CPP SPM

Release v1.1.5dev

the CPP SPM pipeline dev team

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CONTENT

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↪style=flat-square)](https://github.com/cpp-lln-lab/CPP_SPM#contributors)
```

CHAPTER

ONE

CPP SPM

This is a Matlab / Octave toolbox to perform MRI data analysis on a BIDS data set using SPM12.

1.1 Installation and set up

```
git clone \
    --recurse-submodules \
    https://github.com/cpp-lln-lab/CPP_SPM.git
```

To get the latest version that is on the `dev` branch.

```
git clone \
    --recurse-submodules \
    --branch dev \
    https://github.com/cpp-lln-lab/CPP_SPM.git
```

To start using CPP_SPM, you just need to initialize it for this MATLAB / Octave session with::

```
cpp_spm()
```

Please see our documentation for more info.

1.2 Usage

For some of its functionality cpp_spm has a BIDS app like API:

1.2.1 Preprocessing

```
cpp_spm(bids_dir, output_dir, 'participant', ...
        'action', 'preprocess', ...
        'task', {...})
```

1.2.2 GLM

```
cpp_spm(bids_dir, output_dir, 'participant', ...
        'action', 'preprocess', ...
        'preproc_dir', preproc_dir, ...
        'model_file', model_file)
```

Please see our documentation for more info.

1.3 Features

1.3.1 Preprocessing

If your data is fairly "typical" (for example whole brain coverage functional data with one associated anatomical scan for each subject), you might be better off running fmriprep on your data.

If you have more exotic data that cannot be handled well by fmriprep then CPP_SPM has some automated workflows to perform amongst other things:

- slice timing correction
- spatial preprocessing:
  - realignment OR realignm and unwarp
  - coregistration `func` to `anat`,
  - `anat` segmentation and skull stripping
  - (optional) normalization to SPM's MNI space
- smoothing
- fieldmaps processing and voxel displacement map creation (work in progress)

All preprocessed outputs are saved as BIDS derivatives with BIDS compliant filenames.

1.3.2 Statistics

The model specification are set up using the BIDS stats model and can be used to perform:

- whole GLM at the subject level
- whole brain GLM at the group level à la SPM (meaning using a summary statistics approach).
- ROI based GLM (using marsbar)
- model selection (with the MACS toolbox)

1.3.3 Quality control:

- functional data (work in progress)
- GLM auto-correlation check

Please see our documentation for more info.

1.4 Citation

```
@software{CPP_SPM,
  author  = {Gau, Rémi and Barilari, Marco and Battal, Ceren and Rezk, Mohamed and
↪Collignon, Olivier and Gurtubay, Ane and Falagiarda, Federica and MacLean, Michèle
↪and Cerpelloni, Filippo},
  license = {GPL-3.0},
  title   = {CPP SPM},
  url     = {https://github.com/cpp-lln-lab/CPP_SPM},
  version = {1.1.5dev},
  doi     = {https://doi.org/10.5281/zenodo.3554331},
}
```

1.5 Contributors

Thanks goes to these wonderful people (emoji key):

This project follows the all-contributors specification. Contributions of any kind welcome!

CHAPTER

TWO

INSTALLATION

2.1 Dependencies

This SPM toolbox runs with Matlab and Octave.

Dependencies	Minimum required	Used for testing in CI
MATLAB	2014	2020 on Ubuntu 20.04
Octave	4.2.2	4.2.2 on Ubuntu 20.04
SPM12	7219	7771

Some functionalities require some extra SPM toolbox to work: for example the ALI toolbox for brain lesion segmentation.

2.1.1 Octave compatibility

The following features do not yet work with Octave:

- anatomicalQA
- functionalQA
- slice_display toolbox
- rsHRF workflow

Not (yet) tested with Octave:

- MACS toolbox workflow for model selection
- ALI toolbox workflow for model selection

2.2 Installation

If you are only going to use this toolbox for a new analysis and you are not planning to edit the code base of CPP_SPM itself, we STRONGLY suggest you use this template repository to create a new project with a basic structure of folders and with the CPP_SPM code already set up.

Otherwise you can clone the repo with all its dependencies with the following git command:

```
git clone \
    --recurse-submodules \
    https://github.com/cpp-lln-lab/CPP_SPM.git
```

If you need the latest development, then you must clone from the `dev` branch:

```
git clone \
    --branch dev \
    --recurse-submodules \
    https://github.com/cpp-lln-lab/CPP_SPM.git
```

If you just need the code without the commit history download and unzip, you can fin the latest version from HERE.

2.3 Initialization

In general DO NOT ADD CPP SPM PERMANENTLY to your MATLAB / Octave path.

You just need to initialize for a given session with:

```
cpp_spm()
```

This will add all the required folders to the path.

You can also remove CPP_SPM from the path with:

```
cpp_spm('action', 'uninit')
```

2.4 Installation on a computing cluster

> For stand alone download https://www.fil.ion.ucl.ac.uk/spm/download/restricted/utopia/
>
> To use SPM docker https://github.com/spm/spm-docker
>
> See FAQ: https://en.wikibooks.org/wiki/SPM/Standalone#Frequently_Asked_Questions

This relies on the fact that SPM and CPM SPM are Octave compatible, so you will be able to run most of CPP SPM on a high performance cluster (HPC) without having to worry about MATLAB licenses.

Of course this assumes that Octave is available on your HPC.

Note that it should also be possible to precompile with MATLAB all the things you want to run, but this is not shown here.

The pre-requisite steps are described in the example below that shows how to set up CPP SPM on one of the HPC of the université catholique de Louvain.

1. SSH into the HPC

Assumes that you have set things up properly. For the UCLouvain see the documentation on this website (which has some good info about using HPC in general).

If you have everything set up it should be almost as easy as opening a terminal and typing:

```
ssh lemaitre3
```

2. Get SPM

You can simply clone the latest version of SPM from github with:

```
git clone https://github.com/spm/spm12.git --depth 1
```

3. Load the Octave modules

This first step might be different on your HPC, so you might have to figure out what the equivalent modules are called on your HPC (in the UCLouvain case you can find the relevant module by typing `module spider octave`)

Once you have found the modules load them:

```
module load releases/2018b
module load Octave/4.4.1-foss-2018b
```

4. Recompile SPM for Octave

You need to recompile SPM to make sure it works with Octave. This relies on running the following Make commands:

```
make -C spm12/src PLATFORM=octave distclean
make -C spm12/src PLATFORM=octave
make -C spm12/src PLATFORM=octave install
```

5. Add SPM to the path

In the example below `$` shows when you are in the bash terminal and `octave:1>` shows when you are in the Octave terminal.

Launch Octave:

```
$ octave

GNU Octave, version 4.4.1
Copyright (C) 2018 John W. Eaton and others.
This is free software; see the source code for copying conditions.
There is ABSOLUTELY NO WARRANTY; not even for MERCHANTABILITY or
FITNESS FOR A PARTICULAR PURPOSE.  For details, type 'warranty'.

Octave was configured for "x86_64-pc-linux-gnu".

Additional information about Octave is available at https://www.octave.org.

Please contribute if you find this software useful.
For more information, visit https://www.octave.org/get-involved.html

Read https://www.octave.org/bugs.html to learn how to submit bug reports.
For information about changes from previous versions, type 'news'.
```

Add the SPM12 folder to the path and save the path:

```
octave:1> addpath(fullfile(pwd, 'spm12'))
octave:2> savepath
octave:3> exit
```

5. Install CPP SPM

As before install and run an initialization:

```
git clone \
  -b dev \
  --recurse-submodules \
  https://github.com/cpp-lln-lab/CPP_SPM.git
```

Warning: There are some warnings thrown during initialization:

```
octave:1> initCppSpm
warning: addpath: /home/users/r/g/rgau/CPP_SPM/lib/spmup/utlilities/home/users/r/g/
↪rgau/CPP_SPM/lib/spm_2_bids: No such file or directory
warning: called from initCppSpm at line 67 column 5
warning: function /home/users/r/g/rgau/CPP_SPM/lib/spmup/external/cubehelix.m␣
↪shadows a core library function
warning: called from initCppSpm at line 67 column 5
warning: addpath: /home/users/r/g/rgau/CPP_SPM/src/workflows/stats/home/users/r/g/
↪rgau/CPP_SPM/lib/spmup: No such file or directory
```

As well as many warnings of the type:

```
sh: makeinfo: command not found
warning: doc_cache_create: unusable help text found in file 'analyze75info'
```

CHAPTER

THREE

BIDS APP API

src.messages.**cppSpmHelp**()

General intro function for CPP SPM

Note:

- all parameters use snake_case
- most invalid calls simply initialize CPP SPM

bids apps calls

generic call:

```
cpp_spm(bids_dir, output_dir, analysis_level, ...
        'action', 'some_action')
```

Obligatory parameters

Parameters

- **bids_dir** (*path*) – path to a raw BIDS dataset
- **output_dir** (*path*) – path where to output data
- **analysis_level** (*string*) – can either be `'subject'` or `'dataset'`
- **action** (*string*) – defines the pipeline to run; can be any of:
  - `'preprocess'`
  - `'stats'`

Optional parameters common to all actions

Parameters

- **participant_label** – cell of participants labels. For example: `{'01', '03', '08'}`. Can be a regular expression.
- **dry_run** (*logical*) – Defaults to `false`
- **bids_filter_file** (*path to JSON file or structure*) –
- **options** (*path to JSON file or structure*) –
- **verbosity** (*positive scalar*) – can be `0`, `1` or `2`. Defaults to `2`
- **space** (*cell string*) – Defaults to `{'individual', 'IXI549Space'}`

PREPROCESSING:

```
cpp_spm(bids_dir, output_dir, 'participant', ...
        'action', 'preprocess', ...
        'task', {...})
```

Obligatory parameters

Parameters

- **task** (*cell string*) – only one task
- **dummy_scans** (*positive scalar*) – Number of dummy scans to remove. Defaults to 0

Optional parameters

Parameters

- **anat_only** (*logical*) –
- **ignore** (*cell string*) – can be any of {'fieldmaps', 'slicetiming', 'unwarp'}
- **fwhm** (*positive scalar*) – smoothing to apply to the preprocessed data

STATS:

```
cpp_spm(bids_dir, output_dir, 'participant', ...
        'action', 'preprocess', ...
        'preproc_dir', preproc_dir, ...
        'model_file', model_file)
```

Obligatory parameters

Parameters

- **preproc_dir** (*path*) – path to preprocessed data
- **model_file** (*path to JSON file or structure*) –

Optional parameters

Parameters

- **roi_based** (*logical*) –
- **task** (*cell string*) –

low level calls

USAGE:

```
% initialise (add relevant folders to path)
cpp_spm

% equivalent to
cpp_spm('action', 'init')

% uninitialise (remove relevant folders from path)
cpp_spm('action', 'uninit')

% also adds folder for testing to the path
cpp_spm('action', 'dev')

% tried to update the current branch from the upstream repository
```

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```
cpp_spm('action', 'update')

% misc
cpp_spm('action', 'version')
cpp_spm('action', 'run_tests')
```

CHAPTER

FOUR

SET UP

4.1 Configuration of the pipeline

4.1.1 Options

Most of the options you have chosen for your analysis will be set in a variable `opt` an Octave/Matlab structure.

The content of that structure can be defined:

- "at run" time in a script or a function (that often called `getOption`)
- in a separate json file that can be loaded with `src/utils/loadAndCheckOptions.m()`.

You can find examples of both in the `demos` folder. You can also find a template function for `getOption` in the `templates` folder.

Check the *Pipeline defaults* page to see the available options and their defaults.

Selecting groups and subjects

The way to select certain subjects is summarised in the documentation of the `src/utils/getSubjectList()` function.

`src.bids.`**`getSubjectList`**(*BIDS*, *opt*)

Returns the subjects to analyze in `opt.subjects`

USAGE:

```
opt = getSubjectList(BIDS, opt)
```

Parameters

- **BIDS** (*structure*) – output of bids.layout
- **opt** (*structure*) – Options chosen for the analysis. See `checkOptions()`.

Returns

- **opt** (structure)

If no group or subject is speficied in `opt` then all subjects are included. This is equivalent to the default:

```
opt.groups = {''};
opt.subjects = {[]};
```

If you want to run the analysis of some subjects only based on the group they belong to **as defined in the ``participants.tsv``** file, you can do it like this:

```
opt.groups = {'control'};
```

This will run the pipeline on all the `control` subjects.

If your subject label is `blnd02` (as in `sub-blnd02`) but its group affiliation in the `participants.tsv` says `control`, then this subject will NOT be included if you run the pipeline with `opt.groups = {'blnd'}`.

If you have more than 2 groups you can specify them like this:

```
opt.groups = {'cont', 'cat'};
```

You can also directly specify the subject label for the participants you want to run:

```
opt.subjects = {'01', 'cont01', 'cat02', 'ctrl02', 'blind01'};
```

And you can combine both methods:

```
opt.groups = {'blind'};
opt.subjects = {'ctrl01'};
```

This will include all `blind` subjects and `sub-ctrl01`.

Setting directories

Below are some example on how to specify input and output directories.

Note: It will be easier and make your code more portable, if you use relative path for your directory setting.

For preprocessing

For a given folder structure:

```
my_fmri_project
   ├── code
   │   └── getOptionPreproc.m
   ├── outputs/derivatives
   └── inputs
       └── raw
```

Example content of `getOptionPreproc` file:

```
opt.pipeline.type = 'preproc';

this_dir = fileparts(mfilename('fullpath'));

opt.dir.raw = fullfile(this_dir, '..' 'inputs', 'raw');
opt.dir.derivatives = fullfile(this_dir, '..', 'outputs', 'derivatives');
```

For statistics

To run a GLM, CPP SPM gets the images and confound time series from a preprocessed derivatives BIDS dataset (from fMRIprep or CPP SPM) and the `events.tsv` files from a raw BIDS dataset.

For a given folder structure:

```
my_fmri_project
   ├── code
   │   └── getOptionStats.m
   ├── outputs/derivatives
   └── inputs
       ├── fmriprep
       └── raw
```

Example content of `getOptionStats` file:

```
opt.pipeline.type = 'stats';

this_dir = fileparts(mfilename('fullpath'));

opt.dir.raw = fullfile(this_dir, '..', 'inputs', 'raw');
opt.dir.preproc = fullfile(this_dir, '..', 'inputs', 'fmriprep');
opt.dir.derivatives = fullfile(this_dir, '..', 'outputs', 'derivatives');
```

The actual `opt.dir.input` and `opt.dir.output` folders will usually be set automatically when running:

```
opt = checkOptions(opt)
```

But you can set those by hand if you prefer.

4.1.2 BIDS model JSON files

This files allow you to specify the GLM to run and which contrasts to run. It follows BIDS statistical model

The model JSON file that describes:

- out to prepare the regressors for the GLM: `Transformation`
- the design matrix: `X`
- the contrasts to compute: `contrasts`
- several other options

It also allows to specify those for different levels of the analysis:

- run
- subject
- dataset

An example of JSON file could look something like that:

```
{
    "Name": "Basic model",
    "Description": "model for motion localizer",
    "Input": {
        "space": "IXI549Space",
        "task": "motionloc"
    },
    "Nodes": [
        {
            "Level": "Run",
```

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```
            "Transformations": {
                "Transformer": "cpp_spm",
                "Instructions": [
                    {
                        "Name": "Subtract",
                        "Input": [
                            "trial_type.motion",
                            "trial_type.static"
                        ],
                        "Value": 3,
                        "Output": [
                            "motion",
                            "static"
                        ]
                    }
                ]
            },
            "Model": {
                "Type": "glm",
                "X": [
                    "motion",
                    "static",
                    "trans_?",
                    "rot_?",
                    "*outlier*"
                ],
                "HRF": {
                    "Variables": [
                        "motion",
                        "static"
                    ],
                    "Model": "DoubleGamma"
                },
                "Options": {
                    "HighPassFilterCutoffHz": 0.0078,
                    "Mask": ""
                },
                "Software": {
                    "SPM": {
                        "HRFderivatives": "Temporal",
                        "SerialCorrelation": "FAST"
                    }
                }
            },
            "DummyContrasts": {
                "Test": "t",
                "Contrasts": [
                  "motion",
                  "static"
                ]
              },
            "Contrasts": [
                {
                    "Name": "motion_vs_static",
                    "ConditionList": [
                        "motion",
                        "static"
```

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```
                    ],
                    "weights": [
                        1,
                        -1
                    ],
                    "type": "t"
                }
            ]
        }
    ]
}
```

Here are what the different section mean:

```
"Input": {
    "space": "IXI549Space",
    "task": "motionloc"
}
```

This allows you to specify input images you want to include based on the BIDS entities in their name, like the task (can be more than one) or the MNI space your images are in (here `IXI549Space` is for SPM 12 typical MNI space.

