Brain Imaging Data Structure Specification

v1.4.0

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Contents

Chapter 1

The Brain Imaging Data Structure

This resource defines the Brain Imaging Data Structure (BIDS) specification, including the core specification as well as many modality-specific extensions.

To get started, check out the introduction. If you'd like more information on how to adapt your own datasets to match the BIDS specification, we recommend exploring the bids-specification starter kit.

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

Chapter 2

Introduction

Motivation

Neuroimaging experiments result in complicated data that can be arranged in many different ways. So far there is no consensus how to organize and share data obtained in neuroimaging experiments. Even two researchers working in the same lab can opt to arrange their data in a different way. Lack of consensus (or a standard) leads to misunderstandings and time wasted on rearranging data or rewriting scripts expecting certain structure. Here we describe a simple and easy-to-adopt way of organising neuroimaging and behavioral data. By using this standard you will benefit in the following ways:

- It will be easy for another researcher to work on your data. To understand the organisation of the files and their format you will only need to refer them to this document. This is especially important if you are running your own lab and anticipate more than one person working on the same data over time. By using BIDS you will save time trying to understand and reuse data acquired by a graduate student or postdoc that has already left the lab.
- There are a growing number of data analysis software packages that can understand data organised according to BIDS (see http://bids.neuroimaging.io for the most up to date list).
- Databases such as OpenNeuro.org accept datasets organised according to BIDS. If you ever plan to share your data publicly (nowadays some journals require this) you can minimize the additional time and energy spent on publication, and speed up the curation process by using BIDS to structure and describe your data right after acquisition.
- Validation tools such as the BIDS Validator can check your dataset integrity and help you easily spot missing values.

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

Extensions

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

Citing BIDS

When referring to BIDS in context of academic literature please cite:

> 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. Sci Data 3, 160044.

as well as other papers describing specific BIDS extensions (see below).

BIDS has also a Research Resource Identifier (RRID) - `RRID:SCR_016124` - which you can also include in your manuscript in addition to citing the paper.

Chapter 3

Common principles

Definitions

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

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

1. **Dataset** - a set of neuroimaging and behavioral data acquired for a purpose of a particular study. A dataset consists of data acquired from one or more subjects, possibly from multiple sessions.
2. **Subject** - a person or animal participating in the study. Used interchangeably with term **Participant**.
3. **Session** - a logical grouping of neuroimaging and behavioral data consistent across subjects. Session can (but doesn’t have to) be synonymous to a visit in a longitudinal study. In general, subjects will stay in the scanner during one session. However, for example, if a subject has to leave the scanner room and then be re-positioned on the scanner bed, the set of MRI acquisitions will still be considered as a session and match sessions acquired in other subjects. Similarly, in situations where different data types are obtained over several visits (for example fMRI on one day followed by DWI the day after) those can be grouped in one session. Defining multiple sessions is appropriate when several identical or similar data acquisitions are planned and performed on all -or most- subjects, often in the case of some intervention between sessions (e.g., training).
4. **Data acquisition** - a continuous uninterrupted block of time during which a brain scanning instrument was acquiring data according to particular scanning sequence/protocol.
5. **Data type** - a functional group of different types of data. In BIDS we define eight data types: `func` (task based and resting state functional MRI), `dwi` (diffusion weighted imaging), `fmap` (field inhomogeneity mapping data such as field maps), `anat` (structural imaging such as T1, T2, etc.), `meg` (magnetoencephalography), `eeg` (electroencephalography), `ieeg` (intracranial electroencephalography), `beh` (behavioral).
6. **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.
7. **Event** - a stimulus or subject response recorded during a task. Each event has an onset time and duration. Note that not all tasks will have recorded events (e.g., “resting state”).
8. **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.
9. **`<index>`** - a numeric value, possibly prefixed with arbitrary number of 0s for consistent indentation, e.g., it is `01` in `run-01` following `run-<index>` specification.

10. `<label>` - an alphanumeric value, possibly prefixed with arbitrary number of 0s for consistent indentation, e.g., it is `rest` in `task-rest` following `task-<label>` specification.
11. **`suffix`** - an alphanumeric value, located after the `key-value_` pairs (thus after the final `_`), right before the **File extension**, e.g., it is `eeg` in `sub-05_task-matchingpennies_eeg.vhdr`.
12. **File extension** - a portion of the the file name 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.

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 file name 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 file name specified in the standard. This standard aspires to describe a majority of datasets, but acknowledges that there will be cases that do not fit. In such cases one can include additional files and subfolders to the existing folder structure following common sense. For example one may want to include eye tracking data in a vendor specific format that is not covered by this standard. The most sensible place to put it is next to the continuous recording file with the same naming scheme but different extensions. The solutions will change from case to case and publicly available datasets will be reviewed to include common data types in the future releases of the BIDS specification.

File name structure

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

For a data file that was collected in a given `session` from a given `subject`, the file name will begin with the string `sub-<label>_ses-<label>`.

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

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

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.

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). This specification currently does not go into details of recommending a particular naming scheme for including different types of source data (raw event logs, parameter files, etc. before conversion to BIDS). However, in the case that these data are to be included:

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

Alternatively one can organize their data in the following way

```
my_dataset/
  sourcedata/
    ...
  rawdata/
    dataset_description.json
    participants.tsv
    sub-01/
    sub-02/
    ...
  derivatives/
    pipeline_1/
    pipeline_2/
    ...
```

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

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

Storage of derived datasets

Derivatives can be stored/distributed in two ways:

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

   Example of derivatives with one directory per pipeline:

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

   Example of a pipeline with split derivative directories:

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

   Example of a pipeline with nested derivative directories:

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

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

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

```
my_processed_data/
  code/
    processing_pipeline-1.0.0.img
    hpc_submitter.sh
    ...
  sourcedata/
    dataset_description.json
    participants.tsv
    sub-01/
    sub-02/
    ...
  dataset_description.json
  sub-01/
  sub-02/
  ...
```

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

Non-compliant deriatives

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

The Inheritance Principle

Any metadata file (`.json`, `.bvec`, `.tsv`, etc.) may be defined at any directory level, but no more than one applicable file may be defined at a given level (Example 1). The values from the top level are inherited by all lower levels unless they are overridden by a file at the lower level. For example, `sub-*_task-rest_bold.json` may be specified at the participant level, setting TR to a specific value. If one of the runs has a different TR than the one specified in that file, another `sub-*_task-rest_bold.json` file can be placed within that specific series directory specifying the TR for that specific run. There is no notion of "unsetting" a key/value pair. Once a key/value pair is set in a given level in the dataset, lower down in the hierarchy that key/value pair will always have some assigned value. Files for a particular participant can exist only at participant level directory, i.e `/dataset/sub-*[/ses-*]/sub-*_T1w.json`. Similarly, any file that is not specific to a participant is to be declared only at top level of dataset for eg: `task-sist_bold.json` must be placed under `/dataset/task-sist_bold.json`

Example 1: Two JSON files that are erroneously at the same level

```
sub-01/
    ses-test/
        sub-01_ses-test_task-overtverbgeneration_bold.json
        sub-01_ses-test_task-overtverbgeneration_run-2_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
```

In the above example, two JSON files are listed under `sub-01/ses-test/`, which are each applicable to `sub-01_ses-test_task-overtverbgeneration_run-2_bold.nii.gz`, violating the constraint that no more than one file may be defined at a given level of the directory structure. Instead `sub-01_ses-test_task-overtverbgeneration_run-2_bold.json` should have been under `sub-01/ses-test/func/`.

Example 2: Multiple `runs` and `recs` with same acquisition (`acq`) parameters

```
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_rec-recon1_bold.nii.gz
        sub-01_task-xyz_acq-test1_rec-recon2_bold.nii.gz
        sub-01_task-xyz_acq-test1_bold.json
```

For the above example, all NIfTI files are acquired with same scanning parameters (`acq-test1`). Hence a JSON file describing the acq parameters will apply to different runs and rec files. Also if the JSON file (`task-xyz_acq-test1_bold.json`) is defined at dataset top level directory, it will be applicable to all task runs with `test1` acquisition parameter.

Example 3: Multiple JSON files at different levels for same task and acquisition parameters

```
task-xyz_acq-test1_bold.json
sub-01/
    anat/
    func/
        sub-01_task-xyz_acq-test1_run-1_bold.nii.gz
        sub-01_task-xyz_acq-test1_rec-recon1_bold.nii.gz
        sub-01_task-xyz_acq-test1_rec-recon2_bold.nii.gz
        sub-01_task-xyz_acq-test1_bold.json
```

In the above example, the fields from the `task-xyz_acq-test1_bold.json` file at the top directory will apply to all bold runs. However, if there is a key with different value in the `sub-01/func/sub-01_task-xyz_acq-test1_bold.json` file defined at a deeper level, that value will be applicable for that particular run/task NIfTI file/s. In other words, the `.json` file at the deeper level overrides values that are potentially also defined in the `.json` at a more shallow level. If the `.json` file at the more shallow level contains key-value-pairs that are not present in the `.json` file at the deeper level, these key-value-pairs are inherited by the `.json` file at the deeper level (but NOT vice versa!).

Good practice recommendations

Try to avoid excessive amount of overrides. Do not specify a field value in the upper levels if lower levels have more or less even distribution of multiple possible values. E.g., if a field `X` has one value for all `ses-01/` and another for all `ses-02/` it better not to be defined at all in the `.json` at the upper level.

File Formation specification

Imaging files

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

Tabular files

Tabular data MUST be saved as tab delimited values (`.tsv`) files, i.e., CSV files where commas are replaced by tabs. Tabs MUST be true tab characters and MUST NOT be a series of space characters. Each TSV file MUST start with a header line listing the names of all columns (with the exception of physiological and other continuous recordings). Names MUST be separated with tabs. It is RECOMMENDED that the column names in the header of the TSV file are written in `snake_case` with the first letter in lower case (e.g., `variable_name`, not `Variable_name`). String values containing tabs MUST be escaped using double quotes. Missing and non-applicable values MUST be coded as `n/a`. Numerical values MUST employ the dot (`.`) as decimal separator and MAY be specified in scientific notation, using `e` or `E` to separate the significand from the exponent. TSV files MUST be in UTF-8 encoding.

Example:

```
onset duration  response_time correct stop_trial  go_trial
200 200 0 n/a n/a n/a
```

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:

Field name	Definition
LongName	Long (unabbreviated) name of the column.
Description	Description of the column.
Levels	For categorical variables: a dictionary of possible values (keys) and their descriptions (values).
Units	Measurement units. `[<prefix symbol>] <unit symbol>` format following the SI standard is RECOMMENDED (see units section.
TermURL	URL pointing to a formal definition of this type of data in an ontology available on the web.

Example:

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

```
  "bmi": {
    "LongName": "Body mass index",
    "Units": "kilograms per squared meters",
    "TermURL": "http://purl.bioontology.org/ontology/SNOMEDCT/60621009"
  }
}
```

Key/value files (dictionaries)

JavaScript Object Notation (JSON) files MUST be used for storing key/value pairs. JSON files MUST be in UTF-8 encoding. Extensive documentation of the format can be found here: http://json.org/. 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: http://jsoneditoronline.org. It is RECOMMENDED that keys in a JSON file are written in CamelCase with the first letter in upper case (e.g., `SamplingFrequency`, not `samplingFrequency`). Note however, when a JSON file is used as an accompanying sidecar file for a TSV file, the keys linking a TSV column with their description in the JSON file need to follow the exact formatting as in the TSV file.

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

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

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

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

Participant names and other labels

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

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

Units

All units SHOULD be specified as per International System of Units (abbreviated as SI, from the French Système international (d'unités)) and can be SI units or SI derived units. In case there are valid reasons to deviate from SI units or SI derived units, the units MUST be specified in the sidecar JSON file. In case data is expressed in SI units or SI derived units, the units MAY be specified in the sidecar JSON file. In case non-standard prefixes are added to SI or non-SI units, these non-standard prefixed units MUST be specified in the JSON file. See Appendix V for a list of standard units and prefixes.

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.

Describing dates and timestamps:

- Date time information MUST be expressed in the following format `YYYY-MM-DDThh:mm:ss` (one of the ISO8601 date-time formats). For example: `2009-06-15T13:45:30`
- Time stamp information MUST be expressed in the following format: `13:45:30`
- Dates can be shifted by a random number of days for privacy protection reasons. To distinguish real dates from shifted dates always use year 1925 or earlier when including shifted years. For longitudinal studies please remember to shift dates within one subject by the same number of days to maintain the interval information. Example: `1867-06-15T13:45:30`
- 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, e.g., when scanning babies.

Directory structure

Single session example

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

```
sub-control01/
    anat/
        sub-control01_T1w.nii.gz
        sub-control01_T1w.json
        sub-control01_T2w.nii.gz
        sub-control01_T2w.json
    func/
        sub-control01_task-nback_bold.nii.gz
        sub-control01_task-nback_bold.json
        sub-control01_task-nback_events.tsv
        sub-control01_task-nback_physio.tsv.gz
        sub-control01_task-nback_physio.json
        sub-control01_task-nback_sbref.nii.gz
    dwi/
        sub-control01_dwi.nii.gz
        sub-control01_dwi.bval
        sub-control01_dwi.bvec
    fmap/
        sub-control01_phasediff.nii.gz
        sub-control01_phasediff.json
        sub-control01_magnitude1.nii.gz
        sub-control01_scans.tsv
code/
    deface.py
derivatives/
README
participants.tsv
dataset_description.json
CHANGES
```

Unspecified data

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

Non-standard files and directories should be named with care. Future BIDS efforts may standardize new entities and suffixes, changing the meaning of file names 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 file names.

Chapter 4

Modality agnostic files

Dataset description

Templates:

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

`dataset_description.json`

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

Field name	Definition
Name	REQUIRED. Name of the dataset.
BIDSVersion	REQUIRED. The version of the BIDS standard that was used.
DatasetType	RECOMMENDED. The interpretaton of the dataset. MUST be one of `"raw"` or `"derivative"`. For backwards compatibility, the default value is `"raw"`.
License	RECOMMENDED. The license for the dataset. The use of license name abbreviations is RECOMMENDED for specifying a license (see Appendix II). The corresponding full license text MAY be specified in an additional `LICENSE` file.
Authors	OPTIONAL. List of individuals who contributed to the creation/curation of the dataset.
Acknowledgements	OPTIONAL. Text acknowledging contributions of individuals or institutions beyond those listed in Authors or Funding.
HowToAcknowledge	OPTIONAL. 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. List of sources of funding (grant numbers).
EthicsApprovals	OPTIONAL. List of ethics committee approvals of the research protocols and/or protocol identifiers.
ReferencesAndLinks	OPTIONAL. List of references to publication that contain information on the dataset, or links.
DatasetDOI	OPTIONAL. The Document Object Identifier of the dataset (not the corresponding paper).

Example:

```
{
```

```
  "Name": "The mother of all experiments",
  "BIDSVersion": "1.4.0",
  "DatasetType": "raw",
  "License": "CC0",
  "Authors": [
    "Paul Broca",
    "Carl Wernicke"
  ],
  "Acknowledgements": "Special thanks to Korbinian Brodmann for help in formatting this dataset in BIDS. We thank Alan Lloyd Hodgkin and Andrew Huxley for helpful comments and discussions about the experiment and manuscript; Hermann Ludwig Helmholtz for administrative support; and Claudius Galenus for providing data for the medial-to-lateral index analysis.",
  "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. http://doi.org/1920.8/jndata.2015.7"
  ],
  "DatasetDOI": "10.0.2.3/dfjj.10"
}
```

Derived dataset and pipeline description

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

In addition to the keys for raw BIDS datasets, derived BIDS datasets include the following REQUIRED and RECOMMENDED `dataset_description.json` keys:

Key name	**Description**
GeneratedBy	REQUIRED. List of objects with at least one element.
SourceDatasets	RECOMMENDED. A list of objects specifying the locations and relevant attributes of all source datasets. Valid fields in each object include `URL`, `DOI`, and `Version`.

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

Key name	**Description**
Name	REQUIRED. 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. Version of the pipeline.
Description	OPTIONAL. Plain-text description of the pipeline or process that generated the outputs. RECOMMENDED if `Name` is `"Manual"`.
CodeURL	OPTIONAL. URL where the code used to generate the derivatives may be found.

Key name	Description
Container	OPTIONAL. Object specifying the location and relevant attributes of software container image used to produce the derivative. Valid fields in this object include `Type`, `Tag` and `URI`.

Example:

```
{
  "Name": "FMRIPREP Outputs",
  "BIDSVersion": "1.4.0",
  "DatasetType": "derivative",
  "GeneratedBy": [
    {
      "Name": "fmriprep",
      "Version": "1.4.1",
      "Container": {
        "Type": "docker",
        "Tag": "poldracklab/fmriprep:1.4.1"
        }
    },
    {
      "Name": "Manual",
      "Description": "Re-added RepetitionTime metadata to bold.json files"
    }
  ],
  "SourceDatasets": [
    {
      "DOI": "10.18112/openneuro.ds000114.v1.0.1",
      "URL": "https://openneuro.org/datasets/ds000114/versions/1.0.1",
      "Version": "1.0.1"
    }
  ]
}
```

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

README

In addition a free form text file (`README`) describing the dataset in more details SHOULD be provided. The `README` file MUST be either in ASCII or UTF-8 encoding.

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: http://search.cpan.org/~haarg/CPAN-Changes-0.400002/lib/CPAN/Changes/Spec.pod. The `CHANGES` file MUST be either in ASCII or UTF-8 encoding.

Example:

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

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

LICENSE

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

Participants file

Template:

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

The purpose of this RECOMMENDED file is to describe properties of participants such as age, sex, handedness etc. In case of single-session studies, this file has one compulsory column `participant_id` that consists of `sub-<label>`, followed by a list of optional columns describing participants. Each participant MUST be described by one and only one row.

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

- `age`: numeric value in years (float or integer value)
- `sex`: string value indicating phenotypical sex, one of ”male”, ”female”, ”other”
  - for ”male”, use one of these values: `male`, `m`, `M`, `MALE`, `Male`
  - for ”female”, use one of these values: `female`, `f`, `F`, `FEMALE`, `Female`
  - for ”other”, use one of these values: `other`, `o`, `O`, `OTHER`, `Other`
- `handedness`: string value indicating one of ”left”, ”right”, ”ambidextrous”
  - for ”left”, use one of these values: `left`, `l`, `L`, `LEFT`, `Left`
  - for ”right”, use one of these values: `right`, `r`, `R`, `RIGHT`, `Right`
  - for ”ambidextrous”, use one of these values: `ambidextrous`, `a`, `A`, `AMBIDEXTROUS`, `Ambidextrous`

Throughout BIDS you can indicate missing values with `n/a` (i.e., ”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`, and `handedness`, such as `group` in this example, or when a different age unit is needed (e.g., gestational weeks). If no `units` is provided for age, it will be assumed to be in years relative to date of birth.

`participants.json` example:

```
{
    "age": {
        "Description": "age of the participant",
        "Units": "years"
    },
    "sex": {
        "Description": "sex of the participant as reported by the participant",
        "Levels": {
            "M": "male",
            "F": "female"
```

```
        }
    },
    "handedness": {
        "Description": "handedness of the participant as reported by the participant",
        "Levels": {
            "left": "left",
            "right": "right"
        }
    },
    "group": {
        "Description": "experimental group the participant belonged to",
        "Levels": {
            "read": "participants who read an inspirational text before the experiment",
            "write": "participants who wrote an inspirational text before the experiment"
        }
    }
}
```

Phenotypic and assessment data

Template:

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

Optional: Yes

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

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

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

As with all other tabular data, the additional phenotypic information files MAY be accompanied by a JSON file describing the columns in detail (see Tabular files). In addition to the column description, a section describing the measurement tool (as a whole) MAY be added under the name `MeasurementToolMetadata`. This section consists of two keys:

- `Description`: A free text description of the measurement tool
- `TermURL`: A link to an entity in an ontology corresponding to this tool.

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

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

```
      "1": "YES",
      "2": "NO"
    }
  }
}
```

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

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

Scans file

Template:

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

Optional: Yes

The purpose of this file is to describe timing and other properties of each imaging acquisition sequence (each run `.nii[.gz]` file) within one session. Each `.nii[.gz]` file should be described by at most one row. Relative paths to files should be used under a compulsory `filename` header. If acquisition time is included it should be under `acq_time` header. Datetime should be expressed in the following format `2009-06-15T13:45:30[.000000]` (year, month, day, hour (24h), minute, second, and optionally fractional second; this is equivalent to the RFC3339 ”date-time” format, time zone is always assumed as local time). No specific precision is required for fractional seconds, but the precision SHOULD be consistent across the dataset For anonymization purposes all dates within one subject should be shifted by a randomly chosen (but consistent across all runs etc.) number of days. This way relative timing would be preserved, but chances of identifying a person based on the date and time of their scan would be decreased. Dates that are shifted for anonymization purposes should be set to a year 1925 or earlier to clearly distinguish them from unmodified data. Shifting dates is RECOMMENDED, but not required.

