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# Muscle BIDS in QMRITools

For an explanation of the BIDS we refer to <https://bids.neuroimaging.io/index.html> or for a detailed overview of the standard to <https://bids-specification.readthedocs.io/en/stable/>.

An explanation of naming conventions related to BIDS in QMRITools can be found on <https://www.qmritools.com/bids/files_folders/> and a full list of the entities and suffixes QMRITools uses can be found on <https://www.qmritools.com/bids/ents_suffs/>.

## Setting up a study

To use the QMRITools BIDS processing pipeline a study folder must be made. The data that goes into this folder is accompanied by a configuration file that specifies the configuration of the BIDS processing pipeline. Although this can be done for existing datasets it is highly recommended to think about processing and analysis methods during the design of the study. Taking the proccing into account as early as possible helps with automation and quality assurance.

### The source data

The source data is dicom. The data in the dicom source folder is ordered in folders. Each folder is defined as “subjectName” or “subjectName\_sessionName”. If no session name is given the session name “\_001” is given.

The list of datasets names and sessions is based on the folder names in this source folder and can be viewed using the function `*SelectSubjects*`.

### Define a config file

Which data to expect, which data is converted and howe the data is processed is all defined in a configuration file named “config.json” which is placed in the root folder of the BIDS dataset.

The config file is linked to the study design. Automated processing is only feasible if data is consistent. There is some functionality to handle data exceptions. However if the data is not structured and standardized converting data from dicom to BIDS format is manual labor.

For specifications of the config file look at the section about the config file.

## Running the BIDS pipeline

The BIDS pipeline within QMRITools currently consists of 7 functions that fall under 4 different categories that will be further explained in this section.

1. Data conversion to BIDS
   1. *BidsDcmToNii*
   2. *MuscleBidsConvert*
2. Data processing
   1. *MuscleBidsProcess*
3. Data post processing
   1. *MuscleBidsMerge*
   2. *MuscelBidsSegment*
   3. *MuscleBidsTractography*
4. Data Analysis
   1. *MuscleBidsAnalsys*

### BidsDcmToNii

This function converts the dicom data to raw nii files using dcm2niix

### MuscleBidsConvert

This function coverts the raw nii files to muscle BIDS data files based on the specifications given in the “config.json” file

### MuscleBidsProcess

This function processes all the datatypes given in the “config.json” file. Currently processing pipelines for DTI/IVIM, T2mapping and Dixon imaging are implemented. Extra processing pipelines are added based on running studies. There is no roadmap for which functionality to be added.

### MuscleBidsMerge

This function merges all data specified in the “config.json”. The merging consists of two distinct steps first it joins data chunks if needed, next all data types are placed into a common space.

For muscle imaging most muscle don’t fit into a single FOV therefore most of the time data is acquired in multiple chunks that have to be joined together. How to Join the data is specified for each data type separately.

Secondly, all data is registered to a common space. The target of the common space can be specified per data type. Commonly this will be the same target for all contrast and is the one data type on which muscle segmentation is performed. Data is always processed in native space by `*MuscleBidsProcess*` after which all derived parameters maps are moved to the common space. Which derived parameters that are taken along is defined in the “config.json” per data type.

### MuscleBidsSegment

This function performs automated segmentation of the datatypes specified in the “config.json”. Without segmentations `*MuscleBidsTractography*` can only partially run and `*MuscleBidsAnalysis`* cannot be performed. This step can be omitted if manual segmentations are added to the dataset.

### MuscleBidsTractography

This function performs tractography of the datatype “dti” is specified. By default, this step always performs whole volume tractography which is always performed in native space, since the diffusion tensor is always kept in native resolution. If segmentations are present this function can also segment the fiber tracts into tracts per muscle. This step also includes calculating seed density maps, tract density maps, tract length maps, tract angle maps and tract curvature maps. Without a segmentation file these steps cannot be performed.

### MuscleBidsAnalsys

This function analysis all the data generated by the BIDS processing and summarizes it in an xls file per dataset. It also can generate images of all specified contrasts. After each dataset is analyzed all analysis files are combined in one final xls file combining the data of all datasets.

Which parameters to analyze and which images to produce is specified in the “config.json” file.

# Muscle BIDS Config file

The config file specifies what data to expect, what data to process and how the data should be processed. The config file uses the json format and can be viewed using the function `*ViewConfigFile*`.