Then the model has a `Nodes` array where each objectin defines what is to be done at a given `Level` (`Run`, `Subject`, `Dataset`)

```
"Nodes": [
    {
        "Level": "Run",
```

The `Transformations` object allows you to define what you want to do to some variables, before you put them in the design matrix. Here this shows how to subtract 3 seconds from the event onsets of the conditions listed in the `trial_type` columns of the `events.tsv` file, and put the output in a variable called `motion` and `static`.

```
"Transformations": {
    "Transformer": "cpp_spm",
    "Instructions": [
        {
            "Name": "Subtract",
            "Input": [
                "trial_type.motion",
                "trial_type.static"
            ],
            "Value": 3,
            "Output": [
                "motion",
                "static"
            ]
        }
    ]
}
```

Then comes the model object,

`X` defines the variables that have to be put in the design matrix. Here `trans_?` means any of the translation parameters (in this case `trans_x`, `trans_y`, `trans_z`) from the realignment that are stored in `_confounds.tsv` files. Similarly `*outlier*` means that any "scrubbing" regressors created by fMRIprep or CPP SPM to detect motion outlier or potential dummy scans will be included (those regressors are also in the `_confounds.tsv` files).

Note: Following standard Unix-style glob rules, "*" is interpreted to match 0 or more alphanumeric characters, and "?" is interpreted to match exactly one alphanumeric character.

`HRF` specifies which variables of X have to be convolved and what HRF model to use to do so.

```
"Model": {
    "Type": "glm",
    "X": [
        "motion",
        "static",
        "trans_?",
        "rot_?",
        "*outlier*"
    ],
    "HRF": {
        "Variables": [
            "motion",
            "static"
        ],
        "Model": "DoubleGamma"
    }
```

Then we have the contrasts definition where `DummyContrasts` compute the contrasts against baseline for the condition `motion` and `static` and where `Contrasts` compute the t-contrats for "motion greater than static" with these given weights.

```
"DummyContrasts": {
    "Test": "t",
    "Contrasts": [
      "motion",
      "static"
    ]
  },
"Contrasts": [
    {
        "Name": "motion_gt_static",
        "ConditionList": [
            "motion",
            "static"
        ],
        "weights": [
            1,
            -1
        ],
        "type": "t"
    }
]
```

4.1.3 Create an empty BIDS model

```
model = createEmptyModel()
bids.util.jsonwrite('model-empty_smdl.json', model)
```

4.1.4 Create a default BIDS model for a dataset

```
path_to_dataset = fullfile(pwd, 'data', 'raw');
BIDS = bids.layout(path_to_dataset);

opt.taskName = 'myFascinatingTask';

createDefaultStatsModel(BIDS, opt);
```

CHAPTER

FIVE

PIPELINE DEFAULTS

Defaults of the pipeline.

5.1 checkOptions

src.defaults.**checkOptions**(*opt*)

Check the option inputs and add any missing field with some defaults

USAGE:

```
opt = checkOptions(opt)
```

Parameters **opt** (*structure*) – structure or json filename containing the options.

Returns

- **opt** the option structure with missing values filled in by the defaults.

IMPORTANT OPTIONS (with their defaults):

- **generic**
  - `opt.dir`: TODO EXPLAIN
  - `opt.groups = {''}` - group of subjects to analyze
  - `opt.subjects = {[]}` - suject to run in each group space where we conduct the analysis are located. See `setDerivativesDir()` for more information.
  - `opt.space = {'individual', 'IXI549Space'}` - Space where we conduct the analysis
  - `opt.taskName`
  - `opt.query = struct('modality', {{'anat', 'func'}})` - a structure used to specify subset of files to only run analysis on. Default = `struct('modality', {{'anat', 'func'}})` See `bids.query` to see how to specify.

    Warning: `opt.query` might be progressively deprecated in favor of `opt.bidsFilterFile` that allows using different filters for T1w and bold data.

  - `opt.bidsFilterFile` - Sets how to define a typical images "bold", "T1w"... in terms of their bids entities. The default value is:

```
struct( ...
    'fmap', struct('modality', 'fmap'), ...
    'bold', struct('modality', 'func', 'suffix', 'bold'), ...
    't2w',  struct('modality', 'anat', 'suffix', 'T2w'), ...
    't1w',  struct('modality', 'anat', 'space', '', 'suffix', 'T1w'), .
↪..
    'roi',  struct('modality', 'roi', 'suffix', 'mask'));
```

- **preprocessing**
  - `opt.realign.useUnwarp = true`
  - `opt.useFieldmaps = true` - when set to `true` the preprocessing pipeline will look for the voxel displacement maps (created by `bidsCreateVDM()`) and will use them for realign and unwarp.
  - `opt.fwhm.func = 6` - FWHM to apply to the preprocessed functional images.
- **statistics**
  - `opt.model.file = ''` - path to the BIDS model file that contains the model to speficy and the contrasts to compute.
  - `opt.fwhm.contrast = 6` - FWHM to apply to the contrast images before bringing them at the group level.
  - `'opt.model.designOnly'` = if set to `true`, the GLM will be set up without associating any data to it. Can be useful for quick design matrix inspection before running estimation.

OTHER OPTIONS (with their defaults):

- **generic**
  - `opt.verbosity = 1;` - Set it to `0` if you want to see less output on the prompt.
  - `opt.dryRun = false` - Set it to `true` in case you don't want to run the analysis.
  - `opt.pipeline.type = 'preproc'` - Switch it to `stats` when running GLMs.
  - `opt.pipeline.name`
  - `opt.zeropad = 2` - number of zeros used for padding subject numbers, in case subjects should be fetched by their number `1` and not their label `01'`.
  - `opt.rename = true` - to skip renaming files with `bidsRename()`. Mostly for debugging as the ouput files won't be usable by any of the stats workflows.
  - `opt.msg.color = blue` - default font color of the prompt messages.
- **preprocessing**
  - `opt.anatOnly = false` - to only preprocess the anatomical file
  - `opt.segment.force = false` - set to `true` to ignore previous output of the segmentation and force to run it again
  - `opt.skullstrip.mean = false` - to skulstrip mean functional image
  - `opt.skullstrip.threshold = 0.75` - Threshold used for the skull stripping. Any voxel with `p(grayMatter) + p(whiteMatter) + p(CSF) > threshold` will be included in the mask.
  - `opt.skullstrip.do = true` - Set to `true` to skip skullstripping
  - `opt.stc.skip = false` - boolean flag to skip slice time correction or not.

  - `opt.stc.referenceSlice = []` - reference slice for the slice timing correction. If left emtpy the mid-volume acquisition time point will be selected at run time.
  - `opt.stc.sliceOrder = []` - To be used if SPM can't extract slice info. NOT RECOMMENDED, if you know the order in which slices were acquired, you should be able to recompute slice timing and add it to the json files in your BIDS data set.
  - `opt.funcVoxelDims = []` - Voxel dimensions to use for resampling of functional data at normalization.

- **preprocessing QA** (see `functionalQA`)

  `opt.QA.func` contains a lot of options used by `spmup_first_level_qa`

  - `opt.QA.func.carpetPlot = true` to plot carpet plot
  - `opt.QA.func.MotionParameters = 'on'`
  - `opt.QA.func.FramewiseDisplacement = 'on'`
  - `opt.QA.func.Voltera = 'on'`
  - `opt.QA.func.Globals = 'on'`
  - `opt.QA.func.Movie = 'on'` ; set it to `off` to skip generating movies of the time series
  - `opt.QA.func.Basics = 'on'`

- **statistics**

  - `opt.glm.roibased.do = false` must be set to `true` to use the `bidsRoiBasedGLM` workflow
  - `opt.glm.useDummyRegressor = false` to add dummy regressors when a condition is missing from a run. See `bidsModelSelection()` for more information.
  - `opt.glm.maxNbVols = Inf` sets the maximum number of volumes to include in a run in a subject level GLM. This can be useful if some time series have more volumes than necessary.
  - `opt.glm.keepResiduals = false` keeps the subject level GLM residuals
  - `opt.QA.glm.do = false` - If set to `true` the residual images of a GLM at the subject levels will be used to estimate if there is any remaining structure in the GLM residuals (the power spectra are not flat) that could indicate the subject level results are likely confounded. See `plot_power_spectra_of_GLM_residuals.m` and Accurate autocorrelation modeling substantially improves fMRI reliability for more info.

`src.defaults.`**`setDirectories`**`(`*`opt`*`)`

USAGE:

```
opt = setDirectories(opt)
```

5.2 spm_my_defaults

Some more SPM options can be set in the `src.defaults.spm_my_defaults.m()`.

`src.defaults.`**`spm_my_defaults`**`()`

USAGE:

```
spm_my_defaults()
```

This is where we set the defautls we want to use. These will overide the spm defaults. When "not enough" information is specified in the batch files, SPM falls back on the defaults to fill in the blanks. This allows to make the script simpler.

5.2.1 auto-correlation modelisation

Use of FAST and not AR1 for auto-correlation modelisation.

Using FAST does not seem to affect results on time series with "normal" TRs but improves results when using sequences: it is therefore used by default in this pipeline.

Olszowy, W., Aston, J., Rua, C. et al.
Accurate autocorrelation modeling substantially improves fMRI reliability.
Nat Commun 10, 1220 (2019).
https://doi.org/10.1038/s41467-019-09230-w

Note that if you wanted to change this setting you could do so via the `Software` object of the BIDS stats model:

```
{
"Name": "auditory",
"BIDSModelVersion": "1.0.0",
"Description": "contrasts to compute for the FIL MoAE dataset",
"Input": {
    "task": "auditory"
},
"Nodes": [
    {
    "Level": "Run",
    "Name": "run_level",
    "Model": {
        "X": [
        "trial_type.listening"
        ],
        "Type": "glm",
        "Software": {
            "SPM": {
                "SerialCorrelation": "AR(1)",
                "HRFderivatives": "none"
            }
        }
    }
    }
]
}
```

5.3 spm to BIDS filename conversion

src.defaults.**set_spm_2_bids_defaults**(*opt*)
set default map for renaming for cpp_bids

USAGE:

```
opt = set_spm_2_bids_defaults(opt)
```

Further renaming mapping can then be added, changed or removed through the `opt.spm_2_bids object`.

5.4 list of defaults

CHAPTER

SIX

DEMOS

```
demos/
    ├── face_repetition
    ├── lesion_detection
    ├── MoAE
    ├── openneuro
    ├── tSNR
    └── vismotion
```

The demos show show you different way to use CPP_SPM.

6.1 MoAE

```
/demos/MoAE
    ├── models
    └── options
```

This "Mother of All Experiments" is based on the block design dataset of SPM.

In the `options` folder has several examples of how to encode the options of your analysis in a json file.

In the `models` shows the BIDS statistical model used to run the GLM of this demo.

`demos.MoAE.`**`moae_01_preproc`**
: This script will download the dataset from the FIL for the block design SPM tutorial and will run the basic preprocessing.

  (C) Copyright 2019 Remi Gau

`demos.MoAE.`**`moae_02_stats`**
: This script will run the FFX and contrasts on it of the MoAE dataset

  Results might be a bit different from those in the manual as some default options are slightly different in this pipeline (e.g use of FAST instead of AR(1), motion regressors added)

  (C) Copyright 2019 Remi Gau

`demos.MoAE.`**`moae_03_create_roi_extract_data`**
: This script shows how to create a ROI and extract data from it.

  FYI: this is "double dipping" as we use the same data to create the ROI we are going to extract the value from.

  (C) Copyright 2021 Remi Gau

`demos.MoAE.`**`moae_04_slice_display`**
: This script shows how to display the results of a GLM by having on the same image:

- the beta estimates
- the t statistics
- ROI contours

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6.2 Face repetition

This is based on the event related design dataset of SPM.

demos.face_repetition.**face_rep_01_preproc_func**
This script will download the face repetition dataset from SPM and will run the basic preprocessing.

(C) Copyright 2019 Remi Gau

demos.face_repetition.**face_rep_02_stats**
This script will run the FFX and contrasts on the the face repetition dataset from SPM.

Results might be a bit different from those in the manual as some default options are slightly different in this pipeline (e.g use of FAST instead of AR(1). . .)

(C) Copyright 2019 Remi Gau

demos.face_repetition.**face_rep_03_roi_analysis**
Creates a ROI in MNI space from the retinotopic probablistic atlas.

Creates its equivalent in subject space (inverse normalization).

Then uses marsbar to run a ROI based GLM

(C) Copyright 2019 Remi Gau

demos.face_repetition.**face_rep_anat**
This show how an anat only pipeline would look like.

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demos.face_repetition.**face_rep_resolution**
This script runs preprocessing with different final spatial resolution in MNI space It then runs the subject level GLMs

This can show how to script several analysis within the CPP_SPM framework

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6.3 vismotion

Small demo using the data from a visual motion localizer to show how to set up an analysis with CPP SPM from scratch with datalad.

CHAPTER

SEVEN

ARCHITECTURE

At the highest levels CPP SPM is organized in workflows: they all start with the prefix `bids` (for example `bidsRealignReslice`) and are in the folder *`src.workflows`* Workflows typical run on all the subjects specified in the `options` structure (see the *Set up* section).

Most workflows run by creating matlab batches that are saved as `.mat` files in a `jobs` then passed to the SPM jobman to run. To do this the workflows call "bacth creating functions" that all start with the prefix `setBatch` (for example `setBatchCoregistration`). and are in the folder *`src.batches`*.

Many workflows include some post-processing steps (like file renaming) after the execution of the batch, so in many cases the output of running just the batch and running the whole workflow will be different.

Preprocessing, *Statistics* and *Fieldmaps* handling have their own document pages.

Other workflows, batches and related helper functions are listed below.

7.1 Workflows

7.1.1 HRF estimation

Relies on the resting-state HRF toolbox.

`src.workflows.`**`bidsRsHrf`**(*opt*)

Use the rsHRF to estimate the HRF from resting state data.

USAGE:

```
bidsRsHrf(opt)
```

Parameters **`opt`** (*`structure`*) – structure or json filename containing the options. See `checkOptions()` and `loadAndCheckOptions()`.

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7.1.2 Other

src.workflows.**bidsCopyInputFolder**(*opt*, *unzip*)

Copies the folders from the raw folder to the derivatives folder, and will copy the dataset description and task json files to the derivatives directory.

Then it will search the derivatives directory for any zipped *.gz image and uncompress the files for the task of interest.

USAGE:

```
bidsCopyInputFolder(opt, [unzip = true])
```

Parameters

- **opt** (*structure*) – structure or json filename containing the options. See checkOptions() and loadAndCheckOptions().
- **unZip** (*boolean*) –

See also: bids.copy_to_derivative

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src.workflows.**bidsRename**(*opt*)

Renames SPM output into BIDS compatible files.

USAGE:

```
bidsRename(opt)
```

Parameters **opt** (*structure*) – structure or json filename containing the options. See checkOptions() and loadAndCheckOptions().

See the spm_2_bids submodule and defaults.set_spm_2_bids_defaults for more info.

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7.1.3 Worflow helper functions

To be used if you want to create a new workflow.

src.workflows.**setUpWorkflow**(*opt*, *workflowName*, *bidsDir*)

Calls some common functions to:

- check the configuraton,
- remove some old files from an eventual previous crash
- loads the layout of the BIDS dataset
- tries to open a graphic window

USAGE:

```
[BIDS, opt, group] = setUpWorkflow(opt, workflowName, [bidsDir])
```

Parameters

- **opt** (*structure*) – structure or json filename containing the options. See `checkOptions` and `loadAndCheckOptions`.
- **workflowName** (*string*) – name that will be printed on screen
- **bidsDir** –
- **bidsDir** – string

Returns

- **BIDS** (structure) returned by `getData`
- **opt** options checked
- **group**

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`src.workflows.`**saveAndRunWorkflow**(*matlabbatch*, *batchName*, *opt*, *subLabel*)

Saves the SPM matlabbatch and runs it

USAGE:

```
saveAndRunWorkflow(matlabbatch, batchName, opt, [subLabel])
```

Parameters

- **matlabbatch** (*structure*) – list of SPM batches
- **batchName** (*string*) – name of the batch
- **opt** (*structure*) – structure or json filename containing the options. See `checkOptions` and `loadAndCheckOptions`.
- **subLabel** (*string*) – subject label

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`src.workflows.`**cleanUpWorkflow**(*opt*)

USAGE:

```
cleanUpWorkflow(opt)
```

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`src.workflows.`**returnDependency**(*opt*, *type*)

Use to create dependencies between batches in workflows.

