufacturer’s native file format, we encourage users to provide the additional metadata in the sidecar JSON file.

Terminology: Electrodes vs. Channels

For proper documentation of EMG recording metadata it is important to understand the difference between an electrode and a channel: an EMG electrode is a single point of electrical contact with the body, whereas a channel is the combination of the analog differential amplifier (which combines signals from two electrode sources) and the analog-to-digital converter, which results in a potential difference (voltage) that forms the actual data stored in the EMG dataset. We employ the following short definitions:

- Electrode: A single point of contact between the acquisition system and the recording site (whether on the skin surface or intramuscular). Multiple electrodes can be organized as 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 forth.

This distinction is especially important for EMG because a common type of EMG device (often erroneously called a "bipolar electrode") comprises two electrodes at a fixed distance, wired such that the electrode pair is necessarily converted to a single channel by the amplifier (in other words, one of the electrodes necessarily acts as the reference for the other). In other kinds of devices, researchers may have control over which electrode(s) to use as the reference for each channel.

Note also that although the reference and ground electrodes are often referred to as channels, in most common EMG systems they are not recorded by themselves. Therefore they are usually not represented as channels in the data.

## Describing sensor locations

Each EMG-BIDS dataset SHOULD include sensor location information that is as accurate as possible given the measurement means available to the researcher(s). Below are examples ranging from most accurate to least accurate, which can serve as a guide to where sensor placement information should be stored in the dataset.

1. Electrode locations and anatomical landmarks are digitized with a 3D localizer device such as Polhemus FasTrak or a 3D scanner. 3D coordinates for each electrode are given in `x,y,z` columns of `*_electrodes.tsv`, and the coordinate system definition is given in `*_coordsystem.json`.
2. Electrode locations are measured relative to nearby anatomical landmarks using a flexible measuring tape. 2D or 3D coordinates for each electrode are given in `x, y`, and (optionally) `z` columns of `*_electrodes.tsv`, and the coordinate system definition in `*_coordsystem.json` specifies the axis directions with reference to those anatomical landmarks.
3. The arrangement of electrodes in a group or grid is measured (or known from the device manufacturer), and is provided in `x, y`, and (optionally) `z` columns of `*_electrodes.tsv`, with a device-internal "child" coordinate system defined in a `*_coordsystem.json` file. An anatomically-defined "parent" coordinate system is also defined in a different `*_coordsystem.json` file, and the name and coordinates of one electrode (the "anchor" electrode) from each "child" group or grid is provided in the "parent" coordinate system. This allows the approximate anatomical locations of all electrodes to be calculated by treating the device-internal coordinates as offsets from the anchor coordinate. The two `*_coordsystem.json` files are distinguished by the `space` entity in their filenames; the labels used for that entity may be arbitrary (for example, `*_space-grid_coordsystem.json` for the child coordinate system, and `*_space-forearm_coordsystem.json` for the parent coordinate system).
4. Individual electrode locations are chosen by visual inspection, palpation, or functional localizers. No measured coordinates are provided; placement information is given either in the `EMGPlacementSchemeDescription` field of `*_emg.json` (when the placement approach is the same for all sensors), or in the `placement_description` column of `*_channels.tsv` (when the placement approach varied across sensors).

More details on each of these scenarios is given below in the Channels description, Electrodes description, and Coordinate system sections.

A fifth scenario unique to EMG involves location information that is fairly accurate (as in scenarios (1) and (2) above) but it locates bipolar sensor devices rather than electrodes. In this case, researchers SHOULD provide `*_electrodes.tsv` even though information about the individual electrode contacts is not available. Rather, each entry from `*_channels.tsv` should have a corresponding row in `*_electrodes.tsv` where the location information is given, and `*_coordsystem.json` should also be provided (as in scenarios (1) or (2) above).

## EMG in combination with other modalities

When EMG is recorded alongside other BIDS modalities (such as EEG or motion), researchers SHOULD define how recordings are synchronized. Options include:

- Recording time stamps from a common clock source on the LATENCY channel of each modality's acquisition device.
- Recording experimental events (usually as TTL pulses) on dedicated channels of each modality's acquisition devices.
- Storing the acquisition time (relative to a common clock source) of the first data point of each modality's recording in the `acq_time` column of the `*_scans.tsv` file. Note that the BIDS date time format allows optional fractional seconds, which SHOULD be used to maximize the precision of the synchronization.
- Record the start- and stop-time of one modality's recording (relative to the other modality's clock) in the `*_events.tsv` file for the other modality.

It is up to the user to decide which approach is most appropriate given their experimental setup, and to identify which modality will serve as the 'main' clock source for synchronization purposes (or whether a separate external clock source is used).

Sidecar JSON (\*\_emg.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.

These fields MUST be present:

Key name	Requirement Level	Data type	Description
EMGPlacementScheme	REQUIRED	string	The way in which electrode placement locations were determined. If electrode locations are provided as coordinates in *_electrodes.tsv in reference to a coordinate system defined in *_coordsystem.json, then specify "Measured". If approach to placement varied across sensor devices, specify "ChannelSpecific" and include placement details in the placement_scheme column of *_channels.tsv. If a standardized electrode placement procedure (for example, SENIAM 8) was followed, or if an ad-hoc procedure was followed, specify "Other" and provide details in EMGPlacementSchemeDescription. Must be one of: "ChannelSpecific", "Measured", "Other".

Key name	Requirement Level	Data type	Description
EMGPlacementSchemeDescription	OPTIONAL, but REQUIRED if EMGPlacementScheme is "Other"	string	Additional details of the approach to EMG sensor placement. Descriptions SHOULD NOT simply give the name of the targeted muscle (use the <code>target_muscle</code> column in <code>*_channels.tsv</code> for that), but rather SHOULD reflect the process used by the researcher(s) when placing electrodes. For example, EMG electrode sites may be chosen by measured distance from anatomical landmarks, by visual reference to (parts of) target muscles, by palpation of the skin to locate target muscles, or by functional localization (temporary electrode placement at several sites during prescribed behavior, until a site yielding strong EMG signal is found).
EMGReference	REQUIRED	string	Description of the approach to signal referencing. If the same signal source is used as reference for all channels (often called a "monopolar" recording), specify the signal source (typically an electrode name). If different channels have different reference electrodes, this field SHOULD contain the string "ChannelSpecific" and each channel's reference SHOULD be given in the <code>reference</code> column of <code>*_channels.tsv</code> . For bipolar recording devices (where a single sensor unit contains two rigidly separated contacts, and the paired contacts are not listed independently in <code>*_electrodes.tsv</code> ), this field SHOULD be "Bipolar".

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 <code>channels.tsv</code> 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).
RecordingType	REQUIRED	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".
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"}}).

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.

These fields SHOULD be present:



Key name	Requirement Level	Data type	Description
EMGChannelCount	RECOMMENDED	integer	Number of EMG channels. Must be a number greater than or equal to 0.
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"}}.
RecordingDuration	RECOMMENDED	number	Length of the recording in seconds (for example, 3600).

These fields MAY be present:

Key name	Requirement Level	Data type	Description
ElectrodeMaterial	OPTIONAL	string	Material of the electrode (for example, Tin, Ag/AgCl, Gold). If multiple sensor devices with heterogeneous electrode materials are recorded into the same data file, electrode material SHOULD be recorded in the <code>material</code> column of <code>*_electrodes.tsv</code> instead. If instead those devices were recorded into separate data files (distinguished for example by the <code>recording</code> entity), separate <code>*_emg.json</code> files (similarly distinguished) MAY be included, each with their own <code>ElectrodeMaterial</code> values.
ElectrodeType	OPTIONAL	string	Type of the electrode (for example, cup, ring, clip-on, wire, needle).
EMGGround	OPTIONAL	string	Description of the location of the ground electrode (for example, "right radial styloid process").

Key name	Requirement Level	Data type	Description
EpochLength	OPTIONAL, but RECOMMENDED if RecordingType is "epoched"	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.
Gain	OPTIONAL	number	Signal gain from an in-line amplifier, applied between the EMG sensor/device and the data acquisition computer. See also Preamplification.
InterelectrodeDistance	OPTIONAL	number	Distance between pairs or grids of electrodes rigidly attached to the same sensor device. If multiple sensor devices with heterogeneous inter-electrode distances are recorded into the same data file, inter-electrode distance SHOULD be recorded in the <code>interelectrode_distance</code> column of <code>*_electrodes.tsv</code> instead. If instead those devices were recorded into separate data files (distinguished for example by the <code>recording</code> entity), separate <code>*_emg.json</code> files (similarly distinguished) MAY be included, each with their own <code>InterelectrodeDistance</code> values.
Preamplification	OPTIONAL	number	Amplification built into an EMG bipolar sensor, electrode grid, or other device. See also Gain.
SkinPreparation	OPTIONAL	string	How skin was prepared prior to sensor device placement, for example, "alcohol wipe" or "abrasive gel".

Key name	Requirement Level	Data type	Description
SubjectArtefactDescription	OPTIONAL	string	Freeform description of the observed subject artifact 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.
TriggerChannelCount	OPTIONAL	integer	Number of channels for digital (binary TTL) triggers or analog equivalents (TTL in volt). Corresponds to the TRIG channel type. Must be a number greater than or equal to 0.

## Hardware information

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.
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.
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 <code>_electrodes.tsv</code> file.

Key name	Requirement Level	Data type	Description
ElectrodeManufacturersModelName	RECOMMENDED	string	If different electrode types are used, please use the corresponding table in the <code>_electrodes.tsv</code> file.

## Task information

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 filename MAY be derived from this "TaskName" field by removing all non-alphanumeric or + characters (that is, all except those matching <code>[0-9a-zA-Z+]</code> ), and potentially replacing spaces with + to ease readability. For example "TaskName" "faces n-back" or "head nodding" could correspond to task labels <code>faces+n+back</code> or <code>facesnback</code> and <code>head+nodding</code> or <code>headnodding</code> , respectively. A RECOMMENDED convention is to name resting state task using labels beginning with <code>rest</code> .
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, to distinguish resting positions with different postures (for example, "seated", "reclined").

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, "treatment", "control", or "sleep").

## 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.
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 \*\_emg.json

```
{
  "EMGChannelCount":4,
  "EMGGround":"n/a",
  "EMGPlacementScheme":"Other",
  "EMGPlacementSchemeDescription":"midpoint between cubital fossa and radial styloid process",
  "EMGReference":"4 reference electrodes built-in to device, placed near the midpoint between radial and ulnar styloid processes on the volar surface",
  "HardwareFilters":{"Highpass RC filter": {"Half amplitude cutoff (Hz)": 0.0159, "Roll-off": "6dB0ctave"}},
  "InstitutionAddress":"9500 Gilman Drive 0559, La Jolla, CA 92093",
  "InstitutionalDepartmentName":"Swartz Center for Computational Neuroscience",
  "InstitutionName":"University of California San Diego",
  "Instructions":"Jump straight upward as high as you can, while keeping your arms at your sides.",
  "Manufacturer":"Delsys",
  "ManufacturersModelName":"Trigno® Galileo",
  "PowerLineFrequency":60,
  "RecordingDuration":123.456,
  "RecordingType":"continuous",
  "SamplingFrequency":1000,
  "SoftwareFilters":"n/a",
  "TaskDescription":"jumping with stationary arms",
  "TaskName":"jumping"
}
```

Channels description (\*\_channels.tsv)

Template:

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

Legend:

- <matches> is a placeholder to denote an arbitrary (and valid) sequence of entities and labels at the beginning of the filename (only BIDS "raw").
- <source-entities> is a placeholder to denote an arbitrary sequence of entities and labels at the beginning of the filename matching a source file from which the file derives (only BIDS-Derivatives).
- Filename entities or directories between square brackets (for example, [\_ses-<label>]) are OPTIONAL.
- Some entities may only allow specific values, in which case those values are listed in <>, separated by |.
- \_<suffix> means that there are several (>6) valid suffixes for this filename pattern.
- .<extension> means that there are several (>6) valid extensions for this file type.
- [.gz] means that both the unzipped and gzipped versions of the extension are valid.

A channel is represented by one time series recorded with the recording system. Although this information can often be extracted from the EMG 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  $\geq 1000$  Hz). Hence, the \*\_channels.tsv file is RECOMMENDED. Channels SHOULD appear in the table in the same order they do in the EMG data file. Additional columns MAY be included 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:

Column name	Requirement Level	Data type	Description
name	REQUIRED	string	Label of the channel. Values in name MUST be unique.This column must appear first in the file.
type	REQUIRED	string	Type of channel; MUST use the channel types listed below. Note that the type MUST be in upper-case. This column must appear second in the file.For a list of valid values for this column, see the type.
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). This column must appear third in the file.

Column name	Requirement Level	Data type	Description
description	OPTIONAL	string	Brief free-text description of the channel, or other information of interest. This column may appear anywhere in the file.
sampling_frequency	OPTIONAL	number	Sampling rate of the channel in Hz. This column may appear anywhere in the file.
signal_electrode	RECOMMENDED	string	The name of the electrode from which the <b>reference</b> 's signal is subtracted to yield the channel's data. For channels originating from bipolar devices, the <b>signal_electrode</b> MAY be the same as the channel <b>name</b> . This column may appear anywhere in the file.
reference	RECOMMENDED	string	The reference for the given channel. When the reference is an electrode in <b>*_electrodes.tsv</b> , use the name of that electrode. For channels originating from bipolar devices, use "bipolar". For non-EMG channels (for example, trigger channels, microphones) use "n/a". This column may appear anywhere in the file.
group	RECOMMENDED	string or number	Which group the electrode or channel belongs to (typically this indicates electrodes or bipolar channels on the same grid, strip, or other device). This column may appear anywhere in the file.
target_muscle	RECOMMENDED	string	Name of the muscle(s) from which the EMG signal in this channel is believed to originate. When exact muscle is unknown (such as when using electrode grids that cover multiple muscles), groups of muscles may be named instead (for example "flexors of the left forearm"). This column may appear anywhere in the file.

Column name	Requirement Level	Data type	Description
placement_scheme	RECOMMENDED	string	A description of the electrode placement procedure used. See description of the <code>EMGPlacementScheme</code> field in <code>*_emg.json</code> . This column may appear anywhere in the file. Must be one of: "measured", "other".
placement_description	RECOMMENDED	string	Additional details of the approach to EMG sensor placement. See description of the <code>EMGPlacementSchemeDescription</code> field in <code>*_emg.json</code> . This column may appear anywhere in the file.
interelectrode_distance	RECOMMENDED	number	Distance between adjacent electrodes (in a pair or grid) that are rigidly attached to the same sensor device, or between the <code>signal_electrode</code> and its <code>reference</code> when each is independently placed. This column may appear anywhere in the file.
low_cutoff	OPTIONAL	number	Frequencies used for the high-pass filter applied to the channel in Hz. If no high-pass filter applied, use <code>n/a</code> . This column may appear anywhere in the file.
high_cutoff	OPTIONAL	number	Frequencies used for the low-pass filter applied to the channel in Hz. If no low-pass filter applied, use <code>n/a</code> . Note that hardware anti-aliasing in A/D conversion of all MEG/EEG/EMG electronics applies a low-pass filter; specify its frequency here if applicable. This column may appear anywhere in the file. Must be a number greater than or equal to 0.



Column name	Requirement Level	Data type	Description
notch	OPTIONAL	string	Frequencies used for the notch filter applied to the channel, in Hz. If notch filters are applied at multiple frequencies, these frequencies MAY be specified as a list, for example, [60, 120, 180]. If no notch filter was applied, use n/a. This column may appear anywhere in the file.
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]. This column may appear anywhere in the file. Must be one of: "good", "bad".
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 the status column. This column may appear anywhere in the file.
Additional Columns	OPTIONAL	n/a	Additional columns are allowed if they are defined in the associated metadata file.

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

Keyword	Description
ECG	ElectroCardioGram (heart)
EMG	ElectroMyoGram (muscle)
EOG	Generic EOG channel if HEOG or VEOG information not available
HEOG	Horizontal EOG

Keyword	Description
LATENCY	Latency of sample, in seconds from recording onset, typically from an external clock source. See <code>acq_time</code> column of the respective <code>*_scans.tsv</code> file. MUST be in form of <code>s[.000000]</code> , where <code>s</code> reflects whole seconds, and <code>.000000</code> reflects OPTIONAL fractional seconds.
MISC	Miscellaneous
REF	Reference channel
SYSCLOCK	Elapsed time since trial/recording start, as provided by the recording device.
TRIG	Analog (TTL in Volt) or digital (binary TTL) trigger channel
VEOG	Vertical EOG (electrooculogram)

Examples of common free-form text for the `description` column (these should occur without enclosing quotation marks):

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

Example `*_channels.tsv`

See also the corresponding `electrodes.tsv` example.

name	type	units	signal_electrode	reference	target_muscle
emg1	EMG	V	E1	E2	anterior belly of the digastric
emg2	EMG	V	E3	E4	levator angulis oris, zygomaticus major
emg3	EMG	V	E5	E6	platysma
emg4	EMG	V	E7	E8	obicularis oris

Electrodes description (`*_electrodes.tsv`)

Template:

```
sub-<label>/
  [ses-<label>/]
    emg/
      sub-<label>[_ses-<label>][_task-<label>][_acq-<label>][_run-<index>][_recording-<label>]_electrodes.json
      sub-<label>[_ses-<label>][_task-<label>][_acq-<label>][_run-<index>][_recording-<label>]_electrodes.tsv
```

Legend:

- `<matches>` is a placeholder to denote an arbitrary (and valid) sequence of entities and labels at the beginning of the filename (only BIDS "raw").
- `<source-entities>` is a placeholder to denote an arbitrary sequence of entities and labels at the beginning of the filename matching a source file from which the file derives (only BIDS-Derivatives).
- Filename entities or directories between square brackets (for example, `[_ses-<label>]`) are OPTIONAL.
- Some entities may only allow specific values, in which case those values are listed in `<>`, separated by `|`.
- `_<suffix>` means that there are several ( $>6$ ) valid suffixes for this filename pattern.
- `_<extension>` means that there are several ( $>6$ ) valid extensions for this file type.
- `[.gz]` means that both the unzipped and gzipped versions of the extension are valid.

File that gives the measured location, size, and other properties of EMG electrodes. If an `*_electrodes.tsv` file is specified, a `*_coordsystem.json` file MUST be specified as well.

Electrode locations may be specified in one of four ways:

1. Coordinates and landmarks digitized in situ. When 3D electrode locations are digitized in situ, the origin, orientation, and measurement unit of the coordinate system MUST be recorded in Cartesian coordinates according to the `EMGCoordinateSystem` and `EMGCoordinateUnits` fields in `*_coordsystem.json`, as described in the Coordinate Systems Appendix. In such cases, `EMGCoordinateSystem` SHOULD be specified as `Other`, the `EMGCoordinateSystemDescription` SHOULD contain a description of the origin and axis orientations of the 3D coordinate system, and the `coordinate_system` column in `*_electrodes.tsv` may be omitted.
2. Measured coordinates in a single coordinate system defined by anatomical landmarks. This approach is suitable for individual electrodes placed close together on a single body part. In this case the `*_coordsystem.json` file MUST contain fields `EMGCoordinateSystem`, `EMGCoordinateUnits`, and `EMGCoordinateSystemDescription` as described in (1) above. For example, 4 electrodes all placed on the forearm (2 on the volar surface and 2 on the dorsal surface) could be located with coordinates in the following coordinate system:
  - `x`: radial styloid process (RSP) → ulnar styloid process (USP);
  - `y`: olecranon process → cubital fossa;
  - `z`: RSP-USP → lateral humerus epicondyle

It may be possible to omit the `z` column when all electrodes are on the same surface (in the above example, if all electrodes were on the volar surface and none were on the dorsal surface). Though it would be possible to omit both `z` and `y` if all electrodes are colinear along the anatomically defined `x` axis, the `y` column is required and thus researchers SHOULD enter 0 for all entries in column `y` in such cases. In this case (of a single coordinate system for all electrodes) the `coordinate_system` column in `*_electrodes.tsv` may be omitted as in (1) above.

3. Measured coordinates in multiple anatomically-defined coordinate systems. This approach is suitable for individual electrodes placed on multiple body parts. In this case there MUST be multiple `*_coordsystem.json` files (distinguished by the `space` entity) for each coordinate system, each of which MUST contain the fields `EMGCoordinateSystem`, `EMGCoordinateUnits`, and `EMGCoordinateSystemDescription` as described in (1) above. Additionally, the `coordinate_system` column in `*_electrodes.tsv` MUST indicate which named coordinate system the coordinate values in that row reflect, by referencing the label of the `space` entity for the corresponding `*_coordsystem.json` file. For example, `*_space-lowerLeg_coordsystem.json` may specify a coordinate system defined by lower leg landmarks for electrodes below the knee, and another called `*_space-thigh_coordsystem.json` defined by upper-leg landmarks for electrodes above the knee. In such a case, entries in the `coordinate_system` column of `*_electrodes.tsv` MUST specify either `"lowerLeg"` or `"thigh"`. As in (2) above, enter 0 for the `y` column values if all electrodes are colinear along the defined `x` axis.
4. Measured coordinates in "nested" coordinate systems. This approach is suitable for large electrode grids or similar devices. In this case, measured 2D locations in the `x` and `y` columns define the geometry of an electrode grid or group, relative to an arbitrary device-internal origin and axes (this is the "child" coordi-

nate system, defined for example in a file `*_space-dorsalGrid_coordsystem.json`). The group's placement on the body is then described by selecting an "anchor" electrode and providing its coordinates within a "parent" coordinate system defined in reference to subject anatomy (as in (2) above), in a separate file such as `*_space-forearm_coordsystem.json`. Each coordinate system file **MUST** contain the fields `EMGCoordinateSystem`, `EMGCoordinateUnits`, and `EMGCoordinateSystemDescription` as described in (1) above. Additionally, each child coordinate system file **MUST** contain an entry `ParentCoordinateSystem` giving the value of the `space` entity for the file that defines the parent (anatomical) coordinate system, and entries `AnchorElectrode` and `AnchorCoordinates` that name an electrode and provide its coordinates in the parent coordinate system (respectively). For example, a coordinate system called "forearm" defined by forearm anatomical landmarks (as in (2) above) could be the parent coordinate system for two electrode grids placed on the volar and dorsal surfaces of the forearm. Each grid would have its own coordinate system file (named, for example, `*_space-dorsalGrid_coordsystem.json` and `*_space-volarGrid_coordsystem.json`) in which coordinates of each electrode are relative to a device-internal origin, such as the lower-leftmost electrode when the device is in a specified orientation. In such a scenario, entries in the `coordinate_system` column of `*_electrodes.tsv` **MUST** specify either "volarGrid" or "dorsalGrid" for electrodes within each grid (electrodes external to the grid, such as separate reference or ground electrodes, **MAY** specify a different value in the `coordinate_system` column: typically this will be the parent coordinate system or a different anatomically defined coordinate system as in (2) above). Note that the parent coordinate system may be defined in different units than the child coordinate system; for example, if an anchor electrode was placed 50% of the distance between the ulnar styloid process and cubital fossa, the unit of the parent coordinate system is "percent" and `AnchorCoordinates` would have a value of 50 for the x coordinate in `*_space-volarGrid_coordsystem.json`. Meanwhile, the x column of `*_electrodes.tsv` gives the device-internal coordinates of the grid electrodes, which may be in a different unit such as "mm". See the `coordsystem.json` section for further details.

For details of how to specify the coordinate systems in each of these cases, see the `coordsystem.json` section.

Required columns

The order of the required columns in the `*_electrodes.tsv` file **MUST** be as listed below.

Column name	Requirement Level	Data type	Description
name	REQUIRED	string	Name of the electrode contact point. The combination of <code>name</code> and <code>group</code> <b>MUST</b> be unique. This column must appear first in the file.
x	REQUIRED	number	Recorded position along the x-axis. This column must appear second in the file.
y	REQUIRED	number	Recorded position along the y-axis. This column must appear third in the file.
z	OPTIONAL	number	Recorded position along the z-axis. This column must appear fourth in the file.
coordinate_system	RECOMMENDED	string	Name of the coordinate system defined in <code>coordsystem.json</code> in which the electrode's x, y, and (optionally) z coordinates are given. This column must appear fifth in the file.

Column name	Requirement Level	Data type	Description
type	RECOMMENDED	string	Type of the electrode (for example, cup, ring, clip-on, wire, needle). This column may appear anywhere in the file.
material	RECOMMENDED	string	Material of the electrode (for example, Tin, Ag/AgCl, Gold). This column may appear anywhere in the file.
impedance	RECOMMENDED	number	Impedance of the electrode, units MUST be in kOhm. This column may appear anywhere in the file.
group	RECOMMENDED	string or number	Which group the electrode or channel belongs to (typically this indicates electrodes or bipolar channels on the same grid, strip, or other device). The combination of name and group MUST be unique.This column may appear anywhere in the file.
Additional Columns	OPTIONAL	n/a	Additional columns are allowed if they are defined in the associated metadata file.

The `recording-<label>` entity MUST be used to indicate simultaneous acquisition of data from multiple EMG devices, in cases where the devices store data in separate data files. For example:

```
sub-01/
  ses-01/
    emg/
      sub-01_ses-01_recording-RectusFemoris_electrodes.tsv
      sub-01_ses-01_recording-VastusLateralis_electrodes.tsv
      sub-01_ses-01_recording-VastusMedialis_electrodes.tsv
```

Above, acquisitions are labeled with the target muscle, but other naming schemes are also appropriate. For example, if bipolar and grid EMG devices are used simultaneously, acquisitions may be labeled "bipolar" and "grid", or use the device manufacturer names. For cases of multiple devices recording simultaneously into the same data file, the `group` column MUST be used to distinguish which electrodes belong to which device.

Except in cases of simultaneous acquisitions from different devices into different data files (as mentioned above), `*_electrodes.tsv` files SHOULD NOT be duplicated for each data file, for example, during multiple runs of a task. The inheritance principle MUST be used to find the appropriate electrode positions for a given data file. If electrodes are repositioned, it is RECOMMENDED to use multiple sessions to indicate this.

### Example \*\_electrodes.tsv

Example \*\_electrodes.tsv for a 2 by 2 grid of EMG electrodes with 2.5 mm electrode diameter and 10 mm inter-electrode distance.

name	x	y	coordinate_system	group	diameter
001	0.0	0.0	VolarForearm	grid1	2.5
002	10.0	0.0	VolarForearm	grid1	2.5
003	0.0	10.0	VolarForearm	grid1	2.5
004	10.0	10.0	VolarForearm	grid1	2.5
001	0.0	0.0	DorsalForearm	grid2	2.5
002	10.0	0.0	DorsalForearm	grid2	2.5
003	0.0	10.0	DorsalForearm	grid2	2.5
004	10.0	10.0	DorsalForearm	grid2	2.5

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

Template:

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

Legend:

- <matches> is a placeholder to denote an arbitrary (and valid) sequence of entities and labels at the beginning of the filename (only BIDS "raw").
- <source-entities> is a placeholder to denote an arbitrary sequence of entities and labels at the beginning of the filename matching a source file from which the file derives (only BIDS-Derivatives).
- Filename entities or directories between square brackets (for example, [\_ses-<label>]) are OPTIONAL.
- Some entities may only allow specific values, in which case those values are listed in <>, separated by |.
- \_<suffix> means that there are several (>6) valid suffixes for this filename pattern.
- .<extension> means that there are several (>6) valid extensions for this file type.
- [.gz] means that both the unzipped and gzipped versions of the extension are valid.

This \*\_coordsystem.json file contains the coordinate system in which electrode positions are expressed. Associated photos can also be provided. The \*\_coordsystem.json is REQUIRED if the optional \*\_electrodes.tsv is specified; please see the electrodes description section for important guidance regarding how to specify electrode location.

Fields relating to the EMG coordinate system(s):

Key name	Requirement Level	Data type	Description
EMGCoordinateSystem	REQUIRED	string	Defines the coordinate system for the EMG sensors. See the EMGCoordinateSystem for a list of restricted keywords for coordinate systems. If "Other", provide definition of the coordinate system in EMGCoordinateSystemDescription. "Other" is the only valid value until standardized names become available for EMG coordinate systems. Must be one of: "Other".
EMGCoordinateUnits	REQUIRED	string	Units of the coordinates of EMGCoordinateSystem. Must be one of: "m", "mm", "cm", "percent", "n/a".
EMGCoordinateSystemDescription	RECOMMENDED, but REQUIRED if EMGCoordinateSystem is "Other"	string	Free-form text description of the coordinate system, typically defining the origin and positive x,y,z axis directions, relative to anatomical landmarks. May also include a link to a documentation page or paper describing the system in greater detail.
ParentCoordinateSystem	OPTIONAL	string	The name of a JSON mapping key that defines the parent (anatomical) coordinate system in which this child (device) coordinate system is anchored.
AnchorCoordinates	OPTIONAL, but REQUIRED if ParentCoordinateSystem is present	array of numbers	Coordinates of the AnchorElectrode in the parent (anatomical) coordinate system. This should be an array of numbers of length 3, in the units given in EMGCoordinateSystemUnits within the JSON object named in ParentCoordinateSystem.
AnchorElectrode	OPTIONAL, but REQUIRED if ParentCoordinateSystem is present	string	Name of the electrode in the child (device) coordinate system whose coordinates in the parent (anatomical) coordinate system are given in AnchorCoordinates.

The `recording-<label>` entity MUST be used to indicate simultaneous acquisition of data from multiple EMG devices, in cases where the devices store data in separate data files. Except in cases of simultaneous acquisitions from different devices into different data files (as just mentioned), `*_coordsystem.json` files SHOULD NOT be duplicated for each data file, for example, during multiple runs of a task. However, multiple `*_coordsystem.json` files distinguished by the `space` entity MUST be used to describe separate anatomically-defined coordinate systems (for example, to situate devices in reference to landmarks on different limbs). Multiple `*_coordsystem.json` files distinguished by the `space` entity MUST also be used to describe nested coordinate systems that give the relative positions of groups or grids of electrodes mounted to a single device and situate that "child" coordinate system within an anatomically-defined "parent" coordinate system that situates the placement multi-electrode device on the body. The inheritance principle MUST be used to find the appropriate coordinate system description for a given data file.

#### Example 1: `*_coordsystem.json` for digitized electrode positions

Here, a coordinate system is defined based on digitized cranial landmarks, and is suitable for EMG electrodes on the face whose locations are digitized with the same equipment as the cranial landmarks:

```
{
  "EMGCoordinateSystem": "Other",
  "EMGCoordinateSystemDescription": "x: left helix-tragus junction (LHJ) → right helix-tragus junction (RHJ); y:inion → nasion; z: midpoint between
  "EMGCoordinateSystemUnits": "m"
}
```

#### Example 2: `*_coordsystem.json` for measured electrode positions in a single coordinate system defined by anatomical landmarks

Here, a coordinate system is defined based on percentage of distances between anatomical landmarks of the forearm, and is suitable for localizing individual electrodes on the same body part:

```
{
  "EMGCoordinateSystem": "Other",
  "EMGCoordinateSystemDescription": "x: radial styloid process (RSP) → ulnar styloid process (USP); y: oleacranon process → cubital fossa; z: RSP-USP
  "EMGCoordinateSystemUnits": "percent"
}
```

#### Example 3: multiple `*_coordsystem.json` files for measured electrode positions in multiple anatomically-defined coordinate systems

Here, separate anatomically-based coordinate systems are defined for electrodes above and below the elbow joint, and each is given a unique name ("Forearm" or "Humerus") which can be referenced in the `coordinate_system` column of `*_electrodes.tsv`:

```
json title="*_space-Forearm_coordsystem.json" {      "EMGCoordinateSystem": "Other",      "EMGCoordinateSystemDescription": "x: radial styloid
process (RSP) → ulnar styloid process (USP); y: oleacranon process → cubital fossa; z: RSP-USP → lateral humerus epicondyle",      "EMGCoordinateSystemU
"percent" }

json title="*_space-Humerus_coordsystem.json" {      "EMGCoordinateSystem": "Other",      "EMGCoordinateSystemDescription": "x: medial humerus
epicondyle (MHE) → lateral humerus epicondyle (LHE), y: oleacranon process → cubital fossa, z: MHE-LHE → greater humerus tubercule",      "EMGCoordinate
"percent" }
```



## Example 4: multiple \*\_coordsystem.json files for nested/anchored coordinate systems

Here, coordinate systems for the relative locations of electrodes in grids or groups are given in "child" coordinate systems ("BicepGrid", "VolarForearmGrid", "DorsalForearmGrid"), each of which is anchored to a "parent" coordinate system that is defined anatomically:

```
json title="*_space-BicepGrid_coordsystem.json" {      "EMGCoordinateSystem": "Other",      "EMGCoordinateSystemDescription": "x-axis left → right, y-axis bottom → top, when grid is oriented with leads at the bottom",      "EMGCoordinateSystemUnits": "mm",      "ParentCoordinateSystem": "Humerus",      "AnchorCoordinates": [40, 70, 0],      "AnchorElectrode": "E1" }

json title="*_space-VolarForearmGrid_coordsystem.json" {      "EMGCoordinateSystem": "Other",      "EMGCoordinateSystemDescription": "x-axis left → right, y-axis bottom → top, when grid is oriented with leads at the bottom",      "EMGCoordinateSystemUnits": "mm",      "ParentCoordinateSystem": "Forearm",      "AnchorCoordinates": [25, 50, 10],      "AnchorElectrode": "E1" }

json title="*_space-DorsalForearmGrid_coordsystem.json" {      "EMGCoordinateSystem": "Other",      "EMGCoordinateSystemDescription": "x-axis left → right, y-axis bottom → top, when grid is oriented with leads at the bottom",      "EMGCoordinateSystemUnits": "mm",      "ParentCoordinateSystem": "Forearm",      "AnchorCoordinates": [75, 0, 90],      "AnchorElectrode": "E1", }

json title="*_space-Forearm_coordsystem.json" {      "EMGCoordinateSystem": "Other",      "EMGCoordinateSystemDescription": "x: radial styloid process (RSP) → ulnar styloid process (USP); y: oleacranon process → cubital fossa; z: RSP-USP → lateral humerus epicondyle",      "EMGCoordinateSystemUnits": "percent" }

json title="*_space-Humerus_coordsystem.json" {      "EMGCoordinateSystem": "Other",      "EMGCoordinateSystemDescription": "x: medial humerus epicondyle (MHE) → lateral humerus epicondyle (LHE), y: oleacranon process → cubital fossa, z: MHE-LHE → greater humerus tubercule",      "EMGCoordinateSystemUnits": "percent" }
```

## Photos of the electrode positions (\*\_photo.<extension>)

Template:

```
sub-<label>/
  [ses-<label>/]
    emg/
      sub-<label>[_ses-<label>][_acq-<label>][_recording-<label>]_photo.jpg
      sub-<label>[_ses-<label>][_acq-<label>][_recording-<label>]_photo.png
      sub-<label>[_ses-<label>][_acq-<label>][_recording-<label>]_photo.tif
```

Legend:

- <matches> is a placeholder to denote an arbitrary (and valid) sequence of entities and labels at the beginning of the filename (only BIDS "raw").
- <source-entities> is a placeholder to denote an arbitrary sequence of entities and labels at the beginning of the filename matching a source file from which the file derives (only BIDS-Derivatives).
- Filename entities or directories between square brackets (for example, [\_ses-<label>]) are OPTIONAL.
- Some entities may only allow specific values, in which case those values are listed in <>, separated by |.
- \_<suffix> means that there are several (>6) valid suffixes for this filename pattern.

- `.<extension>` means that there are several (>6) valid extensions for this file type.
- `[.gz]` means that both the unzipped and gzipped versions of the extension are valid.

Photos of the electrode locations are OPTIONAL. Photos SHOULD include sufficient surrounding context to distinguish anatomical location. For example, photographs of electrodes on the limbs should include at least one adjacent joint. Photos may need to be cropped and/or blurred to conceal identifying features or entirely omitted prior to dataset distribution, depending on obtained consent.

If there are photos of the electrodes, the `recording-<label>` entity MAY be specified, if separate photos are provided of each EMG device and the devices recorded into separate data files. The `ses-<label>` entity may be used to specify when the photo was taken.

#### Example `*_photo.<extension>`

```
sub-01/  
  ses-01/  
    sub-01_ses-01_recording-DorsalForearmGrid_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. Raw data are data that have been curated into BIDS from a non-BIDS source. If a dataset is derived from at least one other valid BIDS dataset, then it is a derivative dataset.

Examples:

A defaced T1w image would typically be made during the curation process and is thus under raw

```
sourcedata/pre-deface/sub-01/anat/sub-01_T1w.nii.gz  
sub-01/anat/sub-01_T1w.nii.gz
```

A defaced T1w image could also, in theory, be derived from a BIDS dataset and would thus be under derivatives

```
sub-01/anat/sub-01_T1w.nii.gz  
derivatives/defaced/sub-01/anat/sub-01_desc-defaced_T1w.nii.gz
```

## Derivatives storage and directory structure

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>.<extension>` (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>` entity 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>`.

## File format specification

Derived data may be resampled into structures that are not well-handled by the raw data formats. In this section, we describe standard formats that SHOULD be adhered to when appropriate, and the extensions they should have.

### GIFTI Surface Data Format

The [GIFTI](#) format is an XML-based structure containing one or more data arrays, and is well-suited to describing surface geometry and parcellations.

The following extension table is reproduced in part from Section 9.0 of the [GIFTI specification](#), indicating the expected extensions of different data arrays or combinations of data arrays.

Intent	Extension
Coordinates	<code>.coord.gii</code>
Functional	<code>.func.gii</code>

Intent	Extension
Labels	.label.gii
RGB or RGBA	.rgba.gii
Shape	.shape.gii
Surface	.surf.gii
Tensors	.tensor.gii
Time Series	.time.gii
Topology	.topo.gii
Vector	.vector.gii

Unless otherwise stated, bare .gii extensions SHOULD NOT be used for GIFTI files.

# 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 using Sources; 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. Using paths specified relative to the dataset root is Sources.

Key name	Requirement Level	Data type	Description
RawSources	RawSources	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. This field is DEPRECATED, and this metadata SHOULD be recorded in the Sources field using RawSources to distinguish sources from different datasets.

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 Sources metadata, and \_desc-<label> is used (the last entity before the suffix) 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
{
  "Sources": ["bids:raw:sub-01/func/sub-01_task-rest_bold.nii.gz"]
}
```

Note that "raw" must appear in the DatasetLinks metadata in dataset\_description.json. For example, in the case that the given derivatives dataset is nested within the "derivatives" directory of a raw dataset, the entry in DatasetLinks may say: "raw": "../..".

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 Sources.

```
{
  "Sources": [
    "bids:raw:sub-01/func/sub-01_task-rest_bold.nii.gz",
    "bids:raw: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 may include both the local, derivative file, and the raw original file.

```
{
  "Sources": [
    "bids:sub-01/anat/sub-01_desc-preproc_T1w.nii.gz",
    "bids:raw: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	String or object describing the reference image to which the current image is aligned. 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][]	This can be used to point to a specific file. Paths written relative to the root of the derivative dataset are [DEPRECATED][] in favor of [BIDS URIs][].

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": "bids::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. Here referred to via "https" [URIs][].

```
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>/
    [ses-<label>/]
      <datatype>/
        <source-entities>[_space-<space>][_desc-<label>][_suffix>.<extension>]
```

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).

## descriptions.tsv

Template:

```
[sub-<label>/]
  [ses-<label>/]
    [sub-<label>_] [ses-<label>_] descriptions.tsv
    [sub-<label>_] [ses-<label>_] descriptions.json
```

Optional: Yes

To keep a record of processing steps applied to the data, a **descriptions.tsv** file MAY be used. The **descriptions.tsv** file consists of one row for each unique **desc-<label>** entity used in the dataset and a set of REQUIRED and OPTIONAL columns:

Column name	Requirement Level	Data type	Description
desc_id	REQUIRED	string	A desc-<label> entity present in the derivatives dataset. The desc_id column contains the labels used with the desc_id, within the particular nesting that the descriptions.tsv file is placed. For example, if the descriptions.tsv file is placed at the root of the derivative dataset, its desc_id column SHOULD contain all labels of the desc entity) used across the entire derivative dataset. Values in desc_id MUST be unique. This column must appear first in the file.
description	REQUIRED	string	Free-form text description of the entity's label (defined in <entity>_id column). The corresponding label column is desc_id. This column must appear second in the file.
Additional Columns	OPTIONAL	n/a	Additional columns are allowed.

This file MAY be located at the root of the derivative dataset, or at the subject or session level ([Inheritance Principle](#)).

The use of descriptions.tsv files together with the desc entity are helpful to document how files are generated, even if their use may not be sufficient to provide full computational reproducibility.