The config file contains 4 main sections:

1. **Folders**: the names of the folders that will be used during processing.
2. **Conversion**: how to convert form dicom to nii
3. **Datasets**: The data description, how to process and how to post process each datatype
4. **Analysis**: How to analyze

Currently QMRITools BIDS processing deviates from the bids standard since it places each processing step into a separate source folder, instead of keeping it al together. This choice is made since it allows easier debugging and tracing of each processing step.

## Config file Sections

Here we provide a general description of each of the config file sections. For Datasets and Analysis, a more elaborate explanation of all possible settings is given in the corresponding sections later in this manual.

### Folders

This is a mandatory section for all processing steps. In total 5 folders can be specified. Which folders need to be specified depends on how far you use the BIDS functions. If no folders are specified, default folder names are used.

1. **dicomData**: this is the folder in which the source dicom data is stored. This is only needed for the `*BidsDcmToNii*` step.
2. **rawData**: this folder contains the raw and converted nii files generated by `*BidsDcmToNii`* and `*MuscleBidsConvert`*. After these two functions are completed the rawData contains the BIDS dataset. This folder is the input for the `*MuscleBidsProcess`* step.
3. **derivedData**: This is the output folder of the `*MuscleBidsProcces`* step. It will contain all processed datasets in native space. This is the input folder of the `*MuscleBidsMerge`* step.
4. **mergeData**: This is the output folder of the MuscleBidsMerge step. It will contain all datasets in the common space needed for segmentation, tractography and analysis. The `*MuscleBidsSegment*` and `*MuscleBidsTractography*` will used this function as their input and output folders.
5. **Analysis**: This is the output folder of the `*MuscleBidsAnalysis*` step. It will contain all xls files and images generated during this step.

### Conversion

This is an optional section where the version of dcm2niix can be specified. QMRITools allows to chose from different versions as specified in the “PacletInfo.wl” files of QMRITools. In most cases this setting is omitted and by default the latest version of dcm2niix is used.

### Datasets

This is the most complicated and important section of the config file. Here every step of the BIDS processing steps is configured and defined. For each datatype present in the study the names, types, processing, merging, segmentation and tractography settings must be defined. Each data type starts with the data description which contains the data labels, class, type and suffix which are each mandatory. In theory some of these fields can be derived from the data properties, however, having the used specify this explicitly helps with the study design and prevents possible confusion.

1. **Label**: The name of the dataset(s) to be processed. This is the protocol name of the nii data as defined in its json file. To view which protocol names exist in the raw data, (after `*BidsDcmToNii`* but before `*MuscleBidsConvert`*) the function `*ViewProtocolNames*` can be used.
2. **Class**: This the defines how the data will be treated during processing. The class can be “Chunks” or ”Acquisitions”. When the class “Chunks” is given the chunks will be joined during the `*MuscleBidsMerge`* step into one single Acquisition.
3. **Type**: The type of data that was acquired, the type will define in which sub folder the data will be stored. The types “T1w”, “T1w-FS”, “T2w” and “T2w-FS” will go to the “anat” folder, they types “megre” goes to the “dix” folder, the types “mese”, “T1”, “T2”, ” wT2” go to the “quant” folder, and the type “dwi” goes to the “dwi” folder. The data type is the first suffix added to the bids file name after the entities.
4. **Suffix**: The second suffix added to the bids file name which is used for file identification during processing. It is mandatory to specify and is recommended to be “dix”, “dti” or “t2” for Dixon data, DWI data or T2 mapping data respectively.

Next the Datasets section can contain any of the 4 following sub sections which are each explained in detail in “Config section: datasets”:

1. **Process**: Defines the Method and settings on how the data can be processed.
2. **Merging**: Defines how data should be merged for multi chunk data and which contrast is considered the common subject space.
3. **Segment**: Defines if for this data type a segmentation needs to be performed. Currently only automated Leg segmentation based on out phase Dixon data is implemented.
4. **Tractography**: Defines if and how tractography needs to be performed for DTI data.

### Analysis

The final section of the config file specifies how the data or a subselection of the should be analyzed. This section can contain any of the 3 follwing sub sections which are each explained in detail in the “Config section: Analysis”:

1. **Segmentation**: Defines which segmentation file is going to be used for per muscle analysis.
2. **Analysis**: Defines the contrast types and its derived parameters that need to be analyzed.
3. **Images**: Defines which images should be created and how they should look like.

## Config section: datasets

### Data descriptions

### Processing

### Merging

### Segment

### Tractography

## Config section: analysis

### Segmentation

### Analysis

### Images