USAGE:

```
dep = returnDependency(opt, type)
```

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7.2 Batches

src.batches.**setBatchSelectAnat**(*matlabbatch*, *BIDS*, *opt*, *subLabel*)
Creates a batch to set an anatomical image

USAGE:

```
matlabbatch = setBatchSelectAnat(matlabbatch, BIDS, opt, subLabel)
```

Parameters

- **matlabbatch** (*structure*) – list of SPM batches
- **BIDS** (*structure*) – BIDS layout returned by `getData`.
- **opt** (*structure*) – structure or json filename containing the options. See `checkOptions()` and `loadAndCheckOptions()`.
- **subLabel** (*string*) – subject label

Returns

matlabbatch (structure)

matlabbatch = setBatchSelectAnat(matlabbatch, BIDS, opt, subLabel)

- image type = opt.bidsFilterFiler.t1w.suffix (default = T1w)
- session to select the anat from = opt.bidsFilterFiler.t1w.ses (default = 1)

We assume that the first anat of that type is the "correct" one

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src.batches.**setBatchPrintFigure**(*matlabbatch*, *opt*, *figureName*)
template to creae new setBatch functions

USAGE:

```
matlabbatch = setBatchPrintFigure(matlabbatch, figureName)
```

Parameters

- **matlabbatch** –
- **figureName** (*string*) –

Returns

- **matlabbatch** (structure) The matlabbatch ready to run the spm job

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src.batches.**setBatchMeanAnatAndMask**(*matlabbatch*, *opt*, *outputDir*)
Creates batxh to create mean anatomical image and a group mask

USAGE:

```
matlabbatch = setBatchMeanAnatAndMask(matlabbatch, opt, funcFWHM, outputDir)
```

Parameters

- **matlabbatch** (*structure*) –
- **opt** (*structure*) – Options chosen for the analysis. See `checkOptions()`.
- **outputDir** (*tring*) –

Returns

- **matlabbatch** (structure)

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`src.batches.`**`setBatchRsHRF`**(*matlabbatch*, *BIDS*, *opt*, *subLabel*)

Set the batch for realign / realign and reslice / realign and unwarp

USAGE:

```
matlabbatch = setBatchRsHRF(matlabbatch, BIDS, opt, subLabel)
```

Parameters

- **matlabbatch** (*structure*) – SPM batch
- **BIDS** (*structure*) – BIDS layout returned by `getData`.
- **opt** (*structure*) – Options chosen for the analysis. See `checkOptions()`.
- **subLabel** (*string*) – subject label

Returns

- **matlabbatch** (structure) (dimension)

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`src.batches.`**`setBatchImageCalculation`**(*varargin*)

Set a batch for a image calculation

USAGE:

```
matlabbatch = setBatchImageCalculation(matlabbatch, input, output, outDir,␣
↪expression)
```

Parameters

- **matlabbatch** (*structure*) –
- **input** (*cell*) – list of images
- **output** (*string*) – name of the output file
- **outDir** (*string*) – output directory
- **expression** (*string*) – mathematical expression to apply (for example '(i1+i2)>3')
- **expression** – data type that must be one of the following: - 'uint8' - 'int16' (default) - 'int32' - 'float32' - 'float64' - 'int8' - 'uint16' - 'uint32'

See `spm_cfg_imcalc.m` for more information:

```
``edit(fullfile(spm('dir'), 'config', 'spm_cfg_imcalc.m'))``
```

Returns

- **matlabbatch**

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src.batches.**setBatch3Dto4D**(*matlabbatch*, *opt*, *volumesList*, *RT*, *outputName*, *dataType*)
Set the batch for 3D to 4D conversion

USAGE:

```
matlabbatch = setBatch3Dto4D(matlabbatch, volumesList, RT, [outputName],␣
↪[dataType])
```

Parameters

- **matlabbatch** (*structure*) –
- **volumesList** (*array*) – List of volumes to be converted in a single 4D brain
- **outputName** (*string*) – The string that will be used to save the 4D brain
- **dataType** (*integer*) – It identifies the data format conversion
- **RT** (*float*) – It identifies the TR in seconds of the volumes to be written in the 4D file header

Returns

- **matlabbatch** (structure) The matlabbatch ready to run the spm job

dataType:

- 0: SAME
- 2: UINT8 - unsigned char
- 4: INT16 - signed short
- 8: INT32 - signed int
- 16: FLOAT32 - single prec. float
- 64: FLOAT64 - double prec. float

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src.batches.**saveMatlabBatch**(*matlabbatch*, *batchType*, *opt*, *subLabel*)
#ok<INUSL>

Saves the matlabbatch job in a .m file. Environment information are saved in a .json file.

% USAGE:

```
saveMatlabBatch(matlabbatch, batchType, opt, [subLabel])
```

Parameters

- **matlabbatch** (*structure*) –
- **batchType** (*string*) –
- **opt** (*structure*) – Options chosen for the analysis. See checkOptions().

- **subLabel** (*string*) –

The .m file can directly be loaded with the SPM batch or run directly by SPM standalone or SPM docker.

The .json file also contains heaps of info about the "environment" used to set up that batch including the version of:

- OS,
- MATLAB or Octave,
- SPM,
- CPP_SPM

This can be useful for methods writing though if the the batch is generated in one environment and run in another (for example set up the batch with Octave on Mac OS and run the batch with Docker SPM), then this information will be of little value in terms of computational reproducibility.

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src.batches.lesion.**setBatchLesionOverlapMap**(*matlabbatch*, *BIDS*, *opt*, *subLabel*)
Creates a batch for the lesion overlap map

USAGE:

```
matlabbatch = setBatchLesionOverlapMap(matlabbatch, BIDS, opt, subLabel)
```

Parameters **matlabbatch** (*structure*) – list of SPM batches

Returns

- **matlabbatch** (structure)

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src.batches.lesion.**setBatchLesionSegmentation**(*matlabbatch*, *BIDS*, *opt*, *subLabel*)
Creates a batch to segment the anatomical image for lesion detection

USAGE:

```
matlabbatch = setBatchSegmentationDetectLesion(matlabbatch, BIDS, opt, subLabel)
```

Parameters **matlabbatch** (*structure*) – list of SPM batches

Returns

- **matlabbatch** (structure)

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src.batches.lesion.**setBatchLesionAbnormalitiesDetection**(*matlabbatch*, *opt*, *images*)
Creates a batch to detect lesion abnormalities

USAGE:

```
matlabbatch = setBatchLesionAbnormalitiesDetection(matlabbatch, BIDS, opt,␣
↪subLabel)
```

Parameters **matlabbatch** (*structure*) – list of SPM batches

Returns

- **matlabbatch** (structure)

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7.3 Low level functions description

7.3.1 BIDS related functions

src.bids.**initBids**(*varargin*)
Initialize a BIDS dataset and updates dataset description.

USAGE:

```
initBids(opt, 'description', '', 'force', false)
```

Parameters **opt** (*structure*) – obligatory argument.

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src.bids.**addStcToQuery**(*BIDS*, *opt*, *subLabel*)
USAGE:

```
opt = addStcToQuery(opt, subLabel)
```

In case slice timing correction was performed this update the query to fetch the correct files for realignment.

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src.bids.**removeEmptyQueryFields**(*query*)

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src.bids.**getROIs**(*varargin*)
Get the rois from :

- the group folder when running analysis in MNI space
- the `sub-*/roi/sub-subLabel` folder when in individual space

USAGE:

```
[roiList, roiFolder] = getROIs(opt, subLabel)
```

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src.bids.**getData**(*varargin*)
Reads the specified BIDS data set and updates the list of subjects to analyze.

USAGE:

```
[BIDS, opt] = getData(opt, bidsDir)
```

Parameters

- **opt** (*structure*) – Options chosen for the analysis. See `checkOptions()`.

- **bidsDir** (*string*) – the directory where the data is ; default is : `fullfile(opt.dataDir, '..', 'derivatives', 'cpp_spm')`

Returns

- **opt** (structure)
- **BIDS** (structure)

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`src.bids.`**`getInfo`**(*BIDS*, *subLabel*, *opt*, *info*, *varargin*)

Wrapper function to fetch specific info in a BIDS structure returned by spm_bids.

USAGE:

```
varargout = getInfo(BIDS, subLabel, opt, info, varargin)
```

If info = `sessions`, this returns name of the sessions and their number:

```
[sessions, nbSessions] = getInfo(BIDS, subLabel, opt, 'sessions')
```

If info = `runs`, this returns name of the runs and their number for a specified session:

```
[runs, nbRuns] = getInfo(BIDS, subLabel, opt, 'runs', sessionID)
```

If info = `filename`, this returns the name of the file for a specified session and run:

```
filenames = getInfo(BIDS, subLabel, opt, 'filename', sessionID, runID, suffix)
```

Parameters

- **BIDS** (*structure*) – returned by bids.layout when exploring a BIDS data set.
- **subLabel** (*string*) – label of the subject ; in BIDS lingo that means that for a file name `sub-02_task-foo_bold.nii` the subLabel will be the string `02`
- **opt** (*structure*) – Used to find the task name and to pass extra `query` options.
- **info** (*string*) – `sessions`, `runs`, `filename`.
- **sessionLabel** (*string*) – session label (for *ses-001*, the label will be *001*)
- **runIdx** (*string*) – run index label (for *run-001*, the label will be *001*)
- **suffix** (*string*) – datatype (`bold`, `events`, `physio`)

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`src.bids.`**`getSubjectList`**(*BIDS*, *opt*)

Returns the subjects to analyze in `opt.subjects`

USAGE:

```
opt = getSubjectList(BIDS, opt)
```

Parameters

- **BIDS** (*structure*) – output of bids.layout
- **opt** (*structure*) – Options chosen for the analysis. See `checkOptions()`.

Returns

- **opt** (structure)

If no group or subject is speficied in `opt` then all subjects are included. This is equivalent to the default:

```
opt.groups = {''};
opt.subjects = {[]};
```

If you want to run the analysis of some subjects only based on the group they belong to **as defined in the ``participants.tsv``** file, you can do it like this:

```
opt.groups = {'control'};
```

This will run the pipeline on all the `control` subjects.

If your subject label is `blnd02` (as in `sub-blnd02`) but its group affiliation in the `participants.tsv` says `control`, then this subject will NOT be included if you run the pipeline with `opt.groups = {'blnd'}`.

If you have more than 2 groups you can specify them like this:

```
opt.groups = {'cont', 'cat'};
```

You can also directly specify the subject label for the participants you want to run:

```
opt.subjects = {'01', 'cont01', 'cat02', 'ctrl02', 'blind01'};
```

And you can combine both methods:

```
opt.groups = {'blind'};
opt.subjects = {'ctrl01'};
```

This will include all `blind` subjects and `sub-ctrl01`.

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`src.bids.`**`getAndCheckRepetitionTime`**(*varargin*)

Gets the repetition time for a given bids.query filter (for several files) Throws an error if it returns empty or finds inconsistent repetition times.

USAGE:

```
repetitionTime = getAndCheckRepetitionTime(BIDS, filter)
```

Parameters

- **`BIDS`** (*structure*) – obligatory argument.
- **`filter`** (*structure*) – obligatory argument.

Returns

- **repetitionTime** (float) (1x1)

Example:

```
filter = opt.query;
filter.sub =  subLabel;
filter.suffix = 'bold';
```

(continues on next page)

(continued from previous page)

```
filter.extension = {'.nii', '.nii.gz'};
filter.prefix = '';
filter.task = opt.taskName;

TR = getAndCheckRepetitionTime(BIDS, filter);
```

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src.bids.**getAndCheckSliceOrder**(*BIDS*, *opt*, *filter*)

Get the slice order information from the BIDS metadata. If inconsistent slice timing is found across files it returns empty and throws a warning.

USAGE:

```
sliceOrder = getAndCheckSliceOrder(opt)
```

Parameters

- **BIDS** (*structure*) – output of `getData` or `bids.layout`
- **opt** (*structure*) – Options chosen for the analysis. See `checkOptions()`.
- **opt** – filter for `bids.query`.

Returns

- **sliceOrder** a vector of the time when each slice was acquired in in a volume or indicating the order of acquisition of the slices.

`getAndCheckSliceOrder` will try to read the `opt` structure for any relevant information about slice timing. If this is empty, it queries the BIDS dataset to ee if there is any consistent slice timing information for a given `filter`

See also: bidsSTC, setBatchSTC

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src.bids.**getTpmFilename**(*BIDS*, *anatImage*, *res*, *space*)

Gets the fullpath filenames of the tissue probability maps (TPM)

USAGE:

```
[gm, wm, csf] = getTpmFilenames(BIDS, opt, subLabel, space, res)
```

Parameters

- **BIDS** (*structure*) –
- **opt** –
- **opt** – structure
- **anatImage** –
- **anatImage** – string
- **space** –
- **space** – string
- **res** –

- **res** – string

Returns

- **gm** (string) grey matter TPM
- **wm** (string) white matter TPM
- **csf** (string) csf matter TPM

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src.bids.**getMeanFuncFilename**(*BIDS*, *subLabel*, *opt*)

Get the filename and the directory of an mean functional file.

USAGE:

```
[meanImage, meanFuncDir] = getMeanFuncFilename(BIDS, subLabel, opt)
```

Parameters

- **BIDS** (*structure*) –
- **subLabel** (*string*) –
- **opt** (*structure*) – Options chosen for the analysis. See `checkOptions()`.

Returns

- **meanImage** (string)
- **meanFuncDir** (string)

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src.bids.**getBoldFilename**(*varargin*)

Get the filename and the directory of a bold file for a given session / run.

Unzips the file if necessary.

USAGE:

```
[boldFilename, subFuncDataDir] = getBoldFilename(BIDS, subLabel, sessionID, runID,
↪ opt)
```

Parameters

- **BIDS** (*structure*) – returned by bids.layout when exploring a BIDS data set.
- **subLabel** (*string*) – label of the subject ; in BIDS lingo that means that for a file name `sub-02_task-foo_bold.nii` the subLabel will be the string `02`
- **sessionID** (*string*) – session label (for *ses-001*, the label will be *001*)
- **runID** (*string*) – run index label (for *run-001*, the label will be *001*)
- **opt** (*structure*) – Mostly used to find the task name.

Returns

- **boldFilename** (string)
- **subFuncDataDir** (string)

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src.bids.**getAnatFilename**(*BIDS*, *opt*, *subLabel*)

Get the filename and the directory of an anat file for a given session and run. Unzips the file if necessary.

It several images are available it will take the first one it finds.

USAGE:

```
[anatImage, anatDataDir] = getAnatFilename(BIDS, subLabel, opt)
```

Parameters

- **BIDS** (*structure*) –
- **subLabel** –
- **subLabel** – string
- **opt** – structure

Returns

- **anatImage** (string)
- **anatDataDir** (string)

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7.3.2 Input / Output

src.IO.**saveOptions**(*opt*)

Saves options in a JSON file in a `cfg` folder.

USAGE:

```
saveOptions(opt)
```

Parameters **opt** (*structure*) – Options chosen for the analysis. See `checkOptions()`.

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src.IO.**loadAndCheckOptions**(*optionJsonFile*)

Loads the json file provided describing the options of an analysis. It then checks its content and fills any missing fields with the defaults.

If no argument is provived, it checks in the current directory for any `opt_task-*.json` files and loads the most recent one by name (using the `date-` key).

USAGE:

```
opt = loadAndCheckOptions(optionJsonFile)
```

Parameters **optionJsonFile** (*string*) – Fullpath to the json file describing the options of an analysis. It can also be an `opt` structure containing the options.

Returns

opt (structure) Options chosen for the analysis. See `checkOptions()`.

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src.IO.**overwriteDir**(*directory*, *opt*)

(C) Copyright 2021 CPP_SPM developers

src.IO.**createDerivativeDir**(*opt*)

Creates the derivative folder if it does not exist.

USAGE:

```
opt = createDerivativeDir(opt)
```

Parameters **opt** (*structure*) – Options chosen for the analysis. See `checkOptions()`.

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src.IO.**saveSpmScript**(*varargin*)

Saves a matlabbatch as .m file

USAGE:

```
outputFilename = saveSpmScript(input, outputFilename)
```

Parameters

- **input** – a `matlabbatch` variable (cell) or the fullpath to a `.mat` file containing such `matlabbatch` variable.
- **outputFilename** (*path*) – optional. Path to output file

Returns

- **outputFilename** (path)

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src.IO.**unzipAndReturnsFullpathName**(*fullpathName*, *opt*)

Unzips a file if necessary

USAGE:

```
unzippedFullpathName = unzipAndReturnsFullpathName(fullpathName)
```

Parameters **fullpathName** (*string array*) –

Returns

- **unzippedFullpathName** (string)

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src.IO.**onsetsMatToTsv**(*varargin*)

Takes an SPM _onset.mat file and converts it to a _onsets.mat file.