Additional fields can include external behavioral measures relevant to the scan. For example vigilance questionnaire score administered after a resting state scan.

Example:

```
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
```

Code

Template: `code/*`

Source code of scripts that were used to prepare the dataset (for example if it was anonymized or defaced) MAY be stored here.1 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.

1Storing 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).

Chapter 5

Magnetic Resonance Imaging

Common metadata fields

MR Data described in sections 8.3.x 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" by Ben Inglis:

Scanner Hardware

Field name	Definition
Manufacturer	RECOMMENDED. Manufacturer of the equipment that produced the composite instances. Corresponds to DICOM Tag 0008, 0070 `Manufacturer`
ManufacturersModelName	RECOMMENDED. Manufacturer's model name of the equipment that produced the composite instances. Corresponds to DICOM Tag 0008, 1090 `Manufacturers Model Name`
DeviceSerialNumber	RECOMMENDED. The serial number of the equipment that produced the composite instances. Corresponds to DICOM Tag 0018, 1000 `DeviceSerialNumber`. 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. Institution defined name of the machine that produced the composite instances. Corresponds to DICOM Tag 0008, 1010 `Station Name`
SoftwareVersions	RECOMMENDED. Manufacturer's designation of software version of the equipment that produced the composite instances. Corresponds to DICOM Tag 0018, 1020 `Software Versions`
HardcopyDeviceSoftwareVersion	(Deprecated) Manufacturer's designation of the software of the device that created this Hardcopy Image (the printer). Corresponds to DICOM Tag 0018, 101A `Hardcopy Device Software Version`
MagneticFieldStrength	RECOMMENDED. Nominal field strength of MR magnet in Tesla. Corresponds to DICOM Tag 0018,0087 `Magnetic Field Strength`
ReceiveCoilName	RECOMMENDED. Information describing the receiver coil. Corresponds to DICOM Tag 0018, 1250 `Receive Coil Name`, although not all vendors populate that DICOM Tag, in which case this field can be derived from an appropriate private DICOM field

Field name	Definition
ReceiveCoilActiveElements	RECOMMENDED. Information describing the active/selected elements of the receiver coil. This doesn't correspond to a tag in the DICOM ontology. The vendor-defined terminology for active coil elements can go in this field. As an example, 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 (e.g., `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
GradientSetType	RECOMMENDED. It should be possible to infer the gradient coil from the scanner model. If not, e.g. because of a custom upgrade or use of a gradient insert set, then the specifications of the actual gradient coil should be reported independently
MRTransmitCoilSequence	RECOMMENDED. This is a relevant field if a non-standard transmit coil is used. Corresponds to DICOM Tag 0018, 9049 `MR Transmit Coil Sequence`
MatrixCoilMode	RECOMMENDED. (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 (e.g. GRAPPA, SENSE) imaging
CoilCombinationMethod	RECOMMENDED. 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

Sequence Specifics

Field name	Definition
PulseSequenceType	RECOMMENDED. A general description of the pulse sequence used for the scan (i.e. MPRAGE, Gradient Echo EPI, Spin Echo EPI, Multiband gradient echo EPI).
ScanningSequence	RECOMMENDED. Description of the type of data acquired. Corresponds to DICOM Tag 0018, 0020 `Scanning Sequence`.
SequenceVariant	RECOMMENDED. Variant of the ScanningSequence. Corresponds to DICOM Tag 0018, 0021 `Sequence Variant`.
ScanOptions	RECOMMENDED. Parameters of ScanningSequence. Corresponds to DICOM Tag 0018, 0022 `Scan Options`.
SequenceName	RECOMMENDED. Manufacturer's designation of the sequence name. Corresponds to DICOM Tag 0018, 0024 `Sequence Name`.
PulseSequenceDetails	RECOMMENDED. Information beyond pulse sequence type that identifies the specific pulse sequence used (i.e. "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. Boolean stating if the image saved has been corrected for gradient nonlinearities by the scanner sequence.

In-Plane Spatial Encoding

Field name	Definition
NumberShots	RECOMMENDED. The number of RF excitations need to reconstruct a slice or volume. Please mind that this is not the same as Echo Train Length which denotes the number of lines of k-space collected after an excitation.
ParallelReductionFactorInPlane	RECOMMENDED. The parallel imaging (e.g, GRAPPA) factor. Use the denominator of the fraction of k-space encoded for each slice. For example, 2 means half of k-space is encoded. Corresponds to DICOM Tag 0018, 9069 `Parallel Reduction Factor In-plane`.
ParallelAcquisitionTechnique	RECOMMENDED. The type of parallel imaging used (e.g. GRAPPA, SENSE). Corresponds to DICOM Tag 0018, 9078 `Parallel Acquisition Technique`.
PartialFourier	RECOMMENDED. The fraction of partial Fourier information collected. Corresponds to DICOM Tag 0018, 9081 `Partial Fourier`.
PartialFourierDirection	RECOMMENDED. The direction where only partial Fourier information was collected. Corresponds to DICOM Tag 0018, 9036 `Partial Fourier Direction`.
PhaseEncodingDirection	RECOMMENDED. Possible values: `i`, `j`, `k`, `i-`, `j-`, `k-`. The letters `i`, `j`, `k` correspond to the first, second and third axis of the data in the NIFTI file. The polarity of the phase encoding is assumed to go from zero index to maximum index unless `-` sign is present (then the order is reversed - starting from the highest index instead of zero). `PhaseEncodingDirection` is defined as the direction along which phase is was modulated which may result in visible distortions. Note that this is not the same as the DICOM term `InPlanePhaseEncodingDirection` which can have `ROW` or `COL` values. This parameter is REQUIRED if corresponding fieldmap data is present or when using multiple runs with different phase encoding directions (which can be later used for field inhomogeneity correction).
EffectiveEchoSpacing	RECOMMENDED. 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 `DwellTime` parameter below for actual dwell time). It is required for unwarping distortions using field maps. Note that beyond just in-plane acceleration, a variety of other manipulations to the phase encoding need to be accounted for properly, including partial fourier, phase oversampling, phase resolution, phase field-of-view and interpolation.2 This parameter is REQUIRED if corresponding fieldmap data is present.
TotalReadoutTime	RECOMMENDED. This is actually the ”effective” total readout time , defined as the readout duration, specified in seconds, that would have generated data with the given level of distortion. It is NOT the actual, physical duration of the readout train. If `EffectiveEchoSpacing` has been properly computed, it is just `EffectiveEchoSpacing * (ReconMatrixPE - 1)`.3 . This parameter is REQUIRED if corresponding ”field/distortion” maps acquired with opposing phase encoding directions are present (see 8.9.4).

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

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

Timing Parameters

Field name	Definition
EchoTime	RECOMMENDED. The echo time (TE) for the acquisition, specified in seconds. This parameter is REQUIRED if corresponding fieldmap data is present or the data comes from a multi echo sequence. Corresponds to DICOM Tag 0018, 0081 `Echo Time` (please note that the DICOM term is in milliseconds not seconds).
InversionTime	RECOMMENDED. The inversion time (TI) for the acquisition, specified in seconds. Inversion time is the time after the middle of inverting RF pulse to middle of excitation pulse to detect the amount of longitudinal magnetization. Corresponds to DICOM Tag 0018, 0082 `Inversion Time` (please note that the DICOM term is in milliseconds not seconds).
SliceTiming	RECOMMENDED. 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 (in JSON format) 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 (i.e., the final entry in the `SliceTiming` list is the time of acquisition of slice 0). This parameter is REQUIRED for sparse sequences that do not have the `DelayTime` field set. In addition without this parameter slice time correction will not be possible.
SliceEncodingDirection	RECOMMENDED. Possible values: `i`, `j`, `k`, `i-`, `j-`, `k-` (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.
DwellTime	RECOMMENDED. Actual dwell time (in seconds) of the receiver per point in the readout direction, including any oversampling. For Siemens, this corresponds to DICOM field (0019,1018) (in ns). This value is necessary for the optional readout distortion correction of anatomicals in the HCP Pipelines. It also usefully provides a handle on the readout bandwidth, which isn't captured in the other metadata tags. Not to be confused with `EffectiveEchoSpacing`, and the frequent mislabeling of echo spacing (which is spacing in the phase encoding direction) as "dwell time" (which is spacing in the readout direction).

RF & Contrast

Field name	Definition
FlipAngle	RECOMMENDED. Flip angle for the acquisition, specified in degrees. Corresponds to: DICOM Tag 0018, 1314 `Flip Angle`.
MultibandAccelerationFactor	RECOMMENDED. The multiband factor, for multiband acquisitions.
NegativeContrast	OPTIONAL. Boolean (`true` or `false`) value specifying whether increasing voxel intensity (within sample voxels) denotes a decreased value with respect to the contrast suffix. This is commonly the case when Cerebral Blood Volume is estimated via usage of a contrast agent in conjunction with a T2* weighted acquisition protocol.

Slice Acceleration

Field name	Definition
MultibandAccelerationFactor	RECOMMENDED. The multiband factor, for multiband acquisitions.

Anatomical landmarks

Useful for multimodal co-registration with MEG, (S)EEG, TMS, etc.

Field name	Definition
AnatomicalLandmarkCoordinates	RECOMMENDED. 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, (e.g. `{"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]}`).

Institution information

Field name	Definition
InstitutionName	RECOMMENDED. The name of the institution in charge of the equipment that produced the composite instances. Corresponds to DICOM Tag 0008, 0080 `InstitutionName`.
InstitutionAddress	RECOMMENDED. The address of the institution in charge of the equipment that produced the composite instances. Corresponds to DICOM Tag 0008, 0081 `InstitutionAddress`.
InstitutionalDepartmentName	RECOMMENDED. The department in the institution in charge of the equipment that produced the composite instances. Corresponds to DICOM Tag 0008, 1040 `Institutional Department Name`.

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

Anatomy imaging data

Template:

```
sub-<label>/[ses-<label>/]
    anat/
        sub-<label>[_ses-<label>][_acq-<label>][_ce-<label>][_rec-<label>][_run-<index>]_<modality_label>.nii[.gz]
        sub-<label>[_ses-<label>][_acq-<label>][_ce-<label>][_rec-<label>][_run-<index>][_mod-<label>]_defacemask.nii[.gz]
```

Anatomical (structural) data acquired for that participant. Currently supported modalities include:

Name	`modality_label`	Description
T1 weighted	T1w	
T2 weighted	T2w	
T1 Rho map	T1rho	Quantitative T1rho brain imaging https://www.ncbi.nlm.nih.gov/pubmed/24474423 https://www.ncbi.nlm.nih.gov/pmc/articles/PMC4346383/

Name	`modality_label`	Description
T1 map	T1map	quantitative T1 map
T2 map	T2map	quantitative T2 map
T2*	T2star	High resolution T2* image
FLAIR	FLAIR	
FLASH	FLASH	
Proton density	PD	
Proton density map	PDmap	
Combined PD/T2	PDT2	
Inplane T1	inplaneT1	T1-weighted anatomical image matched to functional acquisition
Inplane T2	inplaneT2	T2-weighted anatomical image matched to functional acquisition
Angiography	angio	

The `run` entity

If several scans of the same modality are acquired they MUST be indexed with a key-value pair: `_run-1`, `_run-2`, `_run-3` etc. (only integers are allowed as run labels). When there is only one scan of a given type the run key MAY be omitted. Please note that diffusion imaging data is stored elsewhere (see below).

The `acq` entity

The OPTIONAL `acq-<label>` key/value pair corresponds to a custom label the user MAY use to distinguish a different set of parameters used for acquiring the same modality. For example this should be used when a study includes two T1w images - one full brain low resolution and 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 (e.g. RARE and FLASH for T1w) this field can also be used to make that distinction. At what level of detail to make the distinction (e.g. just between RARE and FLASH, or between RARE, FLASH, and FLASHsubsampled) remains at the discretion of the researcher.

The `ce` entity

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

The `rec` entity

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

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

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:

Field name	Definition
ContrastBolusIngredient	OPTIONAL. Active ingredient of agent. Values MUST be one of: IODINE, GADOLINIUM, CARBON DIOXIDE, BARIUM, XENON Corresponds to DICOM Tag 0018,1048.

Task (including resting state) imaging data

Currently supported image contrasts include:

Name	`contrast_label`	Description
BOLD	bold	Blood-Oxygen-Level Dependent contrast (specialized T2* weighting)
CBV	cbv	Cerebral Blood Volume contrast (specialized T2* weighting or difference between T1 weighted images)
Phase	phase	Phase information associated with magnitude information stored in BOLD contrast

Template:

```
sub-<label>/[ses-<label>/]
    func/
        sub-<label>[_ses-<label>]_task-<label>[_acq-<label>][_ce-<label>][_dir-<label>][_rec-<label>][_run-<index>][_echo-<index>]_<contrast_label>.nii[.gz]
        sub-<label>[_ses-<label>]_task-<label>[_acq-<label>][_ce-<label>][_dir-<label>][_rec-<label>][_run-<index>][_echo-<index>]_sbref.nii[.gz]
```

Imaging data acquired during functional imaging (i.e. imaging which supports rapid temporal repetition). This includes but is not limited to task based fMRI as well as resting state fMRI (i.e. rest is treated as another task). For task based fMRI a corresponding task events file (see below) MUST be provided (please note that this file is not necessary for resting state scans). For multiband acquisitions, one MAY also save the single-band reference image as type `sbref` (e.g. `sub-control01_task-nback_sbref.nii.gz`).

Each task has a unique label that MUST only consist of letters and/or numbers (other characters, including spaces and underscores, are not allowed). Those labels MUST be consistent across subjects and sessions.

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

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

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

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

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

Multi-echo data MUST be split into one file per echo. Each file shares the same name with the exception of the `_echo-<index>` key/value. 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 a form of an integer) of the echo not the echo time value which needs to be stored in the field EchoTime of the separate JSON file.

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

Required fields

Field name	Definition
RepetitionTime	REQUIRED. The time in seconds between the beginning of an acquisition of one volume and the beginning of acquisition of the volume following it (TR). Please note that this definition includes time between scans (when no data has been acquired) in case of sparse acquisition schemes. This value needs to 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` and is derived from DICOM Tag 0018, 0080 and converted to seconds.
VolumeTiming	REQUIRED. The time at which each volume was acquired during the acquisition. It is described using a list of times (in JSON format) referring to the onset of each volume in the BOLD series. The list must have the same length as the BOLD series, and the values must be non-negative and monotonically increasing. This field is mutually exclusive with `RepetitionTime` and `DelayTime`. If defined, this requires acquisition time (TA) be defined via either `SliceTiming` or `AcquisitionDuration` be defined.
TaskName	REQUIRED. Name of the task. No two tasks should have the same name. The task label included in the file name is derived from this TaskName field by removing all non-alphanumeric (`[a-zA-Z0-9]`) characters. For example TaskName `faces n-back` will correspond to task label `facesnback`. A RECOMMENDED convention is to name resting state task using labels beginning with `rest`.

For the fields described above and in the following section, the term ”Volume” refers to a reconstruction of the object being imaged (e.g., 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

Field name	Definition
NumberOfVolumesDiscardedByScanner	RECOMMENDED. 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 doesn’t discard dummy scans would have this set to 0. Please note that the onsets recorded in the _event.tsv file should always refer to the beginning of the acquisition of the first volume in the corresponding imaging file - independent of the value of `NumberOfVolumesDiscardedByScanner` field.
NumberOfVolumesDiscardedByUser	RECOMMENDED. 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 _event.tsv file should always refer to the beginning of the acquisition of the first volume in the corresponding imaging file - independent of the value of `NumberOfVolumesDiscardedByUser` field.

Field name	Definition
DelayTime	RECOMMENDED. User specified time (in seconds) to delay the acquisition of data for the following volume. If the field is not present it is assumed to be set to zero. Corresponds to Siemens CSA header field `lDelayTimeInTR`. This field is REQUIRED for sparse sequences using the `RepetitionTime` field that do not have the `SliceTiming` field set to allowed for accurate calculation of ”acquisition time”. This field is mutually exclusive with `VolumeTiming`.
AcquisitionDuration	RECOMMENDED. Duration (in seconds) of volume acquisition. Corresponds to DICOM Tag 0018,9073 `Acquisition Duration`. This field is REQUIRED for sequences that are described with the `VolumeTiming` field and that do not have the `SliceTiming` field set to allow for accurate calculation of ”acquisition time”. This field is mutually exclusive with `RepetitionTime`.
DelayAfterTrigger	RECOMMENDED. Duration (in seconds) from trigger delivery to scan onset. This delay is commonly caused by adjustments and loading times. This specification is entirely independent of `NumberOfVolumesDiscardedByScanner` or `NumberOfVolumesDiscardedByUser`, as the delay precedes the acquisition.

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

	RepetitionTime	SliceTiming	AcquisitionDuration	DelayTime	VolumeTiming
option A	[X]		[ ]		[ ]
option B	[ ]	[X]		[ ]	[X]
option C	[ ]		[X]	[ ]	[X]
option D	[X]	[X]	[ ]		[ ]
option E	[X]		[ ]	[X]	[ ]

Legend

- [X] --> has to be filled
- [ ] --> has to be left empty
- empty cell --> can be specified but not required

fMRI task information

Field name	Definition
Instructions	RECOMMENDED. Text of the instructions given to participants before the scan. This is especially important in context of resting state fMRI and distinguishing between eyes open and eyes closed paradigms.
TaskDescription	RECOMMENDED. Longer description of the task.
CogAtlasID	RECOMMENDED. URL of the corresponding Cognitive Atlas Task term.
CogPOID	RECOMMENDED. URL of the corresponding CogPO term.

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

Example:

```
sub-control01/
    func/
```

```
        sub-control01_task-nback_bold.json
```

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

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

Diffusion imaging data

Template:

```
sub-<label>/[ses-<label>/]
    dwi/
       sub-<label>[_ses-<label>][_acq-<label>][_dir-<label>][_run-<index>]_dwi.nii[.gz]
       sub-<label>[_ses-<label>][_acq-<label>][_dir-<label>][_run-<index>]_dwi.bval
       sub-<label>[_ses-<label>][_acq-<label>][_dir-<label>][_run-<index>]_dwi.bvec
       sub-<label>[_ses-<label>][_acq-<label>][_dir-<label>][_run-<index>]_dwi.json
       sub-<label>[_ses-<label>][_acq-<label>][_dir-<label>][_run-<index>]_sbref.nii[.gz]
       sub-<label>[_ses-<label>][_acq-<label>][_dir-<label>][_run-<index>]_sbref.json
```

Diffusion-weighted imaging data acquired for that participant. The OPTIONAL `acq-<label>` key/value pair corresponds to a custom label the user may use to distinguish different set of parameters. For example this should be used when a study includes two diffusion images - one single band and one multiband. In such case two files could have the following names: `sub-01_acq-singleband_dwi.nii.gz` and `sub-01_acq-multiband_dwi.nii.gz`, however the user is free to choose any other label than `singleband` and `multiband` as long as they are consistent across subjects and sessions. For multiband acquisitions, one can also save the single-band reference image as type `sbref` (e.g. `dwi/sub-control01_sbref.nii[.gz]`) The bvec and bval files are in the FSL format: The bvec files contain 3 rows with n space-delimited floating-point numbers (corresponding to the n volumes in the relevant NIfTI file). The first row contains the x elements, the second row contains the y elements and third row contains the z elements of a unit vector in the direction of the applied diffusion gradient, where the i-th elements in each row correspond together to the i-th volume with `[0,0,0]` for non-diffusion-weighted volumes. Inherent to the FSL format for bvec specification is the fact that the coordinate system of the bvecs is with respect to the participant (i.e., defined by the axes of the corresponding dwi.nii file) and not the magnet's coordinate system, which means that any rotations applied to dwi.nii also need to be applied to the corresponding bvec file.

bvec example:

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

The bval file contains the b-values (in s/mm2) corresponding to the volumes in the relevant NIfTI file), with 0 designating non-diffusion-weighted volumes, space-delimited.

bval example:

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

`.bval` and `.bvec` files can be saved on any level of the directory structure and thus define those values for all sessions and/or subjects in one place (see Inheritance principle).