Example use of a **descriptions.tsv** file

```
raw/
  CHANGES
  README
  channels.tsv
  dataset_description.json
  participants.tsv
  sub-001/
    eeg/
      sub-001_task-listening_events.tsv
      sub-001_task-listening_events.json
      sub-001_task-listening_eeg.edf
      sub-001_task-listening_eeg.json
```

```
derivatives/  
  descriptions.tsv  
  sub-001/  
    eeg/  
      sub-001_task-listening_desc-Filt_eeg.edf  
      sub-001_task-listening_desc-Filt_eeg.json  
      sub-001_task-listening_desc-FiltDs_eeg.edf  
      sub-001_task-listening_desc-FiltDs_eeg.json  
      sub-001_task-listening_desc-preproc_eeg.edf  
      sub-001_task-listening_desc-preproc_eeg.json
```

Contents of the `descriptions.tsv` file:

```
desc_id description  
desc-Filt    low-pass filtered at 30Hz  
desc-FiltDs low-pass filtered at 30Hz, downsampled to 250Hz  
desc-preproc low-pass filtered at 30Hz, downsampled to 250Hz, and rereferenced to a common average reference
```

# 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>/
    [ses-<label>/]
      <datatype>/
        <source-entities>[_space-<space>] [_res-<label>] [_den-<label>] [_desc-<label>] _<suffix>.<extension>
```

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 <code>res</code> 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 <code>res</code> entity and values should be descriptions of those <code>res</code> values.
Density	REQUIRED if <code>den</code> 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 <code>den</code> entity and values should be descriptions of those <code>den</code> 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>/  
    [ses-<label>]/  
      anat|func|dwi/  
        <source-entities>[_space-<space>][_res-<label>][_label-<label>][_desc-<label>]_mask.json  
        <source-entities>[_space-<space>][_res-<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 a discrete or probabilistic segmentation, then the `label` entity SHOULD be used to specify the masked structure (see Common image-derived labels).

JSON metadata fields:



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".
Sources	RECOMMENDED	array of strings	A list of files with the paths specified using Sources; 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. Using paths specified relative to the dataset root is Sources.
RawSources	RawSources	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. This field is DEPRECATED, and this metadata SHOULD be recorded in the Sources field using RawSources to distinguish sources from different datasets.
Resolution	REQUIRED if <b>res</b> 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 <b>res</b> entity and values should be descriptions of those <b>res</b> values.

Key name	Requirement Level	Data type	Description
Density	REQUIRED if <code>den</code> is present	<code>string</code> or <code>object</code> of <code>strings</code>	Specifies the interpretation of the density keyword. If an object is used, then the keys should be values for the <code>den</code> entity and values should be descriptions of those <code>den</code> values.

Examples:

```
func_loc/  
  sub-001/  
    func/  
      sub-001_task-rest_run-1_space-MNI305_label-PFC_mask.nii.gz  
      sub-001_task-rest_run-1_space-MNI305_label-PFC_mask.json  
manual_masks/  
  sub-001/  
    anat/  
      sub-001_label-tumor_mask.nii.gz  
      sub-001_label-tumor_mask.json
```

## Segmentations

A segmentation is a spatial partition of images and surfaces, such that each location (for example, a voxel or a surface vertex) is identified with one label (discrete) or a combination of labels (probabilistic). Labeled regions may include anatomical structures (for example, tissue classes, white matter tracts, Thalamic nuclei, cortical areas), 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.

If different segmentations coexist within the same directory of the BIDS structure (for example, if they were generated with two alternative tools), the `seg-<label>` entity SHOULD be used for disambiguation.

The `seg-<label>` entity MAY be used in combination with the `atlas-<label>` entity as indicated by the Templates and Atlases section.

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
SpatialReference	RECOMMENDED	string or object	String or object describing the reference image to which the current image is aligned. 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.
Manual	OPTIONAL	boolean	Indicates if the segmentation was performed manually or via an automated process. Must be one of: "true", "false".
CoordinateReportStrategy	OPTIONAL	string	Indicate the method of coordinate reporting in statistically significant clusters. Could be the "peak" statistical coordinate in the cluster or the "center_of_mass" of the cluster. Must be one of: "peak", "center_of_mass", "other".
Resolution	REQUIRED if <b>res</b> 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 <b>res</b> entity and values should be descriptions of those <b>res</b> values.
Density	REQUIRED if <b>den</b> 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 <b>den</b> entity and values should be descriptions of those <b>den</b> values.

## Discrete Segmentations

Discrete segmentations of brain tissue represent regions with unique integer labels. See Common image-derived labels for a description of how integer values map to anatomical structures.

Template:

```
<pipeline-name>/
  sub-<label>/
```

```
[ses-<label>/]
  <data_type>/
    <source-entities>[_space-<space>] [_seg-<label>] [_res-<label>] [_desc-<label>] _dseg.json
    <source-entities>[_space-<space>] [_seg-<label>] [_res-<label>] [_desc-<label>] _dseg.nii.gz]
    <source-entities>[_space-<space>] [_seg-<label>] [_res-<label>] [_desc-<label>] _dseg.tsv
```

For example, we can specify the results of a classic brain tissue segmentation algorithm of a T1w image based on a Gaussian mixture model as:

```
pipeline/
  sub-001/
    anat/
      sub-001_dseg.nii.gz
      sub-001_dseg.json
```

When several segmentations coexist at the same BIDS hierarchy point, `seg-<label>` entity SHOULD be used for disambiguation. For example, if the brain tissue segmentation above will be stored next to segmentations of the eyes:

```
pipeline/
  sub-001/
    anat/
      sub-001_seg-braintissues_dseg.nii.gz
      sub-001_seg-braintissues_dseg.json
      sub-001_seg-eyes_dseg.nii.gz
      sub-001_seg-eyes_dseg.json
```

## 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>/
    [ses-<label>/]
      func|anat|dwi/
        <source-entities>[_space-<space>] [_seg-<label>] [_res-<label>] [_label-<label>] [_desc-<label>] _probseg.json
        <source-entities>[_space-<space>] [_seg-<label>] [_res-<label>] [_label-<label>] [_desc-<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 values for the `label` entity.

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>/
    [ses-<label>/]
      anat/
        <source-entities>[_hemi-{L|R}] [_space-<space>] [_seg-<label>] [_res-<label>] [_den-<label>] [_desc-<label>] _dseg.json
        <source-entities>[_hemi-{L|R}] [_space-<space>] [_seg-<label>] [_den-<label>] [_desc-<label>] _dseg.label.gii
        <source-entities>[_hemi-{L|R}] [_space-<space>] [_seg-<label>] [_res-<label>] [_den-<label>] [_desc-<label>] _dseg.dlabel.nii
        <source-entities>[_hemi-{L|R}] [_space-<space>] [_seg-<label>] [_res-<label>] [_den-<label>] [_desc-<label>] _dseg.tsv
```

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. Values in <b>index</b> MUST be unique.
name	REQUIRED	string	The unique label name.
abbreviation	OPTIONAL	string	The unique label abbreviation
color	OPTIONAL	string	Hexadecimal. Label color for visualization.
mapping	OPTIONAL	integer	Corresponding integer label in the standard BIDS label lookup.
Additional Columns	OPTIONAL	n/a	Additional columns are allowed.

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
```

## Derivatives from atlases

Often, derivatives are atlas-based, meaning, a particular result has been derived from prior knowledge in the form of an atlas. These derivatives follow the specifications above, with the addition of a set of entities that MAY be used to disambiguate the outputs.

Template:

```
<pipeline_name>/  
  sub-<label>/
```

```
<datatype>/
```

```
<source_entities>[_space-<space>][_atlas-<label>][_seg-<label>][_scale-<label>][_res-<label>][_den-<label>][_desc-<label>][_<suffix>].<extension>
```

- `space-<label>` is REQUIRED to disambiguate derivatives defined with respect to different coordinate systems, following the general BIDS-Derivatives specifications.
- `atlas-<label>` is REQUIRED to encode files derived from the atlas identified by the entity's label.
- `seg-<label>` is REQUIRED when a single atlas has several different realizations (for instance, segmentations and parcellations created with different criteria) that need disambiguation.
- `scale-<label>` is REQUIRED to disambiguate different atlas 'scales', when the atlas has more than one 'brain unit' or 'areal resolution', typically relating to the number of regions defined and the area they cover.

For example, derivatives from a single subject segmented with the Automated Anatomical Labeling (AAL) atlas ([Tzourio-Mazoyer et al., 2002](#)).

```
aals-pipeline/  
sub-01/  
  anat/  
    sub-01_atlas-AAL_dseg.json  
    sub-01_atlas-AAL_dseg.nii.gz  
    sub-01_atlas-AAL_dseg.tsv  
    sub-01_atlas-AAL_probseg.nii.gz  
    sub-01_label-brain_mask.nii.gz  
    sub-01_label-head_mask.nii.gz  
    sub-01_T1w.nii.gz  
    sub-01_T1w.json
```

Because the AAL atlas was originally defined in the standardized space of MNI305, it would be unsurprising to find the anatomical reference resampled into the standard space for validation, as well as the spatial transformation file:

```
aals-pipeline/  
sub-001/  
  anat/  
    sub-001_atlas-AAL_dseg.json  
    sub-001_atlas-AAL_dseg.nii.gz  
    sub-001_atlas-AAL_dseg.tsv  
    sub-001_atlas-AAL_probseg.nii.gz  
    sub-001_from-T1w_to-MNI305_mode-image_xfm.h5  
    sub-001_label-brain_mask.nii.gz  
    sub-001_label-head_mask.nii.gz  
    sub-001_space-MNI305_T1w.nii.gz  
    sub-001_space-MNI305_T1w.json  
    sub-001_T1w.nii.gz  
    sub-001_T1w.json
```



Please note that the specification for spatial transforms (BEP 014) is currently under development, and therefore, the specification of transforms files (`sub-01_from-T1w_to-MNI305_mod` in the example above) may change in the future.

In the common case of multiple segmentations and parcellations derived from an atlas, `seg-<label>` SHOULD be used in combination with the `atlas-<label>` entity. Extending on our previous example, when the brain tissue and the eye segmentations are stored next to the results of FreeSurfer's automatic subcortical segmentation ("aseg") using the Destrieux2009 atlas:

```
pipeline/  
  sub-001/  
    anat/  
      sub-001_atlas-Destrieux2009_seg-aseg_dseg.nii.gz  
      sub-001_atlas-Destrieux2009_seg-aseg_dseg.json  
      sub-001_atlas-Destrieux2009_seg-aseg+aparc_dseg.nii.gz  
      sub-001_atlas-Destrieux2009_seg-aseg+aparc_dseg.json  
      sub-001_seg-braintissues_dseg.nii.gz  
      sub-001_seg-braintissues_dseg.json  
      sub-001_seg-eyes_dseg.nii.gz  
      sub-001_seg-eyes_dseg.json
```

Derivatives from several atlases can coexist in a single directory:

```
aals-pipeline/  
  sub-001/  
    anat/  
      sub-001_atlas-AAL_dseg.json  
      sub-001_atlas-AAL_dseg.nii.gz  
      sub-001_atlas-AAL_dseg.tsv  
      sub-001_atlas-AAL_probseg.json  
      sub-001_atlas-AAL_probseg.nii.gz  
      sub-001_atlas-Destrieux2009_seg-aseg+aparc_dseg.json  
      sub-001_atlas-Destrieux2009_seg-aseg+aparc_dseg.nii.gz  
      sub-001_atlas-Destrieux2009_seg-aseg_dseg.json  
      sub-001_atlas-Destrieux2009_seg-aseg_dseg.nii.gz  
      sub-001_seg-braintissues_dseg.json  
      sub-001_seg-braintissues_dseg.nii.gz
```

## Atlas tabular data

Atlases are often distributed with a Look Up Table (LUT) that indexes and labels each node/parcel/region within the atlas. This file will be essential for downstream workflows that generate matrices or other derived files within which node/parcel/region information is required, as the index/label fields will be used to reference the original anatomy the index/labels are derived from. Atlas-derived results SHOULD encode this information with the `dseg.tsv` or `probseg.json` files following the prescriptions of the Common image-derived labels section above. Additional fields can be added with their respective definition/description in the sidecar JSON file.

Template:

```
<pipeline_name>/  
  sub-<label>/  
    <datatype>/  
      <source_entities>[_atlas-<label>][_seg-<label>][_scale-<label>][_desc-<label>]_<suffix>.tsv
```

For example, the participant-level results using the Schaefer 2018 atlas could be structured as follows. Please note that, the `dseg.tsv` files have been moved to the root of the hierarchy following the common principles.

```
bold-pipeline/  
  atlas-Schaefer2018_dseg.json  
  atlas-Schaefer2018_seg-7n_scale-100_dseg.tsv  
  atlas-Schaefer2018_seg-7n_scale-200_dseg.tsv  
  atlas-Schaefer2018_seg-7n_scale-300_dseg.tsv  
  atlas-Schaefer2018_seg-17n_scale-100_dseg.tsv  
  atlas-Schaefer2018_seg-17n_scale-200_dseg.tsv  
  atlas-Schaefer2018_seg-17n_scale-300_dseg.tsv  
  atlas-Schaefer2018_seg-kong17n_scale-100_dseg.tsv  
  atlas-Schaefer2018_seg-kong17n_scale-200_dseg.tsv  
  atlas-Schaefer2018_seg-kong17n_scale-300_dseg.tsv  
  sub-01/  
    anat/  
      sub-01_hemi-L_atlas-Schaefer2018_seg-7n_scale-100_den-164k_dseg.label.gii  
      sub-01_hemi-L_atlas-Schaefer2018_seg-7n_scale-200_den-164k_dseg.label.gii  
      sub-01_hemi-L_atlas-Schaefer2018_seg-7n_scale-300_den-164k_dseg.label.gii  
      sub-01_hemi-L_atlas-Schaefer2018_seg-17n_scale-100_den-164k_dseg.label.gii  
      sub-01_hemi-L_atlas-Schaefer2018_seg-17n_scale-200_den-164k_dseg.label.gii  
      sub-01_hemi-L_atlas-Schaefer2018_seg-17n_scale-300_den-164k_dseg.label.gii  
      sub-01_hemi-L_atlas-Schaefer2018_seg-kong17n_scale-100_den-164k_dseg.label.gii  
      sub-01_hemi-L_atlas-Schaefer2018_seg-kong17n_scale-200_den-164k_dseg.label.gii  
      sub-01_hemi-L_atlas-Schaefer2018_seg-kong17n_scale-300_den-164k_dseg.label.gii  
      ...  
      sub-01_hemi-R_atlas-Schaefer2018_seg-kong17n_scale-300_den-164k_dseg.label.gii  
    bold/  
      sub-01_task-rest_hemi-L_den-164k_bold.func.gii  
      sub-01_task-rest_hemi-R_den-164k_bold.func.gii  
  sub-02/  
    anat/  
      sub-02_hemi-L_atlas-Schaefer2018_seg-7n_scale-100_den-164k_dseg.label.gii  
      sub-02_hemi-L_atlas-Schaefer2018_seg-7n_scale-200_den-164k_dseg.label.gii  
      sub-02_hemi-L_atlas-Schaefer2018_seg-7n_scale-300_den-164k_dseg.label.gii
```

```
sub-02_hemi-L_atlas-Schaefer2018_seg-17n_scale-100_den-164k_dseg.label.gii
sub-02_hemi-L_atlas-Schaefer2018_seg-17n_scale-200_den-164k_dseg.label.gii
sub-02_hemi-L_atlas-Schaefer2018_seg-17n_scale-300_den-164k_dseg.label.gii
sub-02_hemi-L_atlas-Schaefer2018_seg-kong17n_scale-100_den-164k_dseg.label.gii
sub-02_hemi-L_atlas-Schaefer2018_seg-kong17n_scale-200_den-164k_dseg.label.gii
sub-02_hemi-L_atlas-Schaefer2018_seg-kong17n_scale-300_den-164k_dseg.label.gii
...
sub-02_hemi-R_atlas-Schaefer2018_seg-kong17n_scale-300_den-164k_dseg.label.gii
bold/
sub-02_task-rest_hemi-L_den-164k_bold.func.gii
sub-02_task-rest_hemi-R_den-164k_bold.func.gii
```

Example of contents. For example, the file atlas-Schaefer2018\_seg-7n\_scale-100\_dseg.tsv could look like:

```
index  name      color
1    17Networks_LH_VisCent_ExStr_1  #781180
2    17Networks_LH_VisCent_ExStr_2  #781181
3    17Networks_LH_VisCent_ExStr_3  #781182
4    17Networks_LH_VisCent_ExStr_4  #781183
5    17Networks_LH_VisCent_ExStr_5  #781184

...

998 17Networks_RH_TempPar_20    #0d2afb
999 17Networks_RH_TempPar_21    #0d2afc
1000 17Networks_RH_TempPar_22    #0d2afd
```

# Templates and atlases

In the following, we describe how the outcomes of analyses that produce templates and atlases are organized as BIDS-Derivatives.

For outcomes of analyses corresponding to individual subjects that derive from atlases and may refer to spaces other than the original subject's space, please refer to the Derivatives from atlases subsection.

## Derived templates

Many analyses include spatial standardization to pull individuals' data into a common spatial frame. For example, creating an atlas will most likely require the creation of a new template or the integration of existing ones to define a stereotactic space.

For derivatives of template-generating pipelines, which typically aggregate several sessions and/or subjects, the derivatives-specific `tpl-<label>` entity indicates that the spatial frame of analysis is not defined by a single brain image but an aggregation thereof.

The selected `<label>` in the `tpl-<label>` entity is RECOMMENDED for the `space-<label>` entity in downstream derivatives from this particular template (see previous section Derivatives from atlases).

Template:

```
<pipeline-name>/
  tpl-<label>/
    [cohort-<label>/]
      [<datatype>/]
        tpl-<label>[_cohort-<label>][_<entities>]_<suffix>.<extension>
```

where `suffix` is any valid BIDS suffix such as `T1w` or `PET`; and `extension` is a valid BIDS extension such as `nii.gz`, `dscalar.nii.gz`, `dlabel.nii.gz`, `label.gii`, `tsv`, or `json`. Templates and atlases do not establish new suffixes or extensions, but any valid BIDS/BIDS Derivatives filename is permitted in a template directory, substituting `tpl` for `sub` and `cohort` for `ses`.

The `<datatype>/` directory MAY be omitted in the case only one data type (such as `anat/`) is stored under the `tpl-<label>/` directory.

The `cohort-<label>` directory and entity MUST be specified for templates with several cohorts.

In templates/atlasses the `tpl-<label>` and `cohort-<label>` entities are structurally analogous to the `sub-<label>` and `ses-<label>` entities, appearing as both directories and entities. The `cohort-<label>` entity is used to track mappings of arbitrary subject/session pairs.

In BIDS, a template is considered any aggregation of data and the `tpl-` entity replaces the subject-level `sub-` entity when aggregating data across subjects. The `tpl-` entity and `sub-` entity are mutually exclusive in a given file. When the `tpl-` entity is used without the `atlas-` entity, as in the following examples, the imaging data serves as an instantiation of a space. When the `tpl-` entity is used in conjunction with the `atlas-` entity, the intention is to describe aggregations of data in a particular space, as described in the Derived atlases section, below. For uses of the `atlas-` entity without the `tpl-` entity, see Imaging derivatives - Derivatives from atlases.

### Example: Single-cohort template

For the pipeline that generated MNI152Nlin2009cAsym, the outputs could look like the following example:

```
mnii152nlin2009casym-pipeline/  
  tpl-MNI152Nlin2009cAsym/  
    tpl-MNI152Nlin2009cAsym_res-1_T1w.nii.gz  
    tpl-MNI152Nlin2009cAsym_res-1_T1w.json  
    tpl-MNI152Nlin2009cAsym_res-1_label-brain_mask.nii.gz  
    tpl-MNI152Nlin2009cAsym_res-1_label-brain_mask.json  
    tpl-MNI152Nlin2009cAsym_res-1_probseg.nii.gz  
    tpl-MNI152Nlin2009cAsym_res-1_probseg.json  
    tpl-MNI152Nlin2009cAsym_res-2_T1w.nii.gz  
    tpl-MNI152Nlin2009cAsym_res-2_T1w.json  
    tpl-MNI152Nlin2009cAsym_res-2_label-brain_mask.nii.gz  
    tpl-MNI152Nlin2009cAsym_res-2_label-brain_mask.json  
    tpl-MNI152Nlin2009cAsym_res-2_probseg.nii.gz  
    tpl-MNI152Nlin2009cAsym_res-2_probseg.json
```

### Example: Multi-cohort template

In the case that the template-generating pipeline derives results for several cohorts, the file structure must employ the `cohort-<label>` directory and entity.

```
mnipediaticasym-pipeline/  
  tpl-MNIPediatricAsym/  
    cohort-1/  
      tpl-MNIPediatricAsym_cohort-1_T1w.nii.gz  
      tpl-MNIPediatricAsym_cohort-1_T2w.nii.gz  
      tpl-MNIPediatricAsym_cohort-1_PDw.nii.gz  
      tpl-MNIPediatricAsym_cohort-1_desc-brain_mask.nii.gz  
      tpl-MNIPediatricAsym_cohort-1_probseg.nii.gz  
      tpl-MNIPediatricAsym_cohort-1_probseg.json  
    ...  
    cohort-6/
```

```
tpl-MNIPediatricAsym_cohort-6_T1w.nii.gz
tpl-MNIPediatricAsym_cohort-6_T2w.nii.gz
tpl-MNIPediatricAsym_cohort-6_PDw.nii.gz
tpl-MNIPediatricAsym_cohort-6_desc-brain_mask.nii.gz
tpl-MNIPediatricAsym_cohort-6_probseg.nii.gz
tpl-MNIPediatricAsym_cohort-6_probseg.json
```

## Example: Subject-level and template derivatives

Both subject-level and template-level results MAY coexist in a single derivatives dataset. For example, it is possible to share the subject-level results used to generate the template alongside the template:

```
mn152nlin2009casym-pipeline/
  sub-001/
    anat/
      sub-001_from-T1w_to-MNI152Nlin2009cAsym_mode-image_xfm.h5
      sub-001_space-MNI152Nlin2009cAsym_T1w.nii.gz
      sub-001_T1w.nii.gz
    ...
  sub-152/
    anat/
      sub-152_from-T1w_to-MNI152Nlin2009cAsym_mode-image_xfm.h5
      sub-152_space-MNI152Nlin2009cAsym_T1w.nii.gz
      sub-152_T1w.nii.gz
  tpl-MNI152Nlin2009cAsym/
    tpl-MNI152Nlin2009cAsym_res-1_label-brain_mask.nii.gz
    ...
    tpl-MNI152Nlin2009cAsym_res-2_T1w.json
```

Please note that the specification for spatial transforms (BEP 014) is currently under development, and therefore, the specification of transforms files (xfm suffix above) may change in the future.

## Derived atlases

An atlas is structured neuroanatomical or neurofunctional information expressed as spatial annotations, such as anatomical landmarks, segmentations, parcellations, probabilistic maps, or feature maps, typically defined in relation to a space engendered by a specific template. Within BIDS, atlases provide standardized spatially-organized knowledge to label, localize, and interpret data features. Atlases often rely on or embed templates as their reference framework. In BIDS, templates establish the spatial coordinate frames for atlases, independently of whether or not they are considered part of specific atlases' outcomes.

Template:

```
<pipeline_name>/
```

```

atlas-<label>_description.json
tpl-<label>/
  [cohort-<label>/]
  [<datatype>/]
  tpl-<label>[_cohort-<label>][_<entities>]_<suffix>.<extension>

```

## Atlas identification and metadata

The `atlas-<label>_description.json` file provides metadata to uniquely identify, describe and characterize the atlas, as well as give proper attribution to the creators. Atlases **MUST** include `atlas-<label>_description.json` files corresponding to the atlas or atlases in the structure.

The selected `<label>` in the `atlas-<label>_description.json` file is **RECOMMENDED** for the `atlas-<label>` entity in downstream derivatives from this particular atlas (see previous section Derivatives from atlases).

Atlas metadata fields:

Key name	Requirement Level	Data type	Description
Name	REQUIRED	<a href="#">string</a>	Name of the atlas.
License	REQUIRED	<a href="#">string</a>	The license for the dataset. The use of license name abbreviations is <b>RECOMMENDED</b> for specifying a license (see <a href="#">License</a> ). The corresponding full license text <b>MAY</b> be specified in an additional <code>LICENSE</code> file.
Description	RECOMMENDED	<a href="#">string</a>	Free-form natural language description.
Authors	RECOMMENDED	<a href="#">array</a> of <a href="#">strings</a>	List of individuals who contributed to the creation/curation of the dataset.
Curators	OPTIONAL	<a href="#">array</a> of <a href="#">strings</a>	List of curators who helped make the atlas accessible in a database or dataset.
Funding	OPTIONAL	<a href="#">array</a> of <a href="#">strings</a>	List of sources of funding (grant numbers).
ReferencesAndLinks	OPTIONAL	<a href="#">array</a> of <a href="#">strings</a>	List of references to publications that contain information on the dataset. A reference may be textual or a <code>ReferencesAndLinks</code> .

Key name	Requirement Level	Data type	Description
Species	OPTIONAL	string	The <code>species</code> column SHOULD be a binomial species name from the <a href="#">NCBI Taxonomy</a> (for example, <code>homo sapiens</code> , <code>mus musculus</code> , <code>rattus norvegicus</code> ). For backwards compatibility, if <code>species</code> is absent, the participant is assumed to be <code>homo sapiens</code> .
SampleSize	OPTIONAL	number	Number of items (typically, independent participants; although it could also refer to, for example, sessions) that were employed to create the corresponding atlas.
DerivedFrom	OPTIONAL	string	Indicate what data modality the atlas was derived from; for example, "cytoarchitecture", "resting-state", or "task".
LevelType	OPTIONAL	string	Indicate what analysis level the atlas was derived from; for example, "group" or "individual".
RRID	OPTIONAL	string	<a href="#">Research Resource Identifier</a> of the file, dataset or atlas being described.

Example atlas-MyAtlas2025\_description.json:

```
{
  "Name": "A new atlas of the human brain",
  "Authors": [
    "Jane Doe",
    "John Doe"
  ],
  "License": "CC0",
  "RRID": "SCR_002823",
  "Species": "Human"
}
```

Atlas spatial reference

Atlases are often aligned to a common spatial reference to allow for the ready application of atlas data. A file may indicate the spatial reference to which it has been aligned using the `tp1` entity and/or the `SpatialReference` metadata.



The `tpl` entity may take any value in Image-Based Coordinate Systems.

If the `tpl` entity is not in the Standard template identifiers table, then the `SpatialReference` metadata is REQUIRED for files with that entity.

### Example: Deriving templates and atlases

A common use-case of brain templates is establishing stereotaxy for the creation of atlases. For example, the Spatially Unbiased Infratentorial Template (SUIT; [Diedrichsen, 2006](#)), presents an atlas template of the human cerebellum and brainstem based on the anatomy of 20 young healthy individuals.

The authors first developed a template of the cerebellum and brainstem, which is spatially standardized in MNI space. This could be the organization of the template part:

```
suit-pipeline/  
  tpl-SUIT/  
    anat/  
      tpl-SUIT_T1w.nii.gz  
      tpl-SUIT_T1w.json
```

Where `tpl-SUIT_T1w.json` contains (at minimum):

```
{  
  "SpatialReference": "https://templateflow.s3.amazonaws.com/tpl-MNI152NLin6Asym_res-02_T1w.nii.gz"  
}
```

Once the standard space of analysis was prepared, a first atlas was developed in 2009, integrating some segmentations and parcellations:

```
suit-pipeline/  
  atlas-Diedrichsen2009_description.json  
  tpl-SUIT/  
    anat/  
      tpl-SUIT_T1w.nii.gz  
      tpl-SUIT_atlas-Diedrichsen2009_dseg.json  
      tpl-SUIT_atlas-Diedrichsen2009_dseg.nii.gz  
      tpl-SUIT_atlas-Diedrichsen2009_dseg.tsv  
      tpl-SUIT_atlas-Diedrichsen2009_probseg.nii.gz
```

where `atlas-Diedrichsen2009_description.json` could contain:

```
{  
  "Name": "A probabilistic MR atlas of the human cerebellum",  
  "Authors": [  
    "Jörn Diedrichsen",  
    "Joshua H Balsters",  
    "Jonathan Flavell",  
    "Emma Cussans",  
    "Narender Ramnani"
```

```
],
"SampleSize": 20,
"License": "LICENSE file",
"ReferencesAndLinks": [
  "https://doi.org/10.1016/j.neuroimage.2009.01.045",
  "https://github.com/jdiedrichsen/suit"
],
"Species": "Human"
}
```

Later, in 2011 a second atlas was developed integrating new segmentations, so the template dataset can be updated to contain a second atlas:

```
suit-pipeline/
  atlas-Buckner2011_description.json
  atlas-Diedrichsen2009_description.json
  tpl-SUIT/
    anat/
      tpl-SUIT_T1w.nii.gz
      tpl-SUIT_atlas-Buckner2011_dseg.json
      tpl-SUIT_atlas-Buckner2011_seg-17n_dseg.nii.gz
      tpl-SUIT_atlas-Buckner2011_seg-17n_dseg.tsv
      tpl-SUIT_atlas-Buckner2011_seg-17n_desc-confidence_probseg.nii.gz
      tpl-SUIT_atlas-Buckner2011_seg-7n_dseg.nii.gz
      tpl-SUIT_atlas-Buckner2011_seg-7n_dseg.tsv
      tpl-SUIT_atlas-Buckner2011_seg-7n_desc-confidence_probseg.nii.gz
      tpl-SUIT_atlas-Diedrichsen2009_dseg.json
      tpl-SUIT_atlas-Diedrichsen2009_dseg.nii.gz
      tpl-SUIT_atlas-Diedrichsen2009_dseg.tsv
      tpl-SUIT_atlas-Diedrichsen2009_probseg.nii.gz
```

where atlas-Diedrichsen2009\_description.json remains as above, and atlas-Buckner2011\_description.json could contain:

```
{
  "Name": "Atlas of the human cerebellum estimated by intrinsic functional connectivity",
  "Authors": [
    "Randy L Buckner",
    "Fenna M Krienen",
    "Angela Castellanos",
    "Julio C Diaz",
    "B T Thomas Yeo"
  ],
  "SampleSize": 1000,
```

```
"License": "LICENSE file",
"ReferencesAndLinks": [
  "https://doi.org/10.1152/jn.00339.2011",
  "https://github.com/jdiedrichsen/suit"
],
"Species": "Human"
}
```

### Example: Deriving a new atlas referenced in an existing template

For example, the MIAL67ThalamicNuclei ([Najdenovska et al., 2018](#)) atlas-generation pipeline could display the following structure:

```
mial67thalamicnuclei-pipeline/
  atlas-MIAL67ThalamicNuclei_description.json
  sub-01/
    anat/
      sub-01_seg-ThalamicNuclei_dseg.json
      sub-01_seg-ThalamicNuclei_dseg.tsv
      sub-01_seg-ThalamicNuclei_dseg.nii.gz
      sub-01_space-MNI152NLin2009cAsym_T1w.nii.gz
      sub-01_T1w.nii.gz
    ...
  sub-67/
    anat/
      sub-67_seg-ThalamicNuclei_dseg.json
      sub-67_seg-ThalamicNuclei_dseg.tsv
      sub-67_seg-ThalamicNuclei_dseg.nii.gz
      sub-67_space-MNI152NLin2009cAsym_T1w.nii.gz
      sub-67_T1w.nii.gz
  tpl-MNI152NLin2009cAsym/
    anat/
      tpl-MNI152NLin2009cAsym_atlas-MIAL67ThalamicNuclei_dseg.json
      tpl-MNI152NLin2009cAsym_atlas-MIAL67ThalamicNuclei_dseg.tsv
      tpl-MNI152NLin2009cAsym_atlas-MIAL67ThalamicNuclei_res-1_dseg.nii.gz
      tpl-MNI152NLin2009cAsym_atlas-MIAL67ThalamicNuclei_res-1_probseg.nii.gz
```

where the derivatives of anatomical processing of the 67 subjects that were employed to generate the atlas coexist with the template structure.

The inheritance principle applies uniformly, allowing the segmentation metadata be stored only once at the root of the pipeline directory and apply to all the individual subject segmentations:

```
mial67thalamicnuclei-pipeline/
  atlas-MIAL67ThalamicNuclei_description.json
```

```
seg-ThalamicNuclei_dseg.json
seg-ThalamicNuclei_dseg.tsv
sub-01/
  anat/
    sub-01_seg-ThalamicNuclei_dseg.nii.gz
    sub-01_space-MNI152Nlin2009cAsym_T1w.nii.gz
    sub-01_T1w.nii.gz
...
sub-67/
  anat/
    sub-67_seg-ThalamicNuclei_dseg.nii.gz
    sub-67_space-MNI152Nlin2009cAsym_T1w.nii.gz
    sub-67_T1w.nii.gz
tpl-MNI152Nlin2009cAsym/
  anat/
    tpl-MNI152Nlin2009cAsym_atlas-MIAL67ThalamicNuclei_dseg.json
    tpl-MNI152Nlin2009cAsym_atlas-MIAL67ThalamicNuclei_dseg.tsv
    tpl-MNI152Nlin2009cAsym_atlas-MIAL67ThalamicNuclei_res-1_dseg.nii.gz
    tpl-MNI152Nlin2009cAsym_atlas-MIAL67ThalamicNuclei_res-1_probseg.nii.gz
```

In the case the pipeline generated atlas-based segmentations of the original subjects in their native T1w space (for example, to compare with the original segmentation given by `seg-ThalamicNuclei`), the above example translates into:

```
mial67thalamicnuclei-pipeline/
  atlas-MIAL67ThalamicNuclei_description.json
  atlas-MIAL67ThalamicNuclei_dseg.json
  atlas-MIAL67ThalamicNuclei_dseg.tsv
  seg-ThalamicNuclei_dseg.json
  seg-ThalamicNuclei_dseg.tsv
  sub-01/
    anat/
      sub-01_atlas-MIAL67ThalamicNuclei_dseg.nii.gz
      sub-01_seg-ThalamicNuclei_dseg.nii.gz
      sub-01_space-MNI152Nlin2009cAsym_T1w.nii.gz
      sub-01_T1w.nii.gz
...
  sub-67/
    anat/
      sub-67_atlas-MIAL67ThalamicNuclei_dseg.nii.gz
      sub-67_seg-ThalamicNuclei_dseg.nii.gz
      sub-67_space-MNI152Nlin2009cAsym_T1w.nii.gz
```

```
    sub-67_T1w.nii.gz
tpl-MNI152NLin2009cAsym/
  anat/
    tpl-MNI152NLin2009cAsym_atlas-MIAL67ThalamicNuclei_res-1_dseg.nii.gz
    tpl-MNI152NLin2009cAsym_atlas-MIAL67ThalamicNuclei_res-1_probseg.nii.gz
```

### Example: Distributing one atlas aligned to two or more existing templates

This directory structure can be generally applied when the atlas is derived into several template spaces, for example:

```
mial67thalamicnuclei-pipeline/
  atlas-MIAL67ThalamicNuclei_description.json
  atlas-MIAL67ThalamicNuclei_dseg.json
  atlas-MIAL67ThalamicNuclei_dseg.tsv
  atlas-MIAL67ThalamicNuclei_probseg.json
  tpl-MNI152NLin2009cAsym/
    anat/
      tpl-MNI152NLin2009cAsym_atlas-MIAL67ThalamicNuclei_res-1_dseg.nii.gz
      tpl-MNI152NLin2009cAsym_atlas-MIAL67ThalamicNuclei_res-1_probseg.nii.gz
  tpl-MNI152NLin6Asym/
    anat/
      tpl-MNI152NLin6Asym_atlas-MIAL67ThalamicNuclei_res-1_dseg.nii.gz
      tpl-MNI152NLin6Asym_atlas-MIAL67ThalamicNuclei_res-1_probseg.nii.gz
```

# 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
sub-control01_sessions.tsv
participants.tsv
dataset_description.json
README
CHANGES
```

sub-control01\_sessions.tsv content:

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

See this [example dataset](#) that has been formatted using this specification and can be used for practical guidance when curating a new longitudinal dataset.

## 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. This can be done in two ways:

#### Option 2.a: Collate sites at subject level

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 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.

Option 2.b: Use different sessions for different sites

In case of studies such as "Traveling Human Phantom" it is possible to incorporate site within session label. For example `sub-human1/ses-NUY`, `sub-human1/ses-MIT`, `sub-phantom1/ses-NUY`, `sub-phantom1/ses-MIT` and so on.



# Glossary of schema objects

This section compiles the object definitions in the schema.