Onsets are assumed to be in seconds.

USAGE:

```
onsetTsvFile = onsetMatToTsv(onsetMatFile)
```

Parameters **onsetMatFile** (*fullpath*) – obligatory argument.

Returns

- **onsetTsvFile** (path)

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src.IO.**regressorsMatToTsv**(*varargin*)

Takes an SPM _desc-confounds_regressors.mat file and converts it to a _desc-confounds_regressors.tsv file.

USAGE:

```
regressorsTsvFile = regressorsMatToTsv(regressorsMatFile)
```

Parameters **regressorsMatFile** (*fullpath*) – obligatory argument.

Returns

- **regressorsTsvFile** (path)

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src.IO.**renameUnwarpParameter**(*BIDS*, *subLabel*, *opt*)

USAGE:

```
renameUnwarpParameter(BIDS, subLabel, opt)
```

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src.IO.**renameSegmentParameter**(*BIDS*, *subLabel*, *opt*)

USAGE:

```
renameSegmentParameter(BIDS, subLabel, opt)
```

(C) Copyright 2020 CPP_SPM developers

src.IO.**cleanCrash**()

Removes any files left over from a previous unfinished run of the pipeline, like any `*.png` imgages

USAGE:

```
cleanCrash()
```

(C) Copyright 2020 CPP_SPM developers

7.3.3 Utility functions

src.utils.**createDataDictionary**(*tsvContent*)
USAGE:

```
jsonContent = createDataDictionary(tsvContent)
```

(C) Copyright 2020 CPP_SPM developers

src.utils.**createGlmDirName**(*opt*)
USAGE:

```
glmDirName = createGlmDirName(opt)
```

(C) Copyright 2021 CPP_SPM developers

src.utils.**getFuncVoxelDims**(*opt*, *subFuncDataDir*, *fileName*)
Short description of what the function does goes here.

USAGE:

```
[voxDim, opt] = getFuncVoxelDims(opt, subFuncDataDir, fileName)
```

Parameters

- **opt** (*structure*) – Options chosen for the analysis. See `checkOptions()`.
- **subFuncDataDir** –
- **fileName** –

Returns

- **voxDim**
- **opt**

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src.utils.**computeTsnr**(*boldImage*)
calculate temporal SNR from single run of fMRI timeseries data

USAGE:

```
[tsnrImage, volTsnr] = computeTsnr(boldImage)
```

Parameters **boldImage** (*path*) – path to the 4D nifti image. The file must have a BIDS like name (example: `key1_label1_key2-label2_suffic.nii`)

Output:

- tsnrImage: fullpath filename of the tSNR output image
- volTsnr: 3D volume of the tSNR image

Adapted from fmrwhy: https://github.com/jsheunis/fMRwhy/blob/master/fmrwhy/qc/fmrwhy_qc_calculateStats.m

Copyright 2019 Stephan Heunis

src.utils.**rmTrialTypeStr**(*cdtName*)
removes the leading "trial_type." prefix from a string

USAGE:

```
cdtName = rmTrialTypeStr(cdtName)
```

Parameters **cdtName** (*char*) – name of the condition

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src.utils.**setFields**(*structure*, *fieldsToSet*, *overwrite*)
Recursively loop through the fields of a target `structure` and sets the values as defined in the structure `fieldsToSet` if they don't exist.

Content of the target structure can be overwritten by setting the `overwrite```to ``true`.

USAGE:

```
structure = setFields(structure, fieldsToSet, overwrite = false)
```

Parameters

- **structure** –
- **fieldsToSet** (*string*) –
- **overwrite** (*boolean*) –

Returns

- **structure** (structure)

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src.utils.**validationInputFile**(*dir*, *fileNamePattern*, *prefix*)
Looks for file name pattern in a given directory and returns all the files that match that pattern but throws an error if it cannot find any.

A prefix can be added to the filename.

This function is mostly used that a file exists so that an error is thrown early when building a SPM job rather than at run time.

USAGE:

```
files = validationInputFile(dir, fileName, prefix)
```

Parameters

- **dir** (*string*) – Directory where the search will be conducted.
- **fileName** (*string*) – file name pattern. Can be a regular expression except for the starting `^` and ending `$`. For example: `'sub-.*_ses-.*_task-.*_bold.nii'`.
- **prefix** (*string*) – prefix to be added to the filename pattern. This can also be a regular expression (ish). For example ,f looking for the files that start with `c1` or `c2` or `c3`, the prefix can be `c[123]`.

Returns

files (string array) returns the fullpath file list of all the files matching the required pattern.

See also: spm_select

Example: % % tissueProbaMaps = validationInputFile(anatDataDir, anatImage, 'c[12]');

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7.3.4 Print and error handling

src.messages.**printToScreen**(*varargin*)

USAGE:

```
printToScreen(msg, opt, 'format', 'blue')
```

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src.messages.**errorHandling**(*varargin*)

USAGE:

```
errorHandling(functionName, id, msg, tolerant, verbose)
```

Parameters

- **functionName** (*string*) –
- **id** (*string*) – Error or warning id
- **msg** (*string*) – Message to print
- **tolerant** (*boolean*) – If set to `true` errors are converted into warnings
- **verbose** (*boolean*) – If set to `0` or `false` this will silence any warning

EXAMPLE:

```
msg = sprintf('this error happened with this file %s', filename)
id = 'thisError';
errorHandling(mfilename(), id, msg, true, opt.verbosity)
```

adapted from bids-matlab

(C) Copyright 2018 CPP_SPM developers

src.messages.**printWorkflowName**(*workflowName*, *opt*)

(C) Copyright 2019 CPP_SPM developers

src.messages.**printBatchName**(*batchName*, *opt*)

(C) Copyright 2019 CPP_SPM developers

src.messages.**printCredits**(*opt*)

TODO use the .CFF to load contributors

(C) Copyright 2019 CPP_SPM developers

src.messages.**printProcessingSubject**(*iSub*, *subLabel*, *opt*)

(C) Copyright 2019 CPP_SPM developers

7.3.5 Infrastructure related functions

src.infra.**checkDependencies**(*opt*)
Checks that that the right dependencies are installeda and loads the spm defaults.

USAGE:

```
checkDependencies()
```

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src.infra.**checkToolbox**(*varargin*)
Checks that a given SPM toolbox is installed. Possible to install it if necessary.

USAGE:

```
status = checkToolbox(toolboxName, 'verbose', false, 'install', false)
```

Parameters

- **toolboxName** (*string*) – obligatory argument
- **verbose** (*boolean*) – parameter
- **install** (*boolean*) – parameter

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src.infra.**getEnvInfo**(*opt*)
Gets information about the environement and operating system to help generate data descriptors for the derivatives.

USAGE:

```
[OS, generatedBy] = getEnvInfo()
```

Returns

OS (structure) (dimension)

generatedBy (structure) (dimension)

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src.infra.**getVersion**()
Reads the version number of the pipeline from the txt file in the root of the repository.

USAGE:

```
versionNumber = getVersion()
```

Returns

versionNumber (string) Use semantic versioning format (like v0.1.0)

(C) Copyright 2020 CPP_SPM developers

src.infra.**isOctave**()
Returns true if the environment is Octave.

USAGE:

```
retval = isOctave()
```

Returns

retval (boolean)

(C) Copyright 2020 Agah Karakuzu (C) Copyright 2020 CPP_SPM developers

src.infra.**setGraphicWindow**(*opt*)
Short description of what the function does goes here.

USAGE:

```
[interactiveWindow, graphWindow, cmdLine] = setGraphicWindow(opt)
```

Parameters **opt** (*structure*) –

Returns

- **interactiveWindow**
- **graphWindow**
- **cmdLine** (boolean)

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CHAPTER

EIGHT

PREPROCESSING

8.1 Preprocessing workflows

Note: The illustrations in this section mix what the files created by each workflow and the functions and are called by it. In this sense they are not pure DAGs (directed acyclic graphs) as the `*.m` files mentioned in them already exist.

8.1.1 Slice Time Correction

`src.workflows.preproc.`**`bidsSTC`**(*opt*)

Performs the slice timing correction of the functional data.

USAGE:

```
bidsSTC(opt)
```

Parameters **`opt`** (*`structure`*) – structure or json filename containing the options. See `checkOptions()` and `loadAndCheckOptions()`.

STC will be performed using the information provided in the BIDS data set. It will use the mid-volume acquisition time point as as reference.

In general slice order and reference slice is entered in time unit (ms) (this is the BIDS way of doing things) instead of the slice index of the reference slice (the "SPM" way of doing things).

If no slice timing information is available from the file metadata this step will be skipped.

See also: setBatchSTC, getAndCheckSliceOrder

See the documentation for more information about slice timing correction.

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More info available on this page of the SPM wikibook.

Some comments from here on STC, when it should be applied

At what point in the processing stream should you use it?

This is the great open question about slice timing, and it's not super-answerable. Both SPM and AFNI recommend you do it before doing realignment/motion correction, but it's not entirely clear why. The issue is this:

If you do slice timing correction before realignment, you might look down your non-realigned time course for a given voxel on the border of gray matter and CSF, say, and see one TR where the head moved and the voxel sampled from CSF instead of gray. This would results in an interpolation error for that voxel, as it would attempt to interpolate

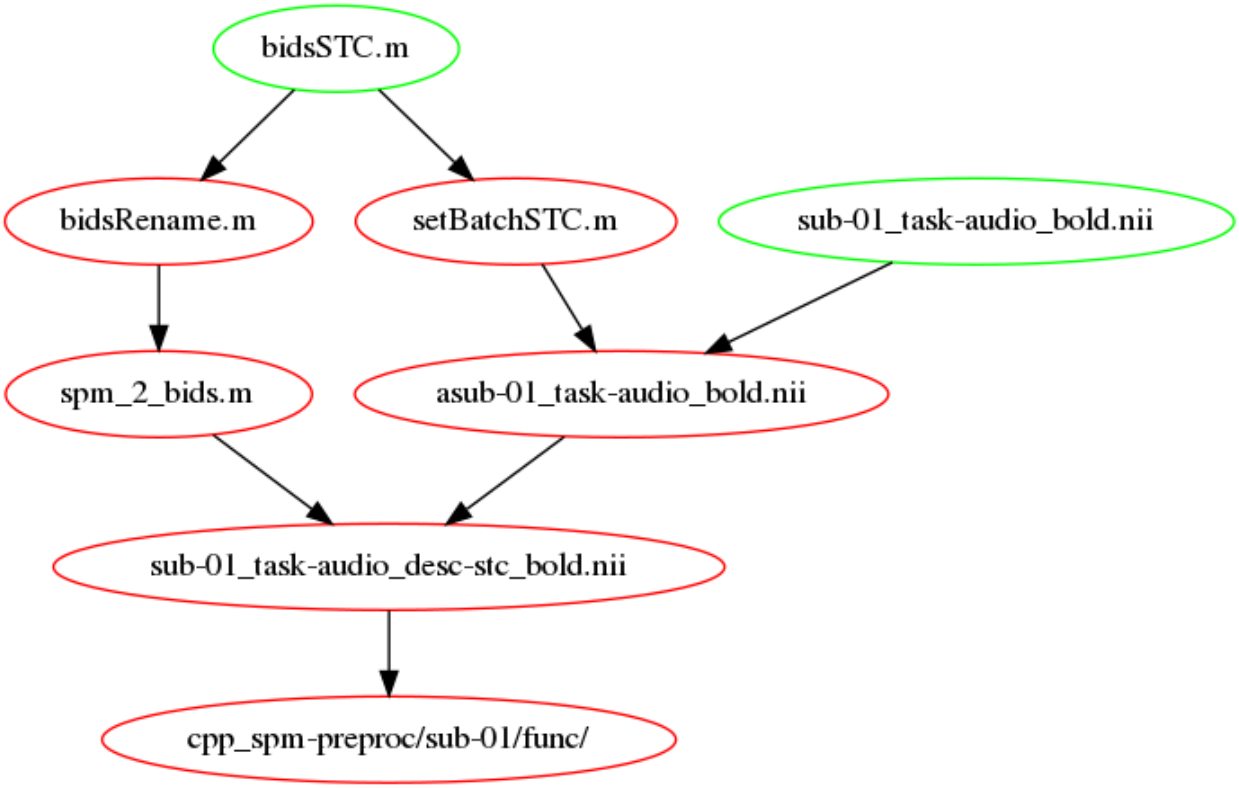

Fig. 1: Slice timing correction workflow

part of that big giant signal into the previous voxel. On the other hand, if you do realignment before slice timing correction, you might shift a voxel or a set of voxels onto a different slice, and then you'd apply the wrong amount of slice timing correction to them when you corrected - you'd be shifting the signal as if it had come from slice 20, say, when it actually came from slice 19, and shouldn't be shifted as much.

There's no way to avoid all the error (short of doing a four-dimensional realignment process combining spatial and temporal correction - Remi's note: fMRIprep does it), but I believe the current thinking is that doing slice timing first minimizes your possible error. The set of voxels subject to such an interpolation error is small, and the interpolation into another TR will also be small and will only affect a few TRs in the time course. By contrast, if one realigns first, many voxels in a slice could be affected at once, and their whole time courses will be affected. I think that's why it makes sense to do slice timing first. That said, here's some articles from the SPM e-mail list that comment helpfully on this subject both ways, and there are even more if you do a search for "slice timing AND before" in the archives of the list.

8.1.2 Spatial Preprocessing

Perform spatial preprocessing by running `bidsSpatialPrepro`

`src.workflows.preproc.`**`bidsSpatialPrepro`**`(`*`opt`*`)`

Performs spatial preprocessing of the functional and anatomical data.

USAGE:

```
bidsSpatialPrepro([opt])
```

Parameters **`opt`** (*`structure`*) – structure or json filename containing the options. See

checkOptions() and loadAndCheckOptions().

The anatomical data are segmented, skull-stripped [and normalized to MNI space].

The functional data are re-aligned (unwarped), coregistered with the anatomical, [and normalized to MNI space].

Assumes that bidsSTC() has already been run if opt.stc.skip is not set to true.

If you want to:

- only do realign and not realign AND unwarp, make sure you set opt.realign.useUnwarp to false.
- normalize the data to MNI space, make sure opt.space includes IXI549Space.

See the *Preprocessing* section of the FAQ to know at what resolution files are resampled during normalization.

If you want to:

- use another type of anatomical data than T1w as a reference or want to specify which anatomical session is to be used as a reference, you can set this in opt.bidsFilterFiler.t1w:

```
opt.bidsFilterFiler.t1w.suffix = 'T1w';
opt.bidsFilterFiler.t1w.ses = 1;
```


The figures below show the bidsSpatialPrepro workflow as it would run using realign and unwarp (default) and with normalization to SPM MNI space (IXI549Space).

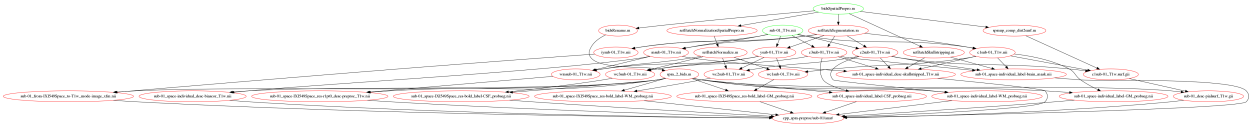

Fig. 2: Anatomical component of the spatial preprocessing workflow

Fig. 3: Functional component of the spatial preprocessing workflow

src.workflows.preproc.**bidsRealignReslice**(*opt*)

Realigns and reslices the functional data of a given task.

USAGE:

```
bidsRealignReslice(opt)
```

Parameters **opt** (*structure*) – structure or json filename containing the options. See checkOptions() and loadAndCheckOptions().

Assumes that bidsSTC() has already been run if opt.stc.skip is not set to true.

src.workflows.preproc.**bidsRealignUnwarp**(*opt*)
Realigns and unwarps the functional data of a given task.

USAGE:

```
bidsRealignReslice(opt)
```

Parameters **opt** (*structure*) – structure or json filename containing the options. See checkOptions() and loadAndCheckOptions().

Assumes that bidsSTC has already been run.

If the bidsCreateVDM() workflow has been run before the voxel displacement maps will be used unless opt.useFieldmaps is set to false.

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8.1.3 Smoothing

Perform smoothing of the functional data by running bidsSmoothing

src.workflows.preproc.**bidsSmoothing**(*opt*)
This performs smoothing to the functional data using a full width half maximum smoothing kernel of size "mm_smoothing".

USAGE:

```
bidsSmoothing(opt)
```

Parameters **opt** (*structure*) – structure or json filename containing the options. See checkOptions() and loadAndCheckOptions().