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
}
```

Fieldmap data

Data acquired to correct for B0 inhomogeneities can come in different forms. The current version of this standard considers four different scenarios. Please note that in all cases fieldmap data can be linked to a specific scan(s) it was acquired for by filling the IntendedFor field in the corresponding JSON file. For example:

```
{
   "IntendedFor": "func/sub-01_task-motor_bold.nii.gz"
}
```

The IntendedFor field may contain one or more filenames with paths relative to the subject subfolder. The path needs to use forward slashes instead of backward slashes. Here's an example with multiple target scans:

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

The IntendedFor field is OPTIONAL and in case the fieldmaps do not correspond to any particular scans it does not have to be filled.

Multiple fieldmaps can be stored. In such case the `_run-1`, `_run-2` should be used. The OPTIONAL `acq-<label>` key/value pair corresponds to a custom label the user may use to distinguish different set of parameters.

Case 1: Phase difference image and at least one magnitude image

Template:

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

OPTIONAL

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

This is a common output for build in fieldmap sequence on Siemens scanners. In this particular case the sidecar JSON file has to define the Echo Times of the two phase images used to create the difference image. `EchoTime1` corresponds to the shorter echo time and `EchoTime2` to the longer echo time. Similarly `_magnitude1` image corresponds to the shorter echo time and the OPTIONAL `_magnitude2` image to the longer echo time. For example:

```
{
   "EchoTime1": 0.00600,
   "EchoTime2": 0.00746,
   "IntendedFor": "func/sub-01_task-motor_bold.nii.gz"
}
```

Case 2: Two phase images and two magnitude images

Template:

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

Similar to the case above, but instead of a precomputed phase difference map two separate phase images are presented. The two sidecar JSON files need to specify corresponding `EchoTime` values. For example:

```
{
   "EchoTime": 0.00746,
   "IntendedFor": "func/sub-01_task-motor_bold.nii.gz"
}
```

Case 3: A real fieldmap image

Template:

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

In some cases (for example GE) the scanner software will output a precomputed fieldmap denoting the B0 inhomogeneities along with a magnitude image used for coregistration. In this case the sidecar JSON file needs to include the units of the fieldmap. The possible options are: `Hz`, `rad/s`, or `Tesla`. For example:

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

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

Template:

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

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. Examples of tools using this kind of images are FSL TOPUP, AFNI 3dqwarp and SPM. In such a case, the phase encoding direction is specified in the corresponding JSON file as one of: `i`, `j`, `k`, `i-`, `j-`, `k-`. For these differentially phase encoded sequences, one also needs to specify the Total Readout Time defined as the time (in seconds) from the center of the first echo to the center of the last echo (aka ”FSL definition” - see here and here how to calculate it). For example

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

`label` value of `_dir-` can be set to arbitrary alphanumeric label (`[a-zA-Z0-9]+` for example `LR` or `AP`) that can help users to distinguish between different files, but should not be used to infer any scanning parameters (such as phase encoding directions) of the corresponding sequence. Please rely only on the JSON file to obtain scanning parameters. _epi files can be a 3D or 4D - in the latter case all timepoints share the same scanning parameters. To indicate which run is intended to be used with which functional or diffusion scan the IntendedFor field in the JSON file should be used.

Chapter 6

Magnetoencephalography

Support for Magnetoencephalography (MEG) was developed as a BIDS Extension Proposal. Please cite the following paper when referring to this part of the standard in context of the academic literature:

> 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. doi: 10.1038/sdata.2018.110

MEG recording data

Template:

```
sub-<label>/
    [ses-<label>]/
      meg/
        sub-<label>[_ses-<label>]_task-<label>[_run-<index>][_proc-<label>]_meg.<
            manufacturer_specific_extension>
        [sub-<label>[_ses-<label>]_task-<label>[_run-<index>][_proc-<label>]_meg.json]
```

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 SHOULD contain details on the Tasks.

Some manufacturers' data storage conventions use folders which contain data files of various nature: for example, CTF's `.ds` format, or BTi/4D. 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. Please refer to Appendix VI for general information on how to deal with such manufacturer specifics and to see more examples.

The `proc` label is analogous to `rec` for MR and denotes a variant of a file that was a result of particular processing performed on the device. This is useful for files produced in particular by Elekta's MaxFilter (e.g.

sss, tsss, trans, quat, mc, etc.), which some installations impose to be run on raw data because of active shielding software corrections before the MEG data can actually be exploited.

Sidecar JSON (`*_meg.json`)

Generic fields MUST be present:

Field name	Definition
TaskName	REQUIRED. Name of the task (for resting state use the `rest` prefix). No two tasks should have the same name. The task label included in the file name is derived from this TaskName field by removing all non-alphanumeric (`[a-zA-Z0-9]`) characters. For example TaskName `faces n-back` will correspond to task label `facesnback`.

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

Field name	Definition
InstitutionName	RECOMMENDED. The name of the institution in charge of the equipment that produced the composite instances.
InstitutionAddress	RECOMMENDED. The address of the institution in charge of the equipment that produced the composite instances.
Manufacturer	RECOMMENDED. Manufacturer of the MEG system (`CTF`, `Elekta/Neuromag`, `BTi/4D`, `KIT/Yokogawa`, `ITAB`, `KRISS`, `Other`). See Appendix VII with preferred names
ManufacturersModelName	RECOMMENDED. Manufacturer's designation of the MEG scanner model (e.g. `CTF-275`). See Appendix VII with preferred names
SoftwareVersions	RECOMMENDED. Manufacturer's designation of the acquisition software.
TaskDescription	RECOMMENDED. Description of the task.
Instructions	RECOMMENDED. Text of the instructions given to participants before the scan. This is not only important for behavioral or cognitive tasks but also in resting state paradigms (e.g. to distinguish between eyes open and eyes closed).
CogAtlasID	RECOMMENDED. URL of the corresponding Cognitive Atlas term that describes the task (e.g. Resting State with eyes closed "http://www.cognitiveatlas.org/task/id/trm_54e69c642d89b")
CogPOID	RECOMMENDED. URL of the corresponding CogPO term that describes the task (e.g. Rest "http://wiki.cogpo.org/index.php?title=Rest")
DeviceSerialNumber	RECOMMENDED. The serial number of the equipment that produced the composite instances. A pseudonym can also be used to prevent the equipment from being identifiable, as long as each pseudonym is unique within the dataset.

Specific MEG fields MUST be present:

Field name	Definition
SamplingFrequency	REQUIRED. Sampling frequency (in Hz) of all the data in the recording, regardless of their type (e.g., 2400)
PowerLineFrequency	REQUIRED. Frequency (in Hz) of the power grid at the geographical location of the MEG instrument (i.e. 50 or 60)
DewarPosition	REQUIRED. Position of the dewar during the MEG scan: `upright`, `supine` or `degrees` of angle from vertical: for example on CTF systems, upright=15°, supine = 90°.

Field name	Definition
SoftwareFilters	REQUIRED. A JSON 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. E.g., `{"SSS": {"frame": "head", "badlimit": 7}, "SpatialCompensation": {"GradientOrder": "Order of the gradient compensation"}}`
DigitizedLandmarks	REQUIRED. Boolean ("true" or "false") value indicating whether anatomical landmark points (i.e. fiducials) are contained within this recording.
DigitizedHeadPoints	REQUIRED. Boolean (`true` or `false`) value indicating whether head points outlining the scalp/face surface are contained within this recording.

SHOULD be present:

Field name	Definition
MEGChannelCount	RECOMMENDED. Number of MEG channels (e.g. 275)
MEGREFChannelCount	RECOMMENDED. Number of MEG reference channels (e.g. 23). For systems without such channels (e.g. Neuromag Vectorview), `MEGREFChannelCount`=0
EEGChannelCount	RECOMMENDED. Number of EEG channels recorded simultaneously (e.g. 21)
ECOGChannelCount	RECOMMENDED. Number of ECoG channels
SEEGChannelCount	RECOMMENDED. Number of SEEG channels
EOGChannelCount	RECOMMENDED. Number of EOG channels
ECGChannelCount	RECOMMENDED. Number of ECG channels
EMGChannelCount	RECOMMENDED. Number of EMG channels
MiscChannelCount	RECOMMENDED. Number of miscellaneous analog channels for auxiliary signals
TriggerChannelCount	RECOMMENDED. Number of channels for digital (TTL bit level) triggers
RecordingDuration	RECOMMENDED. Length of the recording in seconds (e.g. 3600)
RecordingType	RECOMMENDED. Defines whether the recording is `continuous` or `epoched`; this latter limited to time windows about events of interest (e.g., stimulus presentations, subject responses etc.)
EpochLength	RECOMMENDED. Duration of individual epochs in seconds (e.g. 1) in case of epoched data
ContinuousHeadLocalization	RECOMMENDED. Boolean (`true` or `false`) value indicating whether continuous head localisation was performed.
HeadCoilFrequency	RECOMMENDED. List of frequencies (in Hz) used by the head localisation coils ('HLC' in CTF systems, 'HPI' in Elekta, 'COH' in BTi/4D) that track the subject's head position in the MEG helmet (e.g. `[293, 307, 314, 321]`)
MaxMovement	RECOMMENDED. Maximum head movement (in mm) detected during the recording, as measured by the head localisation coils (e.g., 4.8)
SubjectArtefactDescription	RECOMMENDED. Freeform description of the observed subject artefact and its possible cause (e.g. "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. Relative path in BIDS folder structure to empty-room file associated with the subject's MEG recording. The path needs to use forward slashes instead of backward slashes (e.g. `sub-emptyroom/ses-/meg/sub-emptyroom_ses-_task-noise_run-_meg.ds`).
HardwareFilters	RECOMMENDED. A JSON 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. E.g., `{"Highpass RC filter": {"Half amplitude cutoff (Hz)": 0.0159, "Roll-off": "6dB/Octave"}}`

Specific EEG fields (if recorded with MEG) SHOULD be present:

Field name	Definition
EEGPlacementScheme	OPTIONAL. Placement scheme of EEG electrodes. Either the name of a standardised placement system (e.g., ”10-20”) or a list of standardised electrode names (e.g. `["Cz", "Pz"]`).
CapManufacturer	OPTIONAL. Manufacturer of the EEG cap (e.g. `EasyCap`)
CapManufacturersModelName	OPTIONAL. Manufacturer’s designation of the EEG cap model (e.g., `M10`)
EEGReference	OPTIONAL. Description of the type of EEG reference used (e.g., `M1` for left mastoid, `average`, or `longitudinal bipolar`).

By construct, EEG when recorded simultaneously with the same MEG system , should have the same `SamplingFrequency` as MEG. Note that if EEG is recorded with a separate amplifier, it should be stored separately under a new `/eeg` data type (see the EEG specification).

Example:

```
{
  "InstitutionName": "Stanford University",
  "InstitutionAddress": "450 Serra Mall, Stanford, CA 94305-2004, USA",
  "Manufacturer": "CTF",
  "ManufacturersModelName": "CTF-275",
  "DeviceSerialNumber": "11035",
  "SoftwareVersions": "Acq 5.4.2-linux-20070507",
  "PowerLineFrequency": 60,
  "SamplingFrequency": 2400,
  "MEGChannelCount": 270,
  "MEGREFChannelCount": 26,
  "EEGChannelCount": 0,
  "EOGChannelCount": 2,
  "ECGChannelCount": 1,
  "EMGChannelCount": 0,
    "DewarPosition": "upright",
  "SoftwareFilters": {
    "SpatialCompensation": {"GradientOrder": "3rd"}
  },
  "RecordingDuration": 600,
  "RecordingType": "continuous",
  "EpochLength": 0,
  "TaskName": "rest",
  "ContinuousHeadLocalization": true,
  "HeadCoilFrequency": [1470,1530,1590],
  "DigitizedLandmarks": true,
  "DigitizedHeadPoints": true
}
```

Note that the date and time information SHOULD be stored in the Study key file (`scans.tsv`), see Scans file. As it is indicated there, date time information MUST be expressed in the following format `YYYY-MM-DDThh:mm:ss` (ISO8601 date-time format). For example: 2009-06-15T13:45:30. It does not need to be fully detailed, depending on local REB/IRB ethics board policy.

Channels description (`*_channels.tsv`)

Template:

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

This file is RECOMMENDED as it provides easily searchable information across BIDS datasets for e.g., general curation, response to queries or batch analysis. To avoid confusion, the channels SHOULD be listed in the order they appear in the MEG data file. Missing values MUST be indicated with `n/a`.

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

MUST be present:

Column name	Definition
name	REQUIRED. Channel name (e.g., MRT012, MEG023)
type	REQUIRED. Type of channel; MUST use the channel types listed below.
units	REQUIRED. Physical unit of the value represented in this channel, e.g., V for Volt, specified according to the SI unit symbol and possibly prefix symbol (e.g., mV, V), or as a derived SI unit (e.g., fT/cm). For guidelines for Units and Prefixes see Appendix V.

SHOULD be present:

Column name	Definition
description	OPTIONAL. Brief free-text description of the channel, or other information of interest. See examples below.
sampling_frequency	OPTIONAL. Sampling rate of the channel in Hz.
low_cutoff	OPTIONAL. Frequencies used for the high-pass filter applied to the channel in Hz. If no high-pass filter applied, use `n/a`.
high_cutoff	OPTIONAL. Frequencies used for the low-pass filter applied to the channel in Hz. If no low-pass filter applied, use `n/a`. Note that hardware anti-aliasing in A/D conversion of all MEG/EEG electronics applies a low-pass filter; specify its frequency here if applicable.
notch	OPTIONAL. Frequencies used for the notch filter applied to the channel, in Hz. If no notch filter applied, use `n/a`.
software_filters	OPTIONAL. List of temporal and/or spatial software filters applied (e.g. ”SSS”, `"SpatialCompensation"`). Note that parameters should be defined in the general MEG sidecar .json file. Indicate `n/a` in the absence of software filters applied.
status	OPTIONAL. Data quality observed on the channel `(good/bad)`. A channel is considered `bad` if its data quality is compromised by excessive noise. Description of noise type SHOULD be provided in `[status_description]`.
status_description	OPTIONAL. Freeform text description of noise or artifact affecting data quality on the channel. It is meant to explain why the channel was declared bad in `[status]`.

Example:

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

Restricted keyword list for field `type`

Keyword	Definition
MEGMAG	MEG magnetometer
MEGGRADAXIAL	MEG axial gradiometer
MEGGRADPLANAR	MEG planargradiometer
MEGREFMAG	MEG reference magnetometer
MEGREFGRADAXIAL	MEG reference axial gradiometer
MEGREFGRADPLANAR	MEG reference planar gradiometer

Keyword	Definition
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	System Triggers
AUDIO	Audio signal
PD	Photodiode
EYEGAZE	Eye Tracker gaze
PUPIL	Eye Tracker pupil diameter
MISC	Miscellaneous
SYSCLOCK	System time showing elapsed time since trial started
ADC	Analog to Digital input
DAC	Digital to Analog output
HLU	Measured position of head and head coils
FITERR	Fit error signal from each head localization coil
OTHER	Any other type of channel

Example of free text for field `description`

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

Example:

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

Coordinate System JSON (`*_coordsystem.json`)

Template:

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

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

MEG and EEG sensors:

Field name	Description
MEGCoordinateSystem	REQUIRED. Defines the coordinate system for the MEG sensors. See Appendix VIII: preferred names of Coordinate systems. If `Other`, provide definition of the coordinate system in `[MEGCoordinateSystemDescription]`.
MEGCoordinateUnits	REQUIRED. Units of the coordinates of `MEGCoordinateSystem`. MUST be `m`, `cm`, or `mm`.
MEGCoordinateSystemDescription	OPTIONAL. Freeform text description or link to document describing the MEG coordinate system system in detail.

Field name	Description
EEGCoordinateSystem	OPTIONAL. Describes how the coordinates of the EEG sensors are to be interpreted.
EEGCoordinateUnits	OPTIONAL. Units of the coordinates of `EEGCoordinateSystem`. MUST be `m`, `cm`, or `mm`.
EEGCoordinateSystemDescription	OPTIONAL. Freeform text description or link to document describing the EEG coordinate system system in detail.

Head localization coils:

Field name	Description
HeadCoilCoordinates	OPTIONAL. Key:value pairs describing head localization coil labels and their coordinates, interpreted following the `HeadCoilCoordinateSystem`, e.g., {`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 (e.g. for Elekta, Yokogawa systems); in that case generic labels can be used (e.g. {`coil1`: `[12.2,21.3,12.3]`, `coil2`: `[6.7,12.3,8.6]`, `coil3`: `[21.9,11.0,8.1]`}).
HeadCoilCoordinateSystem	OPTIONAL. Defines the coordinate system for the coils. See Appendix VIII: preferred names of Coordinate systems. If ”Other”, provide definition of the coordinate system in `HeadCoilCoordinateSystemDescription`.
HeadCoilCoordinateUnits	OPTIONAL. Units of the coordinates of `HeadCoilCoordinateSystem`. MUST be `m`, `cm`, or `mm`.
HeadCoilCoordinateSystemDescription	OPTIONAL. Freeform text description or link to document describing the Head Coil coordinate system system in detail.

Digitized head points:

Field name	Description
DigitizedHeadPoints	OPTIONAL. Relative path to the file containing the locations of digitized head points collected during the session (e.g., `sub-01_headshape.pos`). RECOMMENDED for all MEG systems, especially for CTF and BTi/4D. For Elekta/Neuromag the head points will be stored in the fif file.
DigitizedHeadPointsCoordinateSystem	OPTIONAL. Defines the coordinate system for the digitized head points. See Appendix VIII: preferred names of Coordinate systems. If `Other`, provide definition of the coordinate system in `DigitizedHeadPointsCoordinateSystemDescription`.
DigitizedHeadPointsCoordinateUnits	OPTIONAL. Units of the coordinates of `DigitizedHeadPointsCoordinateSystem`. MUST be `m`, `cm`, or `mm`.
DigitizedHeadPointsCoordinateSystemDescription	OPTIONAL. Freeform text description or link to document describing the Digitized head Points coordinate system system in detail.

Anatomical MRI:

Field name	Description
IntendedFor	OPTIONAL. Path or list of path relative to the subject subfolder pointing to the structural MRI, possibly of different types if a list is specified, to be used with the MEG recording. The path(s) need(s) to use forward slashes instead of backward slashes (e.g. `ses-/anat/sub-01_T1w.nii.gz`).

Anatomical landmarks:

Field name	Description
AnatomicalLandmarkCoordinates	OPTIONAL. Key:value pairs of the labels and 3-D digitized locations of anatomical landmarks, interpreted following the `AnatomicalLandmarkCoordinateSystem`, e.g., {"NAS": `[12.7,21.3,13.9]`, "LPA": `[5.2,11.3,9.6]`, "RPA": `[20.2,11.3,9.1]`}.
AnatomicalLandmarkCoordinateSystem	OPTIONAL. Defines the coordinate system for the anatomical landmarks. See Appendix VIII: preferred names of Coordinate systems. If `Other`, provide definition of the coordinate system in `AnatomicalLandmarkCoordinateSystemDescription`.
AnatomicalLandmarkCoordinateUnits	OPTIONAL. Units of the coordinates of `AnatomicalLandmarkCoordinateSystem`. MUST be `m`, `cm`, or `mm`.
AnatomicalLandmarkCoordinateSystemDescription	OPTIONAL. Freeform text description or link to document describing the Head Coil coordinate system system in 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 here) - 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 e.g., 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 e.g., "NAS-session1": `[127,213,139]`,"NAS-session2": `[123,220,142]`, etc.

Fiducials information:

Field name	Description
FiducialsDescription	OPTIONAL. A freeform text field documenting the anatomical landmarks that were used and how the head localization coils were placed relative to these. This field can describe, for instance, whether the true anatomical locations of the left and right pre-auricular points were used and digitized, or rather whether they were defined as the intersection between the tragus and the helix (the entry of the ear canal), or any other anatomical description of selected points in the vicinity of the ears.

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

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

Landmark photos (`*_photo.jpg`)

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

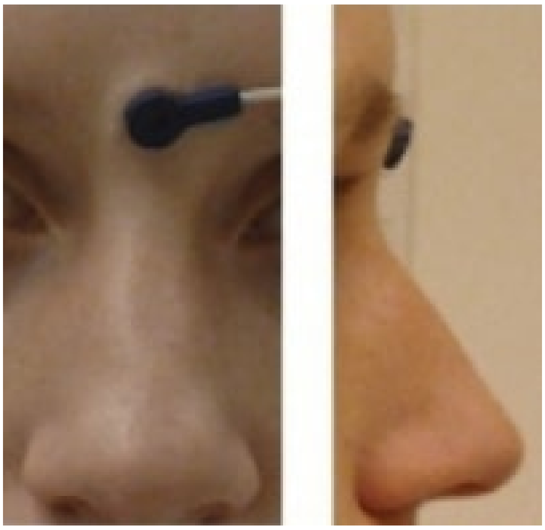
Template:

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

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

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

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



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

Template:

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

This file is RECOMMENDED.

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

Example:

```
sub-control01
    ses-01
        sub-control01_ses-01_acq-HEAD_headshape.pos
        sub-control01_ses-01_acq-ECG_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 environment and system noise. Their collection is RECOMMENDED, before/during/after each session. This data is stored inside a subject folder named `sub-emptyroom`. The `session label` SHOULD be that of the date of the empty-room recording (e.g. `ses-YYYYMMDD`). The `scans .tsv` file containing the date/time of the acquisition SHOULD also be included. Hence, users will be able to retrieve the empty-room recording that best matches a particular session with a participant, based on date/time of recording.