## 4DBti (enums)

Name: 4D BTI

Type: Enums

## ACCEL (enums)

Name: ACCEL

Type: Enums

Schema information:

```
tags:  
- fnirs  
- motion
```

## ACCELChannelCount (metadata)

Name: Acceleration channel count

Type: Metadata

Schema information:

```
minimum: 0  
type: integer
```

## ACPC (enums)

Name: ACPC

Type: Enums

## ADC (enums)

Name: ADC

Type: Enums

Schema information:

```
tags:  
- meg  
- ieeg  
- fnirs
```

## ADC (suffixes)

Name: Apparent diffusion coefficient (ADC)

Type: Suffix

Format: <entities>\_ADC.<extension>

## ANGACCEL (enums)

Name: ANGACCEL

Type: Enums

Schema information:

```
tags:  
- motion
```

## ANGACCELChannelCount (metadata)

Name: Angular acceleration channel count

Type: Metadata

Schema information:

```
minimum: 0
type: integer
```

## AUDIO (enums)

Name: AUDIO

Type: Enums

Schema information:

```
tags:
- eeg
- meg
- ieeg
- fnirs
```

## Absent (enums)

Name: Absent

Type: Enums

## Acknowledgements (metadata)

Name: Acknowledgements

Type: Metadata

Schema information:

```
type: string
```

## AcquisitionDuration (metadata)

Name: Acquisition Duration

Type: Metadata

Schema information:

```
exclusiveMinimum: 0
type: number
unit: s
```

## AcquisitionMode (metadata)

Name: Acquisition Mode

Type: Metadata

Schema information:

```
type: string
```

## AcquisitionVoxelSize (metadata)

Name: Acquisition Voxel Size

Type: Metadata

Schema information:

```
items:
  exclusiveMinimum: 0
  type: number
  unit: mm
maxItems: 3
minItems: 3
type: array
```

## Anaesthesia (metadata)

Name: Anaesthesia

Type: Metadata

Schema information:

```
type: string
```

## AnalyticalApproach (metadata)

Name: Analytical Approach

Type: Metadata

Schema information:

```
anyOf:  
- type: string  
- items:  
  type: string  
  type: array
```

## AnatomicalImage (metadata)

Name: Anatomical Image

Type: Metadata

Schema information:

```
anyOf:  
- format: bids_uri  
  type: string  
- items:  
  format: bids_uri  
  type: string  
  type: array
```

## AnatomicalLandmarkCoordinateSystem (metadata)

Name: Anatomical Landmark Coordinate System

Type: Metadata

Allowed values: CTF, ElektaNeuromag, NeuromagElektaMEGIN, 4DBti, KitYokogawa, ChietiItab, Other, CapTrak, EEGLAB, EEGLAB-HJ, 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

Schema information:

`type: string`

## AnatomicalLandmarkCoordinateSystemDescription (metadata)

Name: Anatomical Landmark Coordinate System Description

Type: Metadata

Schema information:

`type: string`

## AnatomicalLandmarkCoordinateUnits (metadata)

Name: Anatomical Landmark Coordinate Units

Type: Metadata

Allowed values: m, mm, cm, n/a

Schema information:

`type: string`

## AnatomicalLandmarkCoordinates sense 1 (metadata)

Name: Anatomical Landmark Coordinates

Type: Metadata

Schema information:

`additionalProperties:`

```
  items:
    type: number
  maxItems: 3
  minItems: 3
  type: array
type: object
```

## AnatomicalLandmarkCoordinates sense 2 (metadata)

Name: Anatomical Landmark Coordinates

Type: Metadata

Schema information:

```
additionalProperties:
  items:
    type: number
  maxItems: 3
  minItems: 3
  type: array
type: object
```

## AnchorCoordinates (metadata)

Name: Anchor Coordinates

Type: Metadata

Schema information:

```
items:
  type: number
maxItems: 3
minItems: 1
type: array
```

## AnchorElectrode (metadata)

Name: Anchor Electrode

Type: Metadata

Schema information:

```
type: string
```

## Any (extensions)

Name: Any Extension

Type: Extension

Format: <entities>\_<suffix>.\*

## ArterialSpinLabelingType (metadata)

Name: Arterial Spin Labeling Type

Type: Metadata

Allowed values: CASL, PCASL, PASL

Schema information:

```
type: string
```

## AssociatedEmptyRoom (metadata)

Name: Associated Empty Room

Type: Metadata

Schema information:

```
anyOf:  
- items:  
  anyOf:  
    - format: dataset_relative  
      type: string  
    - format: bids_uri  
      type: string  
  type: array  
- format: dataset_relative  
  type: string  
- format: bids_uri  
  type: string
```

## AtlasName (metadata)

Name: Name

Type: Metadata

Schema information:

```
type: string
```



## AtlasSampleSize (metadata)

Name: Atlas' sample size

Type: Metadata

Schema information:

`type: number`

## AttenuationCorrection (metadata)

Name: Attenuation Correction

Type: Metadata

Schema information:

`type: string`

## AttenuationCorrectionMethodReference (metadata)

Name: Attenuation Correction Method Reference

Type: Metadata

Schema information:

`type: string`

## Authors (metadata)

Name: Authors

Type: Metadata

Schema information:

```
items:  
  type: string  
type: array
```

## AverageCalibrationError (metadata)

Name: Average Calibration Error

Type: Metadata

Schema information:

```
type: number
unit: degree
```

## B0FieldIdentifier (metadata)

Name: B0 Field Identifier

Type: Metadata

Schema information:

```
anyOf:
- type: string
- items:
  type: string
  type: array
```

## B0FieldSource (metadata)

Name: B0 Field Source

Type: Metadata

Schema information:

```
anyOf:
- type: string
- items:
  type: string
  type: array
```

## B0ShimmingTechnique (metadata)

Name: B0 Shimming Technique

Type: Metadata

Schema information:

`type: string`

## B1ShimmingTechnique (metadata)

Name: B1 Shimming Technique

Type: Metadata

Schema information:

`type: string`

## BARIUM (enums)

Name: BARIUM

Type: Enums

## BF (suffixes)

Name: Bright-field microscopy

Type: Suffix

Format: `<entities>_BF.<extension>`

## BIDSVersion (metadata)

Name: BIDS Version

Type: Metadata

Schema information:

`type: string`

## BackgroundSuppression (metadata)

Name: Background Suppression

Type: Metadata

Schema information:

```
type: boolean
```

## BackgroundSuppressionNumberPulses (metadata)

Name: Background Suppression Number Pulses

Type: Metadata

Schema information:

```
minimum: 0  
type: number
```

## BackgroundSuppressionPulseTime (metadata)

Name: Background Suppression Pulse Time

Type: Metadata

Schema information:

```
items:  
  minimum: 0  
  type: number  
  unit: s  
type: array
```

## BasedOn (metadata)

Name: Based On

Type: Metadata

Schema information:

```
anyOf:  
- format: participant_relative  
  type: string  
- items:  
  format: participant_relative  
  type: string  
  type: array
```

## BloodDensity (metadata)

Name: Blood Density

Type: Metadata

Schema information:

```
type: number  
unit: g/mL
```

## BodyPart (metadata)

Name: Body Part

Type: Metadata

Schema information:

```
type: string
```

## BodyPartDetails (metadata)

Name: Body Part Details

Type: Metadata

Schema information:

```
type: string
```

## BodyPartDetailsOntology (metadata)

Name: Body Part Details Ontology

Type: Metadata

Schema information:

```
format: uri  
type: string
```

## BolusCutOffDelayTime (metadata)

Name: Bolus Cut Off Delay Time

Type: Metadata

Schema information:

```
anyOf:  
- minimum: 0  
  type: number  
  unit: s  
- items:  
  minimum: 0  
  type: number  
  unit: s  
  type: array
```

## BolusCutOffFlag (metadata)

Name: Bolus Cut Off Flag

Type: Metadata

Schema information:

```
type: boolean
```

## BolusCutOffTechnique (metadata)

Name: Bolus Cut Off Technique

Type: Metadata

Schema information:

```
type: string
```

## Brain (enums)

Name: Brain mask

Type: Enums

## BrainLocation (metadata)

Name: Brain Location

Type: Metadata

Schema information:

`type: string`

## CARBON\_DIOXIDE (enums)

Name: CARBON DIOXIDE

Type: Enums

## CARS (suffixes)

Name: Coherent anti-Stokes Raman spectroscopy

Type: Suffix

Format: `<entities>_CARS.<extension>`

## CASL (enums)

Name: Continuous arterial spin labeling

Type: Enums

## CASLType (metadata)

Name: CASL Type

Type: Metadata

Allowed values: `single-coil`, `double-coil`

Schema information:

`type: string`

## CHANGES (files)

Name: Changelog

Type: Files And Directories

Schema information:

`file_type:` `regular`

## CITATION (files)

Name: CITATION.cff

Type: Files And Directories

Schema information:

`file_type:` `regular`

## COMBINED (enums)

Name: COMBINED

Type: Enums

## CONF (suffixes)

Name: Confocal microscopy

Type: Suffix

Format: `<entities>_CONF.<extension>`

## CTF (enums)

Name: CTF

Type: Enums



## CTF (extensions)

Name: CTF MEG Dataset Directory

Type: Extension

Format: <entities>\_<suffix>.ds/

## CalibrationCount (metadata)

Name: Calibration Count

Type: Metadata

Schema information:

```
minimum: 0
type: integer
```

## CalibrationPosition (metadata)

Name: Calibration Position

Type: Metadata

Schema information:

```
items:
  items:
    type: number
  maxItems: 2
  minItems: 2
  type: array
type: array
```

## CalibrationType (metadata)

Name: Calibration Type

Type: Metadata

Schema information:

```
type: string
```

## CalibrationUnit (metadata)

Name: Calibration Unit

Type: Metadata

Allowed values: pixel, mm, cm

Schema information:

`type: string`

## CapManufacturer (metadata)

Name: Cap Manufacturer

Type: Metadata

Schema information:

`type: string`

## CapManufacturersModelName (metadata)

Name: Cap Manufacturers Model Name

Type: Metadata

Schema information:

`type: string`

## CapTrak (enums)

Name: CapTrak

Type: Enums

## CellType (metadata)

Name: Cell Type

Type: Metadata

Schema information:

`type: string`

## ChemicalShiftOffset (metadata)

Name: Chemical Shift Offset

Type: Metadata

Schema information:

`type: number`

`unit: ppm`

## ChemicalShiftReference (metadata)

Name: Chemical Shift Reference

Type: Metadata

Schema information:

`type: number`

`unit: ppm`

## ChietiItab (enums)

Name: Chieti ITAB

Type: Enums

## Chimap (suffixes)

Name: Quantitative susceptibility map (QSM)

Type: Suffix

Format: `<entities>_Chimap.<extension>`

Schema information:

`unit: ppm`

## ChunkTransformationMatrix (metadata)

Name: Chunk Transformation Matrix

Type: Metadata

Schema information:

```
anyOf:  
- items:  
  items:  
    type: number  
  maxItems: 3  
  minItems: 3  
  type: array  
maxItems: 3  
minItems: 3  
type: array  
- items:  
  items:  
    type: number  
  maxItems: 4  
  minItems: 4  
  type: array  
maxItems: 4  
minItems: 4  
type: array
```

## ChunkTransformationMatrixAxis (metadata)

Name: Chunk Transformation Matrix Axis

Type: Metadata

Schema information:

```
items:  
  type: string  
maxItems: 3  
minItems: 2  
type: array
```

## Code (metadata)

Name: Code

Type: Metadata

Schema information:

```
format: uri  
type: string
```

## CodeMeaning (metadata)

Name: Code Meaning

Type: Metadata

Schema information:

```
type: string
```

## CodeURL (metadata)

Name: Code URL

Type: Metadata

Schema information:

```
format: uri  
type: string
```

## CodeValue (metadata)

Name: Code Value

Type: Metadata

Schema information:

```
type: string
```

## CodingSchemeDesignator (metadata)

Name: Coding Scheme Designator

Type: Metadata

Schema information:

`type: string`

## CodingSchemeVersion (metadata)

Name: Coding Scheme version

Type: Metadata

Schema information:

`type: string`

## CogAtlasID (metadata)

Name: Cognitive Atlas ID

Type: Metadata

Schema information:

`format: uri`

`type: string`

## CogPOID (metadata)

Name: Cognitive Paradigm Ontology ID

Type: Metadata

Schema information:

`format: uri`

`type: string`

## CoilCombinationMethod (metadata)

Name: Coil Combination Method

Type: Metadata

Schema information:

```
type: string
```

## Columns (metadata)

Name: Columns

Type: Metadata

Schema information:

```
items:  
  type: string  
type: array
```

## Container (metadata)

Name: Container

Type: Metadata

Schema information:

```
properties:  
  ContainerTag:  
    description: 'Tag of software container image used to produce the dataset'  
  
    '  
    display_name: Container Tag  
    name: ContainerTag  
    type: string  
  ContainerType:  
    description: 'Type of software container image used to produce the dataset'  
  
    '  
    display_name: Container Type  
    name: ContainerType
```

```
    type: string
ContainerURI:
  description: 'URI for software container image used to produce the dataset
  '
  display_name: Container URI
  format: uri
  name: ContainerURI
  type: string
recommended:
- Type
- Tag
- URI
type: object
```

## ContainerTag (metadata)

Name: Container Tag

Type: Metadata

Schema information:

```
type: string
```

## ContainerType (metadata)

Name: Container Type

Type: Metadata

Schema information:

```
type: string
```

## ContainerURI (metadata)

Name: Container URI

Type: Metadata

Schema information:



```
format: uri  
type: string
```

## ContinuousHeadLocalization (metadata)

Name: Continuous Head Localization

Type: Metadata

Schema information:

```
type: boolean
```

## ContrastBolusIngredient (metadata)

Name: Contrast Bolus Ingredient

Type: Metadata

Allowed values: IODINE, GADOLINIUM, CARBON DIOXIDE, BARIUM, XENON, UNKNOWN, NONE

Schema information:

```
type: string
```

## CoordinateReportStrategy (metadata)

Name: CoordinateReportStrategy

Type: Metadata

Allowed values: peak, center\_of\_mass, other

Schema information:

```
type: string
```

## Curators (metadata)

Name: Curators

Type: Metadata

Schema information:

```
items:  
  type: string  
type: array
```

## DAC (enums)

Name: DAC

Type: Enums

Schema information:

```
tags:  
- meg  
- ieeg  
- fnirs
```

## DBS (enums)

Name: DBS

Type: Enums

Schema information:

```
tags:  
- meg  
- ieeg  
- fnirs
```

## DCOffsetCorrection (metadata)

Name: DC Offset Correction

Type: Metadata

Schema information:

```
type: string
```

## DF (suffixes)

Name: Dark-field microscopy

Type: Suffix

Format: <entities>\_DF.<extension>

## DIC (suffixes)

Name: Differential interference contrast microscopy

Type: Suffix

Format: <entities>\_DIC.<extension>

## DOI (metadata)

Name: DOI

Type: Metadata

Schema information:

`type: string`

## Database (metadata)

Name: Database

Type: Metadata

Schema information:

`format: uri`

`type: string`

## Dataset (metadata)

Name: Dataset

Type: Metadata

Schema information:

```
format: uri
type: string
```

## DatasetDOI (metadata)

Name: DatasetDOI

Type: Metadata

Schema information:

```
format: uri
type: string
```

## DatasetLinks (metadata)

Name: Dataset Links

Type: Metadata

Schema information:

```
additionalProperties:
  format: uri
  type: string
type: object
```

## DatasetType (metadata)

Name: Dataset Type

Type: Metadata

Allowed values: raw, derivative, study

Schema information:

```
type: string
```

## DecayCorrectionFactor (metadata)

Name: Decay Correction Factor

Type: Metadata

Schema information:

```
items:
  type: number
type: array
```

## DeidentificationMethod (metadata)

Name: Deidentification Method

Type: Metadata

Schema information:

```
items:
  type: string
type: array
```

## DeidentificationMethodCodeSequence (metadata)

Name: Deidentification Method Code Sequence

Type: Metadata

Schema information:

```
items:
  properties:
    CodeMeaning:
      description: 'Text that has meaning to a human and conveys the meaning of the
        term

        Corresponds to [DICOM Tag 0008, 0104](https://dicomlookup.com/dicomtags/(0008,0104))
        `Code Meaning`.'
      display_name: Code Meaning
      name: CodeMeaning
      type: string
    CodeValue:
      description: 'An identifier that is unambiguous within the Coding Scheme
```

denoted by Coding Scheme Designator and Coding Scheme Version.

Corresponds to [DICOM Tag 0008, 0100] ([https://dicomlookup.com/dicomtags/\(0008,0100\)](https://dicomlookup.com/dicomtags/(0008,0100)))  
`Code Value`.

```
,
display_name: Code Value
name: CodeValue
type: string
```

CodingSchemeDesignator:

description: 'The identifier of the coding scheme in which the coded entry is defined.'

Corresponds to [DICOM Tag 0008, 0102] ([https://dicomlookup.com/dicomtags/\(0008,0102\)](https://dicomlookup.com/dicomtags/(0008,0102)))

`Coding Scheme Designator`.

```
,
display_name: Coding Scheme Designator
name: CodingSchemeDesignator
type: string
```

CodingSchemeVersion:

description: 'An identifier of the version of the coding scheme if necessary to resolve ambiguity.'

Corresponds to [DICOM Tag 0008, 0103] ([https://dicomlookup.com/dicomtags/\(0008,0103\)](https://dicomlookup.com/dicomtags/(0008,0103)))  
`Coding Scheme Version`.

```
,
display_name: Coding Scheme version
name: CodingSchemeVersion
type: string
```

recommended:

- CodeValue
- CodeMeaning
- CodingSchemeDesignator
- CodingSchemeVersion

type: object

type: array

## DelayAfterTrigger (metadata)

Name: Delay After Trigger

Type: Metadata

Schema information:

```
type: number
unit: s
```

## DelayTime (metadata)

Name: Delay Time

Type: Metadata

Schema information:

```
type: number
unit: s
```

## Delimiter (metadata)

Name: Delimiter

Type: Metadata

Schema information:

```
type: string
```

## Density (metadata)

Name: Density

Type: Metadata

Schema information:

```
anyOf:
- type: string
- additionalProperties:
    type: string
    type: object
```

## Derivative (metadata)

Name: Derivative

Type: Metadata

Schema information:

`type: boolean`

## DerivedFrom (metadata)

Name: DerivedFrom

Type: Metadata

Schema information:

`type: string`

## Description sense 1 (metadata)

Name: Description

Type: Metadata

Schema information:

`type: string`

## Description sense 2 (metadata)

Name: Pipeline Description

Type: Metadata

Schema information:

`type: string`

## Descriptors (metadata)

Name: Descriptors



Type: Metadata

Schema information:

```
anyOf:  
- type: string  
- items:  
  type: string  
  type: array
```

## DetectorType (metadata)

Name: Detector Type

Type: Metadata

Schema information:

```
anyOf:  
- format: unit  
  type: string  
- enum:  
  - mixed  
  type: string
```

## DeviceSerialNumber (metadata)

Name: Device Serial Number

Type: Metadata

Schema information:

```
type: string
```

## DewarPosition (metadata)

Name: Dewar Position

Type: Metadata

Schema information:

```
type: string
```

## DigitizedHeadPoints sense 1 (metadata)

Name: Digitized Head Points

Type: Metadata

Schema information:

`type: boolean`

## DigitizedHeadPoints sense 2 (metadata)

Name: Digitized Head Points

Type: Metadata

Schema information:

`format: file_relative`

`type: string`

## DigitizedHeadPointsCoordinateSystem (metadata)

Name: Digitized Head Points Coordinate System

Type: Metadata

Allowed values: CTF, ElektaNeuromag, NeuromagElektaMEGIN, 4DBti, KitYokogawa, ChietiItab, Other, CapTrak, EEGLAB, EEGLAB-HJ, 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

Schema information:

`type: string`

## DigitizedHeadPointsCoordinateSystemDescription (metadata)

Name: Digitized Head Points Coordinate System Description

Type: Metadata

Schema information:

`type: string`

## DigitizedHeadPointsCoordinateUnits (metadata)

Name: Digitized Head Points Coordinate Units

Type: Metadata

Allowed values: m, mm, cm, n/a

Schema information:

`type: string`

## DigitizedLandmarks (metadata)

Name: Digitized Landmarks

Type: Metadata

Schema information:

`type: boolean`

## Directory (extensions)

Name: Directory

Type: Extension

Format: `<entities>_<suffix>/`

## DispersionConstant (metadata)

Name: Dispersion Constant

Type: Metadata

Schema information:

`type: number`

`unit: s`

## DispersionCorrected (metadata)

Name: Dispersion Corrected

Type: Metadata

Schema information:

`type: boolean`

## DoseCalibrationFactor (metadata)

Name: Dose Calibration Factor

Type: Metadata

Schema information:

`type: number`

## DwellTime (metadata)

Name: Dwell Time

Type: Metadata

Schema information:

`type: number`

`unit: s`

## ECG (enums)

Name: ECG

Type: Enums

Schema information:

`tags:`

- `- eeg`
- `- emg`
- `- meg`
- `- ieeg`
- `- fnirs`

## ECGChannelCount (metadata)

Name: ECG Channel Count

Type: Metadata

Schema information:

```
minimum: 0  
type: integer
```

## ECOG (enums)

Name: ECOG

Type: Enums

Schema information:

```
tags:  
- meg  
- ieeg  
- fnirs
```

## ECOGChannelCount (metadata)

Name: ECOG Channel Count

Type: Metadata

Schema information:

```
minimum: 0  
type: integer
```

## EEG (enums)

Name: EEG

Type: Enums

Schema information:

```
tags:  
- eeg  
- meg  
- ieeg  
- fnirs
```

## EEGChannelCount (metadata)

Name: EEG Channel Count

Type: Metadata

Schema information:

```
minimum: 0  
type: integer
```

## EEGCoordinateSystem (metadata)

Name: EEG Coordinate System

Type: Metadata

Allowed values: CTF, ElektaNeuromag, NeuromagElektaMEGIN, 4DBti, KitYokogawa, ChietiItab, Other, CapTrak, EEGLAB, EEGLAB-HJ, 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

Schema information:

```
type: string
```

## EEGCoordinateSystemDescription (metadata)

Name: EEG Coordinate System Description

Type: Metadata

Schema information:

```
type: string
```

## EEGCoordinateUnits (metadata)

Name: EEG Coordinate Units

Type: Metadata

Allowed values: m, mm, cm, n/a

Schema information:

`type: string`

## EEGGround (metadata)

Name: EEG Ground

Type: Metadata

Schema information:

`type: string`

## EEGLAB (enums)

Name: EEGLAB

Type: Enums

## EEGLAB-HJ (enums)

Name: EEGLAB-HJ

Type: Enums

## EEGPlacementScheme (metadata)

Name: EEG Placement Scheme

Type: Metadata

Schema information:

`type: string`

## EEGReference (metadata)

Name: EEG Reference

Type: Metadata

Schema information:

```
type: string
```

## EMG (enums)

Name: EMG

Type: Enums

Schema information:

```
tags:  
- eeg  
- emg  
- meg  
- ieeg  
- fnirs
```

## EMGChannelCount (metadata)

Name: EMG Channel Count

Type: Metadata

Schema information:

```
minimum: 0  
type: integer
```

## EMGCoordinateSystem (metadata)

Name: EMG Coordinate System

Type: Metadata

Allowed values: Other

Schema information:



`type: string`

## EMGCoordinateSystemDescription (metadata)

Name: EMG Coordinate System Description

Type: Metadata

Schema information:

`type: string`

## EMGCoordinateUnits (metadata)

Name: EMG Coordinate Units

Type: Metadata

Allowed values: m, mm, cm, percent, n/a

Schema information:

`type: string`

## EMGGround (metadata)

Name: EMG Ground

Type: Metadata

Schema information:

`type: string`

## EMGPlacementScheme (metadata)

Name: EMG Placement Scheme

Type: Metadata

Allowed values: ChannelSpecific, Measured, Other

Schema information:

`type: string`

## EMGPlacementSchemeDescription (metadata)

Name: EMG Placement Scheme Description

Type: Metadata

Schema information:

```
type: string
```

## EMGReference (metadata)

Name: EMG Reference

Type: Metadata

Schema information:

```
type: string
```

## EOG (enums)

Name: EOG

Type: Enums

Schema information:

```
tags:  
- eeg  
- emg  
- meg  
- ieeg  
- fnirs
```

## EOGChannelCount (metadata)

Name: EOG Channel Count

Type: Metadata

Schema information:

```
minimum: 0  
type: integer
```

## EYEGAZE (enums)

Name: EYEGAZE

Type: Enums

Schema information:

```
tags:  
- eeg  
- meg  
- ieeg  
- fnirs
```

## EchoAcquisition (metadata)

Name: Echo Acquisition

Type: Metadata

Schema information:

```
type: string
```

## EchoTime sense 1 (metadata)

Name: Echo Time

Type: Metadata

Schema information:

```
anyOf:  
- exclusiveMinimum: 0  
  type: number  
  unit: s  
- items:  
  exclusiveMinimum: 0  
  type: number  
  unit: s  
  type: array
```

## EchoTime sense 2 (metadata)

Name: Echo Time

Type: Metadata

Schema information:

```
exclusiveMinimum: 0  
type: number  
unit: s
```

## EchoTime1 (metadata)

Name: Echo Time1

Type: Metadata

Schema information:

```
exclusiveMinimum: 0  
type: number  
unit: s
```

## EchoTime2 (metadata)

Name: Echo Time2

Type: Metadata

Schema information:

```
exclusiveMinimum: 0  
type: number  
unit: s
```

## EditCondition (metadata)

Name: Editing Condition

Type: Metadata

Schema information:

```
anyOf:  
- type: string  
- items:  
  type: string  
  type: array
```

## EditPulse (metadata)

Name: Editing Pulse

Type: Metadata

Schema information:

```
additionalProperties:  
  properties:  
    FrequencyOffset:  
      anyOf:  
        - type: number  
          unit: ppm  
        - items:  
          type: number  
          unit: ppm  
          type: array  
      description: 'List or value for frequency offset for spectral editing in ppm.  
        See EditPulse  
        '  
      display_name: Frequency Offset  
      name: FrequencyOffset  
    PulseDuration:  
      description: 'Pulse duration if spectral editing was applied, in milliseconds  
        '  
      display_name: Pulse Duration  
      name: PulseDuration  
      type: number  
      unit: ms  
  recommended:  
    - FrequencyOffset  
    - PulseDuration
```

```
type: object  
type: object
```

## EditTarget (metadata)

Name: Editing Target

Type: Metadata

Schema information:

```
anyOf:  
- type: string  
- items:  
  type: string  
  type: array
```

## EffectiveEchoSpacing (metadata)

Name: Effective Echo Spacing

Type: Metadata

Schema information:

```
exclusiveMinimum: 0  
type: number  
unit: s
```

## ElectricalStimulation (metadata)

Name: Electrical Stimulation

Type: Metadata

Schema information:

```
type: boolean
```

## ElectricalStimulationParameters (metadata)

Name: Electrical Stimulation Parameters

Type: Metadata

Schema information:

`type: string`

## ElectrodeManufacturer (metadata)

Name: Electrode Manufacturer

Type: Metadata

Schema information:

`type: string`

## ElectrodeManufacturersModelName (metadata)

Name: Electrode Manufacturers Model Name

Type: Metadata

Schema information:

`type: string`

## ElectrodeMaterial (metadata)

Name: Electrode Material

Type: Metadata

Schema information:

`type: string`

## ElectrodeType (metadata)

Name: Electrode type

Type: Metadata

Schema information:

`type: string`

## ElektaNeuromag (enums)

Name: Elekta Neuromag

Type: Enums

## EncodingTechnique (metadata)

Name: Encoding Technique

Type: Metadata

Schema information:

`type: string`

## Epigenomic (enums)

Name: Epigenomic

Type: Enums

## EpochLength (metadata)

Name: Epoch Length

Type: Metadata

Schema information:

`minimum: 0`  
`type: number`

## Estimate (enums)

Name: Estimate

Type: Enums



## EstimationAlgorithm (metadata)

Name: Estimation Algorithm

Type: Metadata

Schema information:

```
type: string
```

## EstimationReference (metadata)

Name: Estimation Reference

Type: Metadata

Schema information:

```
type: string
```

## EthicsApprovals (metadata)

Name: Ethics Approvals

Type: Metadata

Schema information:

```
items:  
  type: string  
type: array
```

## EyeTrackerDistance (metadata)

Name: Eye-Tracker Distance

Type: Metadata

Schema information:

```
anyOf:  
- type: number  
  unit: m  
- items:  
  type: number
```

```
    unit: m
maxItems: 3
minItems: 3
type: array
```

## EyeTrackingMethod (metadata)

Name: Eye-Tracking Method

Type: Metadata

Schema information:

```
type: string
```

## FA (suffixes)

Name: Fractional Anisotropy image

Type: Suffix

Format: <entities>\_FA.<extension>

## FERMI (enums)

Name: Fermi pulse

Type: Enums

## FITERR (enums)

Name: FITERR

Type: Enums

Schema information:

```
tags:
- meg
- fnirs
```

## FLAIR (suffixes)

Name: Fluid attenuated inversion recovery image

Type: Suffix

Format: <entities>\_FLAIR.<extension>

Schema information:

`unit:` `arbitrary`

## FLASH (suffixes)

Name: Fast-Low-Angle-Shot image

Type: Suffix

Format: <entities>\_FLASH.<extension>

## FLUO (suffixes)

Name: Fluorescence microscopy

Type: Suffix

Format: <entities>\_FLUO.<extension>

## Face (enums)

Name: Face mask

Type: Enums

## FiducialsCoordinateSystem (metadata)

Name: Fiducials Coordinate System

Type: Metadata

Allowed values: CTF, ElektaNeuromag, NeuromagElektaMEGIN, 4DBti, KitYokogawa, ChietiItab, Other, CapTrak, EEGLAB, EEGLAB-HJ, 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

Schema information:

`type: string`

## FiducialsCoordinateSystemDescription (metadata)

Name: Fiducials Coordinate System Description

Type: Metadata

Schema information:

`type: string`

## FiducialsCoordinateUnits (metadata)

Name: Fiducials Coordinate Units

Type: Metadata

Allowed values: m, mm, cm, n/a

Schema information:

`type: string`

## FiducialsCoordinates (metadata)

Name: Fiducials Coordinates

Type: Metadata

Schema information:

`additionalProperties:`

```
  items:
    type: number
  maxItems: 3
  minItems: 3
  type: array
type: object
```

## FiducialsDescription (metadata)

Name: Fiducials Description

Type: Metadata

Schema information:

```
type: string
```

## FlipAngle (metadata)

Name: Flip Angle

Type: Metadata

Schema information:

```
anyOf:  
- exclusiveMinimum: 0  
  maximum: 360  
  type: number  
  unit: degree  
- items:  
  exclusiveMinimum: 0  
  maximum: 360  
  type: number  
  unit: degree  
type: array
```

## Format (metadata)

Name: Value format

Type: Metadata

Allowed values: string, number, integer, boolean, index, label, date, datetime, time, unit, uri, rrid, bids\_uri, dataset\_relative, file\_relative, participant\_relative, stimuli\_relative, hed\_version

Schema information:

```
type: string
```

## FrameAcquisitionDuration (metadata)

Name: Frame Acquisition Duration

Type: Metadata

Schema information:

```
exclusiveMinimum: 0
type: number
unit: s
```

## FrameDuration (metadata)

Name: Frame Duration

Type: Metadata

Schema information:

```
items:
  type: number
type: array
unit: s
```

## FrameTimesStart (metadata)

Name: Frame Times Start

Type: Metadata

Schema information:

```
items:
  type: number
type: array
unit: s
```

## FrequencyOffset (metadata)

Name: Frequency Offset

Type: Metadata

Schema information:

```
anyOf:  
- type: number  
  unit: ppm  
- items:  
  type: number  
  unit: ppm  
type: array
```

## Funding (metadata)

Name: Funding

Type: Metadata

Schema information:

```
items:  
  type: string  
type: array
```

## GADOLINIUM (enums)

Name: GADOLINIUM

Type: Enums

## GAUSSHANN (enums)

Name: Gaussian-Hanning pulse.

Type: Enums

## GAUSSIAN (enums)

Name: Gaussian pulse

Type: Enums

## GRADIENT (enums)

Name: GRADIENT

Type: Enums

## GSR (enums)

Name: GSR

Type: Enums

Schema information:

```
tags:  
- eeg
```

## GYRO (enums)

Name: GYRO

Type: Enums

Schema information:

```
tags:  
- fnirs  
- motion
```

## GYROChannelCount (metadata)

Name: Gyrometer Channel Count

Type: Metadata

Schema information:

```
minimum: 0  
type: integer
```

## Gain (metadata)

Name: Gain



Type: Metadata

Schema information:

```
type: number
unit: arbitrary
```

## GeneratedBy (metadata)

Name: Generated By

Type: Metadata

Schema information:

```
items:
  properties:
    CodeURL:
      description: URL where the code used to generate the dataset may be found.
      display_name: Code URL
      format: uri
      name: CodeURL
      type: string
    Container:
      description: '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`][uri] with [string][] values.

        '
      display_name: Container
      name: Container
      properties:
        ContainerTag:
          description: 'Tag of software container image used to produce the dataset

          '
          display_name: Container Tag
          name: ContainerTag
```

```
    type: string
  ContainerType:
    description: 'Type of software container image used to produce the dataset'

    ,

    display_name: Container Type
    name: ContainerType
    type: string
  ContainerURI:
    description: 'URI for software container image used to produce the dataset'

    ,

    display_name: Container URI
    format: uri
    name: ContainerURI
    type: string
  recommended:
  - Type
  - Tag
  - URI
  type: object
Description:
  description: 'Plain-text description of the pipeline or process that generated
    the outputs.

    RECOMMENDED if `Name` is `"Manual"`.'

    ,

    display_name: Pipeline Description
    name: Description
    type: string
Name:
  description: '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.'
```

```
    |
    display_name: Pipeline Name
    name: Name
    type: string
  Version:
    description: Version of the pipeline
    display_name: Pipeline Version
    name: Version
    type: string
  recommended:
  - Version
  required:
  - Name
  type: object
minItems: 1
type: array
```

## Genetic (enums)

Name: Genetic

Type: Enums

## GeneticLevel (metadata)

Name: Genetic Level

Type: Metadata

Schema information:

```
anyOf:
- enum:
  - Genetic
  - Genomic
  - Epigenomic
  - Transcriptomic
  - Metabolomic
  - Proteomic
  type: string
- items:
```

```
enum:  
- Genetic  
- Genomic  
- Epigenomic  
- Transcriptomic  
- Metabolomic  
- Proteomic  
type: string  
type: array
```

## Genetics (metadata)

Name: Genetics

Type: Metadata

Schema information:

```
properties:  
  Database:  
    description: '[URI](../common-principles.md#uniform-resource-indicator)  
  
    of database where the dataset is hosted.  
  
    '  
    display_name: Database  
    format: uri  
    name: Database  
    type: string  
  Dataset:  
    description: '[URI](../common-principles.md#uniform-resource-indicator)  
  
    where data can be retrieved.  
  
    '  
    display_name: Dataset  
    format: uri  
    name: Dataset  
    type: string  
  Descriptors:  
    anyOf:
```

```
- type: string
- items:
  type: string
  type: array
description: 'List of relevant descriptors (for example, journal articles) for
dataset

using a valid

URI

when possible.

',
display_name: Descriptors
name: Descriptors
required:
- Dataset
type: object
```

## Genomic (enums)

Name: Genomic

Type: Enums

## GradientSetType (metadata)

Name: Gradient Set Type

Type: Metadata

Schema information:

```
type: string
```

## HARD (enums)

Name: Hard pulse

Type: Enums

## HED (columns)

Name: HED

Type: Column

Schema information:

```
type: string
```

## HED (metadata)

Name: HED

Type: Metadata

Schema information:

```
anyOf:  
- type: string  
- additionalProperties:  
  type: string  
  type: object
```

## HEDVersion (metadata)

Name: HED Version

Type: Metadata

Schema information:

```
anyOf:  
- format: hed_version  
  type: string  
- items:  
  format: hed_version  
  type: string  
  type: array
```

## HEOG (enums)

Name: HEOG

Type: Enums

Schema information:

```
tags:  
- eeg  
- emg  
- meg  
- ieeg  
- fnirs
```

## HLU (enums)

Name: HLU

Type: Enums

Schema information:

```
tags:  
- meg  
- fnirs
```

## Haematocrit (metadata)

Name: Haematocrit

Type: Metadata

Schema information:

```
type: number
```

## HardcopyDeviceSoftwareVersion (metadata)

Name: Hardcopy Device Software Version

Type: Metadata

Schema information:

```
type: string
```

## HardwareFilters (metadata)

Name: Hardware Filters

Type: Metadata

Schema information:

```
anyOf:  
- additionalProperties:  
  type: object  
  type: object  
- enum:  
  - n/a  
  type: string
```

## HeadCircumference (metadata)

Name: Head Circumference

Type: Metadata

Schema information:

```
exclusiveMinimum: 0  
type: number  
unit: cm
```

## HeadCoilCoordinateSystem (metadata)

Name: Head Coil Coordinate System

Type: Metadata

Allowed values: CTF, ElektaNeuromag, NeuromagElektaMEGIN, 4DBti, KitYokogawa, ChietiItab, Other, CapTrak, EEGLAB, EEGLAB-HJ, 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

Schema information:

```
type: string
```



## HeadCoilCoordinateSystemDescription (metadata)

Name: Head Coil Coordinate System Description

Type: Metadata

Schema information:

```
type: string
```

## HeadCoilCoordinateUnits (metadata)

Name: Head Coil Coordinate Units

Type: Metadata

Allowed values: m, mm, cm, n/a

Schema information:

```
type: string
```

## HeadCoilCoordinates (metadata)

Name: Head Coil Coordinates

Type: Metadata

Schema information:

```
additionalProperties:
  items:
    type: number
  maxItems: 3
  minItems: 3
  type: array
type: object
```

## HeadCoilFrequency (metadata)

Name: Head Coil Frequency

Type: Metadata

Schema information:

```
anyOf:  
- type: number  
  unit: Hz  
- items:  
  type: number  
  unit: Hz  
  type: array
```

## HeadStabilization (metadata)

Name: Head stabilization

Type: Metadata

Schema information:

```
type: string
```

## HowToAcknowledge (metadata)

Name: How To Acknowledge

Type: Metadata

Schema information:

```
type: string
```

## ICBM452AirSpace (enums)

Name: ICBM452AirSpace

Type: Enums

## ICBM452Warp5Space (enums)

Name: ICBM452Warp5Space

Type: Enums

## IODINE (enums)

Name: IODINE

Type: Enums

## IRT1 (suffixes)

Name: Inversion recovery T1 mapping

Type: Suffix

Format: <entities>\_IRT1.<extension>

## IXI549Space (enums)

Name: IXI549Space

Type: Enums

## ImageAcquisitionProtocol (metadata)

Name: Image Acquisition Protocol

Type: Metadata

Schema information:

`type: string`

## ImageDecayCorrected (metadata)

Name: Image Decay Corrected

Type: Metadata

Schema information:

`type: boolean`

## ImageDecayCorrectionTime (metadata)

Name: Image Decay Correction Time

Type: Metadata

Schema information:

`type: number`  
`unit: s`

## Immersion (metadata)

Name: Immersion

Type: Metadata

Schema information:

`type: string`

## Included (enums)

Name: Included

Type: Enums

## InfusionRadioactivity (metadata)

Name: Infusion Radioactivity

Type: Metadata

Schema information:

`type: number`

## InfusionSpeed (metadata)

Name: Infusion Speed

Type: Metadata

Schema information:

`type: number`

## InfusionSpeedUnits (metadata)

Name: Infusion Speed Units

Type: Metadata

Schema information:

`format: unit`

`type: string`

## InfusionStart (metadata)

Name: Infusion Start

Type: Metadata

Schema information:

`type: number`

`unit: s`

## InjectedMass (metadata)

Name: Injected Mass

Type: Metadata

Schema information:

`anyOf:`

- `- type: number`

- `- enum:`

  - `- n/a`

  - `type: string`

## InjectedMassPerWeight (metadata)

Name: Injected Mass Per Weight

Type: Metadata

Schema information:

`type: number`

## InjectedMassPerWeightUnits (metadata)

Name: Injected Mass Per Weight Units

Type: Metadata

Schema information:

`format: unit`

`type: string`

## InjectedMassUnits (metadata)

Name: Injected Mass Units

Type: Metadata

Schema information:

`anyOf:`

- `- format: unit`

- `type: string`

- `- enum:`

- `- n/a`

- `type: string`

## InjectedRadioactivity (metadata)

Name: Injected Radioactivity

Type: Metadata

Schema information:

`type: number`

## InjectedRadioactivityUnits (metadata)

Name: Injected Radioactivity Units

Type: Metadata

Schema information:

```
format: unit
type: string
```

## InjectedVolume (metadata)

Name: Injected Volume

Type: Metadata

Schema information:

```
type: number
unit: mL
```

## InjectionEnd (metadata)

Name: Injection End

Type: Metadata

Schema information:

```
type: number
unit: s
```

## InjectionStart (metadata)

Name: Injection Start

Type: Metadata

Schema information:

```
type: number
unit: s
```

## InstitutionAddress (metadata)

Name: Institution Address

Type: Metadata

Schema information:

`type: string`

## InstitutionName (metadata)

Name: Institution Name

Type: Metadata

Schema information:

`type: string`

## InstitutionalDepartmentName (metadata)

Name: Institutional Department Name

Type: Metadata

Schema information:

`type: string`

## Instructions (metadata)

Name: Instructions

Type: Metadata

Schema information:

`type: string`

## IntendedFor sense 1 (metadata)

Name: Intended For

Type: Metadata

Schema information:



```
anyOf:
- format: bids_uri
  type: string
- format: participant_relative
  type: string
- items:
  anyOf:
  - format: bids_uri
    type: string
  - format: participant_relative
    type: string
  type: array
```

## IntendedFor sense 2 (metadata)

Name: Intended For

Type: Metadata

Schema information:

```
anyOf:
- format: bids_uri
  type: string
- format: dataset_relative
  type: string
- items:
  anyOf:
  - format: bids_uri
    type: string
  - format: dataset_relative
    type: string
  type: array
```

## InterelectrodeDistance (metadata)

Name: Inter-electrode Distance

Type: Metadata

Schema information:

```
type: number
unit: mm
```

## InversionTime (metadata)

Name: Inversion Time

Type: Metadata

Schema information:

```
exclusiveMinimum: 0
type: number
unit: s
```

## JNTANG (enums)

Name: JNTANG

Type: Enums

Schema information:

```
tags:
- motion
```

## JNTANGChannelCount (metadata)

Name: Joint angle channel count

Type: Metadata

Schema information:

```
minimum: 0
type: integer
```

## Keywords (metadata)

Name: Keywords

Type: Metadata

Schema information:

```
items:  
  type: string  
type: array
```

## KitYokogawa (enums)

Name: KIT/Yokogawa

Type: Enums

## LATENCY (enums)

Name: LATENCY

Type: Enums

Schema information:

```
tags:  
- emg  
- motion
```

## LATENCYChannelCount (metadata)

Name: Latency channel count

Type: Metadata

Schema information:

```
minimum: 0  
type: integer
```

## LICENSE (files)

Name: License

Type: Files And Directories

Schema information:

`file_type: regular`

## LabelingDistance (metadata)

Name: Labeling Distance

Type: Metadata

Schema information:

`type: number`  
`unit: mm`

## LabelingDuration (metadata)

Name: Labeling Duration

Type: Metadata

Schema information:

`anyOf:`  
`- minimum: 0`  
    `type: number`  
    `unit: s`  
`- items:`  
    `minimum: 0`  
    `type: number`  
    `unit: s`  
    `type: array`

## LabelingEfficiency (metadata)

Name: Labeling Efficiency

Type: Metadata

Schema information:

`exclusiveMinimum: 0`  
`type: number`

## LabelingLocationDescription (metadata)

Name: Labeling Location Description

Type: Metadata

Schema information:

```
type: string
```

## LabelingOrientation (metadata)

Name: Labeling Orientation

Type: Metadata

Schema information:

```
items:  
  type: number  
type: array
```

## LabelingPulseAverageB1 (metadata)

Name: Labeling Pulse Average B1

Type: Metadata

Schema information:

```
exclusiveMinimum: 0  
type: number  
unit: uT
```

## LabelingPulseAverageGradient (metadata)

Name: Labeling Pulse Average Gradient

Type: Metadata

Schema information:

```
exclusiveMinimum: 0  
type: number  
unit: mT/m
```

## LabelingPulseDuration (metadata)

Name: Labeling Pulse Duration

Type: Metadata

Schema information:

```
exclusiveMinimum: 0
type: number
unit: ms
```

## LabelingPulseFlipAngle (metadata)

Name: Labeling Pulse Flip Angle

Type: Metadata

Schema information:

```
exclusiveMinimum: 0
maximum: 360
type: number
unit: degree
```

## LabelingPulseInterval (metadata)

Name: Labeling Pulse Interval

Type: Metadata

Schema information:

```
exclusiveMinimum: 0
type: number
unit: ms
```

## LabelingPulseMaximumGradient (metadata)

Name: Labeling Pulse Maximum Gradient

Type: Metadata

Schema information:

```
exclusiveMinimum: 0
type: number
unit: mT/m
```

## LabelingSlabThickness (metadata)

Name: Labeling Slab Thickness

Type: Metadata

Schema information:

```
exclusiveMinimum: 0
type: number
unit: mm
```

## Lesion (enums)

Name: Lesion mask

Type: Enums

## LevelType (metadata)

Name: LevelType

Type: Metadata

Schema information:

```
type: string
```

## Levels (metadata)

Name: Levels

Type: Metadata

Schema information:

```
additionalProperties:
  anyOf:
    - type: string
```

```
- properties:
  Description:
    description: 'Free-form natural language description.'

    '
    display_name: Description
    name: Description
    type: string
  TermURL:
    description: 'URL pointing to a formal definition of this type of data in
      an ontology available on the web.

      For example: https://www.ncbi.nlm.nih.gov/mesh/68008297 for "male".

      '
    display_name: TermURL
    format: uri
    name: TermURL
    type: string
  type: object
type: object
```