Example:

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

`TaskName` in the `*_meg.json` file should be set to ”noise”.

Chapter 7

Electroencephalography

Support for Electroencephalography (EEG) was developed as a BIDS Extension Proposal. Please cite the following paper when referring to this part of the standard in context of the academic literature:

> 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. doi: 10.1038/s41597-019-0104-8

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

- Single session per subject: `eeg_matchingpennies`
- Multiple sessions per subject: `eeg_rishikesh`
- Combined with fMRI: `eeg_rest_fmri`

Further datasets are available from the BIDS examples repository.

EEG recording data

Template:

```
sub-<label>/
    [ses-<label>]/
      eeg/
        sub-<label>[_ses-<label>]_task-<label>[_run-<index>]_eeg.<
            manufacturer_specific_extension>
        sub-<label>[_ses-<label>]_task-<label>[_run-<index>]_eeg.json
```

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:

- European data format (`.edf`)
- BrainVision Core Data Format (`.vhdr`, `.vmrk`, `.eeg`) by Brain Products GmbH
- The format used by the MATLAB toolbox EEGLAB (`.set` and `.fdt` files)
- Biosemi data format (`.bdf`)

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

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

Note the RecordingType, which depends on whether the data stream on disk is interrupted or not. Continuous data is by definition 1 segment without interruption. Epoched data consists of multiple segments that all have the same length (e.g., 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 (e.g., scalp, neural tissue, ...). Multiple electrodes can be organized as caps (for EEG), arrays, grids, leads, strips, probes, shafts, etc.
- 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, etc.

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

Sidecar JSON (`*_eeg.json`)

Generic fields MUST be present:

Field name	Definition
TaskName	REQUIRED. Name of the task (for resting state use the `rest` prefix). No two tasks should have the same name. The task label included in the file name is derived from this TaskName field by removing all non-alphanumeric (`[a-zA-Z0-9]`) characters. For example TaskName `faces n-back` will correspond to task label `facesnback`.

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

Field name	Definition
InstitutionName	RECOMMENDED. The name of the institution in charge of the equipment that produced the composite instances.
InstitutionAddress	RECOMMENDED. The address of the institution in charge of the equipment that produced the composite instances.
Manufacturer	RECOMMENDED. Manufacturer of the EEG system (e.g., `Biosemi`, `Brain Products`, `Neuroscan`).
ManufacturersModelName	RECOMMENDED. Manufacturer's designation of the EEG system model (e.g., `BrainAmp DC`).
SoftwareVersions	RECOMMENDED. Manufacturer's designation of the acquisition software.
TaskDescription	RECOMMENDED. Description of the task.
Instructions	RECOMMENDED. Text of the instructions given to participants before the scan. This is not only important for behavioral or cognitive tasks but also in resting state paradigms (e.g., to distinguish between eyes open and eyes closed).
CogAtlasID	RECOMMENDED. URL of the corresponding Cognitive Atlas term that describes the task (e.g., Resting State with eyes closed "http://www.cognitiveatlas.org/task/id/trm_54e69c642d89b").

Field name	Definition
CogPOID	RECOMMENDED. URL of the corresponding CogPO term that describes the task (e.g., Rest "http://wiki.cogpo.org/index.php?title=Rest") .
DeviceSerialNumber	RECOMMENDED. The serial number of the equipment that produced the composite instances. A pseudonym can also be used to prevent the equipment from being identifiable, as long as each pseudonym is unique within the dataset.

Specific EEG fields MUST be present:

Field name	Definition
EEGReference	REQUIRED. General description of the reference scheme used and (when applicable) of location of the reference electrode in the raw recordings (e.g., "left mastoid", "Cz", "CMS"). If different channels have a different reference, this field should have a general description and the channel specific reference should be defined in the _channels.tsv file.
SamplingFrequency	REQUIRED. Sampling frequency (in Hz) of all the data in the recording, regardless of their type (e.g., 2400).
PowerLineFrequency	REQUIRED. Frequency (in Hz) of the power grid at the geographical location of the EEG instrument (i.e., 50 or 60).
SoftwareFilters	REQUIRED. A JSON 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. E.g., `{"Anti-aliasing filter": {"half-amplitude cutoff (Hz)": 500, "Roll-off": "6dB/Octave"}}`.

SHOULD be present:

Field name	Definition
CapManufacturer	RECOMMENDED. Name of the cap manufacturer (e.g., "EasyCap").
CapManufacturersModelName	RECOMMENDED. Manufacturer's designation of the EEG cap model (e.g., "actiCAP 64 Ch Standard-2").
EEGChannelCount	RECOMMENDED. Number of EEG channels included in the recording (e.g., 128).
ECGChannelCount	RECOMMENDED. Number of ECG channels.
EMGChannelCount	RECOMMENDED. Number of EMG channels.
EOGChannelCount	RECOMMENDED. Number of EOG channels.
MiscChannelCount	RECOMMENDED. Number of miscellaneous analog channels for auxiliary signals.
TriggerChannelCount	RECOMMENDED. Number of channels for digital (TTL bit level) trigger.
RecordingDuration	RECOMMENDED. Length of the recording in seconds (e.g., 3600).
RecordingType	RECOMMENDED. Defines whether the recording is `continuous`, `discontinuous` or `epoched`.
EpochLength	RECOMMENDED. Duration of individual epochs in seconds (e.g., 1) in case of epoched data.
EEGGround	RECOMMENDED. Description of the location of the ground electrode (e.g., "placed on right mastoid (M2)").
HeadCircumference	RECOMMENDED. Circumference of the participants head, expressed in cm (e.g., 58).
EEGPlacementScheme	RECOMMENDED. Placement scheme of EEG electrodes. Either the name of a standardized placement system (e.g., "10-20") or a list of standardized electrode names (e.g., `["Cz", "Pz"]`).

Field name	Definition
HardwareFilters	RECOMMENDED. A JSON 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. E.g., `{"Highpass RC filter": {"Half amplitude cutoff (Hz)": 0.0159, "Roll-off": "6dB/Octave"}}`
SubjectArtefactDescription	RECOMMENDED. Free-form description of the observed subject artifact and its possible cause (e.g., ”Vagus Nerve Stimulator”, ”non-removable implant”). If this field is set to `n/a`, it will be interpreted as absence of major source of artifacts except cardiac and blinks.

Example:

```
{
  "TaskName":"Seeing stuff",
  "TaskDescription":"Subjects see various images for which phase, amplitude spectrum, and color
      vary continuously",
  "Instructions":"Your task is to detect images when they appear for the 2nd time, only then
      press the response button with your right/left hand (counterbalanced across subjects)",
  "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`). As it is indicated there, date time information MUST be expressed in the following format `YYYY-MM-DDThh:mm:ss` (ISO8601 date-time format). For example: 2009-06-15T13:45:30. It does not need to be fully detailed, depending on local REB/IRB ethics board policy.

Channels description (`*_channels.tsv`)

Template:

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

This file is RECOMMENDED as it provides easily searchable information across BIDS datasets for e.g., general curation, response to queries or batch analysis. The required columns are channel `name`, `type` and `units` in this specific order. 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`.

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

MUST be present:

Column name	Definition
name	REQUIRED. Channel name (e.g., FC1, Cz)
type	REQUIRED. Type of channel; MUST use the channel types listed below.
units	REQUIRED. Physical unit of the value represented in this channel, e.g., V for Volt, specified according to the SI unit symbol and possibly prefix symbol (e.g., mV, V), or as a derived SI unit (e.g., fT/cm). For guidelines for Units and Prefixes see Appendix V.

SHOULD be present:

Column name	Definition
description	OPTIONAL. Free-form text description of the channel, or other information of interest. See examples below.
sampling_frequency	OPTIONAL. Sampling rate of the channel in Hz.
reference	OPTIONAL. Name of the reference electrode(s) (not needed when it is common to all channels, in that case it can be specified in `*_eeg.json` as `EEGReference`).
low_cutoff	OPTIONAL. Frequencies used for the high-pass filter applied to the channel in Hz. If no high-pass filter applied, use `n/a`.
high_cutoff	OPTIONAL. 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 EEG electronics applies a low-pass filter; specify its frequency here if applicable.
notch	OPTIONAL. Frequencies used for the notch filter applied to the channel, in Hz. If no notch filter applied, use `n/a`.
status	OPTIONAL. Data quality observed on the channel `(good/bad)`. A channel is considered `bad` if its data quality is compromised by excessive noise. Description of noise type SHOULD be provided in `[status_description]`.
status_description	OPTIONAL. Free-form text description of noise or artifact affecting data quality on the channel. It is meant to explain why the channel was declared bad in `[status]`.

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

Keyword	Description
AUDIO	Audio signal

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

Example of free-form text for field `description`

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

Example:

```
name     type   units   description                     status  status_description
VEOG     VEOG   microV  n/a                             good    n/a
FDI      EMG    microV  left first dorsal interosseous  good    n/a
Cz       EEG    microV  n/a                             bad     high frequency noise
UADC001  MISC   n/a     enevelope of audio signal       good    n/a
```

Electrodes description (`*_electrodes.tsv`)

Template:

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

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

MUST be present:

Column name	Definition
name	REQUIRED. Name of the electrode
x	REQUIRED. Recorded position along the x-axis
y	REQUIRED. Recorded position along the y-axis
z	REQUIRED. Recorded position along the z-axis

SHOULD be present:

Column name	Definition
type	RECOMMENDED. Type of the electrode (e.g., cup, ring, clip-on, wire, needle)
material	RECOMMENDED. Material of the electrode, e.g., Tin, Ag/AgCl, Gold

Column name	Definition
impedance	RECOMMENDED. Impedance of the electrode in kOhm

Example:

```
name  x        y        z        type     material
A1    -0.0707  0.0000   -0.0707  clip-on  Ag/AgCl
F3    -0.0567  0.0677   0.0469   cup      Ag/AgCl
Fz    0.0000   0.0714   0.0699   cup      Ag/AgCl
REF   -0.0742  -0.0200  -0.0100  cup      Ag/AgCl
GND   0.0742   -0.0200  -0.0100  cup      Ag/AgCl
```

The `acq` parameter can be used to indicate acquisition of the same data. For example, this could be the recording of electrode positions with a different electrode position recording device, or repeated digitization before and after the recording.

Coordinate System JSON (`*_coordsystem.json`)

Template:

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

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

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

- Fiducials = 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 = 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: http://www.fieldtriptoolbox.org/faq/how_are_the_lpa_and_rpa_points_defined
- For more information on coordinate systems for coregistration, please visit: http://www.fieldtriptoolbox.org/faq/how_are_the_different_head_and_mri_coordinate_systems_defined

General fields:

Keyword	Description
IntendedFor	OPTIONAL. Relative path to associate the electrodes, landmarks and fiducials to an MRI/CT.

Fields relating to the EEG electrode positions:

Keyword	Description
EEGCoordinateSystem	REQUIRED. Refers to the coordinate system in which the EEG electrode positions are to be interpreted (see Appendix VIII).
EEGCoordinateUnits	REQUIRED. Units in which the coordinates that are listed in the field `EEGCoordinateSystem` are represented (e.g., ”mm”, ”cm”).
EEGCoordinateSystemDescription	RECOMMENDED. 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:

Keyword	Description
FiducialsDescription	OPTIONAL. 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 (e.g., both with Polhemus and with T1w MRI).
FiducialsCoordinates	RECOMMENDED. Key:value pairs of the labels and 3-D digitized position of anatomical landmarks, interpreted following the `FiducialsCoordinateSystem` (e.g., `{"NAS": [12.7,21.3,13.9], "LPA": [5.2,11.3,9.6], "RPA": [20.2,11.3,9.1]}`).
FiducialsCoordinateSystem	RECOMMENDED. Refers to the coordinate space to which the landmarks positions are to be interpreted - preferably the same as the `EEGCoordinateSystem`.
FiducialsCoordinateUnits	RECOMMENDED. Units in which the coordinates that are listed in the field `AnatomicalLandmarkCoordinateSystem` are represented (e.g., ”mm”, ”cm”).
FiducialsCoordinateSystemDescription	RECOMMENDED. 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:

Keyword	Description
AnatomicalLandmarkCoordinates	RECOMMENDED. Key:value pairs of the labels and 3-D digitized position of anatomical landmarks, interpreted following the `AnatomicalLandmarkCoordinateSystem` (e.g., `{"NAS": [12.7,21.3,13.9], "LPA": [5.2,11.3,9.6], "RPA": [20.2,11.3,9.1]}`).
AnatomicalLandmarkCoordinateSystem	RECOMMENDED. Refers to the coordinate space to which the landmarks positions are to be interpreted - preferably the same as the `EEGCoordinateSystem`.
AnatomicalLandmarkCoordinateUnits	RECOMMENDED. Units in which the coordinates that are listed in the field `AnatomicalLandmarkCoordinateSystem` are represented (e.g., ”mm”, ”cm”).
AnatomicalLandmarkCoordinateSystemDescription	RECOMMENDED. Free-form text description of the coordinate system. May also include a link to a documentation page or paper describing the system in greater detail.

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

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

Example:

```
{
  "IntendedFor":"/sub-01/ses-01/anat/sub-01_T1w.nii",
  "EEGCoordinateSystem":"Other",
  "EEGCoordinateUnits":"mm",
  "EEGCoordinateSystemDescription":"RAS orientation: Origin halfway between LPA and RPA,
      positive x-axis towards RPA, positive y-axis orthogonal to x-axis through Nasion,  z-axis
      orthogonal to xy-plane, pointing in superior direction.",
  "FiducialsDescription":"Electrodes and fiducials were digitized with Polhemus, fiducials were
      recorded as the centre of vitamin E capsules sticked on the left/right pre-auricular and
      on the nasion, these are also visible on the T1w MRI"
}
```

Landmark photos (`*_photo.jpg`)

Photos of the anatomical landmarks and/or fiducials.

Template:

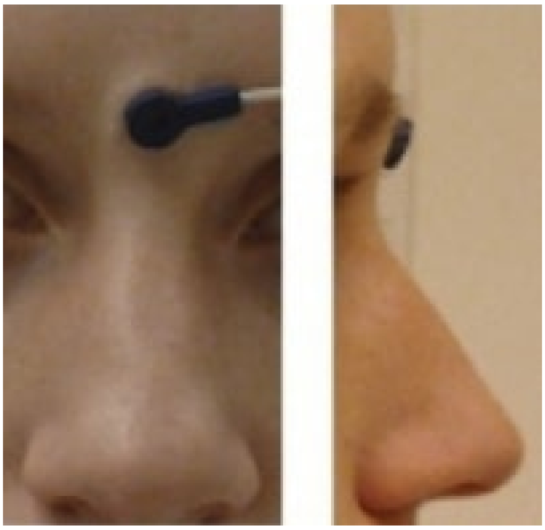
```
sub-<label>/
    [ses-<label>]/
      eeg/
        [sub-<label>[_ses-<label>][_acq-<label>]_photo.jpg]
```

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

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

Example:

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



Chapter 8

Intracranial Electroencephalography

Support for Intracranial Electroencephalography (iEEG) was developed as a BIDS Extension Proposal. Please cite the following paper when referring to this part of the standard in context of the academic literature:

> 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. doi: 10.1038/s41597-019-0105-7

iEEG recording data

Template:

```
sub-<label>/
  [ses-<label>]/
    ieeg/
      sub-<label>[_ses-<label>]_task-<label>[_run-<index>]_ieeg.<manufacturer_specific_extension>
      sub-<label>[_ses-<label>]_task-<label>[_run-<index>]_ieeg.json
```

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:

- European Data Format (`.edf`)
- BrainVision Core Data Format (`.vhdr`, `.eeg`, `.vmrk`) by Brain Products GmbH
- The format used by the MATLAB toolbox EEGLAB (`.set` and `.fdt` files)
- Neurodata Without Borders (`.nwb`)
- MEF3 (`.mef`)

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

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

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

Note the RecordingType, which depends on whether the data stream on disk is interrupted or not. Continuous data is by definition 1 segment without interruption. Epoched data consists of multiple segments that all have the same length (e.g., 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 (e.g., scalp, neural tissue, ...). Multiple electrodes can be organized as arrays, grids, leads, strips, probes, shafts, caps (for EEG), etc.
- 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, etc.

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

Sidecar JSON (`*_ieeg.json`)

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

Generic fields MUST be present:

Field name	Definition
TaskName	REQUIRED. Name of the task (for resting state use the "rest" prefix). No two tasks should have the same name. The task label included in the file name is derived from this TaskName field by removing all non-alphanumeric (`[a-zA-Z0-9]`) characters. For example TaskName `faces n-back` will correspond to task label `facesnback`. Note this 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 (e.g., "rest", "sleep", or "seizure").

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

Field name	Definition
InstitutionName	RECOMMENDED. The name of the institution in charge of the equipment that produced the composite instances.
InstitutionAddress	RECOMMENDED. The address of the institution in charge of the equipment that produced the composite instances.
Manufacturer	RECOMMENDED. Manufacturer of the amplifier system (e.g., "TDT, Blackrock").
ManufacturersModelName	RECOMMENDED. Manufacturer's designation of the iEEG amplifier model.

Field name	Definition
SoftwareVersions	RECOMMENDED. Manufacturer's designation of the acquisition software.
TaskDescription	RECOMMENDED. Longer description of the task.
Instructions	RECOMMENDED. Text of the instructions given to participants before the recording. This is especially important in context of resting state and distinguishing between eyes open and eyes closed paradigms.
CogAtlasID	RECOMMENDED. URL of the corresponding Cognitive Atlas Task term.
CogPOID	RECOMMENDED. URL of the corresponding CogPO term.
DeviceSerialNumber	RECOMMENDED. The serial number of the equipment that produced the composite instances. A pseudonym can also be used to prevent the equipment from being identifiable, as long as each pseudonym is unique within the dataset.

Specific iEEG fields MUST be present:

Field name	Definition
iEEGReference	REQUIRED. General description of the reference scheme used and (when applicable) of location of the reference electrode in the raw recordings (e.g., "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. Sampling frequency (in Hz) of all the iEEG channels in the recording (e.g., 2400). All other channels should have frequency specified as well in the `channels.tsv` file.
PowerLineFrequency	REQUIRED. Frequency (in Hz) of the power grid where the iEEG recording was done (i.e., 50 or 60).
SoftwareFilters	REQUIRED. A JSON 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. E.g., `{"HighPass": {"HalfAmplitudeCutOffHz": 1, "RollOff": "6dB/Octave"}}`

Specific iEEG fields SHOULD be present:

Field name	Definition
DCOffsetCorrection	RECOMMENDED. 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.A JSON 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. E.g., `{"Highpass RC filter": {"Half amplitude cutoff (Hz)": 0.0159, "Roll-off": "6dB/Octave"}}`
ElectrodeManufacturer	RECOMMENDED. can be used if all electrodes are of the same manufacturer (e.g., AD-TECH, DIXI). If electrodes of different manufacturers are used, please use the corresponding table in the _electrodes.tsv file.
ElectrodeManufacturersModelName	RECOMMENDED. If different electrode types are used, please use the corresponding table in the _electrodes.tsv file.
ECOGChannelCount	RECOMMENDED. Number of iEEG surface channels included in the recording (e.g., 120).
SEEGChannelCount	RECOMMENDED. Number of iEEG depth channels included in the recording (e.g., 8).

Field name	Definition
EEGChannelCount	RECOMMENDED. Number of scalp EEG channels recorded simultaneously (e.g., 21).
EOGChannelCount	RECOMMENDED. Number of EOG channels.
ECGChannelCount	RECOMMENDED. Number of ECG channels.
EMGChannelCount	RECOMMENDED. Number of EMG channels.
MiscChannelCount	RECOMMENDED. Number of miscellaneous analog channels for auxiliary signals.
TriggerChannelCount	RECOMMENDED. Number of channels for digital (TTL bit level) triggers.
RecordingDuration	RECOMMENDED. Length of the recording in seconds (e.g., 3600).
RecordingType	RECOMMENDED. Defines whether the recording is ”continuous”, ”discontinuous” or ”epoched”; this latter limited to time windows about events of interest (e.g., stimulus presentations, subject responses etc.)
EpochLength	RECOMMENDED. Duration of individual epochs in seconds (e.g., 1) in case of epoched data. If recording was continuous or discontinuous, leave out the field.
iEEGGround	RECOMMENDED. Description of the location of the ground electrode (”placed on right mastoid (M2)”).
iEEGPlacementScheme	RECOMMENDED. Freeform description of the placement of the iEEG electrodes. Left/right/bilateral/depth/surface (e.g., ”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. Field to describe the way electrodes are grouped into strips, grids or depth probes e.g., {’grid1’: ”10x8 grid on left temporal pole”, ’strip2’: ”1x8 electrode strip on xxx”}.
SubjectArtefactDescription	RECOMMENDED. Freeform description of the observed subject artefact and its possible cause (e.g., ”door open”, ”nurse walked into room at 2 min”, ”seizure at 10 min”). If this field is left empty, it will be interpreted as absence of artifacts.

Specific iEEG fields MAY be present:

Field name	Definition
ElectricalStimulation	OPTIONAL. Boolean field to specify if electrical stimulation was done during the recording (options are ”true” or ”false”). Parameters for event-like stimulation should be specified in the _events.tsv file (see example below).
ElectricalStimulationParameters	OPTIONAL. Free form description of stimulation parameters, such as frequency, shape etc. Specific onsets can be specified in the _events.tsv file. Specific shapes can be described here in freeform text.

Example:

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