## License (metadata)

Name: License

Type: Metadata

Schema information:

```
type: string
```

## LongName (metadata)

Name: Long Name

Type: Metadata

Schema information:

```
type: string
```



## LookLocker (metadata)

Name: Look Locker

Type: Metadata

Schema information:

`type: boolean`

## M0Estimate (metadata)

Name: M0Estimate

Type: Metadata

Schema information:

`exclusiveMinimum: 0`

`type: number`

## M0Type (metadata)

Name: M0Type

Type: Metadata

Allowed values: Separate, Included, Estimate, Absent

Schema information:

`type: string`

## M0map (suffixes)

Name: Equilibrium magnetization (M0) map

Type: Suffix

Format: `<entities>_M0map.<extension>`

Schema information:

`unit: arbitrary`

## MAGN (enums)

Name: MAGN

Type: Enums

Schema information:

```
tags:  
- fnirs  
- motion
```

## MAGNChannelCount (metadata)

Name: Magnetometer Channel Count

Type: Metadata

Schema information:

```
minimum: 0  
type: integer
```

## MEGChannelCount (metadata)

Name: MEG Channel Count

Type: Metadata

Schema information:

```
minimum: 0  
type: integer
```

## MEGCoordinateSystem (metadata)

Name: MEG Coordinate System

Type: Metadata

Allowed values: CTF, ElektaNeuromag, NeuromagElektaMEGIN, 4DBti, KitYokogawa, ChietiItab, Other, CapTrak, EEGLAB, EEGLAB-HJ, 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, UNCIInfant0V21, UNCIInfant1V21, UNCIInfant2V21, UNCIInfant0V22, UNCIInfant1V22, UNCIInfant2V22, UNCIInfant0V23, UNCIInfant1V23, UNCIInfant2V23

Schema information:

`type: string`

## MEGCoordinateSystemDescription (metadata)

Name: MEG Coordinate System Description

Type: Metadata

Schema information:

`type: string`

## MEGCoordinateUnits (metadata)

Name: MEG Coordinate Units

Type: Metadata

Allowed values: m, mm, cm, n/a

Schema information:

`type: string`

## MEGGRADAXIAL (enums)

Name: MEGGRADAXIAL

Type: Enums

Schema information:

`tags:`  
`- meg`  
`- fnirs`

## MEGGRADPLANAR (enums)

Name: MEGGRADPLANAR

Type: Enums

Schema information:

```
tags:  
- meg  
- fnirs
```

## MEGMAG (enums)

Name: MEGMAG

Type: Enums

Schema information:

```
tags:  
- meg  
- fnirs
```

## MEGOTHER (enums)

Name: MEGOTHER

Type: Enums

Schema information:

```
tags:  
- meg  
- ieeg  
- fnirs
```

## MEGRE (suffixes)

Name: Multi-echo Gradient Recalled Echo

Type: Suffix

Format: <entities>\_MEGRE.<extension>

## MEGREFChannelCount (metadata)

Name: MEGREF Channel Count

Type: Metadata

Schema information:

```
minimum: 0
type: integer
```

## MEGREFGRADAXIAL (enums)

Name: MEGREFGRADAXIAL

Type: Enums

Schema information:

```
tags:
- meg
- fnirs
```

## MEGREFGRADPLANAR (enums)

Name: MEGREFGRADPLANAR

Type: Enums

Schema information:

```
tags:
- meg
- fnirs
```

## MEGREFMAG (enums)

Name: MEGREFMAG

Type: Enums

Schema information:

```
tags:  
- meg  
- fnirs
```

## MESE (suffixes)

Name: Multi-echo Spin Echo

Type: Suffix

Format: <entities>\_MESE.<extension>

## MISC (enums)

Name: MISC

Type: Enums

Schema information:

```
tags:  
- eeg  
- emg  
- meg  
- ieeg  
- fnirs  
- motion
```

## MISCChannelCount (metadata)

Name: Miscellaneous channel count

Type: Metadata

Schema information:

```
minimum: 0  
type: integer
```

## MNI152Lin (enums)

Name: MNI152Lin

Type: Enums

## MNI152NLin2009aAsym (enums)

Name: MNI152NLin2009aAsym

Type: Enums

## MNI152NLin2009aSym (enums)

Name: MNI152NLin2009aSym

Type: Enums

## MNI152NLin2009bAsym (enums)

Name: MNI152NLin2009bAsym

Type: Enums

## MNI152NLin2009bSym (enums)

Name: MNI152NLin2009bSym

Type: Enums

## MNI152NLin2009cAsym (enums)

Name: MNI152NLin2009cAsym

Type: Enums

## MNI152NLin2009cSym (enums)

Name: MNI152NLin2009cSym

Type: Enums

## MNI152NLin6Asym (enums)

Name: MNI152NLin6Asym

Type: Enums

## MNI152NLin6Sym (enums)

Name: MNI152NLin6Sym

Type: Enums

## MNI305 (enums)

Name: MNI205

Type: Enums

## MNIColin27 (enums)

Name: MNIColin27

Type: Enums

## MP2RAGE (suffixes)

Name: Magnetization Prepared Two Gradient Echoes

Type: Suffix

Format: `<entities>_MP2RAGE.<extension>`

## MPE (suffixes)

Name: Multi-photon excitation microscopy

Type: Suffix

Format: `<entities>_MPE.<extension>`



## MPM (suffixes)

Name: Multi-parametric Mapping

Type: Suffix

Format: <entities>\_MPM.<extension>

## MRAcquisitionType (metadata)

Name: MR Acquisition Type

Type: Metadata

Allowed values: 1D, 2D, 3D

Schema information:

`type: string`

## MRTransmitCoilSequence (metadata)

Name: MR Transmit Coil Sequence

Type: Metadata

Schema information:

`type: string`

## MTNumberOfPulses (metadata)

Name: MT Number Of Pulses

Type: Metadata

Schema information:

`type: number`

## MTOffsetFrequency (metadata)

Name: MT Offset Frequency

Type: Metadata

Schema information:

`type: number`  
`unit: Hz`

## MTPulseBandwidth (metadata)

Name: MT Pulse Bandwidth

Type: Metadata

Schema information:

`type: number`  
`unit: Hz`

## MTPulseDuration (metadata)

Name: MT Pulse Duration

Type: Metadata

Schema information:

`type: number`  
`unit: s`

## MTPulseShape (metadata)

Name: MT Pulse Shape

Type: Metadata

Allowed values: HARD, GAUSSIAN, GAUSSHANN, SINC, SINCHANN, SINCGAUSS, FERMI

Schema information:

`type: string`

## MTR (suffixes)

Name: Magnetization Transfer Ratio

Type: Suffix

Format: <entities>\_MTR.<extension>

## MTRmap (suffixes)

Name: Magnetization transfer ratio image

Type: Suffix

Format: <entities>\_MTRmap.<extension>

Schema information:

```
maxValue: 100
minValue: 0
unit: arbitrary
```

## MTS (suffixes)

Name: Magnetization transfer saturation

Type: Suffix

Format: <entities>\_MTS.<extension>

## MTState (metadata)

Name: MT State

Type: Metadata

Schema information:

```
type: boolean
```

## MTVmap (suffixes)

Name: Macromolecular tissue volume (MTV) image

Type: Suffix

Format: <entities>\_MTVmap.<extension>

Schema information:

`unit: arbitrary`

## MTsat (suffixes)

Name: Magnetization transfer saturation image

Type: Suffix

Format: <entities>\_MTsat.<extension>

Schema information:

`unit: arbitrary`

## MWFmap (suffixes)

Name: Myelin water fraction image

Type: Suffix

Format: <entities>\_MWFmap.<extension>

Schema information:

`maxValue: 100`

`minValue: 0`

`unit: arbitrary`

## MagneticFieldStrength (metadata)

Name: Magnetic Field Strength

Type: Metadata

Schema information:

`type: number`

## Magnification (metadata)

Name: Magnification

Type: Metadata

Schema information:

`exclusiveMinimum: 0`  
`type: number`

## Manual (metadata)

Name: Manual

Type: Metadata

Schema information:

`type: boolean`

## Manufacturer (metadata)

Name: Manufacturer

Type: Metadata

Schema information:

`type: string`

## ManufacturersModelName (metadata)

Name: Manufacturers Model Name

Type: Metadata

Schema information:

`type: string`

## MatrixCoilMode (metadata)

Name: Matrix Coil Mode

Type: Metadata

Schema information:

```
type: string
```

## MatrixSize (metadata)

Name: Matrix Size

Type: Metadata

Schema information:

```
items:
  minimum: 1
  type: integer
maxItems: 3
minItems: 3
type: array
```

## MaxMovement (metadata)

Name: Max Movement

Type: Metadata

Schema information:

```
type: number
unit: mm
```

## MaximalCalibrationError (metadata)

Name: Maximal Calibration Error

Type: Metadata

Schema information:

```
type: number
unit: degree
```

## Maximum (metadata)

Name: Maximum value

Type: Metadata

Schema information:

```
type: number
```

## MeasurementToolMetadata (metadata)

Name: Measurement Tool Metadata

Type: Metadata

Schema information:

```
properties:
```

```
  Description:
```

```
    description: 'Free-form natural language description.'
```

```
    '
```

```
    display_name: Description
```

```
    name: Description
```

```
    type: string
```

```
  TermURL:
```

```
    description: 'URL pointing to a formal definition of this type of data in an ontology
    available on the web.'
```

```
    For example: https://www.ncbi.nlm.nih.gov/mesh/68008297 for "male".
```

```
    '
```

```
    display_name: TermURL
```

```
    format: uri
```

```
    name: TermURL
```

```
    type: string
```

```
type: object
```

## MetaboliteAvail (metadata)

Name: Metabolite Available

Type: Metadata

Schema information:

`type: boolean`

## MetaboliteMethod (metadata)

Name: Metabolite Method

Type: Metadata

Schema information:

`type: string`

## MetaboliteRecoveryCorrectionApplied (metadata)

Name: Metabolite Recovery Correction Applied

Type: Metadata

Schema information:

`type: boolean`

## Metabolomic (enums)

Name: Metabolomic

Type: Enums

## Minimum (metadata)

Name: Minimum value

Type: Metadata

Schema information:



`type: number`

## MiscChannelCount (metadata)

Name: Misc Channel Count

Type: Metadata

Schema information:

`minimum: 0`  
`type: integer`

## MissingValues (metadata)

Name: MissingValues

Type: Metadata

Schema information:

`type: string`

## MixingTime (metadata)

Name: Mixing Time

Type: Metadata

Schema information:

`type: number`  
`unit: s`

## ModeOfAdministration (metadata)

Name: Mode Of Administration

Type: Metadata

Schema information:

`type: string`

## MolarActivity (metadata)

Name: Molar Activity

Type: Metadata

Schema information:

`type: number`

## MolarActivityMeasTime (metadata)

Name: Molar Activity Measurement Time

Type: Metadata

Schema information:

`format: time`

`type: string`

## MolarActivityUnits (metadata)

Name: Molar Activity Units

Type: Metadata

Schema information:

`format: unit`

`type: string`

## MotionChannelCount (metadata)

Name: Motion Channel Count

Type: Metadata

Schema information:

`minimum: 0`

`type: integer`

## MultibandAccelerationFactor (metadata)

Name: Multiband Acceleration Factor

Type: Metadata

Schema information:

`type: number`

## MultipartID (metadata)

Name: MultipartID

Type: Metadata

Schema information:

`type: string`

## NIHPD (enums)

Name: NIHPD

Type: Enums

## NIRSCWAMPLITUDE (enums)

Name: NIRSCWAMPLITUDE

Type: Enums

Schema information:

`tags:`  
`- fnirs`

## NIRSCWFLUORESCENSEAMPLITUDE (enums)

Name: NIRSCWFLUORESCENSEAMPLITUDE

Type: Enums

Schema information:

```
tags:  
- fnirs
```

## NIRSCWHBO (enums)

Name: NIRSCWHBO

Type: Enums

Schema information:

```
tags:  
- fnirs
```

## NIRSCWHBR (enums)

Name: NIRSCWHBR

Type: Enums

Schema information:

```
tags:  
- fnirs
```

## NIRSCWMUA (enums)

Name: NIRSCWMUA

Type: Enums

Schema information:

```
tags:  
- fnirs
```

## NIRSCWOPTICALDENSITY (enums)

Name: NIRSCWOPTICALDENSITY

Type: Enums

Schema information:

```
tags:  
- fnirs
```

## NIRSChannelCount (metadata)

Name: NIRS Channel Count

Type: Metadata

Schema information:

```
minimum: 0  
type: integer
```

## NIRSCoordinateProcessingDescription (metadata)

Name: NIRS Coordinate Processing Description

Type: Metadata

Schema information:

```
type: string
```

## NIRSCoordinateSystem (metadata)

Name: NIRS Coordinate System

Type: Metadata

Allowed values: CTF, ElektaNeuromag, NeuromagElektaMEGIN, 4DBti, KitYokogawa, ChietiItab, Other, CapTrak, EEGLAB, EEGLAB-HJ, 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

Schema information:

```
type: string
```

## NIRSCoordinateSystemDescription (metadata)

Name: NIRS Coordinate System Description

Type: Metadata

Schema information:

```
type: string
```

## NIRSCoordinateUnits (metadata)

Name: NIRS Coordinate Units

Type: Metadata

Allowed values: m, mm, cm, n/a

Schema information:

```
type: string
```

## NIRSDetectorOptodeCount (metadata)

Name: NIRS Detector Optode Channel Count

Type: Metadata

Schema information:

```
minimum: 1  
type: integer
```

## NIRSPlacementScheme (metadata)

Name: NIRS Placement Scheme

Type: Metadata

Schema information:

```
anyOf:  
- type: string  
- items:  
    type: string  
    type: array
```

## NIRSSourceOptodeCount (metadata)

Name: NIRS Source Optode Count

Type: Metadata

Schema information:

```
minimum: 1  
type: integer
```

## NLO (suffixes)

Name: Nonlinear optical microscopy

Type: Suffix

Format: <entities>\_NLO.<extension>

## Name sense 1 (metadata)

Name: Name

Type: Metadata

Schema information:

```
type: string
```

## Name sense 2 (metadata)

Name: Pipeline Name

Type: Metadata

Schema information:

```
type: string
```

## NegativeContrast (metadata)

Name: Negative Contrast

Type: Metadata

Schema information:

`type: boolean`

## NeuromagElektaMEGIN (enums)

Name: Neuromag Elekta MEGIN

Type: Enums

## None (extensions)

Name: No extension

Type: Extension

Format: <entities>\_<suffix>

## NonlinearGradientCorrection (metadata)

Name: Nonlinear Gradient Correction

Type: Metadata

Schema information:

`type: boolean`

## NumberOfSpectralPoints (metadata)

Name: Number Of Spectral Points

Type: Metadata

Schema information:

`type: integer`

## NumberOfTransients (metadata)

Name: Number Of Transients

Type: Metadata



Schema information:

`type: integer`

## NumberOfVolumesDiscardedByScanner (metadata)

Name: Number Of Volumes Discarded By Scanner

Type: Metadata

Schema information:

`minimum: 0`

`type: integer`

## NumberOfVolumesDiscardedByUser (metadata)

Name: Number Of Volumes Discarded By User

Type: Metadata

Schema information:

`minimum: 0`

`type: integer`

## NumberReceiveCoilActiveElements (metadata)

Name: Number of Receive Coil Active Elements

Type: Metadata

Schema information:

`type: integer`

## NumberShots (metadata)

Name: Number Shots

Type: Metadata

Schema information:

```
anyOf:  
- type: number  
- items:  
  type: number  
  type: array
```

## NumberTransmitCoilActiveElements (metadata)

Name: Number of Transmit Coil Active Elements

Type: Metadata

Schema information:

```
type: integer
```

## NumericalAperture (metadata)

Name: Numerical Aperture

Type: Metadata

Schema information:

```
exclusiveMinimum: 0  
type: number
```

## OASIS30AntsOASISAnts (enums)

Name: OASIS30AntsOASISAnts

Type: Enums

## OASIS30Atropos (enums)

Name: OASIS30Atropos

Type: Enums

## OCT (suffixes)

Name: Optical coherence tomography

Type: Suffix

Format: <entities>\_OCT.<extension>

## OMEBigTiff (extensions)

Name: Open Microscopy Environment BigTIFF

Type: Extension

Format: <entities>\_<suffix>.ome.btf

## OMETiff (extensions)

Name: Open Microscopy Environment Tag Image File Format

Type: Extension

Format: <entities>\_<suffix>.ome.tif

## OMEZARR (extensions)

Name: OME Next Generation File Format

Type: Extension

Format: <entities>\_<suffix>.ome.zarr/

## ORNT (enums)

Name: ORNT

Type: Enums

Schema information:

```
tags:  
- fnirs  
- motion
```

## ORNTChannelCount (metadata)

Name: Orientation Channel Count

Type: Metadata

Schema information:

```
minimum: 0
type: integer
```

## OTHER (enums)

Name: OTHER

Type: Enums

Schema information:

```
tags:
- meg
- fnirs
```

## OneD (enums)

Name: One-dimensional

Type: Enums

## OnsetSource (metadata)

Name: Column Name of the Onset Source

Type: Metadata

Schema information:

```
type: string
```

## OperatingSystem (metadata)

Name: Operating System

Type: Metadata

Schema information:

`type: string`

## Other (enums)

Name: Other

Type: Enums

## OtherAcquisitionParameters (metadata)

Name: Other Acquisition Parameters

Type: Metadata

Schema information:

`type: string`

## OuterVolumeSuppression (metadata)

Name: Outer-Volume Suppression

Type: Metadata

Schema information:

`type: boolean`

## PASL (enums)

Name: Pulsed arterial spin labeling

Type: Enums

## PASLType (metadata)

Name: PASL Type

Type: Metadata

Schema information:

`type: string`

## PC (suffixes)

Name: Phase-contrast microscopy

Type: Suffix

Format: <entities>\_PC.<extension>

## PCASL (enums)

Name: Pseudo-continuous arterial spin labeling

Type: Enums

## PCASLType (metadata)

Name: PCASL Type

Type: Metadata

Allowed values: `balanced`, `unbalanced`

Schema information:

`type: string`

## PD (enums)

Name: PD

Type: Enums

Schema information:

`tags:`  
`- meg`  
`- ieeg`  
`- fnirs`

## PD (suffixes)

Name: Proton density image

Type: Suffix

Format: <entities>\_PD.<extension>

Schema information:

`unit: arbitrary`

## PDT2 (suffixes)

Name: PD and T2 weighted image

Type: Suffix

Format: <entities>\_PDT2.<extension>

Schema information:

`unit: arbitrary`

## PDmap (suffixes)

Name: Proton density image

Type: Suffix

Format: <entities>\_PDmap.<extension>

Schema information:

`unit: arbitrary`

## PDw (suffixes)

Name: Proton density (PD) weighted image

Type: Suffix

Format: <entities>\_PDw.<extension>

Schema information:

`unit: arbitrary`

## PLI (suffixes)

Name: Polarized-light microscopy

Type: Suffix

Format: <entities>\_PLI.<extension>

## POS (enums)

Name: POS

Type: Enums

Schema information:

```
tags:  
- emg  
- motion
```

## POSChannelCount (metadata)

Name: Position Channel Count

Type: Metadata

Schema information:

```
minimum: 0  
type: integer
```

## PPG (enums)

Name: PPG

Type: Enums

Schema information:

```
tags:  
- eeg
```



## PUPIL (enums)

Name: PUPIL

Type: Enums

Schema information:

```
tags:  
- eeg  
- meg  
- ieeg  
- fnirs
```

## ParallelAcquisitionTechnique (metadata)

Name: Parallel Acquisition Technique

Type: Metadata

Schema information:

```
type: string
```

## ParallelReductionFactorInPlane (metadata)

Name: Parallel Reduction Factor In Plane

Type: Metadata

Schema information:

```
type: number
```

## ParallelReductionFactorOutOfPlane (metadata)

Name: Parallel Reduction Factor Out of Plane

Type: Metadata

Schema information:

```
type: number
```

## ParentCoordinateSystem (metadata)

Name: Parent Coordinate System

Type: Metadata

Schema information:

`type: string`

## PartialFourier (metadata)

Name: Partial Fourier

Type: Metadata

Schema information:

`type: number`

## PartialFourierDirection (metadata)

Name: Partial Fourier Direction

Type: Metadata

Schema information:

`type: string`

## PharmaceuticalDoseAmount (metadata)

Name: Pharmaceutical Dose Amount

Type: Metadata

Schema information:

```
anyOf:  
- type: number  
- items:  
    type: number  
  type: array
```

## PharmaceuticalDoseRegimen (metadata)

Name: Pharmaceutical Dose Regimen

Type: Metadata

Schema information:

```
type: string
```

## PharmaceuticalDoseTime (metadata)

Name: Pharmaceutical Dose Time

Type: Metadata

Schema information:

```
anyOf:  
- type: number  
  unit: s  
- items:  
  type: number  
  unit: s  
  type: array
```

## PharmaceuticalDoseUnits (metadata)

Name: Pharmaceutical Dose Units

Type: Metadata

Schema information:

```
format: unit  
type: string
```

## PharmaceuticalName (metadata)

Name: Pharmaceutical Name

Type: Metadata

Schema information:

`type: string`

## PhaseEncodingDirection (metadata)

Name: Phase Encoding Direction

Type: Metadata

Allowed values: i, i-, j, j-, k, k-

Schema information:

`type: string`

## PhotoDescription (metadata)

Name: Photo Description

Type: Metadata

Schema information:

`type: string`

## PhysioType (metadata)

Name: Physiological Recording Type

Type: Metadata

Allowed values: generic, eyetrack

Schema information:

`type: string`

## PhysioTypeEyetrack (enums)

Name: Eye-tracking recording

Type: Enums

## PhysioTypeGeneric (enums)

Name: Generic Physiological Recording

Type: Enums

## PixelSize (metadata)

Name: Pixel Size

Type: Metadata

Schema information:

```
items:  
  minimum: 0  
  type: number  
maxItems: 3  
minItems: 2  
type: array
```

## PixelSizeUnits (metadata)

Name: Pixel Size Units

Type: Metadata

Allowed values: mm, um, nm

Schema information:

```
type: string
```

## Pixels (enums)

Name: Pixels

Type: Enums

## PlasmaAvail (metadata)

Name: Plasma Avail

Type: Metadata

Schema information:

`type: boolean`

## PlasmaFreeFraction (metadata)

Name: Plasma Free Fraction

Type: Metadata

Schema information:

`maximum: 100`

`minimum: 0`

`type: number`

## PlasmaFreeFractionMethod (metadata)

Name: Plasma Free Fraction Method

Type: Metadata

Schema information:

`type: string`

## PostLabelingDelay (metadata)

Name: Post Labeling Delay

Type: Metadata

Schema information:

`anyOf:`

`- minimum: 0`

`type: number`

`unit: s`

`- items:`

`minimum: 0`

`type: number`

```
    unit: s
    type: array
```

## PowerLineFrequency (metadata)

Name: Power Line Frequency

Type: Metadata

Schema information:

```
anyOf:
- exclusiveMinimum: 0
  type: number
  unit: Hz
- enum:
  - n/a
  type: string
```

## Preamplification (metadata)

Name: Preamplification

Type: Metadata

Schema information:

```
type: number
unit: arbitrary
```

## PromptRate (metadata)

Name: Prompt Rate

Type: Metadata

Schema information:

```
items:
  type: number
type: array
```

## Proteomic (enums)

Name: Proteomic

Type: Enums

## PulseDuration (metadata)

Name: Pulse Duration

Type: Metadata

Schema information:

```
type: number
unit: ms
```

## PulseSequenceDetails (metadata)

Name: Pulse Sequence Details

Type: Metadata

Schema information:

```
type: string
```

## PulseSequencePulses (metadata)

Name: Pulse Sequence Pulses

Type: Metadata

Schema information:

```
items:
  type: string
type: array
```

## PulseSequenceTiming (metadata)

Name: Pulse Sequence Timing



Type: Metadata

Schema information:

```
items:  
  type: number  
  unit: s  
type: array
```

## PulseSequenceType (metadata)

Name: Pulse Sequence Type

Type: Metadata

Schema information:

```
type: string
```

## PupilFitMethod (metadata)

Name: Pupil Fit Method

Type: Metadata

Schema information:

```
type: string
```

## Purity (metadata)

Name: Purity

Type: Metadata

Schema information:

```
maximum: 100  
minimum: 0  
type: number
```

## R1map (suffixes)

Name: Longitudinal relaxation rate image

Type: Suffix

Format: <entities>\_R1map.<extension>

Schema information:

`unit: 1/s`

## R2map (suffixes)

Name: True transverse relaxation rate image

Type: Suffix

Format: <entities>\_R2map.<extension>

Schema information:

`unit: 1/s`

## R2starmap (suffixes)

Name: Observed transverse relaxation rate image

Type: Suffix

Format: <entities>\_R2starmap.<extension>

Schema information:

`unit: 1/s`

## RB1COR (suffixes)

Name: RB1COR

Type: Suffix

Format: <entities>\_RB1COR.<extension>

## RB1map (suffixes)

Name: RF receive sensitivity map

Type: Suffix

Format: <entities>\_RB1map.<extension>

Schema information:

`unit:` `arbitrary`

## README (files)

Name: README

Type: Files And Directories

Schema information:

`file_type:` `regular`

## REF (enums)

Name: REF

Type: Enums

Schema information:

`tags:`  
`- eeg`  
`- emg`  
`- ieeg`

## RESP (enums)

Name: RESP

Type: Enums

Schema information:

`tags:`  
`- eeg`

## RF (enums)

Name: RF

Type: Enums

## ROI (enums)

Name: ROI mask

Type: Enums

## RRID (metadata)

Name: RRID

Type: Metadata

Schema information:

```
format: rrid
type: string
```

## RandomRate (metadata)

Name: Random Rate

Type: Metadata

Schema information:

```
items:
  type: number
type: array
```

## RawDataFilters (metadata)

Name: Raw Data Filters

Type: Metadata

Schema information:

```
type: string
```

## RawSources (metadata)

Name: Raw Sources

Type: Metadata

Schema information:

```
items:  
  format: dataset_relative  
  type: string  
type: array
```

## ReceiveCoilActiveElements (metadata)

Name: Receive Coil Active Elements

Type: Metadata

Schema information:

```
type: string
```

## ReceiveCoilName (metadata)

Name: Receive Coil Name

Type: Metadata

Schema information:

```
type: string
```

## ReceiveGain (metadata)

Name: Receive Gain

Type: Metadata

Schema information:

```
anyOf:  
- type: number  
  unit: dB  
- items:  
  type: number  
  unit: dB  
type: array
```

## ReconFilterSize (metadata)

Name: Recon Filter Size

Type: Metadata

Schema information:

```
anyOf:  
- type: number  
  unit: mm  
- items:  
  type: number  
  unit: mm  
type: array
```

## ReconFilterType (metadata)

Name: Recon Filter Type

Type: Metadata

Schema information:

```
anyOf:  
- type: string  
- items:  
  type: string  
type: array
```

## ReconMethodImplementationVersion (metadata)

Name: Recon Method Implementation Version

Type: Metadata

Schema information:

```
type: string
```

## ReconMethodName (metadata)

Name: Recon Method Name

Type: Metadata

Schema information:

```
type: string
```

## ReconMethodParameterLabels (metadata)

Name: Recon Method Parameter Labels

Type: Metadata

Schema information:

```
items:  
  type: string  
type: array
```

## ReconMethodParameterUnits (metadata)

Name: Recon Method Parameter Units

Type: Metadata

Schema information:

```
items:  
  format: unit  
  type: string  
type: array
```

## ReconMethodParameterValues (metadata)

Name: Recon Method Parameter Values

Type: Metadata

Schema information:

```
items:  
  type: number  
type: array
```

## RecordedEye (metadata)

Name: Recorded Eye

Type: Metadata

Allowed values: left, right, cyclopean

Schema information:

```
type: string
```

## RecordingDuration (metadata)

Name: Recording Duration

Type: Metadata

Schema information:

```
type: number  
unit: s
```

## RecordingType (metadata)

Name: Recording Type

Type: Metadata

Allowed values: continuous, epoch, discontinuous

Schema information:

```
type: string
```



## ReferenceSignal (metadata)

Name: Reference Signal

Type: Metadata

Schema information:

```
anyOf:  
- format: bids_uri  
  type: string  
- items:  
  format: bids_uri  
  type: string  
type: array
```

## ReferencesAndLinks (metadata)

Name: References And Links

Type: Metadata

Schema information:

```
items:  
  type: string  
type: array
```

## RepetitionTime (metadata)

Name: Repetition Time

Type: Metadata

Schema information:

```
exclusiveMinimum: 0  
type: number  
unit: s
```

## RepetitionTimeExcitation (metadata)

Name: Repetition Time Excitation

Type: Metadata

Schema information:

```
minimum: 0
type: number
unit: s
```

## RepetitionTimePreparation (metadata)

Name: Repetition Time Preparation

Type: Metadata

Schema information:

```
anyOf:
- minimum: 0
  type: number
  unit: s
- items:
  minimum: 0
  type: number
  unit: s
  type: array
```

## Resolution (metadata)

Name: Resolution

Type: Metadata

Schema information:

```
anyOf:
- type: string
- additionalProperties:
  type: string
  type: object
```

## ResonantNucleus (metadata)

Name: Resonant Nucleus

Type: Metadata

Schema information:

```
anyOf:  
- type: string  
- items:  
  maxItems: 2  
  minItems: 1  
  type: string  
type: array
```

## RotationOrder (metadata)

Name: RotationOrder

Type: Metadata

Allowed values: XYZ, XZY, YXZ, YZX, ZXY, ZYX, n/a

Schema information:

```
type: string
```

## RotationRule (metadata)

Name: Rotation Rule

Type: Metadata

Allowed values: left-hand, right-hand, n/a

Schema information:

```
type: string
```

## S0map (suffixes)

Name: Projected baseline signal amplitude (S0) image

Type: Suffix

Format: <entities>\_S0map.<extension>

## SEEG (enums)

Name: SEEG

Type: Enums

Schema information:

```
tags:  
- meg  
- ieeg  
- fnirs
```

## SEEGChannelCount (metadata)

Name: SEEG Channel Count

Type: Metadata

Schema information:

```
minimum: 0  
type: integer
```

## SEM (suffixes)

Name: Scanning electron microscopy

Type: Suffix

Format: <entities>\_SEM.<extension>

## SINC (enums)

Name: Sinc pulse

Type: Enums

## SINCGAUSS (enums)

Name: Sinc-Gauss pulse

Type: Enums

## SINCHANN (enums)

Name: Sinc-Hanning pulse

Type: Enums

## SPIM (suffixes)

Name: Selective plane illumination microscopy

Type: Suffix

Format: <entities>\_SPIM.<extension>

## SR (suffixes)

Name: Super-resolution microscopy

Type: Suffix

Format: <entities>\_SR.<extension>

## SYSCLOCK (enums)

Name: SYSCLOCK

Type: Enums

Schema information:

```
tags:  
- eeg  
- emg  
- meg  
- ieeg  
- fnirs
```

## SampleCoordinateSystem (metadata)

Name: Coordinate System of the Gaze Position

Type: Metadata

Allowed values: gaze-on-screen, eye-in-head, gaze-in-world, custom

Schema information:

`type: string`

## SampleEmbedding (metadata)

Name: Sample Embedding

Type: Metadata

Schema information:

`type: string`

## SampleEnvironment (metadata)

Name: Sample Environment

Type: Metadata

Allowed values: in vivo, ex vivo, in vitro

Schema information:

`type: string`

## SampleExtractionInstitution (metadata)

Name: Sample Extraction Institution

Type: Metadata

Schema information:

`type: string`

## SampleExtractionProtocol (metadata)

Name: Sample Extraction Protocol

Type: Metadata

Schema information:

`type: string`

## SampleFixation (metadata)

Name: Sample Fixation

Type: Metadata

Schema information:

`type: string`

## SampleOrigin (metadata)

Name: Sample Origin

Type: Metadata

Allowed values: blood, saliva, brain, csf, breast milk, bile, amniotic fluid, other biospecimen

Schema information:

`type: string`

## SamplePrimaryAntibody (metadata)

Name: Sample Primary Antibody

Type: Metadata

Schema information:

```
anyOf:  
- type: string  
- items:  
  type: string  
  type: array
```

## SampleSecondaryAntibody (metadata)

Name: Sample Secondary Antibody

Type: Metadata

Schema information:

```
anyOf:  
- type: string  
- items:  
  type: string  
  type: array
```

## SampleStaining (metadata)

Name: Sample Staining

Type: Metadata

Schema information:

```
anyOf:  
- type: string  
- items:  
  type: string  
  type: array
```

## SamplingFrequency sense 1 (metadata)

Name: Sampling Frequency

Type: Metadata

Schema information:

```
type: number  
unit: Hz
```

## SamplingFrequency sense 2 (metadata)

Name: Sampling Frequency

Type: Metadata

Schema information:

```
anyOf:  
- type: number
```



```
    unit: Hz
- enum:
  - n/a
  type: string
```

## SamplingFrequencyEffective (metadata)

Name: Effective Sampling Frequency

Type: Metadata

Schema information:

```
type: number
unit: Hz
```

## ScaleFactor (metadata)

Name: Scale Factor

Type: Metadata

Schema information:

```
items:
  type: number
type: array
```

## ScanDate (metadata)

Name: Scan Date

Type: Metadata

Schema information:

```
format: date
type: string
```

## ScanOptions (metadata)

Name: Scan Options

Type: Metadata

Schema information:

```
anyOf:  
- type: string  
- items:  
    type: string  
    type: array
```

## ScanRAS (enums)

Name: ScanRAS

Type: Enums

## ScanStart (metadata)

Name: Scan Start

Type: Metadata

Schema information:

```
type: number  
unit: s
```

## ScanningSequence sense 1 (metadata)

Name: Scanning Sequence

Type: Metadata

Schema information:

```
anyOf:  
- type: string  
- items:  
    type: string  
    type: array
```

## ScanningSequence sense 2 (metadata)

Name: Scanning Sequence

Type: Metadata

Allowed values: SVS, MRSI, Unlocalized MRS

Schema information:

```
type: string
```

## ScatterFraction (metadata)

Name: Scatter Fraction

Type: Metadata

Schema information:

```
items:  
  maximum: 100  
  minimum: 0  
  type: number  
type: array
```

## ScreenDistance (metadata)

Name: Screen Distance

Type: Metadata

Schema information:

```
anyOf:  
- type: number  
  unit: m  
- items:  
  type: number  
  maxItems: 3  
  minItems: 3  
  type: array  
- enum:
```

```
- n/a  
type: string
```

## ScreenOrigin (metadata)

Name: Screen Coordinate System's Origin

Type: Metadata

Schema information:

```
items:  
  enum:  
    - top  
    - bottom  
    - left  
    - right  
    - center  
  type: string  
maxItems: 2  
minItems: 2  
type: array
```

## ScreenRefreshRate (metadata)

Name: Screen Refresh Rate

Type: Metadata

Schema information:

```
type: number  
unit: Hz
```

## ScreenResolution (metadata)

Name: Screen Resolution

Type: Metadata

Schema information:

```
anyOf:  
- items:  
  type: integer  
  maxItems: 2  
  minItems: 2  
  type: array  
- enum:  
  - n/a  
  type: string
```

## ScreenSize (metadata)

Name: Screen Size

Type: Metadata

Schema information:

```
anyOf:  
- items:  
  type: number  
  unit: m  
  maxItems: 2  
  minItems: 2  
  type: array  
- enum:  
  - n/a  
  type: string
```

## Separate (enums)

Name: Separate

Type: Enums

## SequenceName (metadata)

Name: Sequence Name

Type: Metadata

Schema information:

```
type: string
```

## SequenceVariant (metadata)

Name: Sequence Variant

Type: Metadata

Schema information:

```
anyOf:  
- type: string  
- items:  
  type: string  
  type: array
```

## ShortChannelCount (metadata)

Name: Short Channel Count

Type: Metadata

Schema information:

```
minimum: 0  
type: integer
```

## SinglesRate (metadata)

Name: Singles Rate

Type: Metadata

Schema information:

```
items:  
  type: number  
type: array
```

## SkinPreparation (metadata)

Name: Skin Preparation

Type: Metadata

Schema information:

`type: string`

## SkullStripped (metadata)

Name: Skull Stripped

Type: Metadata

Schema information:

`type: boolean`

## SliceEncodingDirection (metadata)

Name: Slice Encoding Direction

Type: Metadata

Allowed values: i, i-, j, j-, k, k-

Schema information:

`type: string`

## SliceThickness (metadata)

Name: Slice Thickness

Type: Metadata

Schema information:

`exclusiveMinimum: 0`

`type: number`

`unit: um`

## SliceTiming (metadata)

Name: Slice Timing

Type: Metadata

Schema information:

```
items:  
  minimum: 0  
  type: number  
  unit: s  
type: array
```

## SoftwareFilters (metadata)

Name: Software Filters

Type: Metadata

Schema information:

```
anyOf:  
- additionalProperties:  
  type: object  
  type: object  
- enum:  
  - n/a  
  type: string
```

## SoftwareName (metadata)

Name: Software Name

Type: Metadata

Schema information:

```
type: string
```

## SoftwareRRID (metadata)

Name: SoftwareRRID

Type: Metadata

Schema information:



```
format: rrid
type: string
```

## SoftwareVersion (metadata)

Name: Software Version

Type: Metadata

Schema information:

```
type: string
```

## SoftwareVersions (metadata)

Name: Software Versions

Type: Metadata

Schema information:

```
type: string
```

## SourceDatasets (metadata)

Name: Source Datasets

Type: Metadata

Schema information:

```
items:
  properties:
    DOI:
      description: 'A Digital Object Identifier (DOI) is a persistent, resolvable
        name for a digital resource.

        (see URI)

        '
      display_name: DOI
      name: DOI
      type: string
```

```
URL:
  description: 'A Uniform Resource Locator (URL) is a structured reference to
    an object that

    includes a resource transfer scheme and a location.

    (see URI)

    '
  display_name: URL
  format: uri
  name: URL
  type: string
Version:
  description: Version of the dataset.
  display_name: Dataset Version
  name: Version
  type: string
type: object
type: array
```

## SourceType (metadata)

Name: Source Type

Type: Metadata

Schema information:

```
type: string
```

## Sources (metadata)

Name: Sources

Type: Metadata

Schema information:

```
items:
  format: dataset_relative
```

```
  type: string
type: array
```

## SpatialAxes (metadata)

Name: Spatial axes

Type: Metadata

Schema information:

```
type: string
```

## SpatialReference (metadata)

Name: Spatial Reference

Type: Metadata

Schema information:

```
anyOf:
- enum:
  - orig
  type: string
- format: uri
  type: string
- format: dataset_relative
  type: string
- additionalProperties:
  anyOf:
  - enum:
    - orig
    type: string
  - format: uri
    type: string
  - format: dataset_relative
    type: string
  type: object
```

## Species (metadata)

Name: Species

Type: Metadata

Schema information:

```
type: string
```

## SpecificRadioactivity (metadata)

Name: Specific Radioactivity

Type: Metadata

Schema information:

```
anyOf:  
- type: number  
- enum:  
  - n/a  
  type: string
```

## SpecificRadioactivityMeasTime (metadata)

Name: Specific Radioactivity Measurement Time

Type: Metadata

Schema information:

```
format: time  
type: string
```

## SpecificRadioactivityUnits (metadata)

Name: Specific Radioactivity Units

Type: Metadata

Schema information:

```
anyOf:  
- format: unit  
  type: string  
- enum:  
  - n/a  
  type: string
```

## SpectralWidth (metadata)

Name: Spectral Width

Type: Metadata

Schema information:

```
type: number  
unit: Hz
```

## SpectrometerFrequency (metadata)

Name: Spectrometer Frequency

Type: Metadata

Schema information:

```
anyOf:  
- type: number  
  unit: MHz  
- items:  
  maxItems: 2  
  minItems: 1  
  type: number  
  unit: MHz  
  type: array
```

## SpoilingGradientDuration (metadata)

Name: Spoiling Gradient Duration

Type: Metadata

Schema information:

`type: number`  
`unit: s`

## SpoilingGradientMoment (metadata)

Name: Spoiling Gradient Moment

Type: Metadata

Schema information:

`type: number`  
`unit: mT.s/m`

## SpoilingRFPhaseIncrement (metadata)

Name: Spoiling RF Phase Increment

Type: Metadata

Schema information:

`type: number`  
`unit: degree`

## SpoilingState (metadata)

Name: Spoiling State

Type: Metadata

Schema information:

`type: boolean`

## SpoilingType (metadata)

Name: Spoiling Type

Type: Metadata

Allowed values: RF, GRADIENT, COMBINED

Schema information:

`type: string`

## StartTime (metadata)

Name: Start Time

Type: Metadata

Schema information:

`type: number`

`unit: s`

## StationName (metadata)

Name: Station Name

Type: Metadata

Schema information:

`type: string`

## StimulusPresentation (metadata)

Name: Stimulus Presentation

Type: Metadata

Schema information:

`properties:`

`Code:`

`description: '[URI](../common-principles.md#uniform-resource-indicator)`

`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.`

```
'
display_name: Code
format: uri
name: Code
type: string
OperatingSystem:
  description: 'Operating system used to run the stimuli presentation software

  (for formatting recommendations, see examples below this table).

'
display_name: Operating System
name: OperatingSystem
type: string
ScreenDistance:
  anyOf:
  - type: number
    unit: m
  - items:
    type: number
    maxItems: 3
    minItems: 3
    type: array
  - enum:
    - n/a
    type: string
  description: 'Distance between the participant''s eye and the screen. If no screen
    was used, use `n/a`.

    Distance can either be expressed as a single numeric value indicating the shortest
    distance between

    the participant''s eye and the screen, or a three-coordinates array indicating
    the X, Y, Z distances

    between the participant''s eye and the center of the screen.

'
display_name: Screen Distance
name: ScreenDistance
```



```
ScreenOrigin:
  description: 'Location of the spatial coordinates'' origin for the visual stimuli
    presentation,

    described by a list of two keywords such as ("top", "left") if the coordinates

    refer to the top-left corner of the screen, or ("center", "center") if the position

    (0, 0) is at the center or the screen''s extent.

  '
  display_name: Screen Coordinate System's Origin
  items:
    enum:
      - top
      - bottom
      - left
      - right
      - center
    type: string
  maxItems: 2
  minItems: 2
  name: ScreenOrigin
  type: array
ScreenRefreshRate:
  description: 'Refresh rate of the screen (when used), in Hertz (equivalent to
    frames per second, "FPS").

  '
  display_name: Screen Refresh Rate
  name: ScreenRefreshRate
  type: number
  unit: Hz
ScreenResolution:
  anyOf:
    - items:
        type: integer
      maxItems: 2
      minItems: 2
      type: array
```

```
- enum:
  - n/a
  type: string
description: 'Screen resolution in pixel

(for example `[1920, 1200]` for a screen of 1920-width by 1080-height pixels),

if no screen use `n/a`.

`ScreenResolution` is REQUIRED when the experiment included simultaneous eye-tracking

recordings with `SampleCoordinateSystem` matching `"gaze-on-screen"`.

,
display_name: Screen Resolution
name: ScreenResolution
ScreenSize:
  anyOf:
  - items:
    type: number
    unit: m
    maxItems: 2
    minItems: 2
    type: array
  - enum:
    - n/a
    type: string
description: 'Screen size in m, excluding potential screen borders

(for example `[0.472, 0.295]` for a screen of 47.2-width by 29.5-height cm),

if no screen use `n/a`.

`ScreenSize` is REQUIRED when the experiment included simultaneous eye-tracking

recordings with `SampleCoordinateSystem` matching `"gaze-on-screen"`.

,
display_name: Screen Size
name: ScreenSize
```

```
SoftwareName:
  description: 'Name of the software that was used to present the stimuli.

  '
  display_name: Software Name
  name: SoftwareName
  type: string
SoftwareRRID:
  description: '[Research Resource Identifier](https://rrid.site) 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''.
```

`type: object`

## SubjectArtefactDescription (metadata)

Name: Subject Artifact Description

Type: Metadata

Schema information:

`type: string`

## T1map (suffixes)

Name: Longitudinal relaxation time image

Type: Suffix

Format: `<entities>_T1map.<extension>`

Schema information:

`unit: s`

## T1rho (suffixes)

Name: T1 in rotating frame (T1 rho) image

Type: Suffix

Format: `<entities>_T1rho.<extension>`

Schema information:

`unit: s`

## T1w (suffixes)

Name: T1-weighted image

Type: Suffix

Format: `<entities>_T1w.<extension>`

Schema information:

`unit: arbitrary`

## T2map (suffixes)

Name: True transverse relaxation time image

Type: Suffix

Format: `<entities>_T2map.<extension>`

Schema information:

`unit: s`

## T2star (suffixes)

Name: T2\* image

Type: Suffix

Format: `<entities>_T2star.<extension>`

Schema information:

`anyOf:`

- `unit: arbitrary`
- `unit: s`

## T2starmap (suffixes)

Name: Observed transverse relaxation time image

Type: Suffix

Format: `<entities>_T2starmap.<extension>`

Schema information:

`unit: s`

## T2starw (suffixes)

Name: T2star weighted image

Type: Suffix

Format: <entities>\_T2starw.<extension>

Schema information:

**unit:** arbitrary

## T2w (suffixes)

Name: T2-weighted image

Type: Suffix

Format: <entities>\_T2w.<extension>

Schema information:

**unit:** arbitrary

## TB1AFI (suffixes)

Name: TB1AFI

Type: Suffix

Format: <entities>\_TB1AFI.<extension>

## TB1DAM (suffixes)

Name: TB1DAM

Type: Suffix

Format: <entities>\_TB1DAM.<extension>

## TB1EPI (suffixes)

Name: TB1EPI

Type: Suffix

Format: <entities>\_TB1EPI.<extension>

## TB1RFM (suffixes)

Name: TB1RFM

Type: Suffix

Format: <entities>\_TB1RFM.<extension>

## TB1SRGE (suffixes)

Name: TB1SRGE

Type: Suffix

Format: <entities>\_TB1SRGE.<extension>

## TB1TFL (suffixes)

Name: TB1TFL

Type: Suffix

Format: <entities>\_TB1TFL.<extension>

## TB1map (suffixes)

Name: RF transmit field image

Type: Suffix

Format: <entities>\_TB1map.<extension>

Schema information:

**unit:** arbitrary

## TEM (suffixes)

Name: Transmission electron microscopy

Type: Suffix

Format: <entities>\_TEM.<extension>

## TEMP (enums)

Name: TEMP

Type: Enums

Schema information:

```
tags:  
- eeg
```

## TRIG (enums)

Name: TRIG

Type: Enums

Schema information:

```
tags:  
- eeg  
- emg  
- meg  
- ieeg  
- fnirs
```

## TablePosition (metadata)

Name: Table Position

Type: Metadata

Schema information:

```
items:  
  type: number  
  unit: mm  
maxItems: 3  
minItems: 3  
type: array
```



## Talairach (enums)

Name: Talairach

Type: Enums

## TaskDescription (metadata)

Name: Task Description

Type: Metadata

Schema information:

`type: string`

## TaskName (metadata)

Name: Task Name

Type: Metadata

Schema information:

`type: string`

## TermURL (metadata)

Name: TermURL

Type: Metadata

Schema information:

`format: uri`

`type: string`

## ThreeD (enums)

Name: Three-dimensional

Type: Enums

## TimeZero (metadata)

Name: Time Zero

Type: Metadata

Schema information:

```
format: time
type: string
```

## TissueDeformationScaling (metadata)

Name: Tissue Deformation Scaling

Type: Metadata

Schema information:

```
exclusiveMinimum: 0
type: number
```

## TissueOrigin (metadata)

Name: Tissue Origin

Type: Metadata

Allowed values: gray matter, white matter, csf, meninges, macrovascular, microvascular

Schema information:

```
type: string
```

## TotalAcquiredPairs (metadata)

Name: Total Acquired Pairs

Type: Metadata

Schema information:

```
exclusiveMinimum: 0
type: number
```

## TotalReadoutTime (metadata)

Name: Total Readout Time

Type: Metadata

Schema information:

`type: number`  
`unit: s`

## TracerMolecularWeight (metadata)

Name: Tracer Molecular Weight

Type: Metadata

Schema information:

`type: number`

## TracerMolecularWeightUnits (metadata)

Name: Tracer Molecular Weight Units

Type: Metadata

Schema information:

`format: unit`  
`type: string`

## TracerName (metadata)

Name: Tracer Name

Type: Metadata

Schema information:

`type: string`

## TracerRadLex (metadata)

Name: Tracer Rad Lex

Type: Metadata

Schema information:

`type: string`

## TracerRadionuclide (metadata)

Name: Tracer Radionuclide

Type: Metadata

Schema information:

`type: string`

## TracerSNOMED (metadata)

Name: TracerSNOMED

Type: Metadata

Schema information:

`type: string`

## TrackedPointsCount (metadata)

Name: Tracked Points Count

Type: Metadata

Schema information:

`type: number`

`unit: m`

## TrackingSystemName (metadata)

Name: Tracking System Name

Type: Metadata

Schema information:

`type: string`

## Transcriptomic (enums)

Name: Transcriptomic

Type: Enums

## TriggerChannelCount (metadata)

Name: Trigger Channel Count

Type: Metadata

Schema information:

`minimum: 0`  
`type: integer`

## TubingLength (metadata)

Name: Tubing Length

Type: Metadata

Schema information:

`type: number`  
`unit: m`

## TubingType (metadata)

Name: Tubing Type

Type: Metadata

Schema information:

`type: string`

## TwoD (enums)

Name: Two-dimensional

Type: Enums

## TwoPE (suffixes)

Name: 2-photon excitation microscopy

Type: Suffix

Format: <entities>\_2PE.<extension>

## Type (metadata)

Name: Type

Type: Metadata

Allowed values: Brain, Lesion, Face, ROI

Schema information:

`type: string`

## UNCInfant (enums)

Name: UNCInfant

Type: Enums

## UNCInfant0V21 (enums)

Name: UNCInfant0V21

Type: Enums

## UNCInfant0V22 (enums)

Name: UNCInfant0V22

Type: Enums

## UNCInfant0V23 (enums)

Name: UNCInfant0V23

Type: Enums

## UNCInfant1V21 (enums)

Name: UNCInfant1V21

Type: Enums

## UNCInfant1V22 (enums)

Name: UNCInfant1V22

Type: Enums

## UNCInfant1V23 (enums)

Name: UNCInfant1V23

Type: Enums

## UNCInfant2V21 (enums)

Name: UNCInfant2V21

Type: Enums

## UNCInfant2V22 (enums)

Name: UNCInfant2V22

Type: Enums

## UNCInfant2V23 (enums)

Name: UNCInfant2V23

Type: Enums

## UNIT1 (suffixes)

Name: Homogeneous (flat) T1-weighted MP2RAGE image

Type: Suffix

Format: `<entities>_UNIT1.<extension>`

## URL (metadata)

Name: URL

Type: Metadata

Schema information:

```
format: uri
type: string
```

## Units (metadata)

Name: Units

Type: Metadata

Schema information:

```
format: unit
type: string
```

## VEL (enums)

Name: VEL

Type: Enums

Schema information:



```
tags:  
- motion
```

## VELChannelCount (metadata)

Name: Velocity Channel Count

Type: Metadata

Schema information:

```
minimum: 0  
type: integer
```

## VEOG (enums)

Name: VEOG

Type: Enums

Schema information:

```
tags:  
- eeg  
- emg  
- meg  
- ieeg  
- fnirs
```

## VFA (suffixes)

Name: Variable flip angle

Type: Suffix

Format: <entities>\_VFA.<extension>

## VascularCrushing (metadata)

Name: Vascular Crushing

Type: Metadata

Schema information:

`type: boolean`

## VascularCrushingVENC (metadata)

Name: Vascular Crushing VENC

Type: Metadata

Schema information:

```
anyOf:  
- type: number  
  unit: cm/s  
- items:  
  type: number  
  unit: cm/s  
  type: array
```

## Version sense 1 (metadata)

Name: Dataset Version

Type: Metadata

Schema information:

`type: string`

## Version sense 2 (metadata)

Name: Pipeline Version

Type: Metadata

Schema information:

`type: string`

## VisionCorrection (metadata)

Name: Vision correction

Type: Metadata

Schema information:

```
type: string
```

## VolumeAffineMatrix (metadata)

Name: Volume Affine Matrix

Type: Metadata

Schema information:

```
items:
  items:
    type: number
  maxItems: 4
  minItems: 4
  type: array
maxItems: 4
minItems: 4
type: array
```

## VolumeTiming (metadata)

Name: Volume Timing

Type: Metadata

Schema information:

```
items:
  type: number
  unit: s
minItems: 1
type: array
```

## WaterSuppression (metadata)

Name: Water Suppression

Type: Metadata

Schema information:

`type: boolean`

## WaterSuppressionTechnique (metadata)

Name: Water Suppression Technique

Type: Metadata

Schema information:

`type: string`

## WholeBloodAvail (metadata)

Name: Whole Blood Avail

Type: Metadata

Schema information:

`type: boolean`

## WithdrawalRate (metadata)

Name: Withdrawal Rate

Type: Metadata

Schema information:

`type: number`

`unit: mL/s`

## XENON (enums)

Name: XENON

Type: Enums

## XPCT (suffixes)

Name: X-ray Phase-Contrast Tomography

Type: Suffix

Format: <entities>\_XPCT.<extension>

## abbreviation (columns)

Name: Abbreviation

Type: Column

Schema information:

`type: string`

## acq\_time sense 1 (columns)

Name: Scan acquisition time

Type: Column

Schema information:

`format: datetime`

`type: string`

## acq\_time sense 2 (columns)

Name: Session acquisition time

Type: Column

Schema information:

`format: datetime`

`type: string`

## acquisition (entities)

Name: Acquisition

Type: Entity

Schema information:

`format: label`  
`type: string`

## age (columns)

Name: Subject age

Type: Column

## amniotic\_fluid (enums)

Name: amniotic fluid

Type: Enums

## anat (datatypes)

Name: Anatomical Magnetic Resonance Imaging

Type: Datatype

## angio (suffixes)

Name: Angiogram

Type: Suffix

Format: `<entities>_angio.<extension>`

## asl (suffixes)

Name: Arterial Spin Labeling

Type: Suffix

Format: `<entities>_asl.<extension>`

## aslcontext (suffixes)

Name: Arterial Spin Labeling Context

Type: Suffix

Format: <entities>\_aslcontext.<extension>

## asllabeling (suffixes)

Name: ASL Labeling Screenshot

Type: Suffix

Format: <entities>\_asllabeling.<extension>

## atlas (common\_principles)

Name: Atlas

Type: Common Principle

## atlas (entities)

Name: Atlas

Type: Entity

Schema information:

`format: label`

`type: string`

## ave (extensions)

Name: AVE

Type: Extension

Format: <entities>\_<suffix>.ave

## bad (enums)

Name: bad

Type: Enums

## balanced (enums)

Name: balanced

Type: Enums

## bdf (extensions)

Name: Biosemi Data Format

Type: Extension

Format: <entities>\_<suffix>.bdf

## beh (datatypes)

Name: Behavioral Data

Type: Datatype

## beh (modalities)

Name: Behavioral experiments

Type: Modalities

## beh (suffixes)

Name: Behavioral recording

Type: Suffix

Format: <entities>\_beh.<extension>



## bids\_uri (formats)

Name: BIDS uniform resource indicator

Type: Format

Regular expression: `bids: [0-9a-zA-Z/#:?\_-.]+`

## bile (enums)

Name: Bile

Type: Enums

## blood (enums)

Name: blood

Type: Enums

## blood (suffixes)

Name: Blood recording data

Type: Suffix

Format: `<entities>_blood.<extension>`

## bold (suffixes)

Name: Blood-Oxygen-Level Dependent image

Type: Suffix

Format: `<entities>_bold.<extension>`

## boolean (formats)

Name: Boolean

Type: Format

Regular expression: `(true|false)`

## brain (enums)

Name: brain

Type: Enums

## breast\_milk (enums)

Name: breast milk

Type: Enums

## bval (extensions)

Name: FSL-Format Gradient Amplitudes

Type: Extension

Format: `<entities>_<suffix>.bval`

## bvec (extensions)

Name: FSL-Format Gradient Directions

Type: Extension

Format: `<entities>_<suffix>.bvec`

## calibration (enums)

Name: calibration

Type: Enums

## cardiac (columns)

Name: Cardiac measurement

Type: Column

## cbf (enums)

Name: cbf

Type: Enums

## cbv (suffixes)

Name: Cerebral blood volume image

Type: Suffix

Format: <entities>\_cbv.<extension>

## ceagent (entities)

Name: Contrast Enhancing Agent

Type: Entity

Schema information:

```
format: label
type: string
```

## cell\_free\_sample (enums)

Name: cell-free sample

Type: Enums

## cell\_line (enums)

Name: cell line

Type: Enums

## channel (columns)

Name: Channel

Type: Column

Schema information:

`type: string`

## channels (suffixes)

Name: Channels File

Type: Suffix

Format: `<entities>_channels.<extension>`

## chn (extensions)

Name: KRISS CHN

Type: Extension

Format: `<entities>_<suffix>.chn`

## chunk (entities)

Name: Chunk

Type: Entity

Schema information:

`format: index`

`type: string`

## cloning\_host (enums)

Name: cloning host

Type: Enums

## code (files)

Name: Code

Type: Files And Directories

Schema information:

`file_type: directory`

## cohort (entities)

Name: Cohort

Type: Entity

Schema information:

`format: label`

`type: string`

## colFA (suffixes)

Name: Colored Fractional Anisotropy image

Type: Suffix

Format: `<entities>_colFA.<extension>`

## color (columns)

Name: Color label

Type: Column

Schema information:

`type: string`

`unit: hexadecimal`

## component (columns)

Name: Component

Type: Column

Allowed values: x, y, z, quat\_x, quat\_y, quat\_z, quat\_w

Schema information:

`type: string`

## con (extensions)

Name: KIT/Yokogawa/Ricoh Continuous Data

Type: Extension

Format: `<entities>_<suffix>.con`

## continuous (enums)

Name: Continuous recording

Type: Enums

## control (enums)

Name: control

Type: Enums

## coordinate\_system (columns)

Name: Coordinate System

Type: Column

Schema information:

`type: string`

## coordsystem (suffixes)

Name: Coordinate System File

Type: Suffix

Format: `<entities>_coordsystem.<extension>`

## crosstalk (enums)

Name: crosstalk

Type: Enums

## csf (enums)

Name: CSF

Type: Enums

## dat (extensions)

Name: MEG Fine-Calibration Format

Type: Extension

Format: `<entities>_<suffix>.dat`

## data\_acquisition (common\_principles)

Name: Data acquisition

Type: Common Principle

## data\_type (common\_principles)

Name: Data type

Type: Common Principle

## dataset (common\_principles)

Name: Dataset

Type: Common Principle

## dataset\_description (files)

Name: Dataset Description

Type: Files And Directories

Schema information:

`file_type:` `regular`

## dataset\_relative (formats)

Name: Path relative to the BIDS dataset directory

Type: Format

Regular expression: `(?!/)[0-9a-zA-Z+/_\-.]+`

## date (formats)

Name: Date

Type: Format

Regular expression: `[0-9]{4}-[0-9]{2}-[0-9]{2}([A-Z]{2,4})?`

## datetime (formats)

Name: Datetime

Type: Format

Regular expression: `[0-9]{4}-(?:0[1-9]|1[0-2])-(?:0[1-9]|[12][0-9]|3[01])T(?:2[0-3]|[01][0-9]):[0-5][0-9]:(?:[0-5][0-9]|60)(?:\.[0-9]{1,6})?(?:Z|[-+](?:2[0-3]|`

## defacemask (suffixes)

Name: Defacing Mask

Type: Suffix

Format: `<entities>_defacemask.<extension>`



## deltam (enums)

Name: deltam

Type: Enums

## density (entities)

Name: Density

Type: Entity

Schema information:

`format:` label

`type:` string

## deprecated (common\_principles)

Name: DEPRECATED

Type: Common Principle

## derivative (enums)

Name: derivative

Type: Enums

## derivatives (files)

Name: Derivative data

Type: Files And Directories

Schema information:

`file_type:` directory

## derived\_from (columns)

Name: Derived from

Type: Column

Schema information:

`type: string`

## desc\_id (columns)

Name: Description Label

Type: Column

Schema information:

`type: string`

## description (entities)

Name: Description

Type: Entity

Schema information:

`format: label`

`type: string`

## description (suffixes)

Name: Description file

Type: Suffix

Format: `<entities>_description.<extension>`

## description sense 1 (columns)

Name: Description

Type: Column

Schema information:

`type: string`

## description sense 2 (columns)

Name: Description

Type: Column

Schema information:

`type: string`

## description sense 3 (columns)

Name: Description

Type: Column

Schema information:

`type: string`

## descriptions (suffixes)

Name: Description Entity Definitions

Type: Suffix

Format: `<entities>_descriptions.<extension>`

## detector (enums)

Name: detector

Type: Enums

## detector sense 1 (columns)

Name: Detector Name

Type: Column

Schema information:

`type: string`

## detector\_type (columns)

Name: Detector Type

Type: Column

Schema information:

`type: string`

## dimension (columns)

Name: Dimension

Type: Column

Schema information:

`type: string`

## direction (entities)

Name: Phase-Encoding Direction

Type: Entity

Schema information:

`format: label`

`type: string`

## discontinuous (enums)

Name: Discontinuous recording

Type: Enums

## dlabelnii (extensions)

Name: CIFTI-2 Dense Label File

Type: Extension

Format: `<entities>_<suffix>.dlabel.nii`

## double\_coil (enums)

Name: double-coil

Type: Enums

## dseg (suffixes)

Name: Discrete Segmentation

Type: Suffix

Format: `<entities>_dseg.<extension>`

## duration (columns)

Name: Event duration

Type: Column

Schema information:

```
minimum: 0
type: number
unit: s
```

## dwi (datatypes)

Name: Diffusion-Weighted Imaging

Type: Datatype

## dwi (suffixes)

Name: Diffusion-weighted image

Type: Suffix

Format: <entities>\_dwi.<extension>

## echo (entities)

Name: Echo

Type: Entity

Schema information:

format: index

type: string

## edf (extensions)

Name: European Data Format

Type: Extension

Format: <entities>\_<suffix>.edf

## eeg (datatypes)

Name: Electroencephalography

Type: Datatype

## eeg (extensions)

Name: BrainVision Binary Data

Type: Extension

Format: <entities>\_<suffix>.eeg

## eeg (modalities)

Name: Electroencephalography

Type: Modalities

## eeg (suffixes)

Name: Electroencephalography

Type: Suffix

Format: `<entities>_eeg.<extension>`

## electrodes (suffixes)

Name: Electrodes

Type: Suffix

Format: `<entities>_electrodes.<extension>`

## emg (datatypes)

Name: Electromyography

Type: Datatype

## emg (modalities)

Name: Electromyography

Type: Modalities

## emg (suffixes)

Name: Electromyography

Type: Suffix

Format: `<entities>_emg.<extension>`

## epi (suffixes)

Name: EPI

Type: Suffix

Format: <entities>\_epi.<extension>

## epoched (enums)

Name: Epoched recording

Type: Enums

## event (common\_principles)

Name: Event

Type: Common Principle

## events (suffixes)

Name: Events

Type: Suffix

Format: <entities>\_events.<extension>

## ex\_vivo (enums)

Name: ex vivo

Type: Enums

## expADC (suffixes)

Name: Exponential ADC

Type: Suffix

Format: <entities>\_expADC.<extension>



## extension (common\_principles)

Name: File extension

Type: Common Principle

## fdt (extensions)

Name: EEGLAB FDT

Type: Extension

Format: <entities>\_<suffix>.fdt

## fieldmap (suffixes)

Name: Fieldmap

Type: Suffix

Format: <entities>\_fieldmap.<extension>

## fif (extensions)

Name: Functional Imaging File Format

Type: Extension

Format: <entities>\_<suffix>.fif

## file\_relative (formats)

Name: Path relative to the parent file

Type: Format

Regular expression: (?!/)[0-9a-zA-Z+/\_\-.]+

## filename (columns)

Name: Filename

Type: Column

Schema information:

`format:` participant\_relative  
`type:` string

## flip (entities)

Name: Flip Angle

Type: Entity

Schema information:

`format:` index  
`type:` string

## fmap (datatypes)

Name: Field maps

Type: Datatype

## fsLR (enums)

Name: fsLR

Type: Enums

## fsaverage (enums)

Name: fsaverage

Type: Enums

## fsaverage3 (enums)

Name: fsaverage3

Type: Enums

## fsaverage4 (enums)

Name: fsaverage4

Type: Enums

## fsaverage5 (enums)

Name: fsaverage5

Type: Enums

## fsaverage6 (enums)

Name: fsaverage6

Type: Enums

## fsaverageSym (enums)

Name: fsaverageSym

Type: Enums

## fsaveragesym (enums)

Name: fsaveragesym

Type: Enums

## func (datatypes)

Name: Task-Based Magnetic Resonance Imaging

Type: Datatype

## genetic\_info (files)

Name: Genetic Information

Type: Files And Directories

Schema information:

`file_type:` `regular`

## good (enums)

Name: good

Type: Enums

## gray\_matter (enums)

Name: gray matter

Type: Enums

## group sense 1 (columns)

Name: Channel group

Type: Column

Schema information:

`type:` `string`

## group sense 2 (columns)

Name: Electrode or channel group

Type: Column

Schema information:

`anyOf:`  
`- type:` `string`  
`- type:` `number`

## handedness (columns)

Name: Subject handedness

Type: Column

Allowed values: left, l, L, LEFT, Left, right, r, R, RIGHT, Right, ambidextrous, a, A, AMBIDEXTROUS, Ambidextrous

## headshape (suffixes)

Name: Headshape File

Type: Suffix

Format: <entities>\_headshape.<extension>

## hed\_version (formats)

Name: HED Version

Type: Format

Regular expression: `(?:[a-zA-Z]+:)?(?:[a-zA-Z]+_)?(?:0|[1-9][0-9]*)\.(?:0|[1-9][0-9]*)\.(?:0|[1-9][0-9]*)`

## hemisphere (columns)

Name: Electrode hemisphere

Type: Column

Allowed values: L, R

Schema information:

`type: string`

## hemisphere (entities)

Name: Hemisphere

Type: Entity

Allowed values: L, R

Schema information:

```
format: label  
type: string
```

## high\_cutoff (columns)

Name: High cutoff

Type: Column

Schema information:

```
minimum: 0  
type: number  
unit: Hz
```

## hplc\_recovery\_fractions (columns)

Name: HPLC recovery fractions

Type: Column

Schema information:

```
type: number  
unit: arbitrary
```

## i (enums)

Name: i

Type: Enums

## iEEGCoordinateProcessingDescription (metadata)

Name: iEEG Coordinate Processing Description

Type: Metadata

Schema information:

```
type: string
```

## iEEGCoordinateProcessingReference (metadata)

Name: iEEG Coordinate Processing Reference

Type: Metadata

Schema information:

`type: string`

## iEEGCoordinateSystem (metadata)

Name: iEEG Coordinate System

Type: Metadata

Allowed values: Pixels, ACPC, ScanRAS, Other, ICBM452AirSpace, ICBM452Warp5Space, IXI549Space, fsaverage, fsaverageSym, fsLR, MNIColín27, 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

Schema information:

`type: string`

## iEEGCoordinateSystemDescription (metadata)

Name: iEEG Coordinate System Description

Type: Metadata

Schema information:

`type: string`

## iEEGCoordinateUnits (metadata)

Name: iEEG Coordinate Units

Type: Metadata

Allowed values: pixels, m, mm, cm, n/a

Schema information:

`type: string`

## iEEGElectrodeGroups (metadata)

Name: iEEG Electrode Groups

Type: Metadata

Schema information:

`type: string`

## iEEGGround (metadata)

Name: iEEG Ground

Type: Metadata

Schema information:

`type: string`

## iEEGPlacementScheme (metadata)

Name: iEEG Placement Scheme

Type: Metadata

Schema information:

`type: string`

## iEEGReference (metadata)

Name: iEEG Reference

Type: Metadata

Schema information:

`type: string`

## iMinus (enums)

Name: i-

Type: Enums



## ieeg (datatypes)

Name: Intracranial electroencephalography

Type: Datatype

## ieeg (modalities)

Name: Intracranial Electroencephalography

Type: Modalities

## ieeg (suffixes)

Name: Intracranial Electroencephalography

Type: Suffix

Format: <entities>\_ieeg.<extension>

## imaginary (enums)

Name: Imaginary

Type: Enums

## impedance (columns)

Name: Electrode impedance

Type: Column

Schema information:

**type:** number

**unit:** kOhm

## in\_vitro (enums)

Name: in vitro

Type: Enums

## in\_vitro\_differentiated\_cells (enums)

Name: in vitro differentiated cells

Type: Enums

## in\_vivo (enums)

Name: in vivo

Type: Enums

## index (columns)

Name: Label index

Type: Column

Schema information:

`type: integer`

## index (common\_principles)

Name: index

Type: Common Principle

## index (formats)

Name: Index

Type: Format

Regular expression: `[0-9]+`

## individual (enums)

Name: individual

Type: Enums

## inplaneT1 (suffixes)

Name: Inplane T1

Type: Suffix

Format: <entities>\_inplaneT1.<extension>

Schema information:

`unit:` `arbitrary`

## inplaneT2 (suffixes)

Name: Inplane T2

Type: Suffix

Format: <entities>\_inplaneT2.<extension>

Schema information:

`unit:` `arbitrary`

## integer (formats)

Name: Integer

Type: Format

Regular expression: `*[+-]?\d+ *`

## interelectrode\_distance (columns)

Name: Interelectrode Distance

Type: Column

Schema information:

`type:` `number`

`unit:` `mm`

## inversion (entities)

Name: Inversion Time

Type: Entity

Schema information:

`format: index`  
`type: string`

## j (enums)

Name: j

Type: Enums

## jMinus (enums)

Name: j-

Type: Enums

## jpg (extensions)

Name: Joint Photographic Experts Group Format

Type: Extension

Format: `<entities>_<suffix>.jpg`

## json (extensions)

Name: JavaScript Object Notation

Type: Extension

Format: `<entities>_<suffix>.json`

## k (enums)

Name: k

Type: Enums

## kMinus (enums)

Name: k-

Type: Enums

## kdf (extensions)

Name: KRISS KDF

Type: Extension

Format: <entities>\_<suffix>.kdf

## label (common\_principles)

Name: label

Type: Common Principle

## label (entities)

Name: Label

Type: Entity

Schema information:

`format: label`

`type: string`

## label (enums)

Name: label

Type: Enums

## label (formats)

Name: Label

Type: Format

Regular expression: `[0-9a-zA-Z+]+`

## labelgii (extensions)

Name: GIFTI label/annotation file

Type: Extension

Format: `<entities>_<suffix>.label.gii`

## left\_hand (enums)

Name: left-hand

Type: Enums

## left\_hemisphere (enums)

Name: Left Hemisphere

Type: Enums

## low\_cutoff (columns)

Name: Low cutoff

Type: Column

Schema information:

`type: number`  
`unit: Hz`

## m0scan (enums)

Name: m0scan

Type: Enums

## m0scan (suffixes)

Name: M0 image

Type: Suffix

Format: <entities>\_m0scan.<extension>

## macrovascular (enums)

Name: macrovascular

Type: Enums

## magnitude (enums)

Name: Magnitude

Type: Enums

## magnitude (suffixes)

Name: Magnitude

Type: Suffix

Format: <entities>\_magnitude.<extension>

## magnitude1 (suffixes)

Name: Magnitude

Type: Suffix

Format: <entities>\_magnitude1.<extension>

## magnitude2 (suffixes)

Name: Magnitude

Type: Suffix

Format: <entities>\_magnitude2.<extension>

## manufacturer (columns)

Name: Manufacturer

Type: Column

Schema information:

`type: string`

## mapping (columns)

Name: Label mapping

Type: Column

Schema information:

`type: integer`

## markers (suffixes)

Name: MEG Sensor Coil Positions

Type: Suffix

Format: <entities>\_markers.<extension>

## mask (suffixes)

Name: Binary Mask

Type: Suffix

Format: <entities>\_mask.<extension>



## matches (metaentities)

Name: matches

Type: Meta-Entity

## material (columns)

Name: Electrode material

Type: Column

Schema information:

`type: string`

## md (extensions)

Name: Markdown

Type: Extension

Format: `<entities>_<suffix>.md`

## mefd (extensions)

Name: Multiscale Electrophysiology File Format Version 3.0

Type: Extension

Format: `<entities>_<suffix>.mefd/`

## meg (datatypes)

Name: Magnetoencephalography

Type: Datatype

## meg (modalities)

Name: Magnetoencephalography

Type: Modalities

## meg (suffixes)

Name: Magnetoencephalography

Type: Suffix

Format: <entities>\_meg.<extension>

## meninges (enums)

Name: meninges

Type: Enums

## message (columns)

Name: Message

Type: Column

Schema information:

`type: string`

## metabolite\_parent\_fraction (columns)

Name: Metabolite parent fraction

Type: Column

Schema information:

`maximum: 1`

`minimum: 0`

`type: number`

## metabolite\_polar\_fraction (columns)

Name: Metabolite polar fraction

Type: Column

Schema information:

```
maximum: 1  
minimum: 0  
type: number
```

## mhd (extensions)

Name: ITAB Binary Header

Type: Extension

Format: <entities>\_<suffix>.mhd

## micr (datatypes)

Name: Microscopy

Type: Datatype

## micr (modalities)

Name: Microscopy

Type: Modalities

## microvascular (enums)

Name: microvascular

Type: Enums

## mixed (enums)

Name: mixed

Type: Enums

## modality (common\_principles)

Name: Modality

Type: Common Principle

## modality (entities)

Name: Corresponding Modality

Type: Entity

Schema information:

`format: label`

`type: string`

## motion (datatypes)

Name: Motion

Type: Datatype

## motion (modalities)

Name: Motion

Type: Modalities

## motion (suffixes)

Name: Motion

Type: Suffix

Format: `<entities>_motion.<extension>`

## mri (modalities)

Name: Magnetic Resonance Imaging

Type: Modalities

## mrk (extensions)

Name: MRK

Type: Extension

Format: <entities>\_<suffix>.mrk

## mrs (datatypes)

Name: Magnetic Resonance Spectroscopy

Type: Datatype

## mrs (modalities)

Name: Magnetic Resonance Spectroscopy

Type: Modalities

## mrsl (suffixes)

Name: Magnetic resonance spectroscopy imaging

Type: Suffix

Format: <entities>\_mrsl.<extension>

## mrsref (suffixes)

Name: MRS reference acquisition

Type: Suffix

Format: <entities>\_mrsref.<extension>

## mtransfer (entities)

Name: Magnetization Transfer

Type: Entity

Allowed values: on, off

Schema information:

`format: label`  
`type: string`

## name sense 1 (columns)

Name: Channel name

Type: Column

Schema information:

`type: string`

## name sense 2 (columns)

Name: Electrode name

Type: Column

Schema information:

`type: string`

## name sense 3 (columns)

Name: Optode name

Type: Column

Schema information:

`type: string`

## name sense 4 (columns)

Name: Label name

Type: Column

Schema information:

`type: string`

## nii (extensions)

Name: NIfTI

Type: Extension

Format: `<entities>_<suffix>.nii`

## nii\_gz (extensions)

Name: Compressed NIfTI

Type: Extension

Format: `<entities>_<suffix>.nii.gz`

## nirs (datatypes)

Name: Near-Infrared Spectroscopy

Type: Datatype

## nirs (modalities)

Name: Near-Infrared Spectroscopy

Type: Modalities

## nirs (suffixes)

Name: Near Infrared Spectroscopy

Type: Suffix

Format: `<entities>_nirs.<extension>`

## noRF (enums)

Name: noRF

Type: Enums

## noRF (suffixes)

Name: No Radio Frequency Excitation Scan

Type: Suffix

Format: <entities>\_noRF.<extension>

## notch (columns)

Name: Notch frequencies

Type: Column

Schema information:

`type: string`

## nucleus (entities)

Name: Nucleus

Type: Entity

Schema information:

`format: label`

`type: string`

## number (formats)

Name: Number

Type: Format

Regular expression: `*[+-]?([0-9]+([.][0-9]*)?|[.][0-9]+)([eE][+-]?[0-9]+)? *`



## nwb (extensions)

Name: Neurodata Without Borders Format

Type: Extension

Format: <entities>\_<suffix>.nwb

## off sense 1 (enums)

Name: Off

Type: Enums

## on sense 1 (enums)

Name: On

Type: Enums

## onset sense 1 (columns)

Name: Event onset

Type: Column

Schema information:

**type:** number

**unit:** s

## onset sense 2 (columns)

Name: Onset of events in physiological recordings

Type: Column

Schema information:

**type:** number

## optodes (suffixes)

Name: Optodes

Type: Suffix

Format: `<entities>_optodes.<extension>`

## organoid (enums)

Name: organoid

Type: Enums

## orig (enums)

Name: orig

Type: Enums

## other\_biospecimen (enums)

Name: other biospecimen

Type: Enums

## part (entities)

Name: Part

Type: Entity

Allowed values: `mag`, `phase`, `real`, `imag`

Schema information:

`format:` `label`

`type:` `string`

## participant\_id (columns)

Name: Participant ID

Type: Column

Schema information:

`type:` `string`

## participant\_relative (formats)

Name: Path relative to the participant directory

Type: Format

Regular expression: `(?!/)(?!sub-)[0-9a-zA-Z+/_\-.]+`

## participants (files)

Name: Participant Information

Type: Files And Directories

Schema information:

`file_type:` `regular`

## pathology (columns)

Name: Pathology

Type: Column

## perf (datatypes)

Name: Perfusion imaging

Type: Datatype

## pet (datatypes)

Name: Positron Emission Tomography

Type: Datatype

## pet (modalities)

Name: Positron Emission Tomography

Type: Modalities

## pet (suffixes)

Name: Positron Emission Tomography

Type: Suffix

Format: <entities>\_pet.<extension>

## phase (enums)

Name: Phase

Type: Enums

## phase (suffixes)

Name: Phase image

Type: Suffix

Format: <entities>\_phase.<extension>

Schema information:

```
anyOf:  
- unit: arbitrary  
- unit: rad
```

## phase1 (suffixes)

Name: Phase

Type: Suffix

Format: <entities>\_phase1.<extension>

## phase2 (suffixes)

Name: Phase

Type: Suffix

Format: <entities>\_phase2.<extension>

## phasediff (suffixes)

Name: Phase-difference

Type: Suffix

Format: <entities>\_phasediff.<extension>

## phenotype (datatypes)

Name: Phenotype

Type: Datatype

## phenotype (files)

Name: Phenotype

Type: Files And Directories

Schema information:

`file_type:` `directory`

## photo (suffixes)

Name: Photo File

Type: Suffix

Format: `<entities>_photo.<extension>`

## physio (suffixes)

Name: Physiological recording

Type: Suffix

Format: `<entities>_physio.<extension>`

## physioevents (suffixes)

Name: Physiological events and asynchronous data

Type: Suffix

Format: `<entities>_physioevents.<extension>`

## pixels (enums)

Name: pixels

Type: Enums

## placement sense 1 (columns)

Name: Placement

Type: Column

Schema information:

`type: string`

## placement\_description (columns)

Name: Placement Scheme Description

Type: Column

Schema information:

`type: string`

## placement\_scheme (columns)

Name: Placement Scheme

Type: Column

Allowed values: `measured`, `other`

Schema information:

`type: string`

## plasma\_radioactivity (columns)

Name: Plasma radioactivity

Type: Column

Schema information:

`type: number`

## png (extensions)

Name: Portable Network Graphics

Type: Extension

Format: `<entities>_<suffix>.png`

## pos (extensions)

Name: Head Point Position

Type: Extension

Format: <entities>\_<suffix>.pos

## primary\_cell (enums)

Name: primary cell

Type: Enums

## probseg (suffixes)

Name: Probabilistic Segmentation

Type: Suffix

Format: <entities>\_probseg.<extension>

## processing (entities)

Name: Processed (on device)

Type: Entity

Schema information:

format: label

type: string

## pupil\_size (columns)

Name: Pupil size

Type: Column

Schema information:

type: number

## quat\_w (enums)

Name: quat\_w



Type: Enums

## quat\_x (enums)

Name: quat\_x

Type: Enums

## quat\_y (enums)

Name: quat\_y

Type: Enums

## quat\_z (enums)

Name: quat\_z

Type: Enums

## raw (enums)

Name: raw

Type: Enums

## raw (extensions)

Name: RAW

Type: Extension

Format: `<entities>_<suffix>.raw`

## real (enums)

Name: Real

Type: Enums

## reconstruction (entities)

Name: Reconstruction

Type: Entity

Schema information:

`format: label`  
`type: string`

## recording (entities)

Name: Recording

Type: Entity

Schema information:

`format: label`  
`type: string`

## reference sense 1 (columns)

Name: Electrode reference

Type: Column

Schema information:

`type: string`

## reference sense 2 (columns)

Name: Reference electrode

Type: Column

Schema information:

`type: string`

## reference\_sense 3 (columns)

Name: Electrode reference

Type: Column

Schema information:

`type:` `string`

## reference\_frame (columns)

Name: Reference frame

Type: Column

Schema information:

`type:` `string`

## resolution (entities)

Name: Resolution

Type: Entity

Schema information:

`format:` `label`

`type:` `string`

## respiratory (columns)

Name: Respiratory measurement

Type: Column

## response\_time (columns)

Name: Response time

Type: Column

Schema information:

`type: number`  
`unit: s`

## right\_hand (enums)

Name: right-hand

Type: Enums

## right\_hemisphere (enums)

Name: Right Hemisphere

Type: Enums

## rrid (formats)

Name: Research resource identifier

Type: Format

Regular expression: `RRID: .+_.+`

## rst (extensions)

Name: reStructuredText

Type: Extension

Format: `<entities>_<suffix>.rst`

## run (common\_principles)

Name: Run

Type: Common Principle

## run (entities)

Name: Run

Type: Entity

Schema information:

`format: index`  
`type: string`

## saliva (enums)

Name: saliva

Type: Enums

## sample (common\_principles)

Name: Sample

Type: Common Principle

## sample (entities)

Name: Sample

Type: Entity

Schema information:

`format: label`  
`type: string`

## sample\_id (columns)

Name: Sample ID

Type: Column

Schema information:

`type: string`

## sample\_type (columns)

Name: Sample type

Type: Column

Allowed values: cell line, in vitro differentiated cells, primary cell, cell-free sample, cloning host, tissue, whole organisms, organoid, technical sample

Schema information:

`type: string`

## samples (files)

Name: Sample Information

Type: Files And Directories

Schema information:

`file_type: regular`

## sampling\_frequency (columns)

Name: Channel sampling frequency

Type: Column

Schema information:

`type: number`

`unit: Hz`

## sbref (suffixes)

Name: Single-band reference image

Type: Suffix

Format: `<entities>_sbref.<extension>`

## scale (entities)

Name: Scale

Type: Entity

Schema information:

`format: label`

`type: string`

## scanner (enums)

Name: scanner

Type: Enums

## scans (suffixes)

Name: Scans file

Type: Suffix

Format: `<entities>_scans.<extension>`

## segmentation (entities)

Name: Segmentation

Type: Entity

Schema information:

`format: label`

`type: string`

## session (common\_principles)

Name: Session

Type: Common Principle

## session (entities)

Name: Session

Type: Entity

Schema information:

```
format: label  
type: string
```

## session\_id (columns)

Name: Session ID

Type: Column

Schema information:

```
type: string
```

## sessions (suffixes)

Name: Sessions file

Type: Suffix

Format: <entities>\_sessions.<extension>

## set (extensions)

Name: EEGLAB SET

Type: Extension

Format: <entities>\_<suffix>.set

## sex (columns)

Name: Sex

Type: Column

Allowed values: F, FEMALE, Female, f, female, M, MALE, Male, m, male, O, OTHER, Other, o, other



## short\_channel (columns)

Name: Short Channel

Type: Column

Schema information:

`type: boolean`

## signal\_electrode (columns)

Name: Signal electrode

Type: Column

Schema information:

`type: string`

## single\_coil (enums)

Name: single-coil

Type: Enums

## size (columns)

Name: Electrode size

Type: Column

Schema information:

`type: number`

`unit: mm^2`

## snirf (extensions)

Name: Shared Near Infrared Spectroscopy Format

Type: Extension

Format: `<entities>_<suffix>.snirf`

## software\_filters (columns)

Name: Software filters

Type: Column

Schema information:

`type: string`

## source (enums)

Name: source

Type: Enums

## source\_sense\_1 (columns)

Name: Source name

Type: Column

Schema information:

`type: string`

## source\_sense\_2 (columns)

Name: Source type

Type: Column

Schema information:

`type: string`

## source\_entities (metaentities)

Name: source entities

Type: Meta-Entity

## sourcedata (files)

Name: Source data

Type: Files And Directories

Schema information:

`file_type:` `directory`

## space (common\_principles)

Name: Space

Type: Common Principle

## space (entities)

Name: Space

Type: Entity

Schema information:

`format:` `label`

`type:` `string`

## species (columns)

Name: Species

Type: Column

## split (entities)

Name: Split

Type: Entity

Schema information:

`format:` `index`

`type:` `string`

## sqd (extensions)

Name: SQD

Type: Extension

Format: <entities>\_<suffix>.sqd

## stain (entities)

Name: Stain

Type: Entity

Schema information:

`format: label`

`type: string`

## status (columns)

Name: Channel status

Type: Column

Allowed values: good, bad

Schema information:

`type: string`

## status\_description (columns)

Name: Channel status description

Type: Column

Schema information:

`type: string`

## stim (suffixes)

Name: Continuous recording

Type: Suffix

Format: <entities>\_stim.<extension>

## stim\_file (columns)

Name: Stimulus file

Type: Column

Schema information:

```
format: stimuli_relative  
type: string
```

## stimuli (files)

Name: Stimulus files

Type: Files And Directories

Schema information:

```
file_type: directory
```

## stimuli\_relative (formats)

Name: Path relative to the stimuli directory

Type: Format

Regular expression: (?!/)(?!stimuli/)[0-9a-zA-Z+/\_\-.]+

## strain (columns)

Name: Strain

Type: Column

## strain\_rrid (columns)

Name: Strain RRID

Type: Column

Schema information:

`format:` rrid

`type:` string

## string (formats)

Name: String

Type: Format

Regular expression: .\*

## study sense 1 (enums)

Name: study

Type: Enums

## study sense 2 (enums)

Name: study

Type: Enums

## subject (common\_principles)

Name: Subject

Type: Common Principle

## subject (entities)

Name: Subject

Type: Entity

Schema information:

```
format: label  
type: string
```

## suffix (common\_principles)

Name: suffix

Type: Common Principle

## svs (suffixes)

Name: Single-voxel spectroscopy

Type: Suffix

Format: <entities>\_svs.<extension>

## target\_muscle (columns)

Name: Target muscle

Type: Column

Schema information:

```
type: string
```

## task (common\_principles)

Name: Task

Type: Common Principle

## task (entities)

Name: Task

Type: Entity

Schema information:

`format: label`  
`type: string`

## technical\_sample (enums)

Name: technical sample

Type: Enums

## template (common\_principles)

Name: Template

Type: Common Principle

## template (entities)

Name: Template

Type: Entity

Schema information:

`format: label`  
`type: string`

## template\_x (columns)

Name: X template position

Type: Column

Schema information:

`type: number`

## template\_y (columns)

Name: Y template position

Type: Column



Schema information:

`type: number`

## template\_z (columns)

Name: Z template position

Type: Column

Schema information:

`type: number`

## tif (extensions)

Name: Tag Image File Format

Type: Extension

Format: `<entities>_<suffix>.tif`

## time (columns)

Name: Time

Type: Column

Schema information:

`type: number`

`unit: s`

## time (formats)

Name: Time

Type: Format

Regular expression: `(?:2[0-3] | [01]?[0-9]):[0-5][0-9]:[0-5][0-9]`

## timestamp sense 1 (columns)

Name: Eye-tracking recording timestamp

Type: Column

Schema information:

`type: number`

## tissue (enums)

Name: tissue

Type: Enums

## trace (suffixes)

Name: Trace-weighted diffusion image

Type: Suffix

Format: `<entities>_trace.<extension>`

## tracer (entities)

Name: Tracer

Type: Entity

Schema information:

`format: label`

`type: string`

## tracked\_point sense 1 (columns)

Name: Tracked point channel

Type: Column

Schema information:

`type: string`

## tracksys (entities)

Name: Tracking System

Type: Entity

Schema information:

`format:` `label`

`type:` `string`

## trg (extensions)

Name: KRISS TRG

Type: Extension

Format: `<entities>_<suffix>.trg`

## trial\_type (columns)

Name: Trial type

Type: Column

Schema information:

`type:` `string`

## trigger (columns)

Name: Trigger

Type: Column

## tsv (extensions)

Name: Tab-Delimited

Type: Extension

Format: `<entities>_<suffix>.tsv`

## tsv\_gz (extensions)

Name: Compressed Tab-Delimited

Type: Extension

Format: <entities>\_<suffix>.tsv.gz

## txt (extensions)

Name: Text

Type: Extension

Format: <entities>\_<suffix>.txt

## type sense 1 (columns)

Name: Channel type

Type: Column

Allowed values: ACCEL, ADC, ANGACCEL, AUDIO, DAC, DBS, ECG, ECOG, EEG, EMG, EOG, EYEGAZE, FITERR, GSR, GYRO, HEOG, HLU, JNTANG, LATENCY, MAGN, MEGGRADAXIAL, MEGGRADPLANAR, MEGMAG, MEGOTHER, MEGREFGRADAXIAL, MEGREFGRADPLANAR, MEGREFMAG, MISC, NIRSCWAMPLITUDE, NIRSCWFLUORESCENSEAMPLITUDE, NIRSCWHBO, NIRSCWHBR, NIRSCWMUA, NIRSCWOPTICALDENSITY, ORNT, OTHER, PD, POS, PPG, PUPIL, REF, RESP, SEEG, SYSCLOCK, TEMP, TRIG, VEL, VEOG

Schema information:

type: string

## type sense 2 (columns)

Name: Electrode type

Type: Column

Schema information:

type: string

## type sense 3 (columns)

Name: Type

Type: Column

Allowed values: source, detector

Schema information:

`type: string`

## uCT (suffixes)

Name: Micro-CT

Type: Suffix

Format: <entities>\_uCT.<extension>

## unbalanced (enums)

Name: unbalanced

Type: Enums

## unit (formats)

Name: A standardized unit

Type: Format

Regular expression: .\*

## units sense 1 (columns)

Name: Units

Type: Column

Schema information:

`format: unit`

`type: string`

## units sense 2 (columns)

Name: Units

Type: Column

Schema information:

```
format: unit
type: string
```

## units sense 3 (columns)

Name: Units

Type: Column

Schema information:

```
format: unit
type: string
```

## unknown (enums)

Name: unknown

Type: Enums

## unloc (suffixes)

Name: Unlocalized spectroscopy

Type: Suffix

Format: <entities>\_unloc.<extension>

## uri (formats)

Name: Uniform resource indicator

Type: Format

Regular expression: (([^\:/?#]+):)?(\/(?:[^\/?#]\*)?)(\[^\?#\]\*)(\?(?:\[^\#]\*))?(#(?:.)\*)?

## vhdr (extensions)

Name: BrainVision Text Header

Type: Extension

Format: `<entities>_<suffix>.vhdr`

## vmrk (extensions)

Name: BrainVision Marker

Type: Extension

Format: `<entities>_<suffix>.vmrk`

## volume (entities)

Name: Volume of Interest

Type: Entity

Schema information:

`format: label`

`type: string`

## volume\_type (columns)

Name: ASL volume type

Type: Column

Allowed values: `control`, `label`, `m0scan`, `deltam`, `cbf`, `noRF`

Schema information:

`type: string`

## wavelength\_actual (columns)

Name: Wavelength actual

Type: Column

Schema information:

`type:` `number`

## wavelength\_emission\_actual (columns)

Name: Wavelength emission actual

Type: Column

Schema information:

`type:` `number`

## wavelength\_nominal (columns)

Name: Wavelength nominal

Type: Column

Schema information:

`type:` `number`

## white\_matter (enums)

Name: white matter

Type: Enums

## whole\_blood\_radioactivity (columns)

Name: Whole blood radioactivity

Type: Column

Schema information:

`type:` `number`



## whole\_organisms (enums)

Name: whole organisms

Type: Enums

## x (enums)

Name: x

Type: Enums

## x sense 1 (columns)

Name: X position

Type: Column

Schema information:

`type: number`

## x sense 2 (columns)

Name: X position

Type: Column

Schema information:

`type: number`

## x\_coordinate (columns)

Name: Gaze x-coordinate

Type: Column

Schema information:

`type: number`

## y (enums)

Name: y

Type: Enums

## y sense 1 (columns)

Name: Y position

Type: Column

Schema information:

`type: number`

## y sense 2 (columns)

Name: Y position

Type: Column

Schema information:

`type: number`

## y\_coordinate (columns)

Name: Gaze y-coordinate

Type: Column

Schema information:

`type: number`

## z (enums)

Name: z

Type: Enums

## z sense 1 (columns)

Name: Z position

Type: Column

Schema information:

`type: number`

## z sense 2 (columns)

Name: Z position

Type: Column

Schema information:

`type: number`

# 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](#)).

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](#).

# BIDS schema

The BIDS schema is a machine readable representation of the BIDS standard, written in a custom YAML format. The goal of the schema is to provide a single source for rendering the specification and validating BIDS datasets, reducing the scope for inconsistencies. Third party tools may also use the schema to write code that will adapt to additions to the BIDS standard.

























The BIDS schema is available in two machine readable formats:

- as a set of [YAML](#) files in the [BIDS specification repository](#)
- as a [single dereferenced json file](#)

A didactic walkthrough of the schema can be found in the [BEP Guide](#), and a complete description is available in the [bidsschematools documentation](#). [bidsschematools](#) is a Python package sourced from the specification repository, and includes the necessary code to render the specification and filename validation.

# Contributors

Legend (source: <https://github.com/all-contributors/all-contributors/blob/master/docs/emoji-key.md>)

Emoji	Represents
	Answering Questions (on the mailing list, NeuroStars, GitHub, in person, or otherwise)
	Bug reports
	Blogposts
	Code
	Content (separate from Blogposts, for example Website news)
	Documentation and specification
	Data (example datasets)
	Design
	Examples (for example datasets, use <b>Data</b> )
	Event Organizers
	Financial Support
	Funding/Grant Finders
	Ideas & Planning
	Infrastructure (hosting, build-tools, and so on)
	Maintenance of the BIDS standard
	Mentoring new contributors
	Plugin/utility libraries
	Project management
	Reviewed Pull Requests
	Tools
	Translation
	Tests
	Tutorials
	Talks

Emoji	Represents
📄	User testing (of new features, tools, and so on)
📺	Videos







































































































































































































































































































































































































The following individuals have contributed to the Brain Imaging Data Structure ecosystem (in alphabetical order). If you contributed to the BIDS ecosystem and your name is not listed, please add it.

name	contributions
Aaron Oliver-Taylor	📖
Adam Li	📖💻
Adam Thomas	📖
Adeen Flinker	📖
Adina S. Wagner	🔄💻
Agah Karakuzu	💬📖📺😄💻
Agnese Zazio	📖
Aki Nikolaidis	📖
Alberto Lazari	📖
Alejandro de la Vega	🔥💻⚠️
Alessio Giacomel	📖
Alex Rockhill	📖🔪💻
Alexander Jones	💻🔥
Alexander L. Cohen	🔥💻📖💬
Alexander von Lautz	📖
Alexandre D’Astous	📖💻
Alexandre Gramfort	📖💡
Alexandre Hutton	📖
Alexandre Routier	📖
Alexandru Foias	📖📺
Ali Khan	📖
Alizee Wickenheiser	🔧
Alyssa Dai	💻
Amber R. Hopkins	📖
Ana Fouto	📄
Anders Eklund	📖🔊💻
Andrea Pigorini	📖
Andrew Hoopes	📖
Andrew Jahn	📄
Andrew Janke	📖💻

name	contributions
Anibal Sólón	
Anthony Galassi	
Arianna Sala	
Ariel Rokem	
Arjen Stolk	
Arman Jahanpour	
Arnaud Delorme	
Arnaud Marcoux	
Arshitha Basavaraj	
Ashley G. Gillman	
Athanasia Monika Mowinckel	
Augustijn Vrolijk	
Aysegul Gunduz	
Azeez Adebimpe	
B. Nolan Nichols	
Balint Kincses	
Benjamin Beasley	
Benjamin Dichter	
Benjamin Gagl	
Bertrand Thirion	
Boris Clénet	
Bradley Voytek	
Brent McPherson	
Brett L. Foster	
Brian A. Wandell	
Brian N. Lundstrom	
Camille Maumet	
Carlo Miniussi	
Cecile Madjar	
Chloé Pasturel	
Chris Benjamin	
Chris Gahnström	
Chris Holdgraf	
Chris J. Gorgolewski	
Chris Rorden	
Christian Büchel	
Christian Horea	
Christine Rogers	
Christophe Phillips	
















































































name	contributions
Christopher G. Schwarz	
Christopher J. Honey	
Christopher J. Markiewicz	
Christopher Lee-Messer	
Clara Moreau	
Clint Hansen	
Cody Baker	
Cody C Baker	
Cyril Pernet	
Cyrus Eierud	
D. Sturgeon	
Dan Brady	
Dan Levitas	
Dan Lurie	
Daniel A. Handwerker	
Daniel McCloy	
David Alsop	
David Boas	
David Groppe	
David Keator	
David McAlpine	
David Thomas	
Dejan Draskow	
Desmond Oathes	
Dianne Patterson	
Dimitri Papadopoulos Orfanos	
Dmitry Petrov	
Dora Hermes	
Dorien Huijser	
Dorota Jarecka	
Douglas N. Greve	
Duncan Macleod	
Dung Truong	
Dustin Moraczewski	
Dylan Nielson	
Eduard Ort	
Eleonora Marcantoni	
Elizabeth Bock	
Elizabeth DuPre	

name	contributions
Elke Warmerdam	
Erdal Karaca	
Eric A. Earl	                           
Eric Achten	                           
Eric Bridgeford	                           
Erin W. Dickie	                           
Ethan Blackwood	                           
Eugene P. Duff	                           
Ezequiel Mikulan	                           
Fede Raimondo	                           
Felipe Orihuela-Espina	                           
Fidel Alfaro Almagro	                           
Filip Szczepankiewicz	                           
Filippo Maria Castelli	                           
Franco Pestilli	                           
Franklin W. Feingold	                           
François Tadel	                 

name	contributions
Gustav Nilsson	📖
Hamish Innes-Brown	📖
Hanne D. Hansen	📖
Hanzhang Lu	📖
Hao-Ting Wang	📖👁
Helena Cockx	📖🗨🗨
Henk Mutsaerts	🗨👁📖📖💡🗨📅🔊📱
Hernando Ombao	📖
Hugo Boniface	📖💻
Ilkay Isik	📖
Ilona Lipp	📖
International Neuroinformatics Coordinating Facility	📁🗨
Iris Groen	📖
Isaac To	💻📖
Isla Staden	📖
Jaap von der Aar	📖
Jacob Sanz-Robinson	💻
Jakub Kaczmarzyk	📖🔪🗨
James Gholam	📖
James Kent	🗨💻
Jan Mathijs Schoffelen	📖
Jan Petr	🗨👁📖📖🗨💡🗨📅⚠🔊
Jan Valosek	💻
Jan-Mathijs Schoffelen	📖
Jean-Baptiste Poline	📖🔊🗨📅💻
Jean-Charles Mariani	📖🗨
Jean-Christophe Houde	📖💻
Jean-Dominique Gallezot	📖
Jean-Philippe Lachaux	📖
Jeanette Mumford	📖
Jefferson Casimir	🔪💻📖📖
Jeffrey G. Ojemann	📖
Jeffrey S. Grethe	🗨👁🗨🔊💻
JegouA	💻
Jelle Dalenberg	📖
Jeremy Moreau	📖💡
Jessica A. Turner	📖
Jochem Rieger	📖
John Detre	📖

name	contributions
John Pellman	📖
John T. Wodder	💻
Joke Durnez	📖🔪💻
Jon Haitz Legarreta Gorroño	💻📖
Jonathan C. Lau	📖
Jonathan Winawer	📖
Joost Kuijer	📖
Jose Manuel Saborit	📖
Joseph Wexler	📖💡
Joseph Woods	📖
Julia Guiomar Niso Galán	🧐🔍📄📁🔪🌿💻🧑🏫🗣️📖🔊
Julia Sprenger	📖
Julia-Katharina Pfarr	💻📖🔪🔊🧑🏫
Julien Cohen-Adad	📖🧑🏫🧐
Julio C Hernandez Pavon	📖
Julius Welzel	📖💡🌿💻🧑🏫🧐🗣️📄
Jérémie Fouquet	💻
Kabilar Gunalan	💻
Kai J. Miller	📖
Kangjoo Lee	📖
Katja Heuer	🔪
Kay Robbins	💻📖🌿
Kevin Larcher	🗣️
Kimberly Ray	📖📄🧐📅
Kirstie Whitaker	📖💡🔍🧐🔊🗣️💻
Klara Gregorova	📖
Klaus Gramann	📖🧐
Kris Thielemans	📖
Kristofer Bouchard	📖
Kurt Schilling	📖
Laetitia Fesselier	🔪
Laura and John Arnold Foundation	📄
Leandro Beltrachini	📖
Lee Kamentsky	📖
Lennart Walger	📖
Lennart Wittkuhn	📖
Liberty Hamilton	📖
Luca Pollonini	📖
Luis Hernandez-Garcia	📖📄






































name	contributions
Luke J. Edwards	  
Lyuba Zehl	
Mainak Jas	 
Mana Biabani	
Manjari Narayan	
Manuel Mercier	 
Maqsood Yaqub	
Marc Lalancette	
Marco Castellaro	       
Maria Ermolova	
Maria de la Iglesia	
Marie-Eve Picard	
Marie-Hélène Bourget	   
Mark Mikkelsen	   
Markus Morawski	
Marta Bortoletto	
Martin Craig	
Martin Noergaard	    
Martin Szinte	
Martin Wilson	
Martina Bulgari	
Mary Miedema	
Mateusz Pawlik	     
Mathias Goncalves	  
Mathieu Boudreau	  
Mathieu Dugré	
Mathieu Guay-Paquet	 
Matt Cieslak	
Matt Sanderson	 
Matt Stead	
Matteo Tonietto	
Matthias Günther	
Matthias Van Osch	
Matthieu Chourrout	
Mattia Veronese	
Maureen J Shader	
Maurice Pasternak	
Max A. van den Boom	   
Melanie Ganz-Benjaminsen	      

name	contributions
Melissa Kline Struhl	📖
Michael Chappell	📖🧠📅
Michael Firbank	💻
Michael Hanke	📖😄🔧👁️🔊
Michael P. Harms	📖⚠️🔧
Michael P. Milham	💡🔍
Michael P. Notter	💬📄✅🔊📖
Michael Schirner	📖
Michelle Wang	💻
Mikaël Naveau	👁️
Mohammad Torabi	💻
Monique Denissen	📖💻
Murat Bilgel	📖
Nader Pouratian	📖
Natalia Petridou	📖
Natalie Rotstein	📖
National Institute of Mental Health	📅
Nell Hardcastle	💻📖😄🧠👁️💬
Nicholas Holmes	📖
Nicholas Traut	📖🔧💻
Nick F. Ramsey	📖
Nick Guenther	💻
Nicole C. Swann	📖
Nigel Rogasch	📖
Nikhil Bhagwat	💻
Nikita Beliy	📖
Nima Bigdely Shamlo	📖
Olivier David	📖
Orrin Devinsky	📖
Oscar Esteban	📖🔧😄💬💻
Pamela LaMontagne	📖🔧
Parul Sethi	📖🔧⚠️💻
Patricia Clement	💬👁️💻📖🔧🗑️😄📅⚠️🔊
Patrick Park	📖🔧💬💻
Paul Wighton	📖
Paule-Joanne Toussaint	📖
Peer Herholz	💬📖👁️🔧✅🔊
Petra Ritter	📖
Peyman Najafi	💻🧠📖🔧🔧

name	contributions
Pierre Rioux	👤
Pieter Vandemaele	👤💻
Pradeep Reddy Raamana	💻🔧
Qian Chu	💻👤
R. Cameron Craddock	👤🔊
Reema Gupta	🗣️👤📄📝
Remi Gau	👤💻📄🔊🌟💻👤🔧😊
Richard Höchenberger	👤💻
Richard N. Henson	👤
Robert B. Innis	👤
Robert E. Smith	💻👤
Robert Knight	👤
Robert Luke	💻
Robert Oostenveld	👤🔧🔊🗣️⚠️😊📄🌟📝💻🔧🗣️📁👤📱📖
Roberto Guidotti	👤
Roberto Toro	🔧
Rohan Goyal	👤
Ross W. Blair	💻
Russell A. Poldrack	👤🔍🔊
Rémi Adon	👤
Samir Das	👤
Samuel Garcia	😊👤👤
Samuel Guay	👤🗣️
Samuel Le Meur-Diebolt	👤😊
Samuel Nastase	💻
Sara Elgayar	👤
Sasha D'Ambrosio	👤
Satrajit S. Ghosh	👤💻
Scott Makeig	👤
Sebastian Urchs	💻👤😊🗣️
Sein Jeung	👤💡🌟💻🗣️😊📄🔧📱
Seyed Yahya Shirazi	👤😊💻📄📝🔧🗣️🔧✓
Shashank Bansal	👤
Shiyu Wang	👤
Silvia Isabella	👤
Sjoerd B. Vos	👤
Soichi Hayashi	👤🔧🌟
Sourav Kulkarni	👤
Stefan Appelhoff	👤📄😊🌟💡💻👤⚠️🔊🔧📝🗣️

name	contributions
Stefanie De Smet	📖
Stefano Moia	📖
Stephan Bickel	📖
Steven Meisler	👤📖📱🔗
Suyash Bhogawar	📖🔗⚠️🔗📱
Sylvain Baillet	📖🔍
Sylvain Takerkart	📖
Sébastien Tourbier	👤🔗🔗👤📖
Sören Grothkopp	📖🔗📱
Tal Pal Attia	📖
Tal Yarkoni	📖📖👤🔍🔗🔗🔗🔗🔗🔗
Tamas Spisak	📖
Tamás Józsa	📱
Taylor Khuhn	📖
Taylor Salo	📱📖🔗📖
Teon L. Brooks	📖📖⚠️📱👤🔗🔗🔗
Thomas Deffieux	📖👤
Thomas E. Nichols	📖🔗🔗🔗🔗📖
Thomas Funck	📖
Thomas Kirk	📖
Thomas Okell	📖
Thomas Wachtler	📖🔗🔗
Tibor Auer	📱📖🔗🔗🔗🔗👤
Til Ole Bergmann	📖
Timo Dickscheid	📖
Timotheus Berg	📖👤📱
Tobey Betthauser	📖
Tobias Bengfort	📖
Tom Hampshire	📖
Tor Wager	📖
Torsten Stöter	📖
Travis Riddle	📖🔗🔗
Tristan Glatard	📖📖
Tyler Collins	🔗🔗
Ulrike Bingel	📖
Vanessa Sochat	📖
Vasudev Raguram	📖🔗📖🔗
Victor H. Souza	📖
Vince D. Calhoun	📖



name	contributions
Vittorio Iacovella	
Viviana Siless	
Vladimir Litvak	
Wietske van der Zwaag	 
William Clarke	
William Triplett	
Wouter V. Potters	 
Xiangrui Li	 
Yaroslav O. Halchenko	          
Yaël Balbastre	
Yoni Ashar	 
Yuan Wang	
Zachary Michael	 
Zhi-De Deng	 
ezemikulan	
josator2	
monkeyman192	
patrick-g-h	
tstoeter	
Étienne Bergeron	 

# 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.
<a href="#">PDDL</a>	Open Data Commons Public Domain Dedication and License	License to assign public domain like permissions without giving up the copyright.
<a href="#">CC0</a>	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.

# Entity table

This section compiles the entities (key-value pairs within filenames) 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 (and possibly including + character(s)) (<label>) or numeric (<index>).

A general introduction to entities is given in the section on filename structure, while entity definitions are in the Entities Appendix.

## Magnetic Resonance Imaging

Entity	Subject	Session	Task	Acquisiti	Contrast En- hanc- ing Agent	Reconstr	Phase- Encoding Direc- tion	Run	Correspc Modal- ity	Echo	Flip Angle	Inversio	Magnetiz Trans- fer	Part	Recordir	Chunk
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>	sub-<label>
anat(IR)	REQUIRED	OPTIONAL	OPTIONAL	OPTIONAL	OPTIONAL	OPTIONAL	OPTIONAL	OPTIONAL				REQUIRED		OPTIONAL		OPTIONAL
anat(ME)	REQUIRED	OPTIONAL	OPTIONAL	OPTIONAL	OPTIONAL	OPTIONAL	OPTIONAL	OPTIONAL		REQUIRED				OPTIONAL		OPTIONAL
anat(ME)	REQUIRED	OPTIONAL	OPTIONAL	OPTIONAL	OPTIONAL	OPTIONAL	OPTIONAL	OPTIONAL		REQUIRED				OPTIONAL		OPTIONAL
anat(MP2)	REQUIRED	OPTIONAL	OPTIONAL	OPTIONAL	OPTIONAL	OPTIONAL	OPTIONAL	OPTIONAL		OPTIONAL	OPTIONAL	REQUIRED		OPTIONAL		OPTIONAL
anat(MP)	REQUIRED	OPTIONAL	OPTIONAL	OPTIONAL	OPTIONAL	OPTIONAL	OPTIONAL	OPTIONAL		OPTIONAL	REQUIRED		REQUIRED	OPTIONAL		OPTIONAL
anat(MTR)	REQUIRED	OPTIONAL	OPTIONAL	OPTIONAL	OPTIONAL	OPTIONAL	OPTIONAL	OPTIONAL					REQUIRED	OPTIONAL		OPTIONAL

[illegible]

Entity	Subject	Session	Task	Acquisiti	Contrast En- hanc- ing Agent	Reconstr	Phase- Encoding Direc- tion	Run	Correspc Modal- ity	Echo	Flip Angle	Inversio	Magnetiz Trans- fer	Part	Recordir	Chunk
dwi(ADC REQUIRED OPTIONAL dwi dwi dwi dwi dwi dwi)				OPTIONAL		OPTIONAL	OPTIONAL	OPTIONAL								OPTIONAL
dwi(dwi REQUIRED OPTIONAL dwi)				OPTION		OPTION	OPTION	OPTION						OPTION		OPTIONAL
dwi(physi REQUIRED OPTIONAL dwi dwi)				OPTIONAL		OPTIONAL	OPTIONAL	OPTIONAL								OPTIONAL
fmap(TE REQUIRED OPTIONAL fmap fmap fmap)				OPTION	OPTION	OPTION		OPTION		OPTION	OPTION	OPTION		OPTION		OPTIONAL
fmap(TB1 REQUIRED OPTIONAL fmap)				OPTIONAL	OPTIONAL	OPTIONAL		OPTIONAL			REQUIRED	OPTIONAL		OPTIONAL		OPTIONAL
fmap(TE REQUIRED OPTIONAL fmap)				OPTION	OPTION	OPTION		OPTION		REQUIRED	REQUIRED	OPTION		OPTION		OPTIONAL
fmap(TB1 REQUIRED OPTIONAL fmap)				OPTIONAL	OPTIONAL	OPTIONAL		OPTIONAL		OPTIONAL	REQUIRED	REQUIRED		OPTIONAL		OPTIONAL
fmap(TE REQUIRED OPTIONAL fmap)				OPTION	OPTION	OPTION		OPTION								OPTIONAL
fmap(epi REQUIRED OPTIONAL fmap)				OPTIONAL	OPTIONAL	OPTIONAL	OPTIONAL	OPTIONAL						OPTIONAL		OPTIONAL
fmap(ph REQUIRED OPTIONAL fmap fmap fmap fmap fmap fmap)				OPTION				OPTION								OPTIONAL
func(bold REQUIRED OPTIONAL func func)				REQUIRED	OPTIONAL	REQUIRED	OPTIONAL	OPTIONAL	OPTIONAL	OPTIONAL				OPTIONAL		OPTIONAL
func(eve REQUIRED OPTIONAL func)				REQUIRED	OPTIONAL	REQUIRED	OPTIONAL	OPTIONAL	OPTIONAL	OPTIONAL						OPTIONAL
func(noR REQUIRED OPTIONAL func)				REQUIRED	OPTIONAL	REQUIRED	OPTIONAL	OPTIONAL	OPTIONAL	OPTIONAL				OPTIONAL		OPTIONAL
func(pha REQUIRED OPTIONAL func)				REQUIRED	OPTIONAL	REQUIRED	OPTIONAL	OPTIONAL	OPTIONAL	OPTION						OPTIONAL

Entity	Subject	Session	Task	Acquisiti	Contrast En- hanc- ing Agent	Reconstr	Phase- Encodin g Direc- tion	Run	Correspc Modal- ity	Echo	Flip Angle	Inversio Time	Magnetiz Trans- fer	Part	Recordir	Chunk
func(physio)	REQUIRED	OPTIONAL	REQUIRED	OPTIONAL	OPTIONAL	OPTIONAL	OPTIONAL	OPTIONAL								OPTIONAL
func																
func																
perf(asl)	REQUIRED	OPTIONAL		OPTIONAL		OPTIONAL	OPTIONAL	OPTIONAL		OPTIONAL					OPTIONAL	
perf																
perf(aslcomp)	REQUIRED	OPTIONAL		OPTIONAL		OPTIONAL	OPTIONAL	OPTIONAL								
perf(assl)	REQUIRED	OPTIONAL		OPTIONAL		OPTIONAL		OPTIONAL								
perf(nofunc)	REQUIRED	OPTIONAL		OPTIONAL		OPTIONAL	OPTIONAL	OPTIONAL	OPTIONAL	OPTIONAL					OPTIONAL	
perf(physio)	REQUIRED	OPTIONAL		OPTIONAL		OPTIONAL	OPTIONAL	OPTIONAL								OPTIONAL
perf																
perf																

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(channels eeg)	REQUIRED	OPTIONAL	REQUIRED	OPTIONAL	OPTIONAL		
eeg(coordsystem)	REQUIRED	OPTIONAL	OPTIONAL	OPTIONAL		OPTIONAL	
eeg(electrodes)	REQUIRED	OPTIONAL	OPTIONAL	OPTIONAL	OPTIONAL	OPTIONAL	
eeg(photo)	REQUIRED	OPTIONAL		OPTIONAL			
eeg(physio eeg)	REQUIRED	OPTIONAL	REQUIRED	OPTIONAL	OPTIONAL		OPTIONAL
ieeg(channels ieeg)	REQUIRED	OPTIONAL	REQUIRED	OPTIONAL	OPTIONAL		
ieeg(coordsystem)	REQUIRED	OPTIONAL	OPTIONAL	OPTIONAL		OPTIONAL	
ieeg(electrodes)	REQUIRED	OPTIONAL	OPTIONAL	OPTIONAL	OPTIONAL	OPTIONAL	
ieeg(photo)	REQUIRED	OPTIONAL		OPTIONAL			
ieeg(physio ieeg)	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(channels)	REQUIRED	OPTIONAL	REQUIRED	OPTIONAL	OPTIONAL	OPTIONAL			
meg(coordsystem)	REQUIRED	OPTIONAL	OPTIONAL	OPTIONAL					
meg(electrodes)	REQUIRED	OPTIONAL	OPTIONAL	OPTIONAL	OPTIONAL	OPTIONAL	OPTIONAL		
meg(events)	REQUIRED	OPTIONAL	REQUIRED	OPTIONAL	OPTIONAL				
meg(headshape)	REQUIRED	OPTIONAL		OPTIONAL					
meg)									
meg(markers)	REQUIRED	OPTIONAL	OPTIONAL	OPTIONAL			OPTIONAL		
meg(meg)	REQUIRED	OPTIONAL		REQUIRED					
meg)									
meg(meg)	REQUIRED	OPTIONAL	REQUIRED	OPTIONAL	OPTIONAL	OPTIONAL		OPTIONAL	
meg(physio)	REQUIRED	OPTIONAL	REQUIRED	OPTIONAL	OPTIONAL	OPTIONAL			OPTIONAL
meg meg)									

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(blood)	REQUIRED	OPTIONAL	OPTIONAL	OPTIONAL	OPTIONAL	OPTIONAL	REQUIRED
pet(events pet)	REQUIRED	OPTIONAL	OPTIONAL	OPTIONAL	OPTIONAL	OPTIONAL	
pet(physio pet)	REQUIRED	OPTIONAL	REQUIRED	OPTIONAL	OPTIONAL	OPTIONAL	OPTIONAL
pet)							

Near-Infrared Spectroscopy (NIRS)

Entity	Subject	Session	Task	Acquisition	Run	Recording
Format	sub-<label>	sub-<label>	sub-<label>	sub-<label>	sub-<label>	sub-<label>
nirs(channels nirs)	REQUIRED	OPTIONAL	REQUIRED	OPTIONAL	OPTIONAL	
nirs(coordsystem)	REQUIRED	OPTIONAL	OPTIONAL	OPTIONAL		

Entity	Subject	Session	Task	Acquisition	Run	Recording
nirs(optodes nirs)	REQUIRED	OPTIONAL		OPTIONAL		
nirs(physio nirs nirs)	REQUIRED	OPTIONAL	REQUIRED	OPTIONAL	OPTIONAL	OPTIONAL

Magnetic Resonance Spectroscopy (MRS)

Entity	Subject	Session	Task	Acquisition	Nucleus	Volume of Interest	Reconstructio	Run	Echo	Inversion Time
Format	sub-<label>	sub-<label>	sub-<label>	sub-<label>	sub-<label>	sub-<label>	sub-<label>	sub-<label>	sub-<label>	sub-<label>
mrs(events)	REQUIRED	OPTIONAL	OPTIONAL	OPTIONAL	OPTIONAL	OPTIONAL	OPTIONAL	OPTIONAL		
mrs(svs mrs mrs mrs)	REQUIRED	OPTIONAL	OPTIONAL	OPTIONAL	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(beh beh)	REQUIRED	OPTIONAL	REQUIRED	OPTIONAL	OPTIONAL	
beh(physio beh beh)	REQUIRED	OPTIONAL	REQUIRED	OPTIONAL	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 micr micr micr micr micr micr micr micr micr micr)	REQUIRED	OPTIONAL	REQUIRED	OPTIONAL	OPTIONAL	OPTIONAL	OPTIONAL
micr(photo)	REQUIRED	OPTIONAL	REQUIRED	OPTIONAL			



Motion

Entity	Subject	Session	Task	Tracking System	Acquisition	Run	Recording
Format	sub-<label>	sub-<label>	sub-<label>	sub-<label>	sub-<label>	sub-<label>	sub-<label>
motion(channels motion)	REQUIRED	OPTIONAL	REQUIRED	REQUIRED	OPTIONAL	OPTIONAL	
motion(events)	REQUIRED	OPTIONAL	REQUIRED	OPTIONAL	OPTIONAL	OPTIONAL	
motion(physio motion motion)	REQUIRED	OPTIONAL	REQUIRED	OPTIONAL	OPTIONAL	OPTIONAL	OPTIONAL

# Entities

This section compiles the entities (key-value pairs within filenames) 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.

## tpl

Full name: Template

Format: **tpl**-<label>

Definition: A standardized space of analysis specified or generated by one or more averages of features with respect to which group-level and atlas-derived results are provided. The <label> SHOULD follow the modality-specific conventions listed in the Coordinate Systems Appendix.

## 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).

## cohort

Full name: Cohort

Format: `cohort-<label>`

Definition: A set of subjects sharing one or more common characteristics.

In the context of a template, the `cohort-<label>` entity identifies a subset of subjects or sessions that were used to construct template variations. For example, a developmental template may use scans from participants of different ages, longitudinal sessions of the same participants, or a combination of the two.

## 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>` entity 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: A set of structured activities performed by the participant. Tasks are usually accompanied by stimuli and responses, and can greatly vary in complexity.

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.

While tasks may be repeated across multiple acquisitions, a given task may have different sets of stimuli (for example, randomized order) and participant responses across subjects, sessions, and runs.

The `task-<label>` MUST be consistent across subjects and sessions.

Files with the `task-<label>` entity SHOULD have an associated events file, as well as certain metadata fields in the associated JSON file.

For the purpose of this specification we consider the so-called "resting state" a task, although events files are not expected for resting state data. Additionally, a common convention in the specification is to include the word "rest" in the `task` label for resting state files (for example, `task-rest`).

## tracksys

Full name: Tracking System

Format: `tracksys-<label>`

Definition: The `tracksys-<label>` entity can be used as a key-value pair to label `*_motion.tsv` and `*_motion.json` files. It can also be used to label `*_channel.tsv` or `*_events.tsv` files when they belong to a specific tracking system.

This entity corresponds to the `"TrackingSystemName"` metadata field in a `*_motion.json` file. `tracksys-<label>` entity is a concise string whereas `"TrackingSystemName"` may be longer and more human readable.

## acq

Full name: Acquisition

Format: `acq-<label>`

Definition: The `acq-<label>` entity 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. The level of detail at which the distinction is made (for example, just between `RARE` and `FLASH`, or between `RARE`, `FLASH`, and `FLASHsubsampled`) remains at the discretion of the researcher.

## nuc

Full name: Nucleus

Format: `nuc-<label>`

Definition: The `nuc-<label>` entity can be used to distinguish acquisitions tuned to detect different nuclei. The label is the name of the nucleus or nuclei, which corresponds to DICOM Tag 0018, 9100. If present in the filename, `"ResonantNucleus"` MUST also be included in the associated metadata.

## voi

Full name: Volume of Interest

Format: `voi-<label>`

Definition: The `voi-<label>` entity can be used to distinguish acquisitions localized to different regions. The label SHOULD be the name of the body region or part scanned. If used, the fields "BodyPart" and "BodyPartDetails" MUST be defined in the JSON file. `BodyPartDetailsOntology` is OPTIONAL to also include.

## ce

Full name: Contrast Enhancing Agent

Format: `ce-<label>`

Definition: The `ce-<label>` entity can be used to distinguish sequences using different contrast enhanced images. The label is the name of the contrast agent.

This entity represents the "ContrastBolusIngredient" metadata field. Therefore, if the `ce-<label>` entity is present in a filename, "ContrastBolusIngredient" MAY also be added in the JSON file, with the same label.

## trc

Full name: Tracer

Format: `trc-<label>`

Definition: The `trc-<label>` entity can be used to distinguish sequences using different tracers.

This entity represents the "TracerName" metadata field. Therefore, if the `trc-<label>` entity is present in a filename, "TracerName" MUST be defined in the associated metadata. Please note that the `<label>` does not need to match the actual value of the field.

## 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.

This entity represents the "SampleStaining" metadata field. Therefore, if the `stain-<label>` entity is present in a filename, "SampleStaining" SHOULD be defined in the associated metadata, although the label may be different.

Descriptions of antibodies SHOULD also be indicated in the "SamplePrimaryAntibodies" and/or "SampleSecondaryAntibodies" metadata fields, as appropriate.

## rec

Full name: Reconstruction

Format: `rec-<label>`

Definition: The `rec-<label>` entity 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>` entity can be set to an arbitrary legitimate label (for example, `dir-LR` or `dir-AP`) to distinguish different phase-encoding directions.

This entity represents the "PhaseEncodingDirection" metadata field. Therefore, if the `dir-<label>` entity is present in a filename, "PhaseEncodingDirection" MUST be defined in the associated metadata.

Labels need not follow any particular convention and in case of conflict, JSON metadata MUST take precedence in interpreting an image.

For example, `dir-j0` and `dir-j1` can indicate "PhaseEncodingDirection": "j" and "j-" (or vice versa), identifying the phase-encoding axis while avoiding indicating polarity. However, in case of a dataset indicating `dir-j0` with "PhaseEncodingDirection": "i", the JSON metadata overrides the entity `dir-` setting.

The use of generic labels, such as `dir-reference` and `dir-reversed`, is RECOMMENDED to avoid any possible inconsistency.

To avoid inconsistency, if the `<label>` is AP, PA, LR, RL, SI, or IS, then the "PhaseEncodingDirection" SHOULD correspond to the data axis that most closely aligns with the cardinal direction and orientation. For example, `dir-PA` and `dir-AP` for an image in RAS+ orientation SHOULD have "PhaseEncodingDirection": "j" and "j-", respectively.

## run

Full name: Run

Format: `run-<index>`

Definition: The `run-<index>` entity is used to distinguish separate data acquisitions with the same acquisition parameters and (other) entities.

If several data acquisitions (for example, MRI scans or EEG recordings) 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 indices).

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>` entity 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>` entity MUST be used to distinguish individual files.

This entity represents the "EchoTime" metadata field. Therefore, if the `echo-<index>` entity is present in a filename, "EchoTime" MUST be defined in the associated metadata. Please note that the `<index>` denotes the number/index (in the form of a nonnegative integer), not the "EchoTime" value 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>` entity pair MUST be used to distinguish individual files.

This entity represents the "FlipAngle" metadata field. Therefore, if the `flip-<index>` entity is present in a filename, "FlipAngle" MUST be defined in the associated metadata. Please note that the `<index>` denotes the number/index (in the form of a nonnegative integer), not the "FlipAngle" value 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>` entity MUST be used to distinguish individual files.

This entity represents the "InversionTime" metadata field. Therefore, if the `inv-<index>` entity is present in a filename, "InversionTime" MUST be defined in the associated metadata. Please note that the `<index>` denotes the number/index (in the form of a nonnegative integer), not the "InversionTime" value 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>` entity MUST be used to distinguish individual files.

This entity represents the "MTState" metadata field. Therefore, if the `mt-<label>` entity is present in a filename, "MTState" MUST be defined in the associated metadata. 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>` 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.

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` entity 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 Neuromag/Elekta/MEGIN'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 hemisphere is described by the file. Allowed label values for this entity are L and R, for the left and right hemispheres, respectively.

## space

Full name: Space

Format: `space-<label>`

Definition: The `space-<label>` entity indicates the coordinate system for interpreting spatial coordinates. For sensor-based modalities, such as EEG/MEG/iEEG, the space indicates how sensor positions are reported; for imaging modalities, the space indicates a reference image to which a file has been aligned. A list of common spaces is defined in the Coordinate Systems Appendix, and these SHOULD be used as `<label>` values for data reported in those spaces.

Note that the space entity is broadly applicable to derivative data, but is only defined for a subset of raw data types. For particular use cases, `<label>` may be restricted to a set of enumerated values.

## split

Full name: Split

Format: `split-<index>`

Definition: In the case of long data recordings that exceed a file size of 2Gb, `.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 filenames, 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, all files MUST be listed separately in `scans.tsv` and 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: The `recording-<label>` entity can be used to distinguish continuous recording files.

This entity is commonly applied when continuous recordings are from different acquisition instruments, or have different sampling frequencies or start times. For example, physiological recordings with different sampling frequencies may be distinguished using labels like `recording-100Hz` and `recording-500Hz`.

## chunk

Full name: Chunk

Format: `chunk-<index>`

Definition: The `chunk-<index>` key/value pair is used to distinguish between images of the same physical sample with different fields of view acquired in the same imaging experiment. This entity applies to collections of 2D images, 3D volumes or 4D volume series (for example, diffusion weighted images), and may be used to indicate different anatomical structures or regions of the same structure.

## atlas

Full name: Atlas

Format: `atlas-<label>`

Definition: The `atlas-<label>` entity identifies files that are part of, or derived from, an atlas.

## seg

Full name: Segmentation

Format: `seg-<label>`

Definition: The `seg-<label>` key/value pair corresponds to a custom label the user MAY use to distinguish specific partitions of the data space (segmentations or parcellations).

Segmentations and parcellations MAY or MAY NOT be associated with atlases. Therefore, `seg-<label>` SHOULD NOT be used to designate atlases. Please refer to the template and atlas section for detailed specifications on their combined use. When a segmentation is a realization of an atlas' segmentation or parcellation, `seg-<label>` SHOULD be employed to distinguish them. For example, the [Yeo 2011 atlas](#) is distributed within FreeSurfer with two different parcellations: the 7 networks MAY be described with `seg-7n`, for instance, and the 17 networks MAY correspondingly be described with `seg-17n`.

This entity is only applicable to derivative data.

## scale

Full name: Scale

Format: `scale-<label>`

Definition: The `scale-<label>` key/value pair corresponds to a custom label the user MAY use to distinguish segmentations that entail different levels of regional resolution (scales), often indicated by the number of ROIs. See ([Bijsterbosch et al., 2020](#)) for further details on regional resolution or, as defined by the authors of the manuscript, the brain units.

For example, the [Schaefer 2018 atlas](#) is distributed within FreeSurfer with ten different scales (100, 200, 300, 400, 500, 600, 700, 800, 900, and 1000 regions) for each of its three different parcellations (7 networks, 17 networks, and Kong's variation of 17 networks).

This entity is only applicable to derivative data.

## res

Full name: Resolution

Format: `res-<label>`

Definition: Resolution of regularly sampled N-dimensional data.

This entity represents the "**Resolution**" metadata field. Therefore, if the `res-<label>` entity is present in a filename, "**Resolution**" MUST also be added in the JSON file, to provide interpretation.

This entity is only applicable to derivative data.

## den

Full name: Density

Format: `den-<label>`

Definition: Density of non-parametric surfaces.

This entity represents the "**Density**" metadata field. Therefore, if the `den-<label>` entity is present in a filename, "**Density**" MUST also be added in the JSON file, 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>` entity SHOULD be used.

This entity is only applicable to derivative data.

## 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>][_task-<label>][_acq-<label>][_ce-<label>][_rec-<label>][_run-<index>]_echo-<index>[_part-<mag|phase|real|imag>][_
        sub-<label>[_ses-<label>][_task-<label>][_acq-<label>][_ce-<label>][_rec-<label>][_run-<index>]_echo-<index>[_part-<mag|phase|real|imag>][_
        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>][_run-<index>][_echo-<index>]_flip-<index>[_part-<mag|phase|
        sub-<label>[_ses-<label>][_task-<label>][_acq-<label>][_ce-<label>][_rec-<label>][_run-<index>][_echo-<index>]_flip-<index>[_part-<mag|phase|
        sub-<label>[_ses-<label>][_task-<label>][_acq-<label>][_ce-<label>][_rec-<label>][_run-<index>]_inv-<index>[_part-<mag|phase|real|imag>][_
```

```
sub-<label>[_ses-<label>][_task-<label>][_acq-<label>][_ce-<label>][_rec-<label>][_run-<index>]_inv-<index>[_part-<mag|phase|real|imag>][_c
sub-<label>[_ses-<label>][_task-<label>][_acq-<label>][_ce-<label>][_rec-<label>][_run-<index>][_echo-<index>][_flip-<index>]_inv-<index>[_c
sub-<label>[_ses-<label>][_task-<label>][_acq-<label>][_ce-<label>][_rec-<label>][_run-<index>][_echo-<index>][_flip-<index>]_inv-<index>[_c
sub-<label>[_ses-<label>][_task-<label>][_acq-<label>][_ce-<label>][_rec-<label>][_run-<index>][_echo-<index>][_flip-<index>]_mt-<on|off>[_pa
sub-<label>[_ses-<label>][_task-<label>][_acq-<label>][_ce-<label>][_rec-<label>][_run-<index>][_echo-<index>][_flip-<index>]_mt-<on|off>[_pa
sub-<label>[_ses-<label>][_task-<label>][_acq-<label>][_ce-<label>][_rec-<label>][_run-<index>][_echo-<index>][_flip-<index>]_mt-<on|off>[_pa
sub-<label>[_ses-<label>][_task-<label>][_acq-<label>][_ce-<label>][_rec-<label>][_run-<index>][_echo-<index>][_flip-<index>]_mt-<on|off>[_pa
sub-<label>[_ses-<label>][_task-<label>][_acq-<label>][_ce-<label>][_rec-<label>][_run-<index>]_mt-<on|off>[_part-<mag|phase|real|imag>][_c
sub-<label>[_ses-<label>][_task-<label>][_acq-<label>][_ce-<label>][_rec-<label>][_run-<index>]_mt-<on|off>[_part-<mag|phase|real|imag>][_c
```

Legend:

- <matches> is a placeholder to denote an arbitrary (and valid) sequence of entities and labels at the beginning of the filename (only BIDS "raw").
- <source-entities> is a placeholder to denote an arbitrary sequence of entities and labels at the beginning of the filename matching a source file from which the file derives (only BIDS-Derivatives).
- Filename entities or directories between square brackets (for example, [\_ses-<label>]) are OPTIONAL.
- Some entities may only allow specific values, in which case those values are listed in <>, separated by |.
- \_<suffix> means that there are several (>6) valid suffixes for this filename pattern.
- .<extension> means that there are several (>6) valid extensions for this file type.
- [.gz] means that both the unzipped and gzipped versions of the extension are valid.

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 ( <a href="#">Deoni et al. 2005</a> ).
IRT1	inv, part	Inversion recovery T1 mapping	The IRT1 method involves multiple inversion recovery spin-echo images acquired at different inversion times ( <a href="#">Barral et al. 2010</a> ).
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 ( <a href="#">Marques et al. 2010</a> ).

Suffix	Linking entities	Application	Description
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.
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 ( <a href="#">Helms et al. 2008</a> ).
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 ( <a href="#">Weiskopf et al. 2013</a> ). See <a href="#">here</a> 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>][_c
      sub-<label>[_ses-<label>][_acq-<label>][_ce-<label>][_rec-<label>][_run-<index>]_flip-<index>[_inv-<index>][_part-<mag|phase|real|imag>][_c
      sub-<label>[_ses-<label>][_acq-<label>][_ce-<label>][_rec-<label>][_run-<index>]_echo-<index>_flip-<index>[_inv-<index>][_part-<mag|phase|real|imag>][_c
      sub-<label>[_ses-<label>][_acq-<label>][_ce-<label>][_rec-<label>][_run-<index>]_echo-<index>_flip-<index>[_inv-<index>][_part-<mag|phase|real|imag>][_c
      sub-<label>[_ses-<label>][_acq-<label>][_ce-<label>][_rec-<label>][_run-<index>][_echo-<index>][_flip-<index>][_inv-<index>][_part-<mag|phase|real|imag>][_c
      sub-<label>[_ses-<label>][_acq-<label>][_ce-<label>][_rec-<label>][_run-<index>][_echo-<index>][_flip-<index>][_inv-<index>][_part-<mag|phase|real|imag>][_c
      sub-<label>[_ses-<label>][_acq-<label>][_ce-<label>][_rec-<label>][_run-<index>][_echo-<index>][_flip-<index>][_inv-<index>][_part-<mag|phase|real|imag>][_c
      sub-<label>[_ses-<label>][_acq-<label>][_ce-<label>][_rec-<label>][_run-<index>][_echo-<index>][_flip-<index>][_inv-<index>][_part-<mag|phase|real|imag>][_c
      sub-<label>[_ses-<label>][_acq-<label>][_ce-<label>][_rec-<label>][_run-<index>][_echo-<index>][_flip-<index>][_inv-<index>][_part-<mag|phase|real|imag>][_c
      sub-<label>[_ses-<label>][_acq-<label>][_ce-<label>][_rec-<label>][_run-<index>][_echo-<index>][_flip-<index>][_inv-<index>][_part-<mag|phase|real|imag>][_c
      sub-<label>[_ses-<label>][_acq-<label>][_ce-<label>][_rec-<label>][_run-<index>][_echo-<index>][_flip-<index>][_inv-<index>][_part-<mag|phase|real|imag>][_c
      sub-<label>[_ses-<label>][_acq-<label>][_ce-<label>][_rec-<label>][_run-<index>][_echo-<index>]_flip-<index>_inv-<index>[_part-<mag|phase|real|imag>][_c
      sub-<label>[_ses-<label>][_acq-<label>][_ce-<label>][_rec-<label>][_run-<index>][_echo-<index>]_flip-<index>_inv-<index>[_part-<mag|phase|real|imag>][_c
```

Legend:

- <matches> is a placeholder to denote an arbitrary (and valid) sequence of entities and labels at the beginning of the filename (only BIDS "raw").
- <source-entities> is a placeholder to denote an arbitrary sequence of entities and labels at the beginning of the filename matching a source file from which the file derives (only BIDS-Derivatives).
- Filename entities or directories between square brackets (for example, [\_ses-<label>]) are OPTIONAL.
- Some entities may only allow specific values, in which case those values are listed in <>, separated by |.
- \_<suffix> means that there are several (>6) valid suffixes for this filename pattern.
- .<extension> means that there are several (>6) valid extensions for this file type.
- [.gz] means that both the unzipped and gzipped versions of the extension are valid.

Suffix	Meta-data relevant entity	Application	Description
TB1DAM	flip	Double-angle B1+ mapping	The double-angle B1+ method ( <a href="#">Insko and Bolinger 1993</a> ) 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.



Suffix	Meta-data relevant entity	Application	Description
TB1EPI	flip, echo	B1+ mapping with 3D EPI	This B1+ mapping method ( <a href="#">Jiru and Klose 2006</a> ) 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 ( <a href="#">Yarnykh 2007</a> ) 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 <code>tf1_b1_map</code>	B1+ data acquired using <code>tf1_b1_map</code> product sequence by Siemens based on the method by <a href="#">Chung et al. (2010)</a> . The sequence generates one anatomical image and one scaled flip angle map.
TB1RFM	Please see the qMRI appendix.	Siemens <code>rf_map</code>	B1+ data acquired using <code>rf_map</code> product sequence by Siemens.
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+ ( <a href="#">Eggenchwiler et al. 2011</a> ). This sequence can also be used in conjunction with MP2RAGE T1 mapping to iteratively improve B1+ and T1 map estimation ( <a href="#">Marques &amp; Gruetter 2013</a> ).
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 <a href="#">Papp et al. (2016)</a> .

# 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](#) ( $\mu$ ) or [U+00B5](#) ( $\mu$ )
2. [U+03A9](#) ( $\Omega$ ) or [U+2126](#) ( $\Omega$ )
3. [U+00B0](#) ( $^{\circ}$ )

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  `$\mu$ V`
  - (b) NOT RECOMMENDED: `microV`,  `$\mu$ volt` 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
meter	m	length
kilogram	kg	mass
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	10 <sup>1</sup>
hecto	h	10 <sup>2</sup>
kilo	k	10 <sup>3</sup>
mega	M	10 <sup>6</sup>
giga	G	10 <sup>9</sup>
tera	T	10 <sup>12</sup>
peta	P	10 <sup>15</sup>
exa	E	10 <sup>18</sup>
zetta	Z	10 <sup>21</sup>
yotta	Y	10 <sup>24</sup>

Submultiples

Prefix name	Prefix symbol	Factor
deci	d	10 <sup>-1</sup>
centi	c	10 <sup>-2</sup>
milli	m	10 <sup>-3</sup>
micro	u	10 <sup>-6</sup>
nano	n	10 <sup>-9</sup>
pico	p	10 <sup>-12</sup>
femto	f	10 <sup>-15</sup>
atto	a	10 <sup>-18</sup>
zepto	z	10 <sup>-21</sup>
yocto	y	10 <sup>-24</sup>

# 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 the [HED Schema Browser](#) to view the HED schema and the [HED resources](#) site for additional information.

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 (single term) and long (full path) 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  n/a  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, Red)",
      "stop": "Sensory-event, Visual-presentation, (Square, Blue)"
    }
  },
  "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 the HED annotation for each event (row) by concatenating the annotations for each column, along with the annotation contained directly in a HED column of that row, as described in the next section.

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, Red), (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, such as during manual annotation of artifacts or signal features.

Some acquisition or presentation software systems may produce individual annotations for each event during the experiment. These individualized annotations may be placed into the HED column of the `events.tsv` file when the data is converted into BIDS format.

Dedicated HED tools that assemble the full annotation for events 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 annotations 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 properly validating the HED annotations (for example, using the `bids-validator`).

Example: The following `dataset_description.json` file specifies that the [HED8.4.0.xml](#) file from the `standard_schema/hedxml` directory of the [hed-schemas](#) repository on GitHub should be used to validate the study event annotations.

```
{
  "Name": "A great experiment",
  "BIDSVersion": "1.10.1",
  "HEDVersion": "8.4.0"
}
```

The BIDS validator will generate an error if your dataset uses HED and the `HEDVersion` field is missing from the dataset description file. To avoid this, include a `HEDVersion` field in the `dataset_description.json` if you are using HED annotations.

## Using HED library schemas

HED also allows you to use one or more specialized vocabularies along with or instead of the standard vocabulary. These specialized vocabularies are developed by communities of users and are available in the [hed-schemas](#) GitHub repository. A library schema is specified in the form `<library-name>_<library-version>`.

### Partnered library schemas

A partnered schema is one whose vocabulary trees are merged with its standard schema partner when the schema is released. Thus, the two vocabularies appear as one vocabulary to the annotator. Partnered library schemas were introduced in HED specification version 3.2.0 and are supported by HED standard schema versions  $\geq 8.2.0$ . Each partnered library schema is tied to a specific version of the HED standard schema as specified in its header. A given library schema version is either partnered or standalone.

Note: Whether a particular library schema version is partnered or unpartnered is fixed when the library is released and cannot be changed. For example, [HED-SCORE version 1.0.0](#) is unpartnered, but [HED-SCORE version 2.1.0](#) is partnered with standard schema version 8.4.0.

**Unpartnered library schema example** The following `dataset_description.json` file specifies that the [HED8.1.0.xml](#) standard schema should be used along with the HED-SCORE library schema for clinical neurological annotation located at [HED\\_score\\_1.0.0.xml](#).

```
{
  "Name": "A great experiment",
  "BIDSVersion": "1.10.1",
  "HEDVersion": ["8.4.0", "sc:score_1.0.0"]
}
```

The `sc:` is a user-chosen prefix used to distinguish the source schemas of the terms in the HED annotation. The prefixes MUST be alphanumeric. Any number of prefixed schemas may be used in addition to a non-prefixed one.

The following HED annotation from this dataset uses the `sc:` prefix with `Eye-blink-artifact` and `Seizure-PNES` because these terms are from the HED-SCORE library schema, while `Data-feature` is from the standard HED schema.

`Data-feature, sc:Eye-blink-artifact, sc:Seizure-PNES`

**Single unpartnered library schema example** If only one schema is used for annotation, the prefix can be omitted entirely. The following `dataset_description.json` indicates that only the HED-SCORE library schema version 1.0.0 will be used for HED annotation in this dataset.



```
{  
  "Name": "A great experiment",  
  "BIDSVersion": "1.10.1",  
  "HEDVersion": "score_1.0.0"  
}
```

The corresponding annotations in the dataset do not have a prefix:

Eye-blink-artifact, Seizure-PNES

Partnered library schema example The following `dataset_description.json` file specifies that the HED-SCORE library schema [version 2.1.0](#) is used. This particular library schema version is partnered with the standard schema version [8.4.0](#).

```
{  
  "Name": "A great experiment",  
  "BIDSVersion": "1.10.1",  
  "HEDVersion": "score_2.1.0"  
}
```

The corresponding annotations in the dataset use tags from the HED-SCORE library schema (Seizure-PNES) and from the standard HED (Data-feature and Eye-blink-artifact) as follows:

Data-feature, Eye-blink-artifact, Seizure-PNES

# MEG file formats

Each MEG system brand has specific file organization and data formats. RECOMMENDED values for `manufacturer_specific_extensions`:

Value	Description
<code>ctf</code>	CTF (directory with <code>.ds</code> extension)
<code>fif</code>	Neuromag / Elekta / MEGIN and BabyMEG (file with extension <code>.fif</code> )
<code>4d</code>	BTi / 4D Neuroimaging (directory containing multiple files without extensions)
<code>kit</code>	KIT / Yokogawa / Ricoh (file with extension <code>.sqd</code> , <code>.con</code> , <code>.raw</code> , <code>.ave</code> or <code>.mrk</code> )
<code>kdf</code>	KRISS (file with extension <code>.kdf</code> )
<code>itab</code>	Chieti system (file with extension <code>.raw</code> and <code>.mhd</code> )

Below are specifications for each system brand.

## CTF

Each experimental run with a CTF system yields a directory 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` directory.

```
[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 on the relevant [FieldTrip webpage](#)

## 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` directory, which may be nested inside a `ses-<label>` directory, as shown in the following examples.

Example with single session (omitted session directory)

```
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` subdirectory.

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 directory 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 on the relevant [FieldTrip webpage](#)

## 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>` entity and no more that two marker files may be associated with one raw data file. While the acquisition entity 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 on the relevant [FieldTrip webpage](#)

## KRISS

Each experimental run on the KRISS system produces a file with extension `.kdf`. Additional files can be available in the same directory: 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 Neuromag/Elekta/MEGIN 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.



# 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	<a href="https://www.ctf.com/products">https://www.ctf.com/products</a>
CTF-275	CTF	CTF-275: OMEGA 2000
Neuromag-122	Neuromag/Elekta/Megin	
Elekta Vectorview	Neuromag/Elekta/Megin	102 magnetometers + 204 planar gradiometers
Elekta TRIUX	Neuromag/Elekta/Megin	<a href="https://www.elekta.com/products/neurosurgery/">https://www.elekta.com/products/neurosurgery/</a>
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)

# 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](https://doi.org/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` `CoordSysTypes` 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

- **NeuromagElektMEGIN**: 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: RAS orientation and the origin at the center of the gradient coil for template NifTI images
- The use of **ElektNeuromag** is DEPRECATED. Dataset curators SHOULD use **NeuromagElektMEGIN** instead.

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: RAS orientation and the origin at the center of the gradient coil for template NifTI images

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**
- **NeuromagElektMEGIN**
- **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: RAS orientation and the origin at the center of the gradient coil for template NifTI images

## 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"		<a href="https://www.loni.usc.edu/research/atlas">https://www.loni.usc.edu/research/atlas</a>
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"		<a href="https://www.loni.usc.edu/research/atlas">https://www.loni.usc.edu/research/atlas</a>
IXI549Space	Reference space defined by the average of the "549 (...) subjects from the IXI dataset" linearly transformed to ICBM MNI 452.	SPM12	<a href="https://brain-development.org/">https://brain-development.org/</a>

Coordinate System	Description	Used by	Reference
fsaverage	The <b>fsaverage</b> is a surface reference system (formerly described as fsaverage[3 4 5 6 sym]). Additionally, by convention, <b>fsaverage</b> is used as shorthand for a dual template providing both volumetric and surface coordinates references, where the surface template is <b>fsaverage</b> and the volumetric template corresponds to a FreeSurfer variant of MNI305 space.	Freesurfer	
fsaverageSym	The <b>fsaverageSym</b> is a symmetric surface reference system (formerly described as <b>fsaveragesym</b> ). Additionally, by convention, <b>fsaverageSym</b> is used as shorthand for a dual template providing both volumetric and surface coordinates references, where the surface template is <b>fsaverageSym</b> and the volumetric template corresponds to a FreeSurfer variant of MNI305 space.	Freesurfer	
fsLR	The <b>fsLR</b> is a surface template. Additionally, by convention, <b>fsLR</b> is used as shorthand for a dual template providing both volumetric and surface coordinates references, where the surface template is <b>fsLR</b> and 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	

Coordinate System	Description	Used by	Reference
MNIColin27	Average of 27 T1 scans of a single subject	SPM96	<a href="https://www.bic.mni.mcgill.ca/Services/Atlases/Colin27Highres">https://www.bic.mni.mcgill.ca/Services/Atlases/Colin27Highres</a>
MNI152Lin	Also known as ICBM (version with linear coregistration)	SPM99 to SPM8	<a href="https://www.bic.mni.mcgill.ca/Services/Atlases/ICBM152Lin">https://www.bic.mni.mcgill.ca/Services/Atlases/ICBM152Lin</a>
MNI152NLin2009[a-c][Sym Asym]	Also known as ICBM (non-linear coregistration with 40 iterations, released in 2009). It comes in either three different flavors each in symmetric or asymmetric version.	DARTEL toolbox in SPM12b	<a href="https://www.bic.mni.mcgill.ca/Services/Atlases/ICBM152NLin2009">https://www.bic.mni.mcgill.ca/Services/Atlases/ICBM152NLin2009</a>
MNI152NLin6Sym	Also known as symmetric ICBM 6th generation (non-linear coregistration).	FSL	<a href="https://www.bic.mni.mcgill.ca/Services/Atlases/ICBM152NLin6">https://www.bic.mni.mcgill.ca/Services/Atlases/ICBM152NLin6</a>
MNI152NLin6ASym	A variation of MNI152NLin6Sym built by A. Janke that is released as the MNI template of FSL. Volumetric templates included with <a href="#">HCP-Pipelines</a> correspond to this template too.	HCP-Pipelines	<a href="https://doi.org/10.1016/j.neuroimage.2012.01.024">doi:10.1016/j.neuroimage.2012.01.024</a>
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.		<a href="https://www.bic.mni.mcgill.ca/Services/Atlases/NIHPD-obj1">https://www.bic.mni.mcgill.ca/Services/Atlases/NIHPD-obj1</a>
OASIS30AntsOASISAnts			<a href="https://figshare.com/articles/dataset/ANTs_ANTsR_Brain_Templates/915436">https://figshare.com/articles/dataset/ANTs_ANTsR_Brain_Templates/915436</a>
OASIS30Atropos			<a href="https://mindboggle.info/data.html">https://mindboggle.info/data.html</a>
Talairach	Piecewise linear scaling of the brain is implemented as described in TT88.		<a href="http://talairach.org/">http://talairach.org/</a>
UNCInfant	Infant Brain Atlases from Neonates to 1- and 2-year-olds.		<a href="https://www.nitrc.org/projects/pediatricatlas">https://www.nitrc.org/projects/pediatricatlas</a>

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. <a href="https://www.nitrc.org/projects/pediatricatlas">https://www.nitrc.org/projects/pediatricatlas</a>	UNCInfant

Please note that the template identifiers starting with MNI (for example MNI305) are typically referred to with the umbrella term of MNI Space. The Common Principles deliver a more precise definitions of template, space, and atlas.

### 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 <b>fsnative</b> .
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 <b>RawSources</b> ) after reconstruction and conversion to NIfTI or equivalent for the case of surfaces and dual volume/surface files.



# 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` subdirectory.

List of currently supported collections:

Name	suffix	Description
Inversion recovery T1 mapping	IRT1	The IRT1 method involves multiple inversion recovery spin-echo images acquired at different inversion times ( <a href="#">Barral et al. 2010</a> ).

Name	suffix	Description
Multi-echo Gradient Recalled Echo	MEGRE	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.
Multi-echo Spin Echo	MESE	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.
Magnetization Prepared Two Gradient Echoes	MP2RAGE	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 ( <a href="#">Marques et al. 2010</a> ).
Multi-parametric Mapping	MPM	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 ( <a href="#">Weiskopf et al. 2013</a> ). See <a href="#">here</a> for suggested MPM acquisition protocols.
Magnetization Transfer Ratio	MTR	This method is to calculate a semi-quantitative magnetization transfer ratio map.
Magnetization transfer saturation	MTS	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 ( <a href="#">Helms et al. 2008</a> ).
Variable flip angle	VFA	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 ( <a href="#">Deoni et al. 2005</a> ).

Template:

sub-<label>/

```
[ses-<label>/]
  anat/
    sub-<label>[_ses-<label>][_task-<label>][_acq-<label>][_ce-<label>][_rec-<label>][_run-<index>]_echo-<index>[_part-<mag|phase|real|imag>][_c
    sub-<label>[_ses-<label>][_task-<label>][_acq-<label>][_ce-<label>][_rec-<label>][_run-<index>]_echo-<index>[_part-<mag|phase|real|imag>][_c
    sub-<label>[_ses-<label>][_task-<label>][_acq-<label>][_ce-<label>][_rec-<label>][_dir-<label>][_run-<index>]_echo-<index>[_part-<mag|phase|real|imag>][_c
    sub-<label>[_ses-<label>][_task-<label>][_acq-<label>][_ce-<label>][_rec-<label>][_dir-<label>][_run-<index>]_echo-<index>[_part-<mag|phase|real|imag>][_c
    sub-<label>[_ses-<label>][_task-<label>][_acq-<label>][_ce-<label>][_rec-<label>][_run-<index>]_echo-<index>[_flip-<index>][_part-<mag|phase|real|imag>][_c
    sub-<label>[_ses-<label>][_task-<label>][_acq-<label>][_ce-<label>][_rec-<label>][_run-<index>]_echo-<index>[_flip-<index>][_part-<mag|phase|real|imag>][_c
    sub-<label>[_ses-<label>][_task-<label>][_acq-<label>][_ce-<label>][_rec-<label>][_run-<index>]_inv-<index>[_part-<mag|phase|real|imag>][_c
    sub-<label>[_ses-<label>][_task-<label>][_acq-<label>][_ce-<label>][_rec-<label>][_run-<index>]_inv-<index>[_part-<mag|phase|real|imag>][_c
    sub-<label>[_ses-<label>][_task-<label>][_acq-<label>][_ce-<label>][_rec-<label>][_run-<index>]_echo-<index>[_flip-<index>]_inv-<index>[_part-<mag|phase|real|imag>][_c
    sub-<label>[_ses-<label>][_task-<label>][_acq-<label>][_ce-<label>][_rec-<label>][_run-<index>]_echo-<index>[_flip-<index>]_inv-<index>[_part-<mag|phase|real|imag>][_c
    sub-<label>[_ses-<label>][_task-<label>][_acq-<label>][_ce-<label>][_rec-<label>][_run-<index>]_echo-<index>[_flip-<index>_mt-<on|off>][_part-<mag|phase|real|imag>][_c
    sub-<label>[_ses-<label>][_task-<label>][_acq-<label>][_ce-<label>][_rec-<label>][_run-<index>]_echo-<index>[_flip-<index>_mt-<on|off>][_part-<mag|phase|real|imag>][_c
    sub-<label>[_ses-<label>][_task-<label>][_acq-<label>][_ce-<label>][_rec-<label>][_run-<index>]_echo-<index>[_flip-<index>_mt-<on|off>][_part-<mag|phase|real|imag>][_c
    sub-<label>[_ses-<label>][_task-<label>][_acq-<label>][_ce-<label>][_rec-<label>][_run-<index>]_echo-<index>[_flip-<index>_mt-<on|off>][_part-<mag|phase|real|imag>][_c
    sub-<label>[_ses-<label>][_task-<label>][_acq-<label>][_ce-<label>][_rec-<label>][_run-<index>]_mt-<on|off>[_part-<mag|phase|real|imag>][_c
    sub-<label>[_ses-<label>][_task-<label>][_acq-<label>][_ce-<label>][_rec-<label>][_run-<index>]_mt-<on|off>[_part-<mag|phase|real|imag>][_c
```

Legend:

- <matches> is a placeholder to denote an arbitrary (and valid) sequence of entities and labels at the beginning of the filename (only BIDS "raw").
- <source-entities> is a placeholder to denote an arbitrary sequence of entities and labels at the beginning of the filename matching a source file from which the file derives (only BIDS-Derivatives).
- Filename entities or directories between square brackets (for example, [\_ses-<label>]) are OPTIONAL.
- Some entities may only allow specific values, in which case those values are listed in <>, separated by |.
- \_<suffix> means that there are several (>6) valid suffixes for this filename pattern.
- .<extension> means that there are several (>6) valid extensions for this file type.
- [.gz] means that both the unzipped and gzipped versions of the extension are valid.

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 subdirectory. 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.

## Outputs are quantitative maps

qMRI maps are stored differently depending on the process that generated them. Pre-generated qMRI maps MAY be stored as part of a raw BIDS dataset, whereas they MUST be stored in a derivative BIDS dataset if they were post-generated.

See the example below of a T1map generated from an MP2RAGE file collection using either option.

If the map is post-generated:

```
ds-example/  
  derivatives/  
    qMRI-software-name/  
      sub-01/  
        anat/  
          sub-01_T1map.nii.gz # --> T1 map in a derivative dataset  
          sub-01_T1map.json  
          sub-01_UNIT1.nii.gz # --> UNI T1 in a derivative dataset  
          sub-01_UNIT1.json  
      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
```

If the map is pre-generated, for example, by a Siemens scanner:

```
ds-example/  
  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  
  sub-01_T1map.nii.gz # --> T1 map in a raw dataset  
  sub-01_T1map.json  
  sub-01_UNIT1.nii.gz # --> UNI T1 in a raw dataset  
  sub-01_UNIT1.json
```

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, RepetitionTimePreparation, NumberShots,MagneticFieldStrength	EchoTime
MESE	EchoTime	
MEGRE	EchoTime	
MTR	MTState	
MTS	FlipAngle, MTState, RepetitionTimeExcitation	

File collection	REQUIRED metadata	OPTIONAL metadata
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.

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 directory:

```
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
Sources	RECOMMENDED	array of strings	A list of files with the paths specified using Sources; 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. Using paths specified relative to the dataset root is Sources.
EstimationReference	RECOMMENDED	string	Reference to the study/studies on which the implementation is based.
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 variable. SI units in CMIXF formatting are RECOMMENDED (see Units).
BasedOn	BasedOn	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. This field is DEPRECATED, and this metadata SHOULD be recorded in the Sources field using BasedOn to distinguish sources from different datasets.

Example:

```
sub-01_T1map.nii.gz
sub-01_T1map.json
sub-01_T1map.json:
{
```



```
<<Parameter injected by the software/pipeline>>

"Sources":["bids:raw:sub-01/anat/sub-01_flip-1_VFA.nii.gz",
          "bids:raw:sub-01/anat/sub-01_flip-2_VFA.nii.gz",
          "bids:raw:sub-01/anat/sub-01_flip-3_VFA.nii.gz",
          "bids:raw:sub-01/anat/sub-01_flip-4_VFA.nii.gz",
          "bids:raw:sub-01/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",
"ManufacturersModelName": "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 ( <b>entity/fixed</b> )	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 SHOULD be stored under the `anat` in a raw BIDS dataset 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 MUST be stored in a derivative BIDS dataset 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](#).

# 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  $\text{deltaM} = \text{control} - \text{label}$  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\_type `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`:

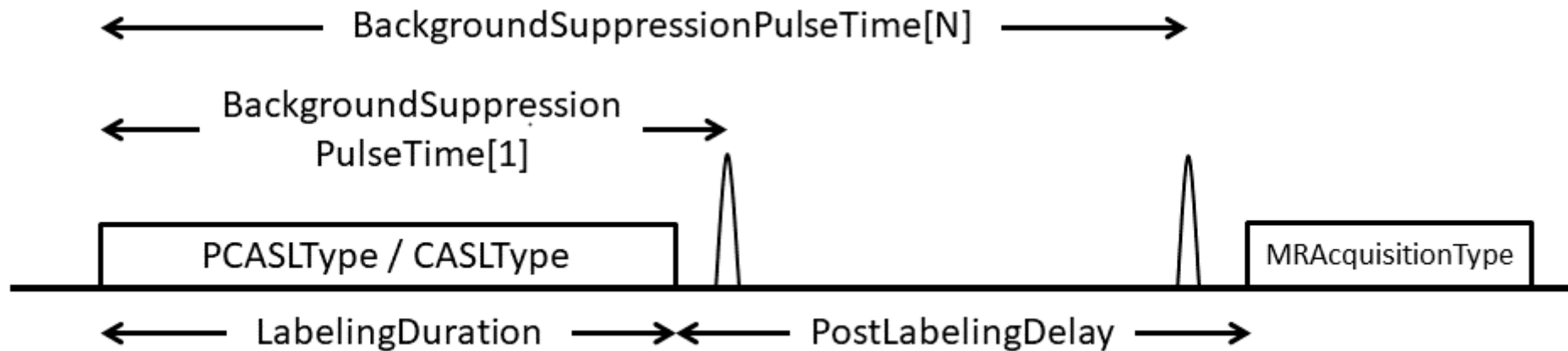
```
volume_type
cbf
m0scan
```

## 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](#).

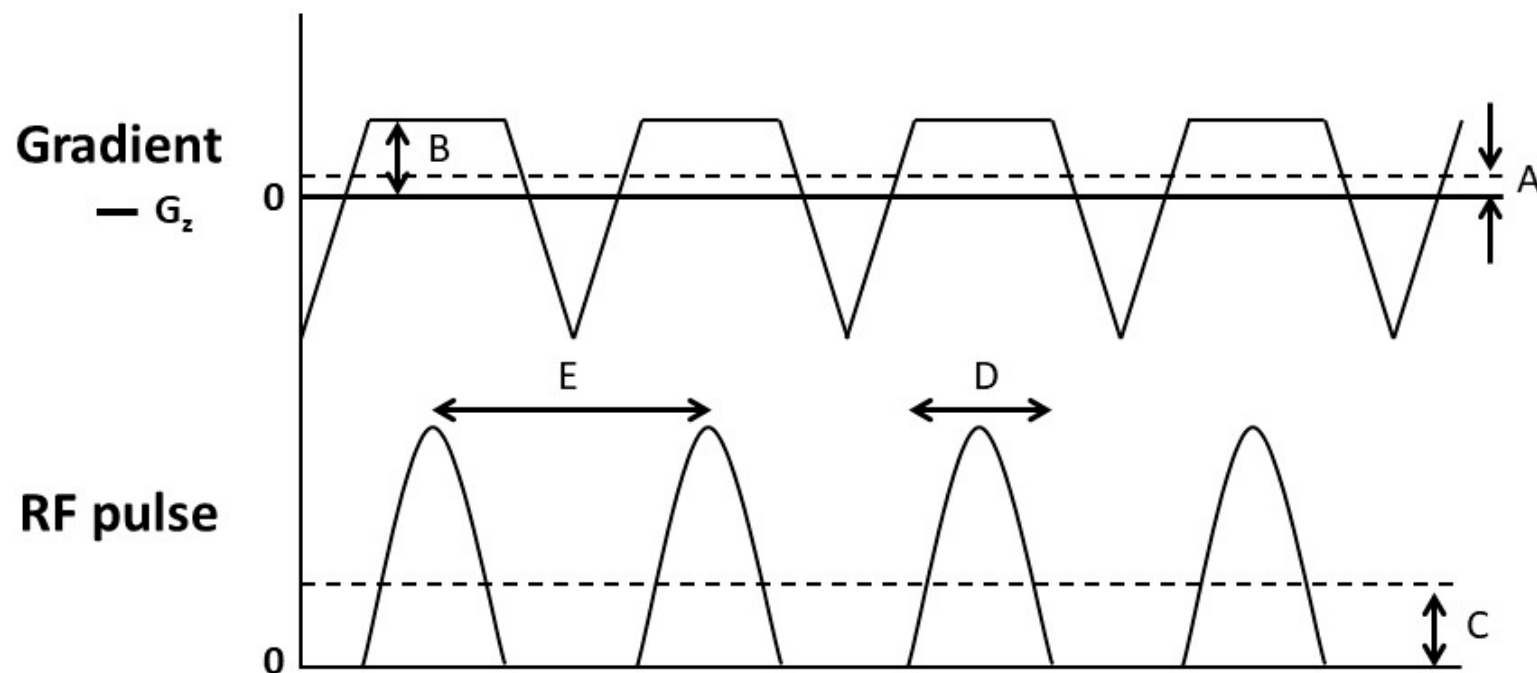
(P)CASL sequence

# (P)CASL



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` is RECOMMENDED if `BackgroundSuppression` was applied. This is 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`).