```
  "PowerLineFrequency":60,
  "SoftwareFilters":"n/a",
  "DCOffsetCorrection":0,
  "HardwareFilters":{"Highpass RC filter": {"Half amplitude cutoff (Hz)": 0.0159, "Roll-off": "6
      dBOctave"}},
  "ElectrodeManufacturer":"AdTech",
  "ECOGChannelCount":120,
  "SEEGChannelCount":0,
  "EEGChannelCount":0,
  "EOGChannelCount":0,
  "ECGChannelCount":0,
  "EMGChannelCount":0,
  "MiscChannelCount":0,
  "TriggerChannelCount":0,
  "RecordingDuration":233.639,
  "RecordingType":"continuous",
  "iEEGGround":"placed on the right mastoid",
  "iEEGPlacementScheme":"right occipital temporal surface",
  "ElectricalStimulation":false
}
```

Note that the date and time information SHOULD be stored in the Study key file (`scans.tsv`). As it is indicated there, date time information MUST be expressed in the following format `YYYY-MM-DDThh:mm:ss` (ISO8601 date-time format). For example: 2009-06-15T13:45:30. It does not need to be fully detailed, depending on local REB/IRB ethics board policy.

Channels description (`*_channels.tsv`)

Template:

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

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

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

MUST be present:

Column name	Definition
name	REQUIRED. Label of the channel. The label must correspond to _electrodes.tsv name and all ieeg type channels are required to have a position. The reference channel name MAY be provided in the reference column.
type	REQUIRED. Type of channel, see below for adequate keywords in this field.
units	REQUIRED. Physical unit of the value represented in this channel, e.g., V for Volt, specified according to the SI unit symbol and possibly prefix symbol (e.g., mV, V), or as a derived SI unit (e.g., fT/cm). For guidelines for Units and Prefixes see Appendix V.
low_cutoff	REQUIRED. Frequencies used for the low pass filter applied to the channel in Hz. If no low pass filter was applied, use `n/a`. Note that anti-alias is a low pass filter, specify its frequencies here if applicable.

Column name	Definition
high_cutoff	REQUIRED. Frequencies used for the high pass filter applied to the channel in Hz. If no high pass filter applied, use `n/a`.

SHOULD be present:

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

Example `sub-01_channels.tsv`:

```
name  type  units low_cutoff  high_cutoff status  status_description
LT01  ECOG   V    300         0.11        good    n/a
LT02  ECOG   V    300         0.11        bad     broken
H01   SEEG   V    300         0.11        bad     line_noise
ECG1  ECG    V    n/a         0.11        good    n/a
TR1   TRIG  n/a   n/a         n/a         good    n/a
```

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

Keyword	Description
EEG	Electrode channel from electroencephalogram
ECOG	Electrode channel from electrocorticogram (intracranial)
SEEG	Electrode channel from stereo-electroencephalogram (intracranial)
DBS	Electrode channel from deep brain stimulation electrode (intracranial)
VEOG	Vertical EOG (electrooculogram)
HEOG	Horizontal EOG
EOG	Generic EOG channel if HEOG or VEOG information not available
ECG	ElectroCardioGram (heart)
EMG	ElectroMyoGram (muscle)
TRIG	System Triggers
AUDIO	Audio signal
PD	Photodiode
EYEGAZE	Eye Tracker gaze
PUPIL	Eye Tracker pupil diameter
MISC	Miscellaneous

Keyword	Description
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

The free text field for the channel description can for example be specified as intracranial, stimulus, response, vertical EOG, horizontal EOG, skin conductance, eyetracker, etc.

Electrode description (`*_electrodes.tsv`)

Template:

```
sub-<label>/
    [ses-<label>]/
      ieeg/
         sub-<label>[_ses-<label>][_space-<label>]_electrodes.tsv
```

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

The optional space label (`*[_space-<label>]_electrodes.tsv`) can be used to indicate the way in which electrode positions are interpreted. The space label needs to be taken from the list in Appendix VIII

For examples:

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

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

For example:

- `sub-01_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.

MUST be present:

Column name	Definition
name	REQUIRED. Name of the electrode contact point.
x	REQUIRED. X position. The positions of the center of each electrode in xyz space. Units are in millimeters or pixels and are specified in _*space-_electrode.json.
y	REQUIRED. Y position.
z	REQUIRED. Z position. If electrodes are in 2D space this should be a column of n/a values.
size	REQUIRED. Surface area of the electrode, in mm^2.

SHOULD be present:

Column name	Definition
material	OPTIONAL. Material of the electrodes.
manufacturer	OPTIONAL. Recommended field to specify the manufacturer for each electrode. Can be used if electrodes were manufactured by more than one company.

Column name	Definition
group	OPTIONAL. Optional field to specify the group that the electrode is a part of. Note that any group specified here should match a group specified in `_channels.tsv`.
hemisphere	OPTIONAL. Optional field to specify the hemisphere in which the electrode is placed, one of `['L' or 'R']` (use capital).

MAY be present:

Column name	Definition
type	OPTIONAL. Optional type of the electrode, e.g., cup, ring, clip-on, wire, needle, ...
impedance	OPTIONAL. Impedance of the electrode in kOhm.
dimension	OPTIONAL. Size of the group (grid/strip/probe) that this electrode belongs to. Must be of form `[AxB]` with the smallest dimension first (e.g., `[1x8]`).

Example:

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

Coordinate System JSON (`*_coordsystem.json`)

Template:

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

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

General fields:

Field name	Definition
IntendedFor	RECOMMENDED. This can be an MRI/CT or a file containing the operative photo, x-ray or drawing with path relative to the project folder. 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**: `sub-<label>/ses-<label>/anat/sub-01_T1w.nii.gz` **Surface**: `/derivatives/surfaces/sub-<label>/ses-<label>/anat/sub-01_T1w_pial.R.surf.gii` **Operative photo**: `/sub-<label>/ses-<label>/ieeg/sub-0001_ses-01_acq-photo1_photo.jpg` **Talairach**: `/derivatives/surfaces/sub-Talairach/ses-01/anat/sub-Talairach_T1w_pial.R.surf.gii`

Fields relating to the iEEG electrode positions:

Field name	Definition
iEEGCoordinateSystem	REQUIRED. Defines the coordinate system for the iEEG electrodes. See Appendix VIII for a list of restricted keywords. 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 2D coordinate systems
iEEGCoordinateUnits	REQUIRED. Units of the _electrodes.tsv, MUST be ”m”, ”mm”, ”cm” or ”pixels”.
iEEGCoordinateSystemDescription	RECOMMENDED. Freeform text description or link to document describing the iEEG coordinate system system in detail (e.g., ”Coordinate system with the origin at anterior commissure (AC), negative y-axis going through the posterior commissure (PC), z-axis going to a mid-hemisperic point which lies superior to the AC-PC line, x-axis going to the right”).
iEEGCoordinateProcessingDescription	RECOMMENDED. Has any post-processing (such as projection) been done on the electrode positions (e.g., ”surface_projection”, ”none”).
iEEGCoordinateProcessingReference	RECOMMENDED. A reference to a paper that defines in more detail the method used to localize the electrodes and to post-process the electrode positions. .

Recommended 3D coordinate systems

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

Allowed 2D coordinate systems

If electrodes are localized in 2D space (only x and y are specified and z is n/a), then the positions in this file must correspond to the locations expressed in pixels on the photo/drawing/rendering of the electrodes on the brain. In this case, 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 (e.g., MRI, CT and MNI), these spaces can be distinguished by the optional `[_space-<label>]` field, see the `*_electrodes.tsv`-section for more information. Note that the `[_space-<label>]` fields must correspond between `*_electrodes.tsv` and `*_coordsystem.json` if they refer to the same data.

Example:

```
{
    "IntendedFor": "/sub-01/ses-01/anat/sub-01_T1w.nii.gz",
    "iEEGCoordinateSystem": "ACPC",
    "iEEGCoordinateUnits": "mm",
    "iEEGCoordinateSystemDescription": "Coordinate system with the origin at anterior commissure
         (AC), negative y-axis going through the posterior commissure (PC), z-axis going to a
        mid-hemisperic point which lies superior to the AC-PC line, x-axis going to the right",
    "iEEGCoordinateProcessingDescription": "surface_projection",
    "iEEGCoordinateProcessingReference": "Hermes et al., 2010 JNeuroMeth"
}
```

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

Template:

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

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.

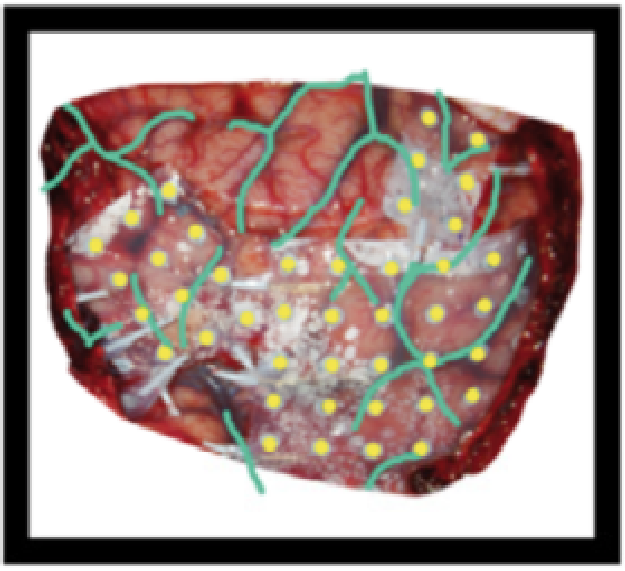
If there are photos of the electrodes, the acquisition field should be specified with:

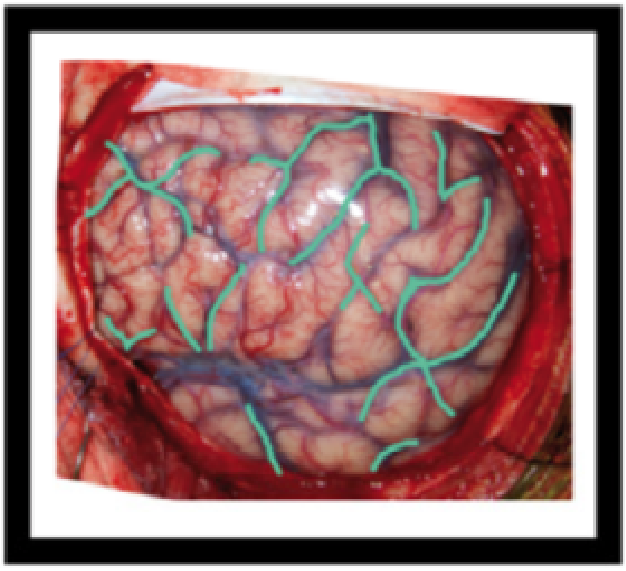
- `*_photo.jpg` in case of an operative photo
- `*_acq-xray#_photo.jpg` in case of an x-ray picture
- `*_acq-drawing#_photo.jpg` in case of a drawing or sketch of electrode placements
- `*_acq-render#_photo.jpg` in case of a rendering

The session label may be used to specify when the photo was taken.

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

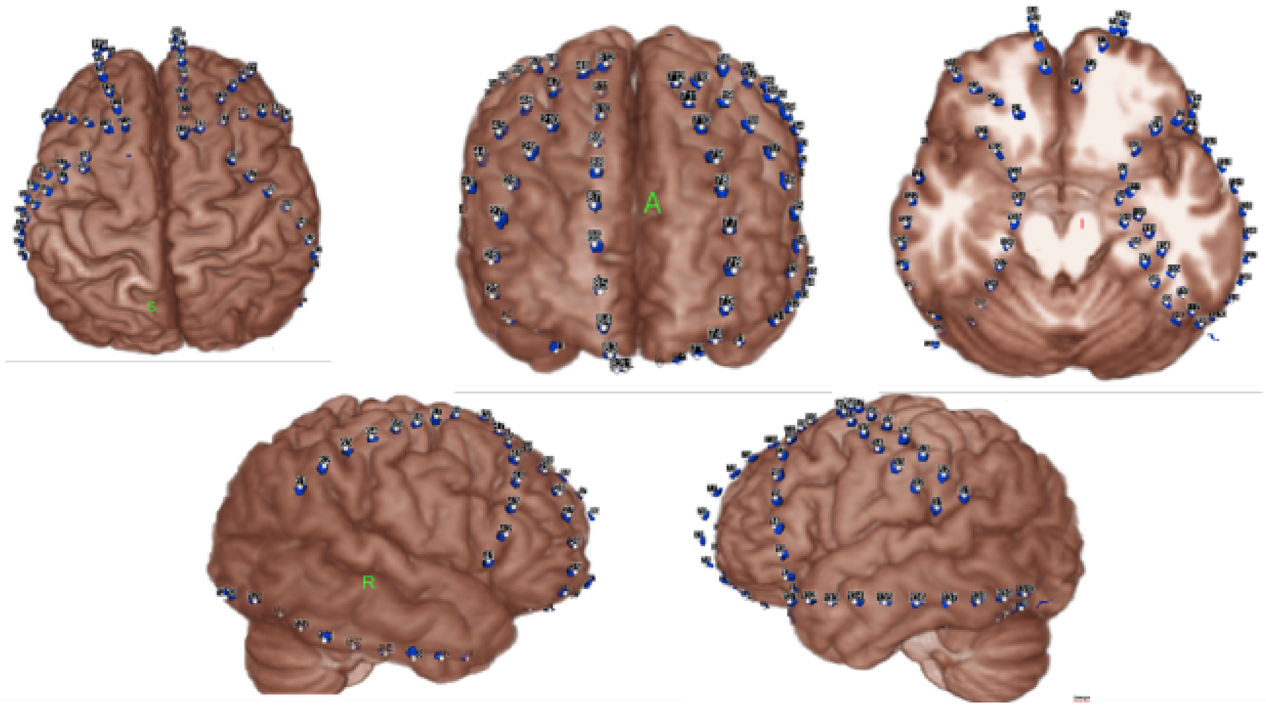
```
    sub-0001_ses-01_acq-photo1_photo.jpg
    sub-0001_ses-01_acq-photo2_photo.jpg
```





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 (e.g., see Burneo JG et al. 2014 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 folder in the `/stimuli/` folder. For example: `/stimuli/electrical_stimulation_functions/biphasic.tsv`

Example:

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

Chapter 9

Task events

Template:

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

Where `<matches>` corresponds to task file name. For example: `sub-control01_task-nback`. It is also possible to have a single _events.tsv file describing events for all participants and runs (see Inheritance Principle). As with all other tabular data, `_events` files may be accompanied by a JSON file describing the columns in detail (see here).

The purpose of this file is to describe timing and other properties of events recorded during the scan. Events MAY be either stimuli presented to the participant or participant responses. A single event file MAY include any combination of stimuli and response events. Events MAY overlap in time. Please mind that this does not imply that only so called ”event related” study designs are supported (in contrast to ”block” designs) - each ”block of events” can be represented by an individual row in the _events.tsv file (with a long duration). Each task events file REQUIRES a corresponding task imaging data file (but a single events file MAY be shared by multiple imaging data files - see Inheritance principle). The tabular files consists of one row per event and a set of REQUIRED and OPTIONAL columns:

Column name	Description
onset	REQUIRED. Onset (in seconds) of the event measured from the beginning of the acquisition of the first volume in the corresponding task imaging data file. If any acquired scans have been discarded before forming the imaging data file, ensure that a time of 0 corresponds to the first image stored. In other words negative numbers in ”onset” are allowed5.
duration	REQUIRED. Duration of the event (measured from onset) in seconds. Must always be either zero or positive. A ”duration” value of zero implies that the delta function or event is so short as to be effectively modeled as an impulse.
sample	OPTIONAL. Onset of the event according to the sampling scheme of the recorded modality (i.e., referring to the raw data file that the `events.tsv` file accompanies).
trial_type	OPTIONAL. 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.
response_time	OPTIONAL. Response time measured in seconds. A negative response time can be used to represent preemptive responses and ”n/a” denotes a missed response.
stim_file	OPTIONAL. Represents the location of the stimulus file (image, video, sound etc.) presented at the given onset time. There are no restrictions on the file formats of the stimuli files, but they should be stored in the /stimuli folder (under the root folder of the dataset; with optional subfolders). The values under the stim_file column correspond to a path relative to ”/stimuli”. For example ”images/cat03.jpg” will be translated to ”/stimuli/images/cat03.jpg”.
value	OPTIONAL. Marker value associated with the event (e.g., the value of a TTL trigger that was recorded at the onset of the event).

Column name	Description
HED	OPTIONAL. Hierarchical Event Descriptor (HED) Tag. See Appendix III for details.

5 For example in case there is an in scanner training phase that begins before the scanning sequence has started events from this sequence should have negative onset time counting down to the beginning of the acquisition of the first volume.

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

In case of multi-echo task run, a single `_events.tsv` file will suffice for all echoes.

Example:

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

```
onset duration  trial_type  response_time stim_file
1.2 0.6 go  1.435 images/red_square.jpg
5.6 0.6 stop  1.739 images/blue_square.jpg
```

References to existing databases can also be encoded using additional columns. Example 2 includes references to the Karolinska Directed Emotional Faces (KDEF) database6:

6http://www.emotionlab.se/resources/kdef

Example:

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

```
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
```

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

```
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
```

Chapter 10

Physiological and other continuous recordings

Template:

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

Optional: Yes

Where `<matches>` corresponds to task file name without the `_bold.nii[.gz]` suffix. For example: `sub-control01_task-nback_run-1`. 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 can be used and placed in the root directory. For example:%60task-movie_stim.tsv.gz‘

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

Field name	Definition
SamplingFrequency	REQUIRED. Sampling frequency in Hz of all columns in the file.
StartTime	REQUIRED. Start time in seconds in relation to the start of acquisition of the first data sample in the corresponding neural dataset (negative values are allowed).
Columns	REQUIRED. Names of columns in file.

Additional metadata may be included as in any TSV file to specify, for example, the units of the recorded time series. Please note that in contrast to other TSV files this one does not include a header line. Instead the name of columns are specified in the JSON file. This is to improve compatibility with existing software (FSL PNM) as well as make support for other file formats possible in the future. Recordings with different sampling frequencies and/or starting times should be stored in separate files. The following naming conventions should be used for column names:

Column name	Definition
cardiac	continuous pulse measurement
respiratory	continuous breathing measurement
trigger	continuous measurement of the scanner trigger signal

Any combination of those three can be included as well as any other stimuli related continuous variables (such as low level image properties in a video watching paradigm).

Physiological recordings (including eye tracking) should use the `_physio` suffix, and signals related to the stimulus should use `_stim` suffix. For motion parameters acquired from scanner side motion correction please use `_physio` suffix.

More than one continuous recording file can be included (with different sampling frequencies). In such case use different labels. For example: `_recording-contrast`, `_recording-saturation`. The full file name could then look like this: `sub-control01_task-nback_run-2_recording-movie_stim.tsv.gz`

For multi-echo data, physio.tsv file is applicable to all echos of particular run. For eg:

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

Example:

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

(after decompression)

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

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

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

Chapter 11

Behavioral experiments (with no MRI)

Template:

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

In addition to logs from behavioral experiments performed along imaging data acquisitions one can also include data from experiments performed outside of the scanner. The results of those experiments can be stored in the `beh` folder using the same formats for event timing (`_events.tsv`), metadata (`_events.json`), physiological (`_physio.tsv.gz`, `_physio.json`) and other continuous recordings (`_stim.tsv.gz`, `_stim.json`) as for tasks performed during MRI acquisitions. Additionally, events files that do not include the mandatory `onset` and `duration` columns can still be included, but should be labeled `_beh.tsv` rather than `_events.tsv`.

Chapter 12

Genetic Descriptor

Support for genetic descriptors was developed as a BIDS Extension Proposal. The extension was primarily developed by Cyril Pernet and Clara Moreau with contributions from Tom Nichols and Jessica Turner.

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.

Dataset Description

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

Datasets linked to a genetic database entry include the following REQUIRED or OPTIONAL `dataset_description.json` keys (a dot in the key name denotes a key in a subdictionary):

Field name	Definition
Genetics.Dataset	REQUIRED. URI where data can be retrieved.
Genetics.Database	OPTIONAL. URI of database where the dataset is hosted.
Genetics.Descriptors	OPTIONAL. List of relevant descriptors (*e.g.*, journal articles) for dataset.

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": ["https://doi.org/10.1016/j.neuroimage.2013.05.041"]
     }
}
```

Subject naming and Participants file

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

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

`participants.tsv` example:

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

Genetic Information

Template:

```
genetic_info.json
```

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

Field name	Definition
GeneticLevel	REQUIRED. String. Describes the level of analysis. Values MUST be one of `Genetic`, `Genomic`, `Epigenomic`, `Transcriptomic`, `Metabolomic`, or `Proteomic`.
AnalyticalApproach	OPTIONAL. String or list of strings. Methodology or methodologies used to analyse the GeneticLevel. Values MUST be taken from the database of Genotypes and Phenotypes (dbGaP) under /Study/Molecular Data Type, for instance `SNP Genotypes (Array)` or `Methylation (CpG)`.
SampleOrigin	REQUIRED. String. Describes from which tissue the genetic information was extracted. Values 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`. Values MUST be one of `gray matter`, `white matter`, `csf`, `meninges`, `macrovascular` or `microvascular`.
BrainLocation	OPTIONAL. String. Refers to the location in space of the `TissueOrigin`. Values may be an MNI coordinate, a label taken from the Allen Brain Atlas, or layer to refer to layer-specific gene expression, which can also tie up with laminar fMRI.
CellType	OPTIONAL. String. Describes the type of cell analyzed. Values SHOULD come from the cell ontology.