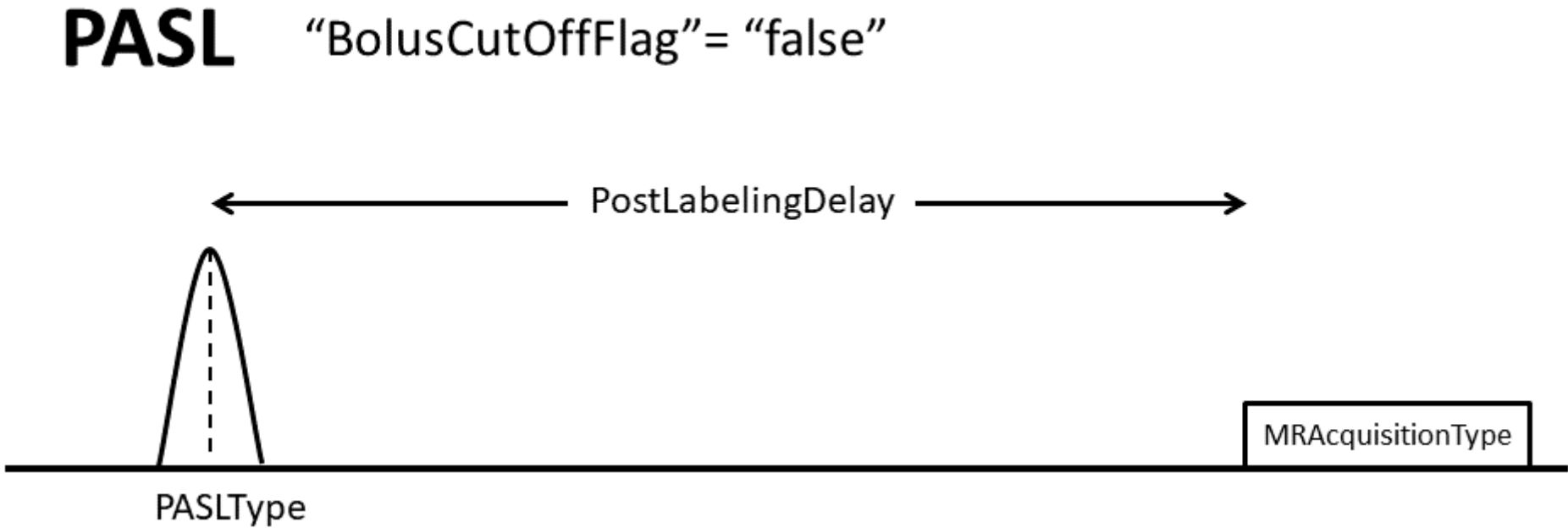
## (P)CASL Labeling Pulses

**PCASL**

- A: LabelingPulseAverageGradient
- B: LabelingPulseMaximumGradient
- C: LabelingPulseAverageB1
- D: LabelingPulseDuration
- E: LabelingPulseInterval

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.

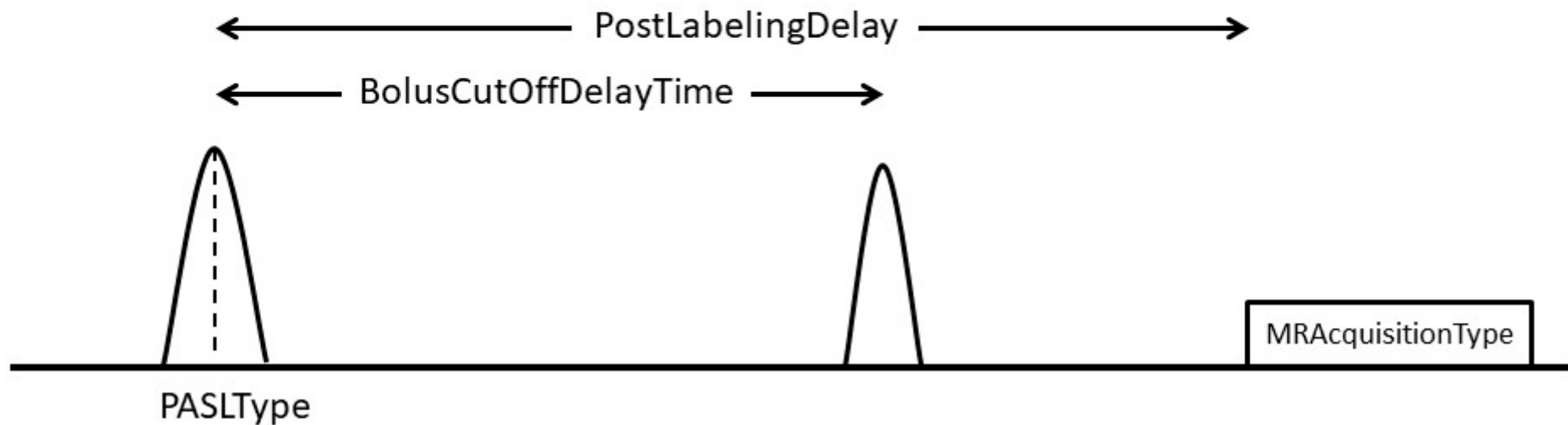
PASL sequence



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.

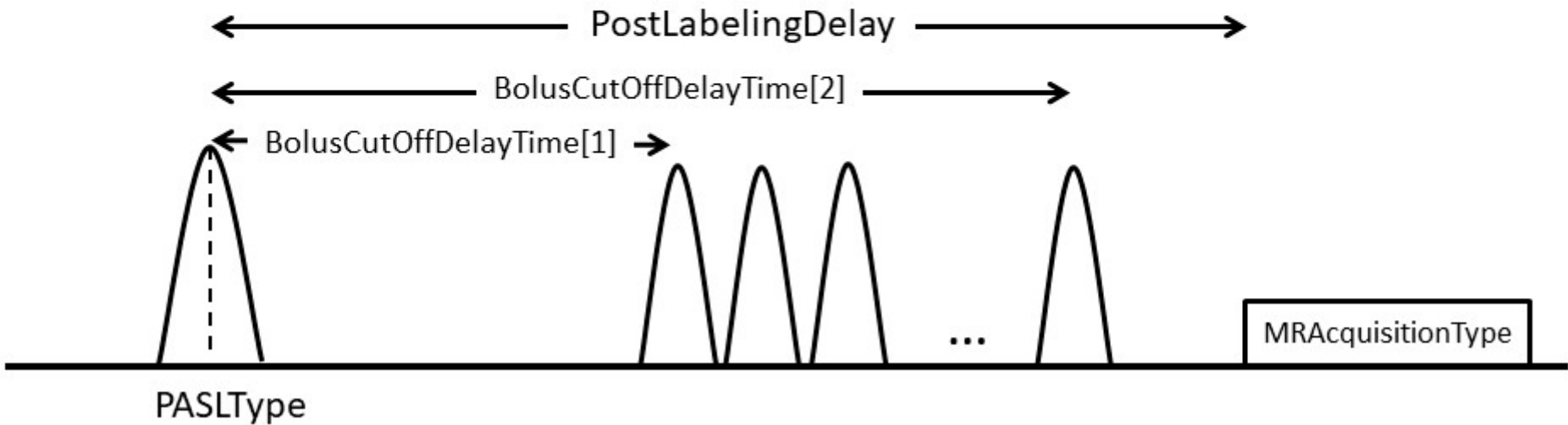


**PASL** “BolusCutOffFlag”= “true”  
“BolusCutOffTechnique”= “QUIPSS-II”



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.

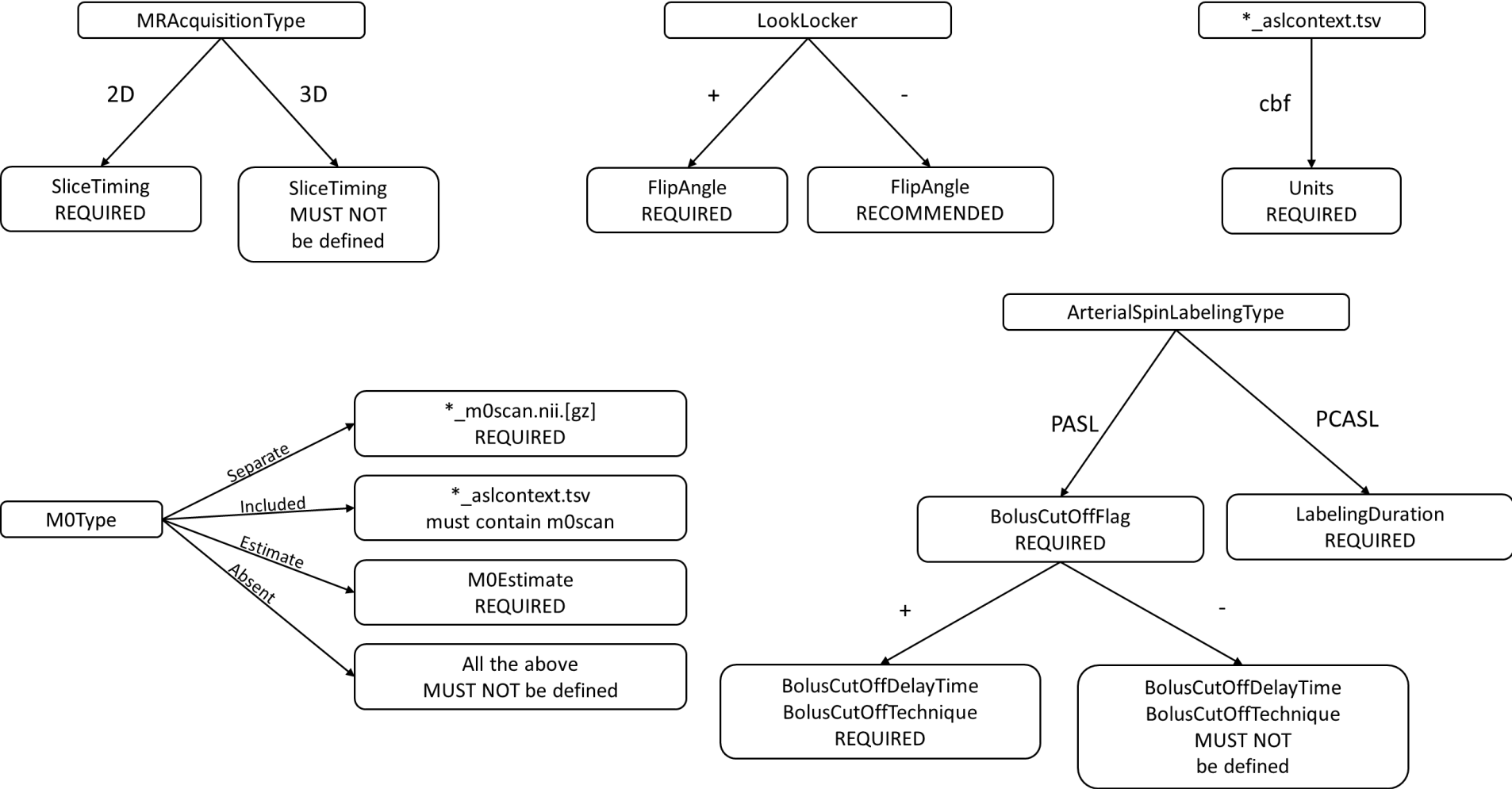
**PASL**    “BolusCutoffFlag”= “true”  
              “BolusCutoffTechnique”= “Q2TIPS”



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.



# 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](https://doi.org/10.1177/0271678X20905433); Norgaard et al. 2019, [doi:10.1016/j.neuroimage.2019.05.055](https://doi.org/10.1016/j.neuroimage.2019.05.055)).

## MRS-MRI correspondence

It is typical to acquire high-resolution 3D anatomical MR images alongside MRS data for voxel/slab placement, co-registration, and partial-volume tissue correction of metabolite concentrations. To avoid incorrectly matching an MRS dataset with a corresponding anatomical MR image, it is RECOMMENDED that the field `AnatomicalImage` be included in the MRS sidecar JSON files.

# Changelog

## v1.11.0 (2026-02-04)

- [ENH] BEP020 - Eye Tracking [#1128](#)
- [ENH] BEP038 - Atlases [#1714](#)
- [ENH] BEP042 - Electromyography (EMG) [#1998](#)
- [ENH] Add another example to inheritance principle for .json without entities [#2019](#) ([yarikoptic](#))
- [ENH] Clarify that "raw dataset" source data in example layout is a raw BIDS dataset [#2210](#) ([yarikoptic](#))
- [ENH] Add human statement to emphasize that \_desc is the last entity [#1915](#) ([yarikoptic](#))
- [ENH] Make Pharmaceutical metadata terms less PET-specific [#2294](#) ([yarikoptic](#))
- [ENH] Updated HED Version to 8.4.0 in examples [#2237](#) ([VisLab](#))
- [ENH] Clarify that "source datasets" do not have to be BIDS, and provide definitions for DOI and URL [#2203](#) ([yarikoptic](#))
- [ENH] Clearly define dual templates (fsaverage, fsaverageSym, and fsLR) in coordinate systems appendix [#1927](#) ([tsalo](#))
- [ENH] Add entity tables for motion, NIRS and MRS [#2209](#) ([JuliusWelzel](#))
- [FIX] Add desc- entity name into descriptions.tsv example [#2281](#) ([yarikoptic](#))
- [FIX] Update navigation with respect to the bids-starter-kit [#2297](#) ([kabilar](#))
- [FIX] Correct bval and clarify bvec descriptions [#2304](#) ([kabilar](#))
- [FIX] Add DWI recommended metadata table [#2308](#) ([kabilar](#))

## v1.10.1 (2025-09-03)

- [ENH] Expand fieldmaps section to include B1 maps, including qMRI maps [#2183](#) ([tsalo](#))
- [ENH] Clarify that task label is not required to derive from TaskName [#2179](#) ([effigies](#))
- [ENH] Remove explicitly worded requirement of events file association with the task [#1440](#) ([yarikoptic](#))
- [ENH] Clarify that recording entity may be used to distinguish recording instruments [#2090](#) ([drammock](#))
- [ENH] Specify that dir- should correspond to PhaseEncodingDirection [#2097](#) ([effigies](#))
- [ENH] Allow direction entity in MESE files [#2100](#) ([tsalo](#))
- [ENH] Add "study" DatasetType to organize a collection of source and derivative datasets [#1972](#) ([yarikoptic](#))

- [ENH] Deprecate 89+ string for default age column, increase expressiveness of column definitions in sidecar files [#2162](#) ([effigies](#))
- [ENH] Update extension citations in Introduction [#2168](#) ([markmikkelsen](#))
- [ENH] Add "Keywords" to `dataset_description.json` [#2158](#) ([markmikkelsen](#))
- [ENH] Update AcquisitionDuration definition to match DICOM, define FrameAcquisitionDuration for sparse sequences [#1974](#) ([effigies](#))
- [ENH] Inheritance Principle: Advise against value overloading. Plan to deprecate support for overloading for BIDS 2.0 [#1834](#) ([Lestropie](#))
- [ENH] Allow `mod-*` entity to relate physio data to MRI data in `anat/` [#1991](#) ([tstoeter](#))
- [ENH] Accept UTC offsets in datetimes [#2001](#) ([effigies](#))
- [ENH] Clarify that electrodes.tsv are REQUIRED for iEEG data [#1896](#) ([effigies](#))
- [ENH] Allow additional columns if defined for various TSV files [#2054](#) ([effigies](#))
- [ENH] Reorganise modality agnostic files section into multiple pages [#2106](#) ([bclenet](#))
- [ENH] Define "phenotype" as a data type not nested inside subjects [#2050](#) ([effigies](#))
- [ENH] Formalize presence of optional docs/ folder [#2104](#) ([yarikoptic](#))
- [ENH] Clarify definition of space entity [#2105](#) ([effigies](#))
- [ENH] Formalize presence of optional logs/ folder [#1962](#) ([yarikoptic](#))
- [ENH] Add `matches` and `source_entity` to glossary and file templates [#1781](#) ([Remi-Gau](#))
- [ENH] Allow plus signs in labels [#1926](#) ([tsalo](#))
- [ENH] Allow participants.tsv to contain a superset of subject directories and subjects listed in phenotype files [#2044](#) ([ericearl](#))
- [ENH] Allow LICENSE files to have .txt, .md, or .rst extensions [#2036](#) ([monique2208](#))
- [ENH] Render code blocks with language "tsv" as tables [#1794](#) ([effigies](#))
- [ENH] Do explicitly "allow" for having dotfiles and explicitly ignore them [#1992](#) ([yarikoptic](#))
- [ENH] Add interpretation of "n/a" onsets in events.tsv files [#1966](#) ([Remi-Gau](#))
- [ENH] Update DWI suffixes to include most common scanner derivatives [#1864](#) ([Lestropie](#))
- [FIX] Update ResonantFrequency and SpectrometerFrequency to support both string/number and arrays [#2172](#) ([markmikkelsen](#))
- [FIX] Rescope or downgrade excess RECOMMENDED fields [#2116](#) ([effigies](#))
- [FIX] Remove incorrect DICOM correspondence of PartialFourier [#2128](#) ([effigies](#))
- [FIX] Re-align the text and the schema for filenames in derivatives [#1567](#) ([mguaypaq](#))
- [FIX] Show example defaced derivative in a pipeline subdirectory [#2065](#) ([robertoostenveld](#))
- [FIX] Remove reference to dicm2nii and point to page with more converters [#2119](#) ([yarikoptic](#))
- [FIX] Fix typos in specification about iEEG photo [#2091](#) ([qian-chu](#))
- [FIX] Allow (but discourage) task, acquisition and run entities for coordsystem.json and electrodes.tsv [#1888](#) ([effigies](#))

## [v1.10.0](#) (2024-09-06)

- [ENH] Add noRF and n/a ASL volume types [1884](#) ([tsalo](#))
- [ENH] Provide baseline definition for behavioral files [1907](#) ([effigies](#))
- [ENH] Add metadata fields for DeIdentificationMethod/CodeSequence for MRI and PET [1772](#) ([CGSchwarzMayo](#))
- [ENH] Apply derivative definition to qMRI appendix [1813](#) ([Remi-Gau](#))
- [ENH] BEP022 - Magnetic Resonance Spectroscopy [1377](#) ([markmikkelsen](#))
- [ENH] MRI: Improve definition of bvec file [1811](#) ([Lestropie](#))
- [ENH] Add TablePosition tag to MRI [1690](#) ([po09i](#))

- [ENH] Add explicit wording on DICOM terms correspondence [1450](#) ([yarikoptic](#))
- [ENH] Generalize Units definition to apply to any variable, including TSV columns [1849](#) ([yarikoptic](#))
- [ENH] Add use of session entity as example of encoding multi-site studies in a single dataset [1803](#) ([yarikoptic](#))
- [ENH] Describe Inheritance Principle in Common Principles [1807](#) ([Lestropie](#))
- [ENH] Use deidentification consistently in place of anonymization [1799](#) ([DimitriPapadopoulos](#))
- [ENH] Allow .bval and .bvec files for pepolar fmaps [1754](#) ([mattcieslak](#))
- [ENH] Add noRF suffix for MR excitation-free noise scans [1451](#) ([tsalo](#))
- [ENH] Add warning about deidentification when sharing sourcedata [1769](#) ([Remi-Gau](#))
- [ENH] Use "Tag XXXX, YYYY" not "Tag (XXXX,YYYY)" for DICOM Tags [1758](#) ([yarikoptic](#))
- [ENH] Add generic metadata from BEP22 to MRI [1396](#) ([Remi-Gau](#))
- [ENH] events.tsv should be sorted by onset values [1732](#) ([Remi-Gau](#))
- [ENH] Add compressed TSV files to the common principles [1749](#) ([oesteban](#))
- [ENH] Add support for HiP-CT [1686](#) ([balbast](#))
- [ENH] Add sample metadata to MRI and PET [1593](#) ([effigies](#))
- [ENH] Clarify the relation of motion.tsv columns to channels.tsv rows [1699](#) ([effigies](#))
- [ENH] Describe parametric images above the suffix table, rather than below [1687](#) ([CPernet](#))
- [FIX] Define a metadata table for TB1EPI [1912](#) ([effigies](#))
- [FIX] Update text to reflect that BackgroundSuppressionPulseTime is recommended [1891](#) ([michaelf500](#))
- [FIX] Remove extra bracket [1865](#) ([kabilar](#))
- [FIX] Change hipCT microscopy suffix to XPCT [1822](#) ([chourroutm](#))
- [FIX] Consistently refer to Neuromag/Elekta/MEGIN [1310](#) ([sappelhoff](#))
- [FIX] Re-add run entity to electrodes.tsv [1722](#) ([effigies](#))
- [FIX] Move rawdata/ into sourcedata/raw in alternative structure example, clarify on naming of datasets themselves [1741](#) ([yarikoptic](#))
- [FIX] Move \_stim.<ext> specification within the Task Events module [1750](#) ([oesteban](#))
- [FIX] Remove mentions of sourcedata in the datatype specific pages [1737](#) ([Remi-Gau](#))
- [FIX] Add missing files in filename template for NIRS [1716](#) ([Remi-Gau](#))
- [FIX] Remove task entity from DWI and PERF time series file templates [1703](#) ([Remi-Gau](#))
- [FIX] Add part-<value> to the PEPOLAR fieldmaps [1685](#) ([oesteban](#))
- [INFRA] Publish schema to Javascript Registry (<https://jsr.io/@bids/schema>) on changes and releases [1899](#) ([effigies](#))
- [INFRA] Introduce metaschema [1787](#) ([bendichter](#))
- [MISC] Restructure MEG empty room example texts [1677](#) ([guiomar](#))

## v1.9.0 (2023-11-20)

- [ENH] Add descriptions.tsv file relating to the desc-<label> entity [#1613](#) ([CPernet](#))
- [INFRA] Publish schema tools API docs to additional ReadTheDocs site [#1491](#) ([bendhouseart](#))
- [ENH] Extend BIDS for Motion data (BEP029) [#981](#) ([JuliusWelzel](#))
- [FIX] mention phenotype dir in folder structure [#1644](#) ([Remi-Gau](#))
- [ENH] add ElectricalStimulation and \*Parameters metadata to MEEG jsons [#1638](#) ([sappelhoff](#))
- [FIX] years and degrees Units and unit to be singular to match the rest [#1631](#) ([yarikoptic](#))

- [FIX] Hierarchical Event Descriptors (HED) page update [#1623](#) ([effigies](#))
- [FIX] Do not require notch frequencies to be parsed as numbers, accommodating multiples [#1605](#) ([effigies](#))
- [ENH] Allow Levels field of column descriptions to be objects with TermURLs for each level [#1603](#) ([Remi-Gau](#))
- [ENH] Add optional low\_cutoff and high\_cutoff columns for fnirs channels.tsv [#1597](#) ([Remi-Gau](#))
- [FIX] Recommend SliceTiming if MRAcquisitionType is "2D" [#1594](#) ([tsalo](#))
- [ENH] Add Level objects to channels.json for motion [#1591](#) ([effigies](#))
- [ENH] Add "chunk" entity to MRI datatype [#1586](#) ([valosekj](#))
- [SCHEMA][ENH] Remove atlas entity and replace it with seg in prep of BEP038 [#1579](#) ([melanieganz](#))
- [FIX] Correct PDw suffix description [#1578](#) ([jeremie-fouquet](#))
- [FIX] improve longitudinal example [#1576](#) ([Remi-Gau](#))
- [INFRA] Adds Kim Ray as maintainer. [#1571](#) ([arokem](#))
- [ENH] Allow for "echo" entity to be used with T1w and other nonparametric anatomical suffixes [#1570](#) ([yarikoptic](#))
- [FIX] Update templates in modality-agnostic-files [#1564](#) ([sappelhoff](#))
- [FIX] Clarify that electrodes.tsv is optional for MEG, for use with simultaneous (i)EEG [#1555](#) ([effigies](#))
- [ENH] Allow UNKNOWN and NONE ContrastBolusIngredients [#1547](#) ([Remi-Gau](#))
- [FIX] Update links to BIDS examples [#1545](#) ([Remi-Gau](#))
- [ENH] add schema in appendix [#1543](#) ([Remi-Gau](#))
- [ENH] add "visual correction" and "head stabilization" metadata [#1539](#) ([Remi-Gau](#))
- [ENH] Clarify meaning of raw vs derivative datasets [#1537](#) ([CPernet](#))
- [FIX] match subject label in folder and filename in func example [#1536](#) ([Remi-Gau](#))
- [FIX] Trail MEG directory formats with / [#1534](#) ([effigies](#))
- [ENH] Permit CITATION.cff as structured alternative to some dataset\_description fields [#1525](#) ([effigies](#))
- [FIX] Add missing column description in physio example [#1514](#) ([sappelhoff](#))
- [ENH] Clarify that data files must be uniquely identified by entities/suffix [#1508](#) ([sappelhoff](#))
- [FIX] Remove references to unspecified aslcontext.json [#1485](#) ([Remi-Gau](#))
- [ENH] Define channel column for events and Delimiter field for column descriptions [#1483](#) ([effigies](#))
- [FIX] Revert index (entity format) definition to be a non-negative number, permitting zero [#1482](#) ([TheChymera](#))
- [FIX] Clean up qMRI RB1COR notes [#1465](#) ([lukeje](#))
- [ENH] Allow fractional seconds in StartTime [#1459](#) ([sappelhoff](#))
- [MISC] consistently list filename templates; ext --> extension; \_photo.jpg --> \_photo.<extension> [#1458](#) ([sappelhoff](#))
- [FIX] Demote sample and value columns in events.tsv from OPTIONAL to arbitrary [#1457](#) ([sappelhoff](#))
- [ENH] Clarify shape of PDT2 images and recommend acq entity for split PDw/T2w images [#1448](#) ([effigies](#))
- [ENH] clarify guiding principles for requirement levels [#1444](#) ([sappelhoff](#))
- [FIX] Clarify that dataset\_description.Genetics object is required for genetics data [#1442](#) ([sappelhoff](#))
- [ENH] Clarify that BIDS specification is in American English [#1439](#) ([yarikoptic](#))
- [MISC] Link to new BEP guidelines. [#1426](#) ([arokem](#))
- [FIX] reorganize anat filename templates [#1419](#) ([Remi-Gau](#))
- [FIX] Rename channels.tsv column: orientation\_component to component [#1417](#) ([sjeung](#))
- [ENH] Some missing docstrings for bidschematools [#1413](#) ([anibalsolon](#))
- [FIX] fixing some minor issues introduced recently [#1411](#) ([yarikoptic](#))



- [ENH] Add paragraph about richness versus distinctness in filenames [#1392](#) (CPernet)
- [FIX] Updated HED score library version [#1390](#) (VisLab)
- [FIX] Updated links and fixed typos in hed appendix [#1383](#) (VisLab)
- [ENH] add screen parameters metadata [#1369](#) (Remi-Gau)
- [MISC] allow for any "recording" file to be listed in \_scans.tsv not just "neural recording" [#1368](#) (yarikoptic)
- [FIX] wrong usage of DOI in SourceDatasets example [#1361](#) (sappelhoff)
- [FIX] make references to Neuromag/Elekta/MEGIN consistent [#1359](#) (sappelhoff)
- [ENH] Add reference for ASL BEP [#1357](#) (Remi-Gau)
- [FIX] remove redundant entity definitions in behavioral page [#1356](#) (Remi-Gau)
- [FIX] add missing processing entity for MEG physio files and render physio filename templates for fNIRS [#1355](#) (Remi-Gau)
- [ENH] Recommend gzip header fields be set to empty values [#1349](#) (kousu)
- [FIX] clarify TriggerChannelCount and TRIG type [#1342](#) (sappelhoff)
- [ENH] Add qMRI fieldmap filename templates [#1336](#) (Remi-Gau)
- [ENH] Introduce GIFTI formats in derivatives [#1333](#) (effigies)
- [ENH] Add ParallelReductionFactorOutOfPlane to MRI metadata [#1221](#) (lukeje)
- [ENH][SCHEMA] Adding an OPTIONAL \_task-<label> to structural MRI acquisitions [#1185](#) (melanieganz)
- [INFRA] use tributors to list contributors and CITATION.cff for referencing [#1115](#) (Remi-Gau)
- [SCHEMA] Add full object definitions for valid values in schema [#919](#) (tsalo)

## v1.8.0 (2022-10-29)

- [ENH] allow for .png and .tif in eeg/ieeg/meg as allowed for micr [#1049](#) (yarikoptic)
- [ENH] Add BIDS URIs and deprecate relative paths, RawSources and (possibly unused) BasedOn [#918](#) (effigies)
- [FIX] Drop the functional and f for NIRS [#1325](#) (rob-luke)
- [FIX][SCHEMA] Add conditionals for PET ReconMethod\* and ReconFilter [#1299](#) (bendhouseart)
- [ENH] use schema to mention which "top directories" are allowed [#1289](#) (Remi-Gau)
- [ENH] Add glossary links to all tables [#1268](#) (tsalo)
- [ENH] Remove redundant entity definitions on MRI page [#1265](#) (tsalo)
- [ENH] Standardize and organize entity descriptions [#1264](#) (tsalo)
- [ENH] Add filename template legend [#1259](#) (Remi-Gau)
- [MISC] Reorder appendices [#1256](#) (tsalo)
- [MISC] Clarify: FieldMap PE technique --> no SPM [#1253](#) (CPernet)
- [MISC] Adding qMRI BIDS article reference (BEP001) [#1251](#) (agahkarakuzu)
- [ENH] Link to filename element definitions in filename templates [#1228](#) (tsalo)
- [MISC] Remove label format and inheritance principle redundancies in fMRI section [#1197](#) (Remi-Gau)
- [ENH] add task metadata to PET [#1196](#) (Remi-Gau)
- [FIX] clarify which file to list in scans.tsv for file formats with multiple files [#1178](#) (sappelhoff)
- [FIX] add recommendation to fully omit non-compulsory data that is n/a [#1171](#) (sappelhoff)
- [FIX] Discourage use of "sample" in events if sampling frequency is ambiguous, add guidelines for precision [#1140](#) (sappelhoff)
- [FIX] Clarify MEG empty-room recommendations [#1125](#) (robertoostenveld)

- [FIX] clarify no blank and duplicated headers in TSV [#1116](#) ([sappelhoff](#))
- [ENH] Added the specification for using HED libraries in BIDS [#1106](#) ([VisLab](#))
- [ENH] Microscopy: NGFF format support [#1104](#) ([TheChymera](#))
- [ENH] Add Microscopy-BIDS citation [#1102](#) ([mariehbouquet](#))
- [FIX] MEG link typo [#1100](#) ([xi](#))
- [FIX] IntendedFor in (i)EEG is dataset relative [#1093](#) ([sappelhoff](#))
- [MISC] make dataset\_description.Authors RECOMMENDED [#1092](#) ([sappelhoff](#))
- [ENH] adding optional \_rec-label to DWI [#1090](#) ([dorahtermes](#))
- [SCHEMA] Conform the schema/rules files consistently [#1078](#) ([ericearl](#))
- [ENH] State of the schema sprint [#1075](#) ([effigies](#))
- SCHEMA: Convert datatype lists to objects [#1074](#) ([effigies](#))
- [SCHEMA] Define common derivatives rules [#1072](#) ([rwblair](#))
- [SCHEMA] Define blood.tsv columns [#1070](#) ([rwblair](#))
- [SCHEMA] Create context schema in meta/ [#1069](#) ([effigies](#))
- [SCHEMA] Replace addendum with description\_addendum [#1066](#) ([tsalo](#))
- [SCHEMA] Encode requirement levels for dataset\_description and genetic\_info [#1064](#) ([effigies](#))
- [SCHEMA] Correlating existing validator issues to schema entries [#1063](#) ([bendhouseart](#))
- [SCHEMA] Specify column requirement levels for several tabular files [#1061](#) ([effigies](#))
- [SCHEMA] Start drafting validation rules for ASL data [#1060](#) ([tsalo](#))
- [SCHEMA] Add MEG, func, and fmap metadata tables [#1054](#) ([tsalo](#))
- [MISC] Preface each macro call with comment [#1052](#) ([Remi-Gau](#))
- [FIX] typo in "rawdata" example [#1045](#) ([sappelhoff](#))
- [MISC] consistently use "directory" instead of "folder" as a term [#1044](#) ([sappelhoff](#))
- [MISC] Update CODEOWNERS [#1040](#) ([erdalkaraca](#))
- [ENH] Allow README file extensions. [#1033](#) ([mateuszpawlik](#))
- [MISC] Rewrite and update html build instructions [#1032](#) ([sappelhoff](#))
- [FIX] Clarify that BIDS standard template data is to be in scanner coordinates (MEG, iEEG, EEG) [#1031](#) ([alexrockhill](#))
- [SCHEMA] Define YAML tables for DWI/ASL/(i)EEG/micr/beh metadata [#1029](#) ([tsalo](#))
- [FIX] Add coordsystem-specific definition of DigitizedHeadPoints [#1023](#) ([tsalo](#))
- [FIX] PET Spec; added known DICOM tags, fixed tag error, updated citation, clarified scale factor. [#1021](#) ([bendhouseart](#))
- [MISC] clarify copyright for logo [#1019](#) ([sappelhoff](#))
- [SCHEMA] Define YAML tables for MRI common metadata fields and anatomy data [#1017](#) ([tsalo](#))
- SCHEMA: Encode first two MR metadata tables as "sidecars.yml" [#1016](#) ([tsalo](#))
- [SCHEMA] Add datatypes field to datatype rule files [#1012](#) ([tsalo](#))
- [FIX] Change recording entity to REQUIRED for pet/blood modality [#1005](#) ([ghisvail](#))
- [ENH] Microscopy: Add IntendedFor metadata field to photo files [#1000](#) ([mariehbouquet](#))
- [ENH] Introduce the atlas entity for derivatives data [#997](#) ([sebastientourbier](#))
- [ENH] Clearly define "entity" in common principles [#947](#) ([Lestropie](#))
- [ENH] BEP030: Functional Near-Infrared Spectroscopy [#802](#) ([rob-luke](#))
- [FIX] Clarify run entity to accommodate multiple imaging modalities [#760](#) ([yarikoptic](#))

## v1.7.0 (2022-02-15)

- [ENH] add metadata to PET calibration factor: "DoseCalibrationFactor" [#825](#) (CPernet)
- [FIX] 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)
- [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)
- [MISC] update steering group composition [#976](#) (Remi-Gau)
- [MISC] 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] Reword front page [#958](#) (arokem)
- [MISC] 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)
- Address BEP031 macro requests [#945](#) (tsalo)
- [FIX] Typo: ECG\_headshape [#942](#) (Moo-Marc)
- [FIX] description: dwi is specialized T2 weighting, not T2\* [#939](#) (sappelhoff)
- [FIX] relax unrealistically strict requirements with iieg channels.tsv 'name' column [#938](#) (sappelhoff)
- [FIX] Add links from derivatives section to entity list [#936](#) (sappelhoff)
- [FIX] Remove repeated words [#934](#) (DimitriPapadopoulos)
- [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)
- [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)
- [FIX] small typo in json example [#897](#) (Remi-Gau)
- [INFRA] Document \*.webm video files as binary [#895](#) (DimitriPapadopoulos)
- [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](#) (mariebourget)

- [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](#))
- [MISC] 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 .lgtn.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](#))
- [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](#))
- [FIX] correct file location of scans.tsv file in example [#824](#) ([ghisvail](#))
- [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](#) ([mariehbouquet](#))
- [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](#) ([mariehbouquet](#))
- [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)

- [ENH] Bep 009: Positron Emission Tomography [#633](#) ([melanieganz](#))
- [FIX] Typos discovered by codespell [#784](#) ([yarikoptic](#))
- [FIX] Rename "Unit" metadata to "Units" for consistency with existing fields [#773](#) ([effigies](#))
- [FIX] typo in pet: institutional -> institutional [#771](#) ([sappelhoff](#))
- [INFRA] install git in linkchecker job [#767](#) ([sappelhoff](#))
- [INFRA] Fix CircleCI workflows [#764](#) ([sappelhoff](#))
- [FIX] Mix up (typo) between fcduals 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](#))
- [MISC] move schema documentation into the schema directory [#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](#))

## v1.5.0 (2021-02-23)

- [ENH] Add "multipart DWI" acquisitions and refactor DWI specifications [#624](#) ([oesteban](#))
- [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](#))
- [MISC] 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](#) ([glmflndn](#))
- [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](#))
- [SCHEMA] Render schema elements in text [#610](#) ([tsalo](#))
- [ENH] Add part entity for complex-valued data [#424](#) ([tsalo](#))

## v1.4.1 (2020-10-13)

- [ENH] Extend date time information to include optional UTC syntax, warn about FIF requirements [#546](#) ([sappelhoff](#))
- [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 \(tsalo\)](#)
- Updating the bep009 with the latest master branch updates [#576 \(melanieganz\)](#)
- [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 \(roberttoostenveld\)](#)
- [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 \(adam2392\)](#)
- [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] 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)

- [ENH] Derived (processed) MR data [#109](#) ([chrisgorgo](#))
- [FIX] Clarify language on unsetting a key/value pair [#495](#) ([nicholst](#))
- [ENH] Add RECOMMENDED DatasetType key to dataset description [#494](#) ([effigies](#))
- [ENH] Clarify mask/dseg/probseg in common derivatives [#489](#) ([effigies](#))
- [ENH] Reorganize derivatives [#488](#) ([effigies](#))
- [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](#))
- [INFRA] add zenodo badge to README [#447](#) ([sappelhoff](#))
- [FIX] fix inconsistencies for task label between sections [#446](#) ([Remi-Gau](#))
- [FIX] update DECISION-MAKING.md document with new governance [#441](#) ([sappelhoff](#))
- [FIX] specify the derivatives pipeline following [#345](#) [#358](#) ([CPernet](#))
- [ENH] Clarify the position toward non-compliant derivative datasets and files [#334](#) ([effigies](#))
- [FIX] Separate out imaging-specific "common derivatives" [#310](#) ([effigies](#))
- [FIX] Revise template-generated coordinate systems [#307](#) ([oesteban](#))
- [ENH] Add `res` and `den` keywords to indicate resolution of resampled data [#301](#) ([oesteban](#))
- [ENH] BEP 003: Common Derivatives [#265](#) ([effigies](#))
- [FIX] use `<label>` for `_desc-` - not some `<value>` + clarify `<value>` [#224](#) ([yarikoptic](#))
- [ENH] Various proposed changes to diffusion derivatives [#205](#) ([Lestropie](#))
- [ENH] Add Glossary of terms/abbreviations used in the specification [#152](#) ([yarikoptic](#))



## v1.3.0 (2020-04-14)

- [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](#))
- [FIX] improve wording on data dictionaries [#410](#) ([sappelhoff](#))
- BEP 18 suggestions [#398](#) ([effigies](#))
- [ENH] BEP 018 - Genetic Information [#395](#) ([effigies](#))
- [FIX] consistent units description between EEG/MEG/iEEG. Clarify (derived) SI units + prefixes [#391](#) ([sappelhoff](#))

## v1.2.2 (2020-02-12)

- [FIX] Normalization of template-generated standard spaces [#306](#) ([oesteban](#))
- [MISC] update contributions by CPernet [#409](#) ([CPernet](#))
- [MISC] Add Sébastien Tourbier to contributors [#394](#) ([sebastientourbier](#))
- [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 directory 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](#) ([jasmmainak](#))
- [MISC] Add BEP027 - BIDS Execution to BEP list [#314](#) ([effigies](#))
- [FIX] Add CBV and phase to Entity table [#312](#) ([tsalo](#))
- [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)

- [INFRA] Add clarification on merge methods to DECISION\_MAKING [#217](#) ([sappelhoff](#))
- [FIX] repair link in anatomical MRI table [#297](#) ([sappelhoff](#))
- [ENH] Clarify requirements in Release Protocol [#294](#) ([franklin-feingold](#))
- [INFRA] 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] 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 directory 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](#))
- [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](#))
- [ENH] clarify decimal sep and numerical notation convention [#143](#) ([sappelhoff](#))
- [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)

- [ENH] Merge bep006 and bep010 [#108](#) ([sappelhoff](#))
- [INFRA] Update Pipfile.lock [#144](#) ([franklin-feingold](#))
- [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](#))
- [MISC] Adding formal decision-making rules [#104](#) ([chrisgorgo](#))
- [FIX] number of small corrections to the specification [#98](#) ([robertoostenveld](#))

## v1.1.2 (2019-01-10)

- [ENH] Global fields in data dictionaries [#117](#) ([chrisgorgo](#))
- [ENH] First(?) good practice recommendation. No excessive overrides in Inheritance principle [#99](#) ([yarikoptic](#))
- [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](#))
- [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](#))
- [FIX] additional table to recap 'volume acquisition timing' [#87](#) ([Remi-Gau](#))
- [FIX] Small typo in "scanning sequence" DICOM Tag [#84](#) ([Remi-Gau](#))
- [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](#))
- [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](#) ([patrick-g-h](#))
- [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 directory 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