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

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

`genetic_info.json` example:

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

```
}
```

Chapter 13

BIDS Derivatives

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

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

Metadata conventions

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

File naming conventions

- Filenames that are permissible for a raw BIDS data type have a privileged status. Any modification of raw files must use a modified filename that does not conflict with the raw filename. Further, any files created as part of a derivative dataset must not match a permissible filename of a valid raw dataset. Stated equivalently, if any filename in a derivative dataset has a name permissible for a raw BIDS data, then that file must be an identical copy of that raw file.
- Each Derivatives filename MUST be of the form: `<source_entities>[_keyword-<value>]_<suffix>.<ext>` (where `<value>` could either be an `<index>` or a `<label>` depending on the keyword; see Definitions)
- When the derivatives chain involves outputs derived from a single raw input, `source_entities` MUST be the entire source filename, with the omission of the source suffix and extension. One exception to this rule is filename entities that are no longer relevant. Depending on the nature of the derivative file, the suffix can either be the same as the source file if that suffix is still appropriate, or a new appropriate value selected from the controlled list.
- There is no prohibition against identical filenames in different derived datasets, although users should be aware of the potential ambiguity this can create and use the sidecar JSON files to detail the specifics of individual files.
- When necessary to distinguish two files that do not otherwise have a distinguishing entity, the `_desc-<label>` keyword-value SHOULD be used. This includes the cases of needing to distinguish both differing

inputs and differing outputs (for example, `_desc-T1w` and `_desc-T2w` to distinguish brain mask files derived from T1w and T2w images; or `_desc-sm4` and `_desc-sm8` to distinguish between outputs generated with two different levels of smoothing).

- When naming files that are not yet standardized, it is RECOMMENDED to use names consistent with BIDS conventions where those conventions apply. For example, if a summary statistic is derived from a given task, the file name SHOULD contain `_task-<label>`.

Chapter 14

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	Description
Description	RECOMMENDED. Free-form natural language description of the nature of the file.
Sources	OPTIONAL. A list of files with the paths specified relative to dataset root; these files were directly used in the creation of this derivative data file. For example, if a derivative A is used in the creation of another derivative B, which is in turn used to generate C in a chain of A->B->C, C should only list B in `Sources`, and B should only list A in `Sources`. However, in case both X and Y are directly used in the creation of Z, then Z should list X and Y in `Sources`, regardless of whether X was used to generate Y.
RawSources	OPTIONAL. A list of paths relative to dataset root pointing to the BIDS-Raw file(s) that were used in the creation of this derivative.

Examples

Preprocessed `bold` NIfTI file in the original coordinate space of the original run. The location of the file in the original datasets is encoded in the `RawSources` metadata, and `desc-<label>` is used to prevent clashing with the original file name.

```
sub-01/func/sub-01_task-rest_desc-preproc_bold.nii.gz
sub-01/func/sub-01_task-rest_desc-preproc_bold.json
```

```
{
    "RawSources": ["sub-01/func/sub-01_task-rest_bold.nii.gz"]
}
```

If this file was generated with prior knowledge from additional sources, such as the same subject's `T1w`, then both files MAY be included in `RawSources`.

```
{
    "RawSources": [
        "sub-01/func/sub-01_task-rest_bold.nii.gz",
        "sub-01/anat/sub-01_T1w.nii.gz"
    ]
}
```

On the other hand, if a preprocessed version of the T1w image was used, and it also occurs in the derivatives, `Sources` and `RawSources` can both be specified.

```
{
    "Sources": [
        "sub-01/anat/sub-01_desc-preproc_T1w.nii.gz"
    ],
    "RawSources": [
        "sub-01/func/sub-01_task-rest_bold.nii.gz"
    ]
}
```

Spatial references

Derivatives are often aligned to a common spatial reference to allow for the comparison of acquired data across runs, sessions, subjects or datasets. A file may indicate the spatial reference to which it has been aligned using the `space` entity and/or the `SpatialReference` metadata.

The `space` entity may take any value in Image-Based Coordinate Systems.

If the `space` entity is omitted, or the space is not in the Standard template identifiers table, then the `SpatialReference` metadata is REQUIRED.

Key name	**Description**
SpatialReference	RECOMMENDED if the derivative is aligned to a standard template listed in Standard template identifiers. REQUIRED otherwise. For images with a single reference, the value MUST be a single string. For images with multiple references, such as surface and volume references, a JSON object MUST be used.

SpatialReference key allowed values

Value	**Description**
`orig`	A (potentially unique) per-image space. Useful for describing the source of transforms from an input image to a target space.
URI or path	This can be used to point to a specific file. Paths are written relative to the root of the derivative dataset.

In the case of images with multiple references, an object must link the relevant structures to reference files. If a single volumetric reference is used for multiple structures, the `VolumeReference` key MAY be used to reduce duplication. For CIFTI-2 images, the relevant structures are BrainStructure values defined in the BrainModel elements found in the CIFTI-2 header.

Examples

Preprocessed `bold` NIfTI file in `individual` coordinate space. Please mind that in this case `SpatialReference` key is REQUIRED.

```
sub-01/func/sub-01_task-rest_space-individual_bold.nii.gz
sub-01/func/sub-01_task-rest_space-individual_bold.json
```

```
{
    "SpatialReference": "sub-01/anat/sub-01_desc-combined_T1w.nii.gz"
}
```

Preprocessed `bold` CIFTI-2 files that have been sampled to the fsLR surface meshes defined in the Conte69 atlas along with the MNI152NLin6Asym template. In this example, because all volumetric structures are sampled to the same reference, the `VolumeReference` key is used as a default, and only the surface references need to be specified by BrainStructure names.

```
sub-01/func/sub-01_task-rest_space-fsLR_den-91k_bold.dtseries.nii
sub-01/func/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-<participant_label>/
        <datatype>/
            <source_entities>[_space-<space>][_desc-<label>]_<suffix>.<ext>
```

Data is considered to be *preprocessed* or *cleaned* if the data type of the input, as expressed by the BIDS `suffix`, is unchanged. By contrast, processing steps that change the number of dimensions are likely to disrupt the propagation of the input's `suffix` and generally, the outcomes of such transformation cannot be considered preprocessed or cleaned data.

Examples of preprocessing:

- Motion-corrected, temporally denoised, and transformed to MNI space BOLD series
- Inhomogeneity corrected and skull stripped T1w files
- Motion-corrected DWI files
- Time-domain filtered EEG data
- MaxFilter (for example, SSS) cleaned MEG data

The `space` keyword is recomended to distinguish files with different underlying coordinate systems or registered to different reference maps. See Spatial references for details. The `desc` (description) keyword 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 (e.g., if a source 4D image is averaged to create a single static volume, a `RepetitionTime` property would no longer be relevant).

Chapter 15

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-<participant_label>/
        <datatype>/
            <source_entities>[_space-<space>][_res-<label>][_den-<label>][_desc-<label>]_<suffix>.<ext>
```

Volumetric preprocessing does not modify the number of dimensions, and so the specifications in Preprocessed or cleaned data apply. The use of surface meshes and volumetric measures sampled to those meshes is sufficiently similar in practice to treat them equivalently.

When two or more instances of a given derivative are provided with resolution or surface sampling density being the only difference between them, then the `res` (for *resolution* of regularly sampled N-D data) and/or `den` (for *density* of non-parametric surfaces) SHOULD be used to avoid name conflicts. Note that only files combining both regularly sampled (e.g., 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	Description
SkullStripped	REQUIRED. Boolean. Whether the volume was skull stripped (non-brain voxels set to zero) or not.
Resolution	REQUIRED if `res` is present. String, or object mapping labels to strings. Specifies the interpretation of the resolution keyword.
Density	REQUIRED if `den` is present. String, or object mapping labels to strings. Specifies the interpretation of the density keyword.

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-<participant_label>/
        anat|func|dwi/
            <source_entities>[_space-<space>][_res-<label>][_den-<label>][_label-<label>][_desc
                -<label>]_mask.nii.gz
```

A binary (1 - inside, 0 - outside) mask in the space defined by `<space>`. If no transformation has taken place, the value of `space` SHOULD be set to `orig`. If the mask is an ROI mask derived from an atlas, then the `label` entity SHOULD be used to specify the masked structure (see Common image-derived labels), and the `Atlas` metadata SHOULD be defined.

JSON metadata fields:

Key name	Description
RawSources	Same as defined in Introduction, but elevated from OPTIONAL to REQUIRED
Type	RECOMMENDED. Short identifier of the mask. Reserved values: `Brain` - brain mask, `Lesion` - lesion mask, `Face` - face mask, `ROI` - ROI mask
Atlas	OPTIONAL. Which atlas (if any) was used to generate the mask. RECOMMENDED if `label` entity is defined.
Resolution	REQUIRED if `res` is present. String, or object mapping labels to strings. Specifies the interpretation of the resolution keyword.
Density	REQUIRED if `den` is present. String, or object mapping labels to strings. Specifies the interpretation of the density keyword.

Examples:

```
func_loc/
    sub-001/
        func/
           sub-001_task-rest_run-1_space-MNI305_desc-PFC_mask.nii.gz
           sub-001_task-rest_run-1_space-MNI305_desc-PFC_mask.json
```

```
manual_masks/
    sub-001/
        anat/
            sub-001_desc-tumor_mask.nii.gz
            sub-001_desc-tumor_mask.json
```

Segmentations

A *segmentation* is a labeling of regions of an image such that each location (for example, a voxel or a surface vertex) is identified with a label or a combination of labels. Labeled regions may include anatomical structures (such as tissue class, Brodmann area or white matter tract), discontiguous, functionally-defined networks, tumors or lesions.

A *discrete segmentation* represents each region with a unique integer label. A *probabilistic segmentation* represents each region as values between 0 and 1 (inclusive) at each location in the image, and one volume/frame per structure may be concatenated in a single file.

Segmentations may be defined in a volume (labeled voxels), a surface (labeled vertices) or a combined volume/-surface space.

The following section describes discrete and probabilistic segmentations of volumes, followed by discrete segmentations of surface/combined spaces. Probabilistic segmentations of surfaces are currently unspecified.

The following metadata fields apply to all segmentation files:

Key name	Description
Manual	OPTIONAL. Boolean. Indicates if the segmenation was performed manually or via an automated process
Atlas	OPTIONAL. Which atlas (if any) was used to derive the segmentation.
Resolution	REQUIRED if `res` is present. String, or object mapping labels to strings. Specifies the interpretation of the resolution keyword.
Density	REQUIRED if `den` is present. String, or object mapping labels to strings. Specifies the interpretation of the density keyword.

Discrete Segmentations

Discrete segmentations of brain tissue represent multiple anatomical structures (such as tissue class or Brodmann area) with a unique integer label in a 3D volume. See Common image-derived labels for a description of how integer values map to anatomical structures.

Template:

```
<pipeline_name>/
    sub-<participant_label>/
        anat|func|dwi/
            <source_entities>[_space-<space>][_res-<label>][_den-<label>]_dseg.nii.gz
```

Example:

```
pipeline/
    sub-001/
        anat/
            sub-001_space-orig_dseg.nii.gz
            sub-001_space-orig_dseg.json
```

A segmentation can be used to generate a binary mask that functions as a discrete ”label” for a single structure. In this case, the mask suffix MUST be used, the `label` entity SHOULD be used to specify the masked structure (see Common image-derived labels), and the `Atlas` metadata SHOULD be defined. For example:

```
pipeline/
    sub-001/
        anat/
            sub-001_space-orig_label-GM_mask.nii.gz
```

Probabilistic Segmentations

Probabilistic segmentations of brain tissue represent a single anatomical structure with values ranging from 0 to 1 in individual 3D volumes or across multiple frames. If a single structure is included, the `label` entity SHOULD be used to specify the structure.

Template:

```
<pipeline_name>/
    sub-<participant_label>/
        func|anat|dwi/
            <source_entities>[_space-<space>][_res-<label>][_den-<label>][_label-<label>]
                _probseg.nii.gz
```

Example:

```
pipeline/
    sub-001/
        anat/
            sub-001_space-orig_label-BG_probseg.nii.gz
            sub-001_space-orig_label-WM_probseg.nii.gz
```

See Common image-derived labels for reserved key values for `label`.

A 4D probabilistic segmentation, in which each frame corresponds to a different tissue class, must provide a label mapping in its JSON sidecar. For example:

```
pipeline/
    sub-001/
        anat/
            sub-001_space-orig_probseg.nii.gz
            sub-001_space-orig_probseg.json
```

The JSON sidecar MUST include the label-map key that specifies a tissue label for each volume:

```
{
    "LabelMap": [
        "BG",
        "WM",
        "GM"
        ]
}
```

Values of `label` SHOULD correspond to abbreviations defined in Common image-derived labels.

Discrete surface segmentations

Discrete surface segmentations (sometimes called *parcellations*) of cortical structures MUST be stored as GIFTI label files, with the extension `.label.gii`. For combined volume/surface spaces, discrete segmentations MUST be stored as CIFTI-2 dense label files, with the extension `.dlabel.nii`.

Template:

```
<pipeline_name>/
    sub-<participant_label>/
        anat/
            <source_entities>[_hemi-{L|R}][_space-<space>][_res-<label>][_den-<label>]_dseg.{
                label.gii|dlabel.nii}
```

The `hemi` tag 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
            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	Description
index	REQUIRED. The label integer index
name	REQUIRED. The unique label name
abbreviation	OPTIONAL. The unique label abbreviation
color	OPTIONAL. Hexadecimal. Label color for visualization
mapping	OPTIONAL. Corresponding integer label in the standard BIDS label lookup

An example, custom `dseg.tsv` that defines three labels:

```
index   name            abbreviation    color       mapping
100     Gray Matter     GM              #ff53bb     1
101     White Matter    WM              #2f8bbe     2
102     Brainstem       BS              #36de72     11
```

The following example `dseg.tsv` defines regions that are not part of the standard BIDS labels:

```
index   name                abbreviation
137     pars opercularis    IFGop
138     pars triangularis   IFGtr
139     pars orbitalis      IFGor
```

Chapter 16

Longitudinal and multi-site studies

Multiple sessions (visits) are encoded by adding an extra layer of directories and file names in the form of `ses-<label>`. Session label can consist only of alphanumeric characters `[a-zA-Z0-9]` and should be consistent across subjects. If numbers are used in session labels we recommend using zero padding (for example `ses-01`, `ses-11` instead of `ses-1`, `ses-11`). This makes results of alphabetical sorting more intuitive. Acquisition time of session can be defined in the sessions file (see below for details).

The extra session layer (at least one `/ses-<label>` subfolder) should be added for all subjects if at least one subject in the dataset has more than one session. Skipping the session layer for only some subjects in the dataset is not allowed. If a `/ses-<label>` subfolder is included as part of the directory hierarchy, then the same `ses-<label>` tag must also be included as part of the file names themselves.

```
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_cont-physio.tsv.gz
            sub-control01_ses-predrug_task-nback_cont-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_cont-physio.tsv.gz
            sub-control01_ses-postdrug_task-nback_cont-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_ses-postdrug_scans.tsv
    sub-control01_sessions.tsv
participants.tsv
dataset_description.json
README
CHANGES
```

Sessions file

Template:

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

Optional: Yes

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

`_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
```

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.

Treat each site/center as a separate dataset

The simplest way of dealing with multiple sites is to treat data from each site as a separate and independent BIDS dataset with a separate participants.tsv and other metadata files. This way you can feed each dataset individually to BIDS Apps and everything should just work.

Option 2: Combining sites/centers into one dataset

Alternatively you can combine data from all sites into one dataset. To identify which site each subjects comes from you can add a `site` column in the `participants.tsv` file indicating the source site. This solution allows you to analyze all of the subjects together in one dataset. One caveat is that subjects from all sites will have to have unique labels. To enforce that and improve readability you can use a subject label prefix identifying the site. For example `sub-NUY001`, `sub-MIT002`, `sub-MPG002` etc. Remember that hyphens and underscores are not allowed in subject labels.

Chapter 17

BIDS Extension Proposals

The BIDS specification can be extended in a backwards compatible way and will evolve over time. This is accomplished with BIDS Extension Proposals (BEPs), which are community-driven processes (see BEP guidelines Google Doc).

On the BIDS homepage you can find a list of extension protocols 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 Google Doc

Chapter 18

Appendix I: Contributors

Legend (source: https://github.com/kentcdodds/all-contributors)

Emoji	Represents
	Answering Questions (on the mailing list, NeuroStars, GitHub, or in person)
	Bug reports
	Blogposts
	Code
	Documentation and specification
	Design
	Examples
	Event Organizers
	Financial Support
	Funding/Grant Finders
	Ideas & Planning
	Infrastructure (Hosting, Build-Tools, etc)
	Plugin/utility libraries
	Reviewed Pull Requests
	Tools
	Translation
	Tests
	Tutorials
	Talks
	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.

- Fidel Alfaro Almagro
- Stefan Appelhoff
- Tibor Auer
- Sylvain Baillet
- Arshitha Basavaraj
- Stephan Bickel
- Elizabeth Bock
- Kristofer Bouchard
- Eric Bridgeford
- Teon L. Brooks
- Suyash Bhogawar
- Vince D. Calhoun
- Alexander L. Cohen
- R. Cameron Craddock
- Sasha D'Ambrosio
- Samir Das

- Olivier David
- Orrin Devinsky
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- Peer Herholz
- Dora Hermes
- Katja Heuer
- Chris Holdgraf
- Christopher J. Honey
- Jean-Christophe Houde
- International Neuroinformatics Coordinating Facility
- Andrew Janke
- Mainak Jas
- Alexander Jones
- David Keator
- James Kent
- Gregory Kiar
- Robert Knight
- Jean-Philippe Lachaux
- Pamela LaMontagne
- Kevin Larcher
- Jonathan C. Lau
- Laura and John Arnold Foundation
- Christopher Lee-Messer
- Jon Haitz Legarreta
- Xiangrui Li
- Vladimir Litvak
- Brian N. Lundstrom
- Dan Lurie
- Camille Maumet
- Christopher J. Markiewicz
- Kai J. Miller
- Jeremy Moreau
- Zachary Michael

- Ezequiel Mikulan
- Michael P. Milham
- Henk Mutsaerts
- National Institute of Mental Health
- Mikael Naveau
- B. Nolan Nichols
- Thomas E. Nichols
- Dylan Nielson
- Guiomar Niso
- Michael P. Notter
- Jeffrey G. Ojemann
- Robert Oostenveld
- Dimitri Papadopoulos Orfanos
- Patrick Park
- Dianne Patterson
- John Pellman
- Cyril Pernet
- Franco Pestilli
- Natalia Petridou
- Dmitry Petrov
- Christophe Phillips
- Gio Piantoni
- Andrea Pigorini
- Russell A. Poldrack
- Jean-Baptiste Poline
- Wouter V. Potters
- Nader Pouratian
- Pradeep Reddy Raamana
- Vasudev Raguram
- Nick F. Ramsey
- Kay Robbins
- Alex Rockhill
- Ariel Rokem
- Matt Sanderson
- Gunnar Schaefer
- Jan-Mathijs Schoffelen
- Robert E. Smith
- Vanessa Sochat
- Arjen Stolk
- Nicole C. Swann
- François Tadel
- Roberto Toro
- Sébastien Tourbier
- William Triplett
- Jessica A. Turner
- Bradley Voytek
- Brian A. Wandell
- Joseph Wexler
- Kirstie Whitaker
- Jonathan Winawer
- Gaël Varoquaux
- Tal Yarkoni
- Lyuba Zehl

Chapter 19

Appendix II: Licenses

This section lists a number of common licenses for datasets and defines suggested abbreviations for use in the dataset metadata specifications.

Please note that this list only serves to provide some examples for possible licenses. The terms of any license should be consistent with the informed consent obtained from participants and any institutional limitations on distribution.

Identifier	License name	Description
PD	Public Domain	No license required for any purpose; the work is not subject to copyright in any jurisdiction.
PDDL	Open Data Commons Public Domain Dedication and License	License to assign public domain like permissions without giving up the copyright: http://opendatacommons.org/licenses/pddl/
CC0	Creative Commons Zero 1.0 Universal.	Use this if you are a holder of copyright or database rights, and you wish to waive all your interests in your work worldwide: http://opendatacommons.org/licenses/cc0/

Chapter 20

Appendix III: Hierarchical Event Descriptors

Hierarchical Event Descriptors (HED) are a controlled vocabulary of terms describing events in a behavioral paradigm. HED was originally developed with EEG in mind, but is applicable to all behavioral experiments. Each level of a hierarchical tag is delimited with a forward slash (`/`). An HED string contains one or more HED tags separated by commas (`,`). Parentheses (brackets, `()`) group tags and enable specification of multiple items and their attributes in a single HED string (see section 2.4 in HED Tagging Strategy Guide). For more information about HED and tools available to validate and match HED strings, please visit www.hedtags.org. Since dedicated fields already exist for the overall task classification in the sidecar JSON files (`CogAtlasID` and `CogPOID`), HED tags from the `Paradigm` HED subcategory should not be used to annotate events.

There are several ways to associate HED annotations with events within the BIDS framework. The most direct way is to use the `HED` column of the _events.tsv file to annotate events:

Example:

```
onset   duration    HED
1.1 n/a Event/Category/Experimental stimulus, Event/Label/CrossFix,  Sensory presentation/Visual
    , Item/Object/2D Shape/Cross
1.3 n/a Event/Category/Participant response, Event/Label/ButtonPress, Action/Button press
...
```

The direct approach requires that each line in the events file must be annotated. Since there are typically thousands of events in each experiment, this method of annotation is usually not convenient unless the annotations are automatically generated. In many experiments, the event instances fall into a much smaller number of categories, and often these categories are labeled with numerical codes or short names. It is therefore more convenient to associate the HED annotations with these categories and allow the analysis tools to make the association with individual event instances during analysis. To use this approach, your _events.tsv file should associate a category (often called an event code) with each event instance. Since BIDS allows an arbitrary number of columns to be included in an _events.tsv file, you can make this association by including columns representing various types of event categories in your _events.tsv file.

Example:

```
onset   duration    mycodes
1.1 n/a Fixation
1.3 n/a Button
1.8 n/a Target
...
```

If you provide an _events.json file somewhere in your data hierarchy that has an HED mapping for `mycodes`, the HED tags associated with a given `mycodes` value can then be associated with the event instances in that category. You may provide a `HED` column and multiple category columns. The union of the relevant HED tags will then be associated with the event instance.

Example:

```
{
    "mycodes": {
        "HED": {
            "Fixation": "Event/Category/Experimental stimulus, Event/Label/CrossFix, Event/Description/A cross appears at screen center to serve as a fixation point, Sensory presentation/Visual, Item/Object/2D Shape/Cross, Attribute/Visual/Fixation point, Attribute/Visual/Rendering type/Screen, Attribute/Location/Screen/Center",
            "Target": "Event/Label/Target image, Event/Description/A white airplane as the RSVP target superimposed on a satellite image is displayed., Event/Category/Experimental stimulus, (Item/Object/Vehicle/Aircraft/Airplane, Participant/Effect/Cognitive/Target, Sensory presentation/Visual/Rendering type/Screen/2D), (Item/Natural scene/Arial/Satellite, Sensory presentation/Visual/Rendering type/Screen/2D)",
            "Button": "..."
        }
    }
}
```

The tags in the `HED` column are often specific to the event instances, while the common properties associated with categories such as `mycodes` are encapsulated in the _events.json dictionary. Downstream tools should not distinguish between tags specified using the different mechanisms. Further, the normal BIDS inheritance principle applies so these data dictionaries can appear higher in the BIDS hierarchy.

Chapter 21

Appendix IV: Entity table

This section compiles the entities (key-value pairs) described throughout this specification, and establishes a common order within a filename. For example, if a file has an acquisition and reconstruction label, the acquisition entity must precede the reconstruction entity. REQUIRED and OPTIONAL entities for a given file type are denoted. Entity formats indicate whether the value is alphanumeric (`<label>`) or numeric (`<index>`).

A general introduction to entities is given in the section on file name structure

Entity	Subject	Session	Task	Acquisition	Contrast Enhancing Agent	Reconstruction	Phase-Encoding Direction	Run	Corresponding modality	Echo	Recording	Processed (on device)	Space	Split
Format	`sub-<label>`	`ses-<label>`	`task-<label>`	`acq-<label>`	`ce-<label>`	`rec-<label>`	`dir-<label>`	`run-<index>`	`mod-<label>`	`echo-<index>`	`recording-<label>`	`proc-<label>`	`space-<label>`	`split-<index>`
anat(T1w T2w T1rho T1map T2map T2star FLAIR FLASH PD PDmap PDT2 inplaneT1 inplaneT2 angio)	REQUIRED	OPTIONAL		OPTIONAL	OPTIONAL	OPTIONAL								
anat(defacemask)	REQUIRED	OPTIONAL		OPTIONAL	OPTIONAL	OPTIONAL			OPTIONAL					
func(bold cbv phase sbref events)	REQUIRED	OPTIONAL	REQUIRED	OPTIONAL	OPTIONAL	OPTIONAL	OPTIONAL	OPTIONAL		OPTIONAL				
func(physio stim)	REQUIRED	OPTIONAL	REQUIRED	OPTIONAL		OPTIONAL		OPTIONAL			OPTIONAL	OPTIONAL		
dwi(dwi bvec bval)	REQUIRED	OPTIONAL		OPTIONAL			OPTIONAL	OPTIONAL						
fmap(phasediff phase1 phase2 magnitude1 magnitude2 magnitude fieldmap)	REQUIRED	OPTIONAL		OPTIONAL				OPTIONAL						
fmap(epi)	REQUIRED	OPTIONAL		OPTIONAL	OPTIONAL		REQUIRED	OPTIONAL						
beh(events stim physio)	REQUIRED	OPTIONAL	REQUIRED											
meg	REQUIRED	OPTIONAL	REQUIRED	OPTIONAL				OPTIONAL				OPTIONAL		OPTIONAL
eeg	REQUIRED	OPTIONAL	REQUIRED	OPTIONAL				OPTIONAL						
ieeg	REQUIRED	OPTIONAL	REQUIRED	OPTIONAL				OPTIONAL						
channels(meg/eeg/ieeg)	REQUIRED	OPTIONAL	REQUIRED					OPTIONAL						
headshape(meg)	REQUIRED	OPTIONAL		OPTIONAL									OPTIONAL	
markers(meg)	REQUIRED	OPTIONAL	OPTIONAL	OPTIONAL									OPTIONAL	
photo(meg/eeg/ieeg)	REQUIRED	OPTIONAL		OPTIONAL										
electrodes(eeg/ieeg)	REQUIRED	OPTIONAL		OPTIONAL									OPTIONAL	

Entity	Subject	Session	Task	Acquisition	Contrast Enhancing Agent	Reconstruction	Phase-Encoding Direction	Run	Corresponding modality	Echo	Recording	Processed (on device)	Space	Split
events(meg/eeg/ieeg)	REQUIRED	OPTIONAL	REQUIRED					OPTIONAL						

Chapter 22

Appendix V: Units

Following the International System of Units (SI, abbreviated from the French Système international (d'unités))

Unit name	Unit symbol	Quantity name
metre	m	length
kilogram	kg	mass
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	Ω	resistance, impedance, reactance
siemens	S	electrical conductance
weber	Wb	magnetic flux
tesla	T	magnetic flux density
henry	H	inductance
degree Celsius	°C	temperature relative to 273.15 K
lumen	lm	luminous flux
lux	lx	illuminance
becquerel	Bq	radioactivity (decays per unit time)
gray	Gy	absorbed dose (of ionizing radiation)
sievert	Sv	equivalent dose (of ionizing radiation)
katal	kat	catalytic activity

Prefixes

Multiples

Prefix name	Prefix symbol	Factor
deca	da	101
hecto	h	102

Prefix name	Prefix symbol	Factor
kilo	k	103
mega	M	106
giga	G	109
tera	T	1012
peta	P	1015
exa	E	1018
zetta	Z	1021
yotta	Y	1024

Submultiples

Prefix name	Prefix symbol	Factor
deci	d	10-1
centi	c	10-2
milli	m	10-3
micro	µ	10-6
nano	n	10-9
pico	p	10-12
femto	f	10-15
atto	a	10-18
zepto	z	10-21
yocto	y	10-24

Chapter 23

Appendix VI: MEG file formats

Each MEG system brand has specific file organization and data formats. RECOMMENDED values for `manufacturer_specific_extensions`:

Value	Definition
`ctf`	CTF (folder with `.ds` extension)
`fif`	Neuromag / Elekta / MEGIN and BabyMEG (file with extension `.fif`)
`4d`	BTi / 4D Neuroimaging (folder containing multiple files without extensions)
`kit`	KIT / Yokogawa / Ricoh (file with extension `.sqd`, `.con`, `.raw`, `.ave` or `.mrk`)
`kdf`	KRISS (file with extension `.kdf`)
`itab`	Chieti system (file with extension `.raw` and `.mhd`)

Below are specifications for each system brand.

CTF

Each experimental run with a CTF system yields a folder with a `.ds` extension, containing several files. The OPTIONAL digitized positions of the head points are usually stored in a separate `.pos` file, not necessarily within the `.ds` folder.

```
[sub-<label>[_ses-<label>]_headshape.pos]
sub-<label>[_ses-<label>]_task-<label>[_run-<index>]_meg.ds>
```

CTF's data storage is therefore via directories containing multiple files. The files contained within a `.ds` directory are named such that they match the parent directory, but preserve the original file extension (e.g., `.meg4`, `.res4`, etc.). 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: http://www.fieldtriptoolbox.org/getting_started/ctf

Neuromag/Elekta/MEGIN

Neuromag/Elekta/MEGIN data and Tristan Technologies BabyMEG data is stored with file extension `.fif`. The digitized positions of the head points are saved inside the fif file along with the MEG data, with typically no `_headshape` file.

```
sub-<label>[_ses-<label>]_task-<label>[_run-<index>]_meg.fif
```

Note that we do not provide specifications for cross-talk and fine-calibration matrix files in the current version of BIDS.

Example:

```
sub-control01/
    ses-001/
        sub-control01_ses-001_scans.tsv
        meg/
            sub-control01_ses-001_coordsystem.json
            sub-control01_ses-001_task-rest_run-01_meg.fif
            sub-control01_ses-001_task-rest_run-01_meg.json
            sub-control01_ses-001_task-rest_run-01_channels.tsv
```

After applying the MaxFilter pre-processing tool, files should be renamed with the corresponding label (e.g., `proc-sss`) and placed into a `derivatives` subfolder.

Example:

```
sub-control01_ses-001_task-rest_run-01_proc-sss_meg.fif
sub-control01_ses-001_task-rest_run-01_proc-sss_meg.json
```

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 file names, but also the internal file pointers will be updated.

It is RECOMMENDED that `.fif` files with multiple parts use the `split-<index>` entity to indicate each part.

Example:

```
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

BTi/4D neuroimaging

Each experimental run on a 4D neuroimaging/BTi system results in a folder containing multiple files without extensions.

```
[sub-<label>[_ses-<label>]_headshape.pos]
sub-<label>[_ses-<label>]_task-<label>[_run-<index>]_meg>
```

One SHOULD rename/create a father run specific directory and keep the original files for each run inside (e.g., `c,rfhp0.1Hz`, `config` and `hs_file`).

Example:

```
sub-control01/
    ses-001/
        sub-control01_ses-001_scans.tsv
        meg/
            sub-control01_ses-001_coordsystem.json
            sub-control01_ses-001_headshape.pos
            sub-control01_ses-001_task-rest_run-01_meg
            sub-control01_ses-001_task-rest_run-01_meg.json
            sub-control01_ses-001_task-rest_run-01_channels.tsv
```

Where:

```
sub-control01_ses-001_task-rest_run-01_meg/
    config
    hs_file
    e,rfhp1.0Hz.COH
    c,rfDC
```

More about the 4D neuroimaging/BTi data organization at: http://www.fieldtriptoolbox.org/getting_started/bti

KIT/Yokogawa/Ricoh

Each experimental run on a KIT/Yokogawa/Ricoh system yields a raw (`.sqd`, `.con`) file with its associated marker coil file(s) (`.sqd`, `.mrk`), which contains 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>
```

If there are files with multiple marker coils, the marker files must have the `acq-<label>` parameter and no more that two marker files may be associated with one raw data file. While the acquisition parameter can take any value, it is RECOMMENDED that if the two marker measurements occur before and after the raw data acquisition, `pre` and `post` are used to differentiate the two situations.

More about the KIT/Yokogawa/Ricoh data organization at: http://www.fieldtriptoolbox.org/getting_started/yokogawa

KRISS

Each experimental run on the KRISS system produces a file with extension `.kdf`. Additional files can be available in the same folder: the digitized positions of the head points (`\_digitizer.txt`), the position of the center of the MEG coils (`.chn`) and the event markers (`.trg`).

```
[sub-<label>[_ses-<label>]_headshape.txt]
sub-<label>[_ses-<label>]_task-<label>[_run-<index>]_meg.kdf
sub-<label>[_ses-<label>]_task-<label>[_run-<index>]_meg.chn
sub-<label>[_ses-<label>]_task-<label>[_run-<index>]_meg.trg
sub-<label>[_ses-<label>]_task-<label>[_acq-<label>]_digitizer.txt
```

Example:

```
sub-control01/
    ses-001/
        sub-control01_ses-001_scans.tsv
        meg/
            sub-control01_ses-001_coordsystem.json
            sub-control01_ses-001_headshape.txt
            sub-control01_ses-001_task-rest_run-01_meg
            sub-control01_ses-001_task-rest_run-01_meg.json
            sub-control01_ses-001_task-rest_run-01_channels.tsv
            sub-control01_ses-001_task-rest_run-01_meg.chn
            sub-control01_ses-001_task-rest_run-01_meg.kdf
            sub-control01_ses-001_task-rest_run-01_meg.trg
            sub-control01_ses-001_task-rest_digitizer.txt
```

ITAB

Each experimental run on a ITAB-ARGOS153 system yields a raw (`.raw`) data file plus an associated binary header file (`.mhd`). The raw data file has an ASCII header that contains detailed information about the data acquisition system, followed by binary data. The associated binary header file contains part of the information from the ASCII header, specifically the one needed to process data, plus other information on offline preprocessing performed after data acquisition (e.g., sensor position relative to subject's head, head markers, stimulus information).

Example:

```
sub-control01/
    ses-001/
        sub-control01_ses-001_coordsystem.json
        sub-control01_ses-001_headshape.txt
        sub-control01_ses-001_task-rest_run-01_meg
        sub-control01_ses-001_task-rest_run-01_meg.json
        sub-control01_ses-001_task-rest_run-01_channels.tsv
        sub-control01_ses-001_task-rest_run-01_meg.raw
        sub-control01_ses-001_task-rest_run-01_meg.raw.mhd
```

Aalto MEG–MRI

For stand-alone MEG data, the Aalto hybrid device uses the standard `.fif` data format and follows the conventions of Elekta/Neuromag as described above. The `.fif` files may contain unreconstructed MRI data. The inclusion of MRI data and information for accurate reconstruction will be fully standardized at a later stage.

Chapter 24

Appendix VII: MEG systems

Perferred names of MEG systems comprise restricted keywords for Manufacturer field in the `*_meg.json` file:

- `CTF`
- `Neuromag/Elekta/Megin`
- `BTi/4D`
- `KIT/Yokogawa/Ricoh`
- `KRISS`
- `ITAB`
- `Aalto/MEG-MRI`
- `Other`

Restricted keywords for ManufacturersModelName field in the `*_meg.json` file:

System Model Name	Manufacturer	Details
CTF-64	CTF	
CTF-151	CTF	https://www.ctf.com/products
CTF-275	CTF	CTF-275: OMEGA 2000
Neuromag-122	Neuromag/Elekta/Megin	
ElektaVectorview	Neuromag/Elekta/Megin	102 magnetometers + 204 planar gradiometers
ElektaTRIUX	Neuromag/Elekta/Megin	https://www.elekta.com/diagnostic-solutions/
4D-Magnes-WH2500	BTi/4D	
4D-Magnes-WH3600	BTi/4D	
KIT-157	KIT/Yokogawa	
KIT-160	KIT/Yokogawa	
KIT-208	KIT/Yokogawa	
ITAB-ARGOS153	ITAB	
Aalto-MEG-MRI-YYYY/MM	Aalto/MEG-MRI	YYYY-MM (year, month; or major version)

Chapter 25

Appendix VIII: Coordinate systems

Introduction

To interpret a coordinate (x, y, z), it is required that you know relative to which origin the coordinates are expressed, you have to know the interpretation of the three axes, and you have to know 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.

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 e.g., 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 (e.g., 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 (origin, orientation) are specified in `XXXCoordinateSystem`, and the units are specified in `XXXCoordinateSystemUnits`.

Allowed values for the `XXXCoordinateSystem` field come from a list of restricted keywords, as listed in the sections below. 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 further details in the `XXXCoordinateSystemDescription` field

MEG Specific Coordinate Systems

Restricted keywords for the `XXXCoordinateSystem` field in the `coordinatesystem.json` file for MEG datasets:

- `CTF`: ALS orientation and the origin between the ears
- `ElektaNeuromag`: RAS orientation and the origin between the ears
- `4DBti`: ALS orientation and the origin between the ears
- `KitYokogawa`: ALS orientation and the origin between the ears
- `ChietiItab`: RAS orientation and the origin between the ears

Note that the short descriptions above do not capture all details, There are detailed extensive descriptions of these EEG coordinate systems on the FieldTrip toolbox web page

EEG Specific Coordinate Systems

Restricted keywords for the `XXXCoordinateSystem` field in the `coordsystem.json` file for EEG datasets:

- `Captrak`: RAS orientation and the origin between the ears

Note that the short descriptions above do not capture all details, There are detailed extensive descriptions of these EEG coordinate systems on the FieldTrip toolbox web page.

iEEG Specific Coordinate Systems

Restricted keywords for the `XXXCoordinateSystem` 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.

Image-based Coordinate Systems

The transformation of the real world geometry to an artificial frame of reference is described in `XXXCoordinateSystem`. 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 `XXXCoordinateSystemUnits` field, the units are assumed to be mm.

Standard template identifiers

Coordinate System	Description
ICBM452AirSpace	Reference space defined by the ”average of 452 T1-weighted MRIs of normal young adult brains” with ”linear transforms of the subjects into the atlas space using a 12-parameter affine transformation” https://www.loni.usc.edu/research/atlases
ICBM452Warp5Space	Reference space defined by the ”average of 452 T1-weighted MRIs of normal young adult brains” ”based on a 5th order polynomial transformation into the atlas space” https://www.loni.usc.edu/research/atlases
IXI549Space	Reference space defined by the average of the ”549 (...) subjects from the IXI dataset” linearly transformed to ICBM MNI 452.Used by SPM12. http://www.brain-development.org/

Coordinate System	Description
fsaverage[3|4|5|6|sym]	DISCOURAGED, please use `fsaverage` without modifiers. Images were sampled to the FreeSurfer surface reconstructed from the subject's T1w image, and registered to an fsaverage template
fsaverage	The `fsaverage` is a **dual template** providing both volumetric and surface coordinates references. The volumetric template corresponds to a FreeSurfer variant of `MNI305` space. The `fsaverage` atlas also defines a surface reference system (formerly described as fsaverage[3|4|5|6|sym]).
fsaverageSym	The `fsaverage` is a **dual template** providing both volumetric and surface coordinates references. The volumetric template corresponds to a FreeSurfer variant of `MNI305` space. The `fsaverageSym` atlas also defines a symmetric surface reference system (formerly described as `fsaveragesym`).
fsLR	The `fsLR` is a **dual template** providing both volumetric and surface coordinates references. The volumetric template corresponds to `MNI152NLin6Asym`. Surface templates are given at several sampling densities: 164k (used by HCP pipelines for 3T and 7T anatomical analysis), 59k (used by HCP pipelines for 7T MRI bold and DWI analysis), 32k (used by HCP pipelines for 3T MRI bold and DWI analysis), or 4k (used by HCP pipelines for MEG analysis) fsaverage_LR surface reconstructed from the T1w image.
MNIColin27	Average of 27 T1 scans of a single subject http://www.bic.mni.mcgill.ca/ServicesAtlases/Colin27Highres
MNI152Lin	Also known as ICBM (version with linear coregistration) http://www.bic.mni.mcgill.ca/ServicesAtlases/ICBM152Lin
MNI152NLin2009[a-c][Sym|Asym]	Also known as ICBM (non-linear coregistration with 40 iterations, released in 2009). It comes in either three different flavours each in symmetric or asymmetric version. http://www.bic.mni.mcgill.ca/ServicesAtlases/ICBM152NLin2009
MNI152NLin6Sym	Also known as symmetric ICBM 6th generation (non-linear coregistration). Used by SPM99 - SPM8. http://www.bic.mni.mcgill.ca/ServicesAtlases/ICBM152NLin6
MNI152NLin6ASym	A variation of `MNI152NLin6Sym` built by A. Janke that is released as the *MNI template* of FSL. Volumetric templates included with HCP-Pipelines correspond to this template too. See 10.1016/j.neuroimage.2012.01.024.
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. http://www.bic.mni.mcgill.ca/ServicesAtlases/NIHPD-obj1
OASIS30AntsOASISAnts	https://figshare.com/articles/ANTs_ANTsR_Brain_Templates/915436
OASIS30Atropos	https://mindboggle.info/data.html
Talairach	Piecewise linear scaling of the brain is implemented as described in TT88. http://www.talairach.org/
UNCInfant	Infant Brain Atlases from Neonates to 1- and 2-year-olds. https://www.nitrc.org/projects/pediatricatlas
UNCInfant[0|1|2]V[21|22|23]	DISCOURAGED, please use `UNCInfant` without modifiers. Infant Brain Atlases from Neonates to 1- and 2-year-olds. https://www.nitrc.org/projects/pediatricatlas

The following template identifiers are retained for backwards compatibility of BIDS implementations. Their use is NOT RECOMMENDED for new BIDS datasets and tooling, but their presence MUST NOT produce a validation error.

Coordinate System	Recommended identifier
fsaverage[3|4|5|6|sym]	fsaverage[|Sym]
UNCInfant[0|1|2]V[21|22|23]	UNCInfant

Nonstandard coordinate system identifiers

The following template identifiers are RECOMMENDED for individual- and study-specific reference spaces. In order for these spaces to be interpretable, `SpatialReference` metadata MUST be provided, as described in Common file level metadata fields.

In the case of multiple study templates, additional names may need to be defined.

Coordinate System	Description
individual	Participant specific anatomical space (for example derived from T1w and/or T2w images). This coordinate system requires specifying an additional, participant-specific file to be fully defined. In context of surfaces this space has been refered to as `fsnative`.
study	Custom space defined using a group/study-specific template. This coordinate system requires specifying an additional file to be fully defined.

Non-template coordinate system identifiers

The `scanner` coordinate system is implicit and assumed by default if the derivative filename does not define **any** `space-<label>`. Please note that `space-scanner` SHOULD NOT be used, it is mentioned in this specification to make its existence explicit.

Coordinate System	Description
scanner	The intrinsic coordinate system of the original image (the first entry of `RawSources`) after reconstruction and conversion to NIfTI or equivalent for the case of surfaces and dual volume/surface files.

Chapter 26

Changelog

v1.4.0 (2020-06-11)

- [FIX] Clarify language on unsetting a key/value pair #495 (nicholst)
- ENH: Add RECOMMENDED DatasetType key to dataset description #494 (effigies)
- Clarify mask/dseg/probseg in common derivatives #489 (effigies)
- Reorganize derivatives #488 (effigies)
- Enh/prov #486 (satra)
- [ENH] optionally allow LICENSE file #483 (sappelhoff)
- [INFRA] linkchecker - ignore github pull and tree URLs #477 (yarikoptic)
- [ENH] Allow fractional seconds in scans file datetimes #470 (tsalo)
- [MISC] Maintainers - `Scope` responsibility #467 (franklin-feingold)
- [FIX] Align tables in MRI section #465 (sappelhoff)
- [FIX] Drop `\_part-` reference from example, introduce `\_split-` entity #460 (sappelhoff)
- [FIX] clarify participants tsv+json with examples and recommendations #459 (sappelhoff)
- [FIX] Remove BESA from list of restricted keywords of EEG coordsystems #457 (sappelhoff)
- [INFRA] add steps for release protocol (PDF upload) #455 (sappelhoff)
- [FIX] Add reference to PDF on front page of specification #452 (nicholst)
- [INFRA] Add conditional for link-checking releases #451 (franklin-feingold)
- [FIX] unordered list formatting in BEP018 #449 (sappelhoff)
- [FIX] fix inconsistencies for task label between sections #446 (Remi-Gau)
- [FIX] update DECISION-MAKING.md document with new governance #441 (sappelhoff)
- [ENH] Add `res` and `den` keywords to indicate resolution of resampled data #301 (oesteban)
- [ENH] BEP 003: Common Derivatives #265 (effigies)
- [ENH] Add Glossary of terms/abbreviations used in the specification #152 (yarikoptic)

v1.3.0 (2020-04-14)

- [INFRA] add zenodo badge to README #447 (sappelhoff)
- Added contributors from VisLab #444 (VisLab)
- FIX: Clarify snake_case+CamelCase in TSV+JSON #442 (sappelhoff)
- [FIX] Eliminate web/online-specific language #437 (nicholst)
- [INFRA] ensure build_docs_pdf CircleCI job runs last #436 (sappelhoff)
- [INFRA] Add issue templates for GitHub #434 (sappelhoff)
- [INFRA] Get latest PDF build from CircleCI artifacts #433 (sappelhoff)
- [INFRA] Update release protocol #432 (franklin-feingold)
- [INFRA] add support for building PDF versions of the spec #431 (Arshitha)
- [ENH] Explicitly mention bids-validator and update link #428 (sappelhoff)
- [INFRA] use new bids-maintenance GitHub account to take over automatic work #426 (sappelhoff)
- [FIX] Unify section titles and table-of-contents entries #422 (nicholst)
- [INFRA] add # before heading in CHANGES #419 (sappelhoff)
- [INFRA] fix heading of auto changelog to be a markdown header #417 (sappelhoff)
- ENH: Add OPTIONAL EthicsApprovals field to dataset description #412 (effigies)
- [ENH] BEP 018 - Genetic Information #395 (effigies)

v1.2.2 (2020-02-12)

- [FIX] improve wording on data dictionaries #410 (sappelhoff)
- [MISC] update contributions by CPernet #409 (CPernet)
- Units2ascii #408 (satra)
- [FIX] Fix typos and formatting #404 (alexandreroutier)
- BEP 18 suggestions #398 (effigies)
- [MISC] Add Sébastien Tourbier to contributors #394 (sebastientourbier)
- [FIX] consistent units description between EEG/MEG/iEEG. Clarify (derived) SI units + prefixes #391 (sappelhoff)
- [MISC] moved list of extension proposals to the main BIDS website #389 (robertoostenveld)
- [FIX] Typos and clarifications #386 (apjanke)
- ENH: 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)
- specify further the pipeline following #345 #358 (CPernet)
- 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)
- RM: rm TOC.md - seems no longer pertinent/used #341 (yarikoptic)
- [MISC] Move the PR template to a separate folder and improve contents #338 (jhlegarreta)
- [INFRA] Find npm requirements file in Circle #336 (franklin-feingold)
- ENH: Clarify the position toward non-compliant derivative datasets and files #334 (effigies)
- [ENH] Clarify phenotypic and assessment data in new section #331 (sappelhoff)
- [MISC] add information about continuous integration checks to PR template #330 (sappelhoff)
- [FIX] Fix `Common principles` `Key/value files` section level #328 (jhlegarreta)
- [INFRA] Set the maximum heading length lint check to `false` #325 (jhlegarreta)
- [FIX] Number explicitly all cases in MRI field map section headers #323 (jhlegarreta)
- [FIX] Add SoftwareFilters to EEG sidecar example #322 (Remi-Gau)
- [MISC] Fixing Travis errors with Remark #320 (franklin-feingold)
- [INFRA] Link to doc builds in CI checks #315 (jasmainak)
- [MISC] Add BEP027 - BIDS Execution to BEP list #314 (effigies)
- [FIX] Add CBV and phase to Entity table #312 (tsalo)
- [FIX] Separate out imaging-specific "common derivatives" #310 (effigies)
- [FIX] Revise template-generated coordinate systems #307 (oesteban)
- [FIX] Normalization of template-generated standard spaces #306 (oesteban)
- [ENH] Release protocol notes #304 (franklin-feingold)
- [INFRA] Adding contributor appendix sentence to PR template #299 (franklin-feingold)
- [ENH] Added discontinuous datatype for EEG and iEEG #286 (wouterpotters)
- [FIX] Clarify paragraph about custom data types #264 (effigies)

v1.2.1 (2019-08-14)

- FIX: repair link in anatomical MRI table #297 (sappelhoff)
- [ENH] Clarify requirements in Release Protocol #294 (franklin-feingold)
- [INFRA+FIX] Use linkchecker (from a dedicated docker image) to check all URLs #293 (yarikoptic)
- [ENH] Adding Contributors and updating contributions #284 (franklin-feingold)
- [MISC] update Code of Conduct contact #281 (franklin-feingold)
- [ENH] Update contributing guide and README to make discussion forums easy to find #279 (emdupre)
- [ENH] Starter Kit dropdown menu #278 (franklin-feingold)
- [ENH] BEP Update #277 (franklin-feingold)
- [INFRA] Update pipenv #274 (sappelhoff)
- [INFRA] Transpose the entity table and link to text anchors describing each entity #272 (sappelhoff)
- [ENH] Add Twitter badge to README and link to website to landing page #268 (franklin-feingold)

- [ENH] adding release guidelines #267 (franklin-feingold)
- [FIX] Common principles: Fix filename in inheritance principle #261 (Lestropie)
- [MISC] update modality references #258 (sappelhoff)
- [INFRA] adding logo to RTD #256 (franklin-feingold)
- [INFRA] add footer, replacing mkdocs/material advert with Github link #250 (sappelhoff)
- [MISC] rename logo files, add a README of where they come from, fix favicon #249 (sappelhoff)
- [MISC] updating MEG doc links, manufacturer names, and adding a missing MEG example #248 (sappelhoff)
- [ENH] Add favicon to RTD #246 (franklin-feingold)
- [MISC] Update Authors in BEP025 #241 (josator2)
- [MISC] Document BEPs that are not active anymore, but have not been merged #240 (sappelhoff)
- [FIX] remove ManufacturersAmplifierModelName (again) #236 (robertoostenveld)
- [INFRA] Update release protocol #235 (effigies)
- [INFRA] Enable version panel for quickly finding previous versions #232 (effigies)
- [FIX] use \<label> for _desc- - not some \<value> + clarify \<value> #224 (yarikoptic)
- [FIX] Clarify Appendix II: The list of licenses only lists examples #222 (sappelhoff)
- [FIX] Trivial column header fix #220 (nicholst)
- [INFRA] Add clarification on merge methods to DECISION_MAKING #217 (sappelhoff)
- [INFRA] Enable permalink urls to appear at (sub)section headings #214 (yarikoptic)
- [INFRA] bump up mkdocs-materials version #211 (sappelhoff)
- [ENH] Various proposed changes to diffusion derivatives #205 (Lestropie)
- [MISC] Fix github username for @chrisgorgo #204 (chrisgorgo)
- [FIX] clarify example 3 in common principles (inheritance) #202 (sappelhoff)
- [MISC] Expand entity table for MEG/EEG/iEEG specific files #198 (sappelhoff)
- [FIX] make iEEG ToC more consistent with MEG and EEG #191 (robertoostenveld)
- [FIX] Clarify use of acq and task parameters in EEG, MEG, and iEEG #188 (sappelhoff)
- [FIX] clarify use of tools for CTF data renaming #187 (sappelhoff)
- [MISC] Add bep006 and bep010 to completed beps and fix links #186 (sappelhoff)
- [FIX] change file for definition of electrical stimulation labels from _electrodes.json to _events.json #185 (ezemikulan)
- [ENH] relax ieeg channel name requirements of letters and numbers only #182 (sappelhoff)
- [FIX] make MEG section headings and ToC consistent to the EEG and iEEG specs #181 (robertoostenveld)
- [FIX] make section headings and ToC consistent between meg and eeg specs #180 (robertoostenveld)
- [MISC] Spelling fixes #179 (DimitriPapadopoulos)
- [ENH] Alternative folder organization for raw, derived, and source data #178 (chrisgorgo)
- [INFRA] Adding instructions for naming PRs #177 (chrisgorgo)
- [MISC] Introducing Stefan Appelhoff as the first Maintainer #176 (chrisgorgo)
- [FIX] Clarify name of ”BrainVision” format #175 (JegouA)
- [FIX] Fixes spelling of continuous #171 (emdupre)
- [FIX] Clarify continuous recording metadata fields #167 (effigies)
- [FIX] changed reference of `dcm2nii` to `dcm2niix` #166 (DimitriPapadopoulos)
- [FIX] Removing a leftover file #162 (chrisgorgo)
- [ENH] Derived (processed) MR data #109 (chrisgorgo)
- [FIX] Specify marker file names for KIT data (MEG) #62 (monkeyman192)
- [FIX] Remove father-level for meg filetypes other than BTi/4D data #19 (teonbrooks)

v1.2.0 (2019-03-04)

- [MISC] Adding Dimitri Papadopoulos Orfanos to the list of contributors #157 (DimitriPapadopoulos)
- RF: use ”specification” not ”protocol” to refer to BIDS #156 (yarikoptic)
- Fix example misalignment #155 (DimitriPapadopoulos)
- Update Pipfile.lock #144 (franklin-feingold)
- [MRG] clarify decimal sep and numerical notation convention #143 (sappelhoff)
- [MRG] clarify encoding of README, CHANGES, TSV, and JSON files #140 (sappelhoff)
- Update site_name and release protocol #137 (franklin-feingold)
- BF: 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)
- Update to Release_Protocol.md #126 (franklin-feingold)
- Update tag naming convention #123 (chrisgorgo)

- [MRG] Merge bep006 and bep010 #108 (sappelhoff)
- Adding formal decision-making rules #104 (chrisgorgo)
- [MRG] number of small corrections to the specification #98 (robertoostenveld)

v1.1.2 (2019-01-10)

- Update 01-contributors.md #120 (oesteban)
- Global fields in data dictionaries #117 (chrisgorgo)
- Propose BEP026 MER #116 (greydongilmore)
- Remove duplicate entries in MEG table #113 (franklin-feingold)
- Propose BEP025 MIDS #110 (josator2)
- repair links #106 (sappelhoff)
- Autogenerate CHANGES.md #103 (franklin-feingold)
- Added contributor information #100 (jgrethe)
- ENH: First(?) good practice recommendation. No excessive overrides in Inheritance principle #99 (yarikoptic)
- adding extensions page #97 (choldgraf)
- Fix up some urls (as detected to be broken/inconsistent #95 (yarikoptic)
- Change BEP numbers to include MRS #94 (Hboni)
- RF harmonize and thus shorten templates etc #93 (yarikoptic)
- put links and some text into README #91 (sappelhoff)
- Add extension proposal in 01-introduction.md #88 (Hboni)
- additional table to recap 'volume acquisition timing' #87 (Remi-Gau)
- Small typo in "scanning sequence" DICOM tag #84 (Remi-Gau)
- Update 01-contributors.md #83 (teonbrooks)
- Added CBV contrast #82 (TheChymera)
- Add CC-BY 4.0 license #81 (KirstieJane)
- Fix Travis break #80 (franklin-feingold)
- ENH: allow _dir for other EPI (func, dwi) sequences #78 (yarikoptic)
- Added appendix to mkdocs and added some internal links #77 (franklin-feingold)
- DOC: added JC Houde as contributor. #76 (jchoude)
- Updated my contributions #75 (nicholst)
- update HED appendix #74 (sappelhoff)
- [MRG] unicode: replace greek mu and omega by micro and ohm signs #73 (sappelhoff)
- Update 01-contributors.md #72 (francopestilli)
- add ce-\<label> for fmri data #70 (dasturge)
- pin pip version #68 (chrisgorgo)
- Fix link in index #46 (chrisgorgo)
- edit contributing md #44 (Park-Patrick)
- Mkdocs configuration and RTD setup #42 (choldgraf)
- Move definitions, compulsory, and raw/derivatives sections to principles #40 (chrisgorgo)
- Remove duplicate section #39 (chrisgorgo)
- mkdocs rendering #36 (chrisgorgo)
- Style consistency #35 (chrisgorgo)
- Renaming files to conform with style guide #34 (chrisgorgo)
- enable travis cache #32 (chrisgorgo)
- FIX - corrected link that is shown for CC0 #31 (robertoostenveld)
- [WIP] added linter integration via travis #30 (chrisgorgo)
- Cleanup #29 (chrisgorgo)
- [MRG] split intro, commons, mr, and meg into folder from specification.md #28 (teonbrooks)
- Add some bids starter kit contributors #27 (KirstieJane)
- Embedded footnotes into text #25 (franklin-feingold)
- Making HED Strategy Guide link prettier #24 (fake-filo)
- Fix/more cleanup #21 (chrisgorgo)
- formatted MEG (8.4) #17 (franklin-feingold)
- small fixes #16 (chrisgorgo)
- Add meg img #14 (sappelhoff)
- [WIP] Cleaning up the specification #13 (chrisgorgo)
- Adding code of conduct #6 (chrisgorgo)
- Renaming the main document #1 (chrisgorgo)

1.1.1

- 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

- 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

- 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

- 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 file names

- Added ability to store stimuli files.
- Clarified the language describing allowed subject labels.
- Added quantitative proton density maps.

1.0.0

- Added ability to specify fieldmaps acquired with multiple parameter sets.
- Added ability to have multiple runs of the same fieldmap.
- Added FLASH anatomical images.

1.0.0-rc4

- Replaced links to neurolex with explicit DICOM Tags.
- Added sourcedata.
- Added data dictionaries.
- Be more explicit about contents of JSON files for structural (anatomical) scans.

1.0.0-rc3

- Renamed PhaseEncodingDirection values from “x”, “y”, “z” to “i”, “j”, “k” to avoid confusion with FSL parameters
- Renamed SliceEncodingDirection values from “x”, “y”, “z” to “i”, “j”, “k”

1.0.0-rc2

- Removed the requirement that TSV files cannot include more than two consecutive spaces.
- Refactor of the definitions sections (copied from the manuscript)
- Make support for uncompressed .nii files more explicit.
- Added BIDSVersion to dataset.json
- Remove the statement that SliceEncodingDirection is necessary for slice time correction
- Change dicom converter recommendation from dcmstack to dcm2nii and dicm2nii following interactions with the community (see https://github.com/moloney/dcmstack/issues/39 and https://github.com/neurolabusc/dcm2niix/issues/4).
- Added section on behavioral experiments with no accompanying MRI acquisition
- Add _magnitude.nii[.gz] image for GE type fieldmaps.
- Replaced EchoTimeDifference with EchoTime1 and EchoTime2 (SPM toolbox requires this input).
- Added support for single band reference image for DWI.
- Added DatasetDOI field in the dataset description.
- Added description of more metadata fields relevant to DWI fieldmap correction.
- PhaseEncodingDirection is now expressed in “x”, “y” etc. instead of “PA” “RL” for DWI scans (so it’s the same as BOLD scans)
- Added rec-<label> flag to BOLD files to distinguish between different reconstruction algorithms (analogous to anatomical scans).

- Added recommendation to use _physio suffix for continuous recordings of motion parameters obtained by the scanner side reconstruction algorithms.

1.0.0-rc1

- Initial release

* *This Change Log was automatically generated by github_changelog_generator*

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- 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.
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- 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