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8.1.4 Others

src.workflows.preproc.**bidsResliceTpmToFunc**(*opt*)
Reslices the tissue probability map (TPMs) from the segmentation to the mean functional and creates a mask for the bold mean image

USAGE:

```
bidsResliceTpmToFunc(opt)
```

Parameters **opt** (*structure*) – structure or json filename containing the options. See checkOptions() and loadAndCheckOptions().

Assumes that the anatomical has already been segmented by bidsSpatialPrepro() or bidsSegmentSkullStrip().

It is necessary to run this workflow before running the functionalQA pipeline as the computation of the tSNR by spmup requires the TPMs to have the same dimension as the functional.

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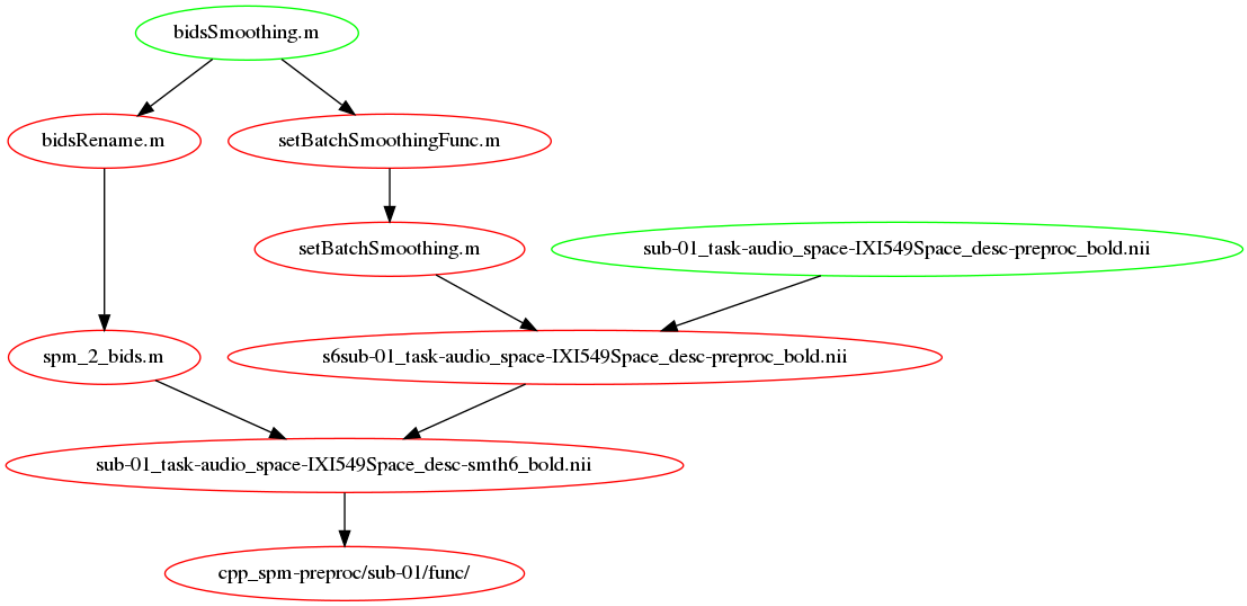

Fig. 4: Smoothing workflow

`src.workflows.preproc.`**`bidsSegmentSkullStrip`**`(`*`opt`*`)`

Segments and skullstrips the anatomical image. This workflow is already included in the bidsSpatialPrepro workflow.

USAGE:

```
bidsSegmentSkullStrip(opt)
```

Parameters **`opt`** (*`structure`*) – structure or json filename containing the options. See `checkOptions()` and `loadAndCheckOptions()`.

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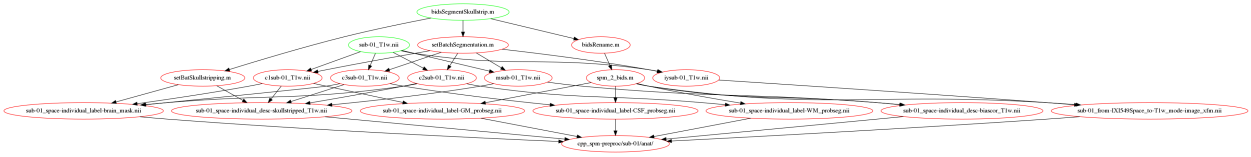

Fig. 5: Segment and skullstrip workflow

`src.workflows.preproc.`**`bidsWholeBrainFuncMask`**`(`*`opt`*`)`

Create segmented-skull stripped mean functional image

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8.2 Preprocessing batches

8.2.1 Slice Time Correction

src.batches.preproc.**setBatchSTC**(*varargin*)

Creates batch for slice timing correction

USAGE:

```
matlabbatch = setBatchSTC(matlabbatch, BIDS, opt, subLabel)
```

Parameters

- **BIDS** (*structure*) – BIDS layout returned by `getData`.
- **opt** (*structure*) – structure or json filename containing the options. See `checkOptions()` and `loadAndCheckOptions()`.
- **subLabel** (*string*) – subject label

Returns

- **matlabbatch** (structure) The matlabbatch ready to run the spm job

Slice timing units is in seconds to be BIDS compliant and not in slice number as is more traditionally the case with SPM.

If no slice order can be found, the slice timing correction will not be performed.

If not specified this function will take the mid-volume time point as reference to do the slice timing correction.

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8.2.2 Spatial Preprocessing

src.batches.preproc.**setBatchRealign**(*varargin*)

Set the batch for realign / realign and reslice / realign and unwarp

USAGE:

```
[matlabbatch, voxDim] = setBatchRealign(matlabbatch, ...
                                        BIDS, ...
                                        opt, ...
                                        subLabel, ...
                                        [action = 'realign'])
```

Parameters

- **matlabbatch** (*cell*) – SPM batch
- **BIDS** (*structure*) – BIDS layout returned by `getData`.
- **opt** (*structure*) – Options chosen for the analysis. See `checkOptions()`.
- **subLabel** (*string*) – subject label
- **action** (*string*) – `realign`, `realignReslice`, `realignUnwarp`, `'reslice'`

Returns

- **matlabbatch** (structure) (dimension)

- **voxDim** (array) (dimension)

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src.batches.preproc.**setBatchReslice**(*matlabbatch*, *opt*, *referenceImg*, *sourceImages*, *interp*)
Set the batch for reslicing source images to the reference image resolution

USAGE:

```
matlabbatch = setBatchReslice(matlabbatch, opt, referenceImg, sourceImages,␣
↪interp)
```

Parameters

- **matlabbatch** (*structure*) – list of SPM batches
- **opt** (*structure*) –
- **referenceImg** (*string or cellstring*) – Reference image (only one image)
- **sourceImages** (*string or cellstring*) – Source images
- **interp** (*integer >= 0*) – type of interpolation to use (default = 4). Nearest neighbour = 0.

Returns

- **matlabbatch** (structure) The matlabbatch ready to run the spm job

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src.batches.preproc.**setBatchSegmentation**(*matlabbatch*, *opt*, *imageToSegment*)
Creates a batch to segment the anatomical image

USAGE:

```
matlabbatch = setBatchSegmentation(matlabbatch, opt)
```

Parameters

- **matlabbatch** (*structure*) – list of SPM batches
- **opt** (*structure*) – structure or json filename containing the options. See `checkOptions()` and `loadAndCheckOptions()`.

Returns

matlabbatch (structure)

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src.batches.preproc.**setBatchSkullStripping**(*matlabbatch*, *BIDS*, *opt*, *subLabel*)
Creates a batch to compute a brain mask based on the tissue probability maps from the segmentation.

USAGE:

```
matlabbatch = setBatchSkullStripping(matlabbatch, BIDS, opt, subLabel)
```

Parameters

- **matlabbatch** (*structure*) – list of SPM batches

- **BIDS** (*structure*) – BIDS layout returned by `getData`.
- **opt** (*structure*) – structure or json filename containing the options. See `checkOptions()` and `loadAndCheckOptions()`.
- **subLabel** (*string*) – subject label

Returns

- **matlabbatch** (structure) The matlabbatch ready to run the spm job

This function will get its inputs from the segmentation batch by reading the dependency from `opt.orderBatches.segment`. If this field is not specified it will try to get the results from the segmentation by relying on the `anat` image returned by `getAnatFilename`.

The threshold for inclusion in the mask can be set by:

```
opt.skullstrip.threshold (default = 0.75)
```

Any voxel with p(grayMatter) + p(whiteMatter) + p(CSF) > threshold will be included in the skull stripping mask.

It is also possible to segment a functional image by setting `opt.skullstrip.mean` to `true`

Skullstripping can be skipped by setting `opt.skullstrip.do` to `false`

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`src.batches.preproc.`**setBatchNormalize**(*matlabbatch*, *deformField*, *voxDim*, *imgToResample*)

Short description of what the function does goes here.

USAGE:

```
matlabbatch = setBatchNormalize(matlabbatch [, deformField] [, voxDim] [,␣
↪imgToResample])
```

Parameters

- **matlabbatch** (*structure*) –
- **deformField** –
- **voxDim** –
- **voxDim** –
- **imgToResample** –
- **imgToResample** –

Returns

- **matlabbatch** (structure)

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`src.batches.preproc.`**setBatchNormalizationSpatialPrepro**(*matlabbatch*, *BIDS*, *opt*, *voxDim*)

Short description of what the function does goes here.

USAGE:

```
matlabbatch = setBatchNormalizationSpatialPrepro(matlabbatch, opt, voxDim)
```

Parameters

- **matlabbatch** (*structure*) –
- **opt** (*array*) –
- **voxDim** –

Returns

- **matlabbatch** (structure)

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src.batches.preproc.**setBatchCoregistrationFuncToAnat**(*matlabbatch*, *BIDS*, *opt*, *subLabel*)

Set the batch for coregistering the functional images to the anatomical image.

USAGE:

```
matlabbatch = setBatchCoregistrationFuncToAnat(matlabbatch, BIDS, subLabel, opt)
```

Parameters

- **matlabbatch** (*structure*) – list of SPM batches
- **BIDS** (*structure*) – BIDS layout returned by `getData`.
- **opt** (*structure*) – structure or json filename containing the options. See `checkOptions()` and `loadAndCheckOptions()`.
- **subLabel** (*string*) – subject label

Returns

- **matlabbatch** (structure) The matlabbatch ready to run the spm job

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src.batches.preproc.**setBatchCoregistration**(*varargin*)

Set the batch for coregistering the source images into the reference image

USAGE:

```
matlabbatch = setBatchCoregistration(matlabbatch, opt, ref, src, other)
```

Parameters

- **matlabbatch** (*structure*) – list of SPM batches
- **opt** (*cell string*) – Other images to apply the coregistration to
- **ref** (*string*) – Reference image
- **src** (*string*) – Source image
- **other** (*cell string*) – Other images to apply the coregistration to

Returns

- **matlabbatch** (structure) The matlabbatch ready to run the spm job

EXAMPLE:

```
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```

src.batches.preproc.**setBatchSaveCoregistrationMatrix**(*matlabbatch*, *BIDS*, *opt*, *subLabel*)

Short description of what the function does goes here.

USAGE:

```
matlabbatch = setBatchSaveCoregistrationMatrix(matlabbatch, BIDS, opt, subLabel)
```

Parameters

- **matlabbatch** (*structure*) –
- **BIDS** (*structure*) – BIDS layout returned by `getData`.
- **opt** (Options chosen for the analysis. See `checkOptions()`.) –
- **subLabel** (*string*) –

Returns

- **matlabbatch**

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8.2.3 Smoothing

src.batches.preproc.**setBatchSmoothConImages**(*matlabbatch*, *opt*)

Creates a batch to smooth all the con images of all subjects

USAGE:

```
matlabbatch = setBatchSmoothConImages(matlabbatch, group, opt)
```

Parameters

- **matlabbatch** –
- **group** –
- **opt** – Options chosen for the analysis. See `checkOptions()`.

Returns

- **matlabbatch**

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src.batches.preproc.**setBatchSmoothingFunc**(*matlabbatch*, *BIDS*, *opt*, *subLabel*)

Short description of what the function does goes here.

USAGE:

```
matlabbatch = setBatchSmoothingFunc(matlabbatch, BIDS, opt, subLabel)
```

Parameters

- **matlabbatch** (*structure*) –

- **BIDS** (*structure*) – BIDS layout returned by `getData`.
- **opt** (*string*) – Options chosen for the analysis. See `checkOptions()`.
- **subLabel** –

Returns

- **matlabbatch** (structure)

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`src.batches.preproc.`**setBatchSmoothing**(*matlabbatch*, *opt*, *images*, *fwhm*, *prefix*)

Small wrapper to create smoothing batch

USAGE:

```
matlabbatch = setBatchSmoothing(matlabbatch, images, fwhm, prefix)
```

Parameters

- **matlabbatch** (*structure*) –
- **images** –
- **fwhm** –
- **prefix** –

Returns

- **matlabbatch** (structure)

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CHAPTER

NINE

FIELDMAPS

In a nutshell, the information we need to create a VDM in SPM (see `calculate VDM` module in SPM batch):

- `blip direction`
- `echo time`
- `total EPI readout time`

Inferring `blip direction` and `echo time` from a dataset that has sufficient metadata is usually simple.

But `total EPI readout time` is not mentioned, so it has to be computed from the information we have, it is not entirely clear how (see the comments with a lot of `???` in `getTotalReadoutTime`).

Things that are yet unclear:

- is it actually possible to compute total EPI readout time that SPM needs from the info in a typical dataset with fieldmaps like `openneuro/ds001168`?
- If it is not then that is an issue because it means some BIDS dataset are not usable with SPM.

Things to keep an eye on: the code from this repo from the fMRIprep team could have answers for us.

`src.workflows.preproc.`**`bidsCreateVDM`**(*opt*)

Creates the voxel displacement maps from the fieldmaps of a BIDS dataset.

USAGE:

```
bidsCreateVDM(opt)
```

Parameters **`opt`** (*`structure`*) – structure or json filename containing the options. See `checkOptions()` and `loadAndCheckOptions()`.

Inspired from spmup `spmup_BIDS_preprocess` (@ commit 198c980d6d7520b1a99) (URL missing)

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`src.batches.preproc.`**`setBatchCoregistrationFmap`**(*matlabbatch*, *BIDS*, *opt*, *subLabel*)

Set the batch for the coregistration of field maps

USAGE:

```
matlabbatch = setBatchCoregistrationFmap(matlabbatch, BIDS, opt, subLabel)
```

Parameters

- **`BIDS`** (*`structure`*) – BIDS layout returned by `getData`.
- **`opt`** (*`structure`*) – structure or json filename containing the options. See `checkOptions()` and `loadAndCheckOptions()`.

- **subLabel** (*string*) –

Returns

- **matlabbatch** (structure) The matlabbatch ready to run the spm job

TODO implement for 'phase12', 'fieldmap', 'epi'

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src.batches.preproc.**setBatchCreateVDMs**(*matlabbatch*, *BIDS*, *opt*, *subLabel*)
Short description of what the function does goes here.

USAGE:

```
matlabbatch = setBatchCreateVDMs(matlabbatch, BIDS, opt, subLabel)
```

Parameters

- **matlabbatch** (*structure*) –
- **BIDS** (*structure*) – BIDS layout returned by `getData`.
- **opt** (*structure*) – structure or json filename containing the options. See `checkOptions()` and `loadAndCheckOptions()`.
- **subLabel** (*string*) – subject label

Returns

- **matlabbatch** (structure) The matlabbatch ready to run the spm job

TODO implement for 'phase12', 'fieldmap', 'epi'

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src.batches.preproc.**setBatchComputeVDM**(*matlabbatch*, *fmapType*, *refImage*)
Short description of what the function does goes here.

USAGE:

```
matlabbatch = setBatchComputeVDM(matlabbatch, fmapType, refImage)
```

Parameters

- **matlabbatch** (*structure*) – list of SPM batches
- **fmapType** –
- **refImage** – Reference image

Returns

- **matlabbatch** (structure) The matlabbatch ready to run the spm job

matlabbatch = setBatchComputeVDM(type)

adapted from spmup get_FM_workflow.m (@ commit 198c980d6d7520b1a996f0e56269e2ceab72cc83)

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src.fieldmaps.**getBlipDirection**(*metadata*)
Gets the total read out time of a sequence.

USAGE:

```
blipDir = getBlipDirection(metadata)
```

Parameters **metadata** (*strcuture*) – image metadata

Returns

- **blipDir**

Used to create the voxel dsiplacement map (VDM) from the fieldmap

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src.fieldmaps.**getMetadataFromIntendedForFunc**(*BIDS*, *fmapMetadata*)
Gets metadata of the associated bold file: - finds the bold file a fmap is intended for, - parse its filename, - get its metadata.

USAGE:

```
[totalReadoutTime, blipDir] = getMetadataFromIntendedForFunc(BIDS, fmapMetadata)
```

Parameters

- **BIDS** (*structure*) – BIDS layout returned by `getData()`.
- **fmapMetadata** (*structure*) –

Returns

totalReadoutTime (type) (dimension)

blipDir (type) (dimension)

At the moment the VDM is created based on the characteristics of the last func file in the IntendedFor field

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src.fieldmaps.**getTotalReadoutTime**(*metadata*)
Gets the total read out time of a sequence. Used to create the voxel dsiplacement map (VDM) from the fieldmap

USAGE:

```
totalReadoutTime = getTotalReadoutTime(metadata)
```

Parameters **metadata** (*strcuture*) – image metadata

Returns

- **totalReadoutTime** (float) in millisecond

Currently this relies on the user adding extra metadata in the json of the functional files as the metadata queried are not "official" BIDS metadata but can usuall be found in the DICOM headers (for example: `PixelBandwidth`)

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src.fieldmaps.**getVdmFile**(*BIDS*, *opt*, *boldFilename*)
returns the voxel displacement map associated with a given bold file

USAGE:

```
vdmFile = getVdmFile(BIDS, opt, boldFilename)
```

Parameters

- **BIDS** (*structure*) –
- **opt** (*string*) – Options chosen for the analysis. See `checkOptions()`.
- **boldFilename** –

Returns

- **vdmFile** (string)

CHAPTER

TEN

STATISTICS

10.1 Statistics workflows

Note: The illustrations in this section mix what the files created by each workflow and the functions and are called by it. In this sense they are not pure DAGs (directed acyclic graphs) as the `*.m` files mentioned in them already exist.

10.1.1 Subject level

`src.workflows.stats.`**`bidsFFX`**(*varargin*)

- specify the subject level fMRI model
- estimates it
- do both in one go
- or compute the contrasts

To run this workflows get the BOLD input images from derivatives BIDS dataset that contains the preprocessed data and get the condition, onsets, durations from the events files in the raw BIDS dataset.

For the model specification, if `opt.model.designOnly` is set to `true`, then it is possible to specify a model with no data: this can useful for debugging or to quickly inspect designs specification.

For the model estimation, it is possible to do some rough QA, by setting `opt.QA.glm.do = true`.

USAGE:

```
bidsFFX(action, opt, 'nodeName', 'run_level')
```

Parameters **`action`** (*`char`*) – Action to be conducted

- `'specify'` to specify the fMRI GLM
- `'specifyAndEstimate'` for fMRI design + estimate
- `'contrasts'` to estimate contrasts.

Parameters

- **`opt`** (*`structure`*) – structure or json filename containing the options. See `checkOptions()` and `loadAndCheckOptions()`.
- **`nodeName`** (*`char`*) – Only for action `'contrasts'`. Specifies which Node to work on.

See also: setBatchSubjectLevelGLMSpec, setBatchSubjectLevelContrasts

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After the specification step an output folder is created. To get the fullpath of that folder you can use:

```
getFFXdir(subLabel, opt)
```

A typical folder will contain:

```
cpp_spm-stats/sub-01/stats/task-audio_space-IXI549Space_FWHM-6
├── SPM.mat
├── sub-01_task-audio_space-IXI549Space_desc-beforeEstimation_designmatrix.png
├── sub-01_task-audio_run-01_desc-confounds_regressors.mat
├── sub-01_task-audio_run-01_desc-confounds_regressors.tsv
├── sub-01_task-audio_run-01_onsets.mat
└── sub-01_task-audio_run-01_onsets.tsv
```

Each run should have a pair of tsv/mat files:

- One that summarises the onsets used for that design.
- One that summarises the regressors confounds used for that design.

In most cases those are going to be a subset of the content:

- of the `_events.tsv` from the raw BIDS dataset
- of the `_regressors.tsv` from the deriratives BIDS dataset containing the preprocessed data.

What part of the _events.tsv and _regressors.tsv gets into the final GLM specification depends on the BIDS statistical model used.

The mat files can directly be ingested by SPM: the TSV files are there for both logging and interoperability.

Fig. 1: Subject level GLM specification workflow for model specification

`src.workflows.stats.`**`bidsConcatBetaTmaps`**(*opt*, *deleteIndBeta*, *deleteIndTmaps*)

Make 4D images of beta and t-maps for the MVPA.

USAGE:

```
concatBetaImgTmaps(opt, [deleteIndBeta = true,] [deleteIndTmaps = true])
```

Parameters

- **opt** (*structure*) – options structure
- **deleteIndBeta** (*(boolean)*) – decide to delete beta-maps
- **deleteIndTmaps** (*(boolean)*) – decide to delete t-maps

A valid BIDS stats model is required for this workflow: this is because the beta images to concatenate are those of the conditions mentioned in the `DummyContrasts` of the RUN level of the BIDS stats model.

When concatenating betamaps:

- Ensures that there is only 1 image per "contrast".
- Creates a tsv that lists the content of the 4D image.
- This TSV is in the subject level GLM folder where the beta map came from.
- This TSV file is named `sub-subLabel_task-taskName_space-space_labelfold.tsv`.

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10.1.2 Group level

`src.workflows.stats.`**bidsRFX**(*varargin*)

- smooths all contrast images created at the subject level

OR

- creates a mean structural image and mean mask over the sample

OR

- specifies and estimates the group level model,
- computes the group level contrasts.

USAGE:

```
bidsRFX(action, opt)
```

Parameters

- **action** (*string*) – Action to be conducted: `'smoothContrasts'` or `'RFX'` or `'meanAnatAndMask'` or `'contrast'`
- **opt** (*structure*) – structure or json filename containing the options. See `checkOptions()` and `loadAndCheckOptions()`.
- **nodeName** (*char*) – name of the BIDS stats model to run analysis on

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10.1.3 Compute results

src.workflows.stats.**bidsResults**(*opt*)

Computes the results for a series of contrast that can be specified at the run, subject or dataset step level (see contrast specification following the BIDS stats model specification).

USAGE:

```
bidsResults(opt)
```

Parameters **opt** (*structure*) – structure or json filename containing the options. See `checkOptions()` and `loadAndCheckOptions()`.

See also: setBatchSubjectLevelResults, setBatchGroupLevelResults

Below is an example of how specify the option structure to getsome speific results outputs for certain contrasts.

See the online documentation for example of those outputs.

The field `opt.results` allows you to get results from several Nodes from the BIDS stats model. So you could run `bidsResults` once to view results from the subject and the dataset level.

Specify a default structure result for this node:

```
opt.results(1) = returnDefaultResultsStructure();
```

Specify the Node name (usually "run_level", "subject_levle" or "dataset_level"):

```
opt.results(1).nodeName = 'subject_level';
```

Specify the name of the contrast whose resul we want to see. This must match one of the existing contrats (dummy contrast or contrast) in the BIDS stats model for that Node:

```
opt.results(1).name = 'listening_1';
```

For each contrat, you can adapt:

- voxel level threshold (`p`) [between 0 and 1]
- cluster level threshold (`k`) [positive integer]
- type of multiple comparison (`MC`):
  - `'FWE'` is the defaut
  - `'FDR'`
  - `'none'`

You can thus specify something different for a second contrast:

```
opt.results(2).name = {'listening_lt_baseline'};
opt.results(2).MC =  'none';
opt.results(2).p = 0.01;
opt.results(2).k = 0;
```

Specify how you want your output (all the following are on `false` by default):

```
% simple figure with glass brain view and result table
opt.results(1).png = true();

% result table as a .csv: very convenient when comes the time to write papers
opt.results(1).csv = true();

% thresholded statistical map
opt.results(1).threshSpm = true();

% binarised thresholded statistical map (useful to create ROIs)
opt.results(1).binary = true();
```

You can also create a montage to view the results on several slices at once:

```
opt.results(1).montage.do = true();

% slices position in mm [a scalar or a vector]
opt.results(1).montage.slices = -0:2:16;

% slices orientation: can be 'axial' 'sagittal' or 'coronal'
% axial is default
opt.results(1).montage.orientation = 'axial';

% path to the image to use as underlay
% Will use the SPM MNI T1 template by default
opt.results(1).montage.background = ...
     fullfile(spm('dir'), 'canonical', 'avg152T1.nii');
```

Finally you can export as a NIDM results zip files.

NIDM results is a standardized results format that is readable by the main neuroimaging softwares (SPM, FSL, AFNI). Think of NIDM as BIDS for your statistical maps. One of the main other advantage is that it makes it VERY easy to share your group results on neurovault (which you should systematically do).

- NIDM paper
- NIDM specification
- *NIDM results viewer for SPM <https://github.com/incf-nidash/nidmresults-spmhtml>*

To generate NIDM results zip file for a given contrats simply:

```
opt.results(1).nidm = true();
```

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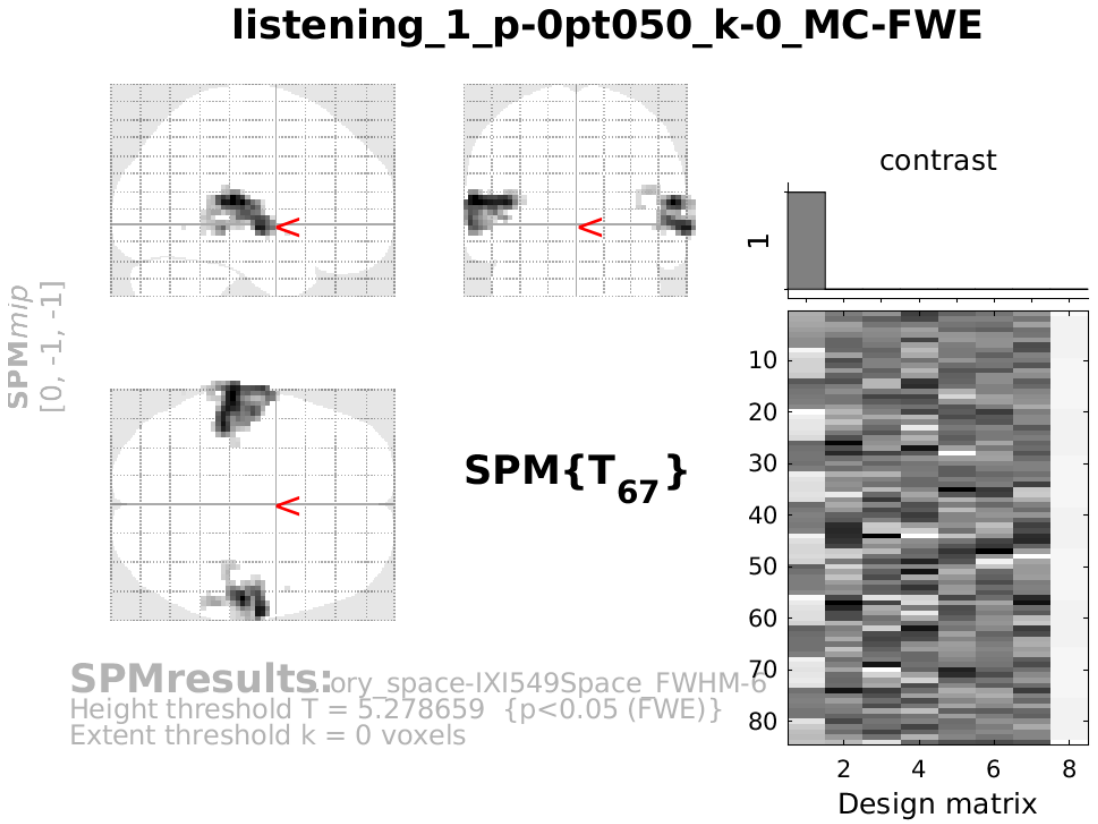
`CSV output example`

CPP SPM also includes the `slice_display` code that allows you to plot on the same figure:

- beta values
- t values
- cluster boundaries
- ROI boundaries

An example of how to use it is available in the `moae_04_slice_display.m` script in the MoAE demo.



Statistics: ***p-values adjusted for search volume***

set-level		cluster-level				peak-level					mm mm mm		
p	c	$p_{FWE-corr}$	$q_{FDR-corr}$	k_E	p_{uncorr}	$p_{FWE-corr}$	$q_{FDR-corr}$	T	(Z_E)	p_{uncorr}			
0.000	5	0.000	0.000	399	0.000	0.000	0.000	12.16	Inf	0.000	-63	-28	11
						0.000	0.000	11.33	Inf	0.000	-45	-34	11
						0.000	0.000	10.12	7.84	0.000	-66	-10	-1
		0.000	0.000	214	0.000	0.000	0.000	12.10	Inf	0.000	57	-22	11
						0.000	0.000	11.29	Inf	0.000	66	-13	-4
						0.000	0.003	7.07	6.09	0.000	60	-37	5
		0.001	0.020	5	0.012	0.006	0.200	5.81	5.21	0.000	69	-25	-4
		0.015	0.221	1	0.221	0.039	0.851	5.35	4.86	0.000	51	5	-7
		0.015	0.221	1	0.221	0.050	0.998	5.28	4.81	0.000	-63	-58	-4

table shows 3 local maxima more than 8.0mm apart

Height threshold: T = 5.28, p = 0.000 (0.050) Degrees of freedom = [1.0, 67.0]
Extent threshold: k = 0 voxels FWHM = 9.9 9.9 8.3 mm mm mm; 3.3 3.3 2.8 {voxels
Expected voxels per cluster, <k> = 0.715 Volume: 1784484 = 66092 voxels = 1953.4 resels
Expected number of clusters, <c> = 0.07 Voxel size: 3.0 3.0 3.0 mm mm mm; (resel = 30.35 vo
FWEp: 5.279, FDRp: 6.440, FWEc: 1, FDRc: 5

Fig. 2: Example of subject level results from the MoAE demo

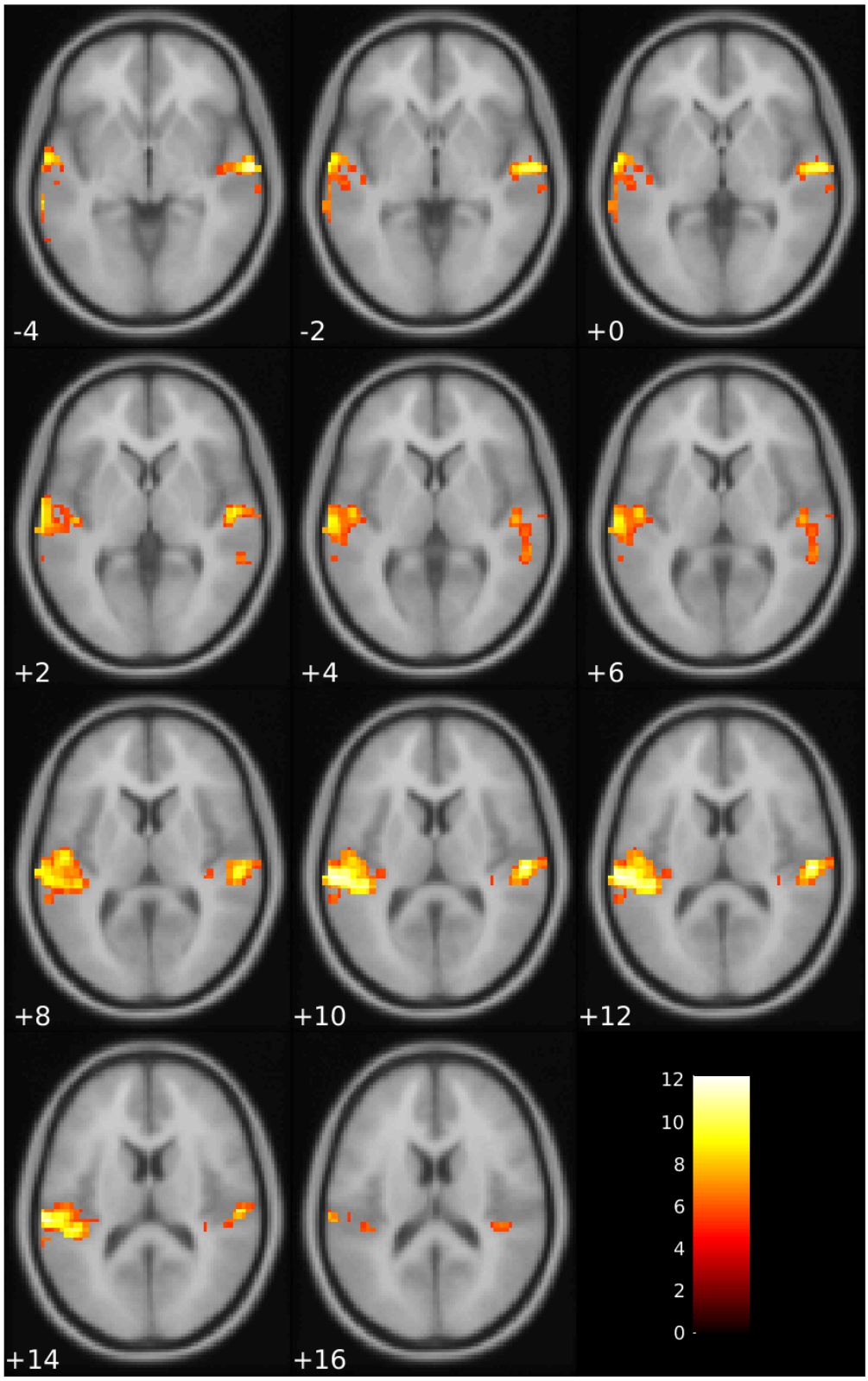


Fig. 3: Example of subject level montage from the MoAE demo

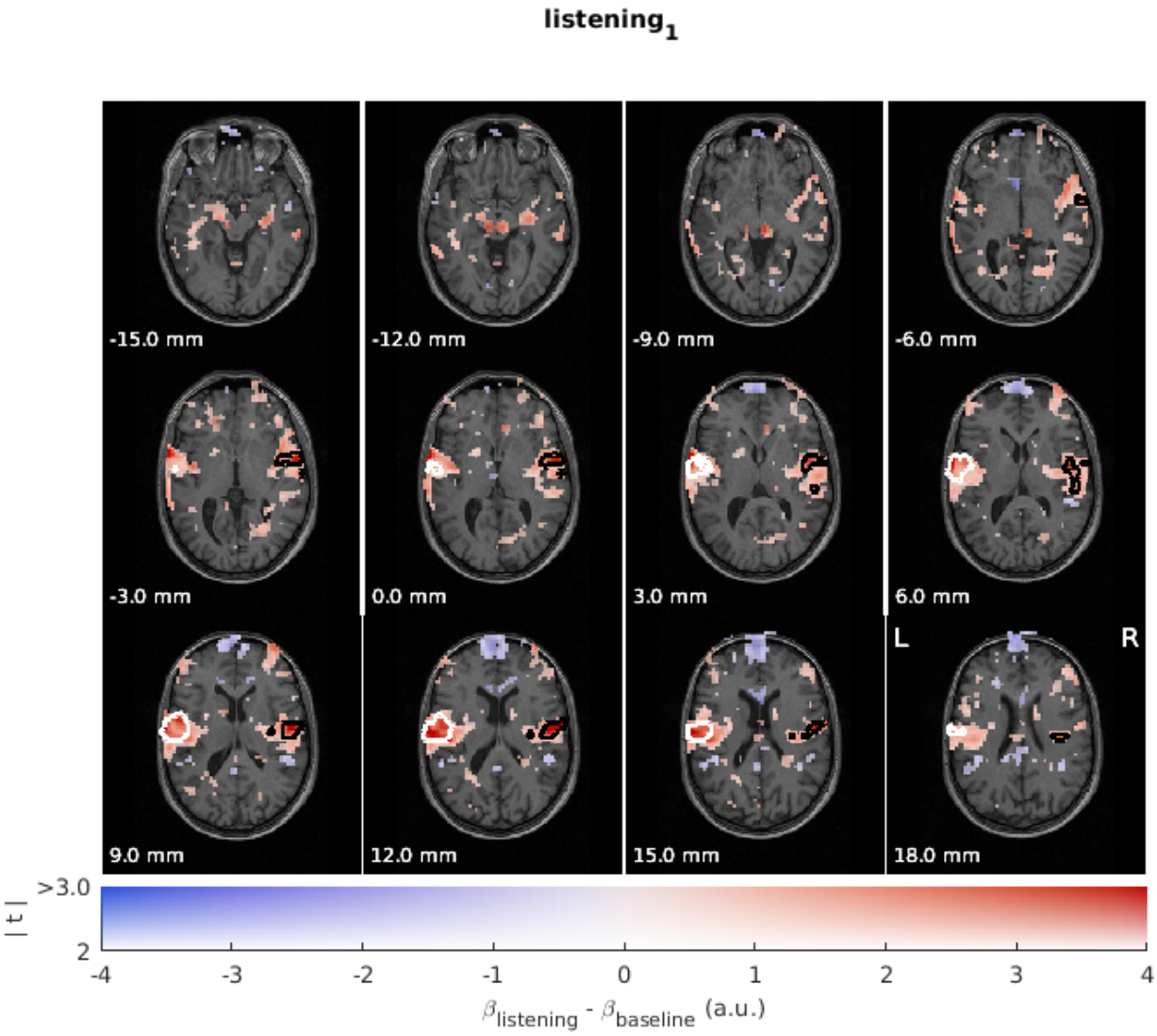


Fig. 4: Example of subject level slice display from the MoAE demo

10.1.4 Model selection

src.workflows.stats.**bidsModelSelection**(*varargin*)

Uses the MACS toolbox to perform model selection.

USAGE:

```
bidsModelSelection(opt, 'action', 'all')
```

Parameters

- **opt** (*structure*) – structure or json filename containing the options. See `checkOptions()` and `loadAndCheckOptions()`.
- **action** (*string*) – any of `'all'`, `'modelSpace'`, `'cvLME'`, `'posterior'`, `'BMS'`

Steps are performed in that order:

1. MA_model_space: defines a model space
2. MA_cvLME_auto: computes cross-validated log model evidence
3. MS_PPs_group_auto: calculate posterior probabilities from cvLMEs
4. MS_BMS_group_auto: perform cross-validated Bayesian model selection
5. MS_SMM_BMS: generate selected models maps from BMS

- `'all'` : performs 1 to 5
- `'modelSpace'`: : performs step 1
- `'cvLME'`: performs steps 1 and 2
- `'posterior'`: performs steps 1 and 3, assuming step 2 has already been run
- `'BMS'`: performs 1, 4 and 5, assuming step 2 and 3 have already been run

This way you can run all steps at once:

```
bidsModelSelection(opt, 'action', 'all');
```

Or in sequence (can be useful to split running cvLME in several batches of subjects)

bidsModelSelection(opt, 'action', 'cvLME'); bidsModelSelection(opt, 'action', 'posterior'); bidsModelSelection(opt, 'action', 'BMS');

Requirements:

- define the list of BIDS stats models in a cell string of fullpaths

```
opt.toolbox.MACS.model.files
```

- all models must have the same `space` and `task` defined in their inputs
- for a given subject / model, all runs must have the same numbers of regressors This requires to create dummy regressors in case some subjects are missing a condition or a confound. This can be done by using the *bidsFFX(opt)* with the option *opt.glm.useDummyRegressor* set to *true*.

Note: Adding dummy (empty) regressors will make your model non-estimable by SPM, where as the MACS toolbox can deal with this.

- specify each model for each subject:

```
opt = opt_stats_subject_level();

opt.glm.useDummyRegressor = true;

models = opt.toolbox.MACS.model.files

for i = 1:numel(models)
  opt.model.file = models{i};
  bidsFFX('specify', opt);
end
```

For more information see the toolbox manual in the folder `lib/MACS/MACS_Manual`.

Links:

- MACS toolbox repo

If you use this workflow, please cite the following paper:

```
@article{soch2018jnm,
  title={MACS - a new SPM toolbox for model assessment, comparison and selection.}
↪,
  author={Soch J, Allefeld C},
  journal={Journal of Neuroscience Methods},
  year={2018},
  volume={306},
  doi={https://doi.org/10.1016/j.jneumeth.2018.05.017}
}
```

If you use cvBMS or cvBMA, please also cite the respective method:

```
@article{soch2016nimg,
  title={How to avoid mismodelling in GLM-based fMRI data analysis:
         cross-validated Bayesian model selection.},
  author={Soch J, Haynes JD, Allefeld C},
  journal={NeuroImage},
  year={2016},
  volume={141},
  doi={https://doi.org/10.1016/j.neuroimage.2016.07.047}
}

@article{soch2017nimg,
  title={How to improve parameter estimates in GLM-based fMRI data analysis:
         cross-validated Bayesian model averaging.},
  author={Soch J, Meyer AP, Haynes JD, Allefeld C},
  journal={NeuroImage},
  year={2017},
  volume={158},
  doi={https://doi.org/10.1016/j.neuroimage.2017.06.056}
}
```

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10.1.5 Region of interest analysis

src.workflows.roi.**bidsCreateROI**(*opt*)

Use CPP_ROI and marsbar to create a ROI in MNI space based on a given atlas and inverse normalize those ROIs in native space if requested.

Parameters **opt** (*structure*) – structure or json filename containing the options. See checkOptions() and loadAndCheckOptions().

USAGE:

```
opt = get_option();
opt.roi.atlas = 'wang';
opt.roi.name = {'V1v', 'V1d'};
opt.roi.space = {'IXI549Space', 'individual'};
opt.dir.stats = fullfile(opt.dir.raw, '..', 'derivatives', 'cpp_spm-stats');

bidsCreateROI(opt);
```

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src.workflows.roi.**bidsRoiBasedGLM**(*opt*)

Will run a GLM within a ROI using MarsBar.

USAGE:

```
bidsRoiBasedGLM(opt)
```

Parameters **opt** (*structure*) – structure or json filename containing the options. See checkOptions() and loadAndCheckOptions().

Will compute the absolute maximum percent signal change and the time course of the events or blocks of contrast specified in the BIDS model and save and plot the results in tsv / json / jpeg files.

Warning: If your blocks are modelled as series of fast paced "short" events, the results of this workflow might be misleading. It might be better to make sure that the each block has a single event with a "long" duration.

Adapted from the MarsBar tutorial: lib/CPP_ROI/lib/marsbar-0.44/examples/batch

See also: bidsCreateRoi, plotRoiTimeCourse, getEventSpecificationRoiGlm

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10.2 Statistics batches

10.2.1 Subject level

src.batches.stats.**setBatchSubjectLevelGLMSpec**(*varargin*)

Sets up the subject level GLM

USAGE:

```
matlabbatch = setBatchSubjectLevelGLMSpec(matlabbatch, BIDS, opt, subLabel)
```

Parameters

- **matlabbatch** (*structure*) –
- **BIDS** (*structure*) –
- **opt** (*structure*) –
- **subLabel** (*char*) –

Returns

- **matlabbatch** (structure)

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src.batches.stats.**setBatchEstimateModel**(*matlabbatch*, *opt*, *nodeName*, *contrastsList*)

Set up the estimate model batch for run/subject or group level GLM

USAGE:

```
matlabbatch = setBatchEstimateModel(matlabbatch, opt)
matlabbatch = setBatchEstimateModel(matlabbatch, opt, nodeName, contrastsList)
```

Parameters

- **matlabbatch** (*structure*) –
- **opt** (*structure*) –
- **nodeName** (*char*) –
- **contrastsList** (*cell string*) –

Returns

- **matlabbatch** (structure)

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10.2.2 Group level model

src.batches.stats.**setBatchContrasts**(*matlabbatch*, *opt*, *spmMatFile*, *consess*)
Short description of what the function does goes here.

USAGE:

```
matlabbatch = setBatchContrasts(matlabbatch, opt, spmMatFile, consess)
```

Parameters

- **matlabbatch** (*cell*) –
- **opt** (*structure*) –
- **spmMatFile** (*string*) –
- **consess** (*cell*) –

Returns

- **matlabbatch** (structure)

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src.batches.stats.**setBatchFactorialDesign**(*matlabbatch*, *opt*, *nodeName*)
Short description of what the function does goes here.

USAGE:

```
matlabbatch = setBatchFactorialDesign(matlabbatch, opt, nodeName)
```

Parameters

- **matlabbatch** (*structure*) –
- **opt** (*structure*) –

nodeName

Returns

- **matlabbatch** (structure)

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src.batches.stats.**setBatchSubjectLevelContrasts**(*matlabbatch*, *opt*, *subLabel*, *nodeName*)
set batch for run and subject level contrasts

USAGE:

```
matlabbatch = setBatchSubjectLevelContrasts(matlabbatch, opt, subLabel, funcFWHM)
```

Parameters

- **matlabbatch** (*structure*) –
- **opt** (*structure*) –
- **subLabel** (*string*) –

Returns

- **matlabbatch**

See also: bidsFFX, specifyContrasts, setBatchContrasts

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src.batches.stats.**setBatchGroupLevelContrasts**(*matlabbatch*, *opt*, *nodeName*)
USAGE:

```
matlabbatch = setBatchGroupLevelContrasts(matlabbatch, opt, nodeName)
```

Parameters

- **matlabbatch** (*structure*) –
- **opt** (*structure*) –
- **nodeName** (*string*) –

Returns

- **matlabbatch**

See also: setBatchContrasts, specifyContrasts, setBatchSubjectLevelContrasts

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10.2.3 Compute results

src.batches.stats.**setBatchResults**(*matlabbatch*, *result*)
Outputs the typical matlabbatch to compute the result for a given contrast

Common for all type of results: run, session, subject, dataset

USAGE:

```
matlabbatch = setBatchResults(matlabbatch, opt, result)
```

Parameters

- **matlabbatch** (*structure*) –
- **results** –

Returns

- **matlabbatch** (structure)

See also: setBatchSubjectLevelResults, setBatchGroupLevelResults

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src.batches.stats.**setBatchSubjectLevelResults**(*varargin*)
USAGE:

```
matlabbatch = setBatchSubjectLevelResults(matlabbatch, opt, subLabel, result)
```

Parameters

- **matlabbatch** (*structure*) –
- **opt** (*structure*) –
- **subLabel** (*string*) –

Returns

- **matlabbatch** (structure)

See also: bidsResults, setBatchResults

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src.batches.stats.**setBatchGroupLevelResults**(*varargin*)

USAGE:

```
matlabbatch = setBatchGroupLevelResults(matlabbatch, opt, result)
```

Parameters

- **matlabbatch** (*structure*) –
- **opt** (*structure*) –
- **result** (*structure*) –

Returns

- **matlabbatch** (structure)

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10.3 Statistics functions

10.3.1 Subject level

src.subject_level.**createAndReturnOnsetFile**(*opt*, *subLabel*, *tsvFile*)

For a given _events.tsv file and _model.json, it creates a _onset.mat file that can directly be used for the GLM specification of a subject level model.

The file is moved directly into the folder of the GLM.

USAGE:

```
onsetFilename = createAndReturnOnsetFile(opt, subLabel, tsvFile)
```

Parameters

- **opt** (*structure*) –
- **subLabel** (*char*) –
- **tsvFile** (*char*) – fullpath name of the tsv file.

Returns

onsetFilename (path) fullpath name of the file created.

See also: convertOnsetTsvToMat

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src.subject_level.**getFFXdir**(*subLabel*, *opt*)

Sets the name the FFX directory and creates it if it does not exist

USAGE:

```
ffxDir = getFFXdir(subLabel, funcFWFM, opt)
```

Parameters

- **subLabel** (*string*) –
- **opt** –
- **opt** – structure

Returns

- **ffxDir** (string)

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src.subject_level.**getBoldFilenameForFFX**(*varargin*)

Gets the filename for this bold run for this task for the FFX setup and check that the file with the right prefix exist

USAGE:

```
boldFilename = getBoldFilenameForFFX(BIDS, opt, subLabel, funcFWHM, iSes, iRun)
```

Parameters

- **BIDS** (*structure*) –
- **opt** (*structure*) –
- **subLabel** (*string*) –
- **iSes** (*integer*) –
- **iRun** (*integer*) –

Returns

- **boldFilename** (string)

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src.subject_level.**deleteResidualImages**(*ffxDir*)

USAGE:

```
deleteResidualImages(ffxDir)
```

Parameters **ffxDir** (*string*) –

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src.subject_level.**specifyContrasts**(*SPM*, *model*, *nodeName*)
Specifies the first level contrasts

USAGE:

```
contrasts = specifyContrasts(SPM, model)
```

Parameters

- **SPM** (*structure*) – content of SPM.mat
- **model** (*bids model object*) –
- **nodeName** (*char*) – name of the node to return name of

Returns

- **contrasts** (structure)

To know the names of the columns of the design matrix, type : `strvcat(SPM.xX.name)`

See also: setBatchSubjectLevelContrasts, setBatchGroupLevelContrasts

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Functions to deal with onsets files and confounds regressors.

src.subject_level.**convertOnsetTsvToMat**(*opt*, *tsvFile*)
Converts an events.tsv file to an onset file suitable for SPM subject level analysis.

Use a BIDS stats model specified in a JSON file to:

- loads events.tsv and apply the Node.Transformations to its content
- extract the trials (onsets, durations) of the conditions that should be convolved as requested from Node.HRF.Variables field

It then stores them in in a .mat file that can be fed directly in an SPM GLM batch as 'Multiple conditions'

Parametric modulation can be specified via an 'amplitude' column in the TSV file. This column created via the use of Node.Transformations. Only polynomial 1 are supported and only 1 modulation per condition is supported. More complex modulation should be precomputed via the Transformations.

USAGE:

```
fullpathOnsetFilename = convertOnsetTsvToMat(opt, tsvFile)
```

Parameters

- **opt** (*structure*) –
- **tsvFile** (*string*) –

if `opt.glm.useDummyRegressor` is set to `true`, any missing condition will be replaced by a DummyRegressor.

Returns

fullpathOnsetFilename (string) name of the output `.mat` file.

See also: createAndReturnOnsetFile, bids.transformers

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src.subject_level.**convertRealignParamToTsv**(*rpTxtFile*, *opt*, *rmInput*)

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src.subject_level.**createAndReturnCounfoundMatFile**(*opt*, *tsvFile*)

Creates an `_regressors.mat` in the subject level GLM folder.

For a given `_regressors.tsv` file and `_model.json`, it creates a `_regressors.mat` file that can directly be used for the GLM specification of a subject level model.

The file is moved directly into the folder of the GLM.

USAGE:

```
counfoundMatFile = createAndReturnCounfoundMatFile(opt, tsvFile)
```

Parameters

- **opt** (*structure*) –
- **tsvFile** (*string*) – fullpath name of the tsv file.

Returns

counfoundMatFile (string) fullpath name of the file created.

See also: setBatchSubjectLevelGLMSpec, createConfounds

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src.subject_level.**getConfoundsRegressorFilename**(*BIDS*, *opt*, *subLabel*, *session*, *run*)

Gets the `_confounds.tsv` for a given subject, session, run

USAGE:

```
realignParamFile = getRealignParamFile(BIDS, subLabel, session, run, opt)
```

Parameters

- **BIDS** (*structure*) – returned by bids.layout when exploring a BIDS data set.
- **subLabel** (*string*) – label of the subject ; in BIDS lingo that means that for a file name `sub-02_task-foo_bold.nii` the subLabel will be the string `02`
- **session** (*string*) – session label (for *ses-001*, the label will be *001*)
- **run** (*string*) – run index label (for *run-001*, the label will be *001*)
- **opt** (*structure*) – Mostly used to find the task name.

Returns

- **filename** (string)

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src.subject_level.**getRealignParamFilename**(*BIDS*, *subLabel*, *session*, *run*, *opt*)

Gets the realignement parameter file produced by SPM (rp_*.txt) for a given subject, session, run

USAGE:

```
realignParamFile = getRealignParamFile(BIDS, subLabel, session, run, opt)
```

Parameters

- **BIDS** (*structure*) – returned by bids.layout when exploring a BIDS data set.
- **subLabel** (*string*) – label of the subject ; in BIDS lingo that means that for a file name `sub-02_task-foo_bold.nii` the subLabel will be the string `02`
- **session** (*string*) – session label (for *ses-001*, the label will be *001*)
- **run** (*string*) – run index label (for *run-001*, the label will be *001*)
- **opt** (*structure*) – Mostly used to find the task name.

Returns

- **realignParamFile** (string)

10.3.2 Group level model

`src.group_level.`**`getRFXdir`**(*opt*, *nodeName*, *contrastName*)

Sets the name the group level analysis directory and creates it if it does not exist

USAGE:

```
rfxDir = getRFXdir(opt)
```

Parameters **opt** (*structure*) – Options chosen for the analysis. See `checkOptions()`.

Returns

rfxDir (string) Fullpath of the group level directory

Typical output:

- `opt.dir.derivatives/cpp_spm-stats/derivatives/cpp_spm-groupStats/cpp_spm-stats`

```
['task-',     model.Input.task, ...
 '_space-'    model.Input.space, ...
 '_FWHM-',    num2str(opt.fwhm.func), ...
 '_conFWHM-', opt.fwhm.contrast, ...
 'desc-', model.Input.Nodes(dataset_level).Name, ...              % optional
 'contrast-', model.Input.Nodes(dataset_level).Contrast(i).Name  % if ~= from
↪"dataset_level"
 ]
```

10.3.3 Compute results

src.results.**defaultOuputNameStruct**(*opt*, *result*)
USAGE:

```
outputName = defaultOuputNameStruct(opt, result)
```

Parameters

- **opt** (*structure*) –
- **result** (*structure*) –

Returns

- **outputName** (structure)

See also: setBatchSubjectLevelResults, bidsResults

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src.results.**setMontage**(*result*)
USAGE:

```
montage = setMontage(result)
```

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CHAPTER

ELEVEN

QUALITY CONTROL

Note: The illustrations in this section mix what the files created by each workflow and the functions and are called by it. In this sense they are not pure DAGs (directed acyclic graphs) as the `*.m` files mentioned in them already exist.

`src.QA.`**`anatomicalQA`**`(`*`opt`*`)`

Computes several metrics for anatomical image.

Is run as part of:

- `bidsSpatialPrepro`

USAGE:

```
anatomicalQA(opt)
```

Parameters **`opt`** (*`structure`*) – Options chosen for the analysis. See `checkOptions()`.

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`src.QA.`**`functionalQA`**`(`*`opt`*`)`

Is run as part of:

- `bidsSpatialPrepro`

USAGE:

```
functionalQA(opt)
```

For each run works on the realigned (and unwarped) data:

- plots motion, global signal, framewise displacement
- make a movie of the realigned time series
- computes additional confounds regressors depending on the options asked
- gets temporal SNR (TODO)
- creates a carpet plot of the data (TODO) ; warning this is slow

Relevant options:

```
opt.QA.func.Basics = 'on';
opt.QA.func.Motion = 'on';
opt.QA.func.FD = 'on';
opt.QA.func.Globals = 'on';
```

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```
opt.QA.func.Movie = 'on';
opt.QA.func.Voltera = 'on';
opt.QA.func.carpetPlot = true;
```

Parameters **opt** (*structure*) – Options chosen for the analysis. See `checkOptions()`.

Warning: Because of a bug in spm_up, if `Voltera = 'on'`, then the confound regressors of framewise displacement, RMS and global signal will not be saved.

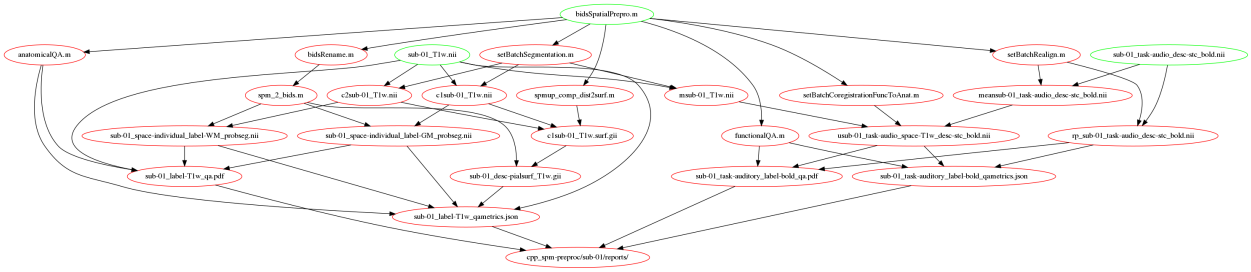

Fig. 1: workflows for QA as part of the spatial preprocessing workflow

`src.QA.`**`computeDesignEfficiency`**(*tsvFile*, *opt*)

Calculate efficiency for fMRI GLMs. Relies on Rik Henson's fMRI_GLM_efficiency function.

For more information on design efficiency, see Jeanette Mumford excellent videos and the dedicated videos from the Principles of fMRI Part 2, Module 7-9.

Warning: This function should NOT be used for proper design efficiency optimization as there are better tools for this.

In general see the BrainPower doc but more specifically the tools below:

- neuropower
- some of the Canlab tools

USAGE:

```
e = computeDesignEfficiency(tsvFile, opt)
```

Parameters

- **tsvFile** (*string*) – Path to a bids _events.tsv file.
- **opt** (*structure*) – Options chosen for the analysis with the content below.

Required:

- `opt.model.file`: path to bids stats model file
- `opt.TR`: inter-scan interval (s) - can be read from the `_bold.json`

Optional:

- `opt.t0`: initial transient (s) to ignore (default = 1)
- `opt.Ns`: number of scans

See also: fMRI_GLM_efficiency

—

EXAMPLE:

```
%% create stats model JSON
json = createEmptyStatsModel();
runStepIdx = 1;
json.Steps{runStepIdx}.Model.X = {'trial_type.cdt_A', 'trial_type.cdt_B'};
json.Steps{runStepIdx}.DummyContrasts = {'trial_type.cdt_A', 'trial_type.cdt_B'};

contrast = struct('type', 't', ...
                  'Name', 'A_gt_B', ...
                  'weights', [1, -1], ...
                  'ConditionList', {{'trial_type.cdt_A', 'trial_type.cdt_B'}});

json.Steps{runStepIdx}.Contrasts = contrast;

bids.util.jsonwrite('smdl.json', json);

%% create events TSV file
conditions = {'cdt_A', 'cdt_B'};
IBI = 5;
ISI = 0.1;
stimDuration = 1.5;
stimPerBlock = 12;
nbBlocks = 10;

trial_type = {};
onset = [];
duration = [];

time = 0;

for iBlock = 1:nbBlocks
  for cdt = 1:numel(conditions)
    for iTrial = 1:stimPerBlock
      trial_type{end + 1} = conditions{cdt};
      onset(end + 1) = time;
      duration(end + 1) = stimDuration;
      time = time + stimDuration + ISI;
    end
    time = time + IBI;
  end
end

tsv = struct('trial_type',  {trial_type}, 'onset', onset, 'duration', duration');

bids.util.tsvwrite('events.tsv', tsv);

opt.TR = 2;

opt.model.file = fullfile(pwd, 'smdl.json');
```

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```
e = computeDesignEfficiency(fullfile(pwd, 'events.tsv'), opt);
```


src.QA.**plotEvents**(*eventsFile*, *modelFile*)

USAGE:

```
plotEvents(eventsFile, modelFile)
```

Parameters

- **eventsFile** (*string*) – Path to a bids _events.tsv file.
- **modelFile** (*structure*) – Optional. Path to a bids statistical model file to filter what events to plot.

EXAMPLE:

```
dataDir = fullpath('bids-examples', 'ds001');

eventsFile = bids.query(dataDir, ...
                        'data', ...
                        'sub', '01', ...
                        'task', 'balloonanalogrisktask', ...
                        'suffix', 'events');

plotEvents(eventsFile{1});
```

CHAPTER

TWELVE

FREQUENTLY ASKED QUESTIONS

12.1 General

12.1.1 What happens if we run same code twice? Are there timestamps on the files or are we overwriting them?

In the vast majority of cases, if you have not touched anything to your options, you will overwrite the output.

Two exceptions that actually have time stamps and are not over-written:

- The matlabbatches saved in the `jobs` folders as `.mat` and `.json` files.
- If you have saved your options with `saveOptions`, then the output `.json` file is saved with a time stamp too. Most of the default `getOptions` templates include `saveOptions` as a last function call.

In most of other cases if you don't want to overwrite previous output, you will have to change the output directory.

For the preprocessing workflows, in general you would have to specify a different `opt.dir.ouput`.

For the statistics workflows, you have a few more options as the name of the output folders includes information that comes from the options and / or the BIDS stats model.

The output folder name (generated by `getFFXdir()` for the subject level and by `getRFXdir()` for the dataset level) should include the FWHM used on the BOLD images as well as info specified in the `Inputs` section of the BIDS stats model JSON file (like the name of the task or the MNI space of the input images).

```
$ ls demos/MoAE/outputs/derivatives/cpp_spm-stats/sub-01/stats

# Folder name for a model on the auditory task in SPM's MNI space
# on data smoothed with a 6mm kernel
task-auditory_space-IXI549Space_FWHM-6
```

But also the GLM folder will include the `Name` of the BIDS stats model as description (`desc`) if this `Name` is not just the name `opt.taskName`.

For example, here with the following BIDS stats model.

```
$ head tests/dummyData/models/model-nback_smdl.json

{
  "Name": "nback MVPA",      # <---- this gets appended to the folder name as␣
↪description
  "BIDSModelVersion": "1.0.0",
  "Description": "for folder naming",
  "Input": {
```

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```
    "task": "nback"
  }
  ...
```

And this code to set things up

```
subLabel = '02';
opt.taskName = 'nback';
opt.space = 'individual';

opt.dir.stats = 'outputs/derivatives/cpp_spm-stats';

ffxDir = getFFXdir(subLabel, opt);
```

Here is the expected output folder name

```
expectedOutput = fullfile(opt.dir.stats, 'sub-02', 'stats', ...
                          'task-nback_space-individual_FWHM-6_desc-nbackMVPA');
```

12.1.2 How can I know that things are set up properly before I run an analysis?

If you want to set things up but not let SPM actually run the batches you can use the option:

`opt.dryRun = true()`

This can be useful when debugging. You may still run into errors when SPM jobman takes over and starts running the batches, but you can at least see if the batches will be constructed without error and then inspect with the SPM GUI to make sure everything is fine.

12.1.3 What is the BIDS way to name and store (Regions of Interest) ROIs?

There is no "official" way to name ROI in BIDS, but you can apply BIDS naming principles to name those.

The closest things to ROI naming are the `masks` for the BIDS derivatives.

Here is an example from the :ref:`face repetition demo`::

```
cpp_spm-roi
├── group
│   ├── hemi-L_space-MNI_label-V1d_desc-wang_mask.json
│   ├── hemi-L_space-MNI_label-V1d_desc-wang_mask.nii
│   ├── hemi-L_space-MNI_label-V1v_desc-wang_mask.json
│   ├── hemi-L_space-MNI_label-V1v_desc-wang_mask.nii
│   ├── hemi-R_space-MNI_label-V1d_desc-wang_mask.json
│   ├── hemi-R_space-MNI_label-V1d_desc-wang_mask.nii
│   ├── hemi-R_space-MNI_label-V1v_desc-wang_mask.json
│   └── hemi-R_space-MNI_label-V1v_desc-wang_mask.nii
└── sub-01
    └── roi
        ├── sub-01_hemi-L_space-individual_label-V1d_desc-wang_mask.nii
        ├── sub-01_hemi-L_space-individual_label-V1v_desc-wang_mask.nii
        ├── sub-01_hemi-R_space-individual_label-V1d_desc-wang_mask.nii
        └── sub-01_hemi-R_space-individual_label-V1v_desc-wang_mask.nii
```

ROIs that are defined in some MNI space are going to be the same across subjects, so you could store a "group" folder (this is not BIDSy but is less redundant than having a copy of the same file for each subject).

The `desc` entity (description) here is used to denotate the atlas the ROI taken from, so if you are building yours from a localizer you might not need to use it.

Ideally you would want to add a JSON file to add metadata about those ROIs.

You can use bids matlab to help you create bids valid filenames.

```
>> name_spec.ext = '.nii';
>> name_spec.suffix = 'mask';
>> name_spec.entities = struct( ...
                               'hemi', 'R', ...
                               'space', 'MNI', ...
                               'label', 'V1v', ...
                               'desc', 'wang');
>> file = bids.File(name_spec);
>> file.filename

   hemi-R_space-MNI_label-V1v_desc-wang_mask.nii
```

12.1.4 How can run my script only only certain files, like just the session `02` for example?

So in general you can select a subset of your data by using the `opt.query`.

This will create a "filter" that bids matlab will use to only "query" and retrieve the subset of files that match the requirement of that filter

In "pure" bids matlab it would look like:

```
BIDS = bids.layout(path_to_my_dataset)
bids.query(BIDS, 'data', opt.query)
```

So if you wanted to run your analysis on say run `02` and `05` of session `02`, you would define your filter like this:

```
opt.query.ses = '02'
opt.query.run = {'02', '05'}
```

12.2 Preprocessing

12.2.1 What images are resampled during preprocessing and to what resolution?

In the spatial preprocessing workflow (`bidsSpatialPrepro`):

1. When no normalization is requested

This is the case when `opt.space = 'individual'`, functional images resolution is not changed. This cannot be overridden.

2. During normalization to MNI

By default, functional images resolution is not changed. Override possible by setting `opt.funcVoxelDims` to the desired resolution.

The anatomical images are resampled at 1 mm.

Tissue probability maps downsampled at resolution of functional images mostly to help with potential with creation of tissue-based mask and also quality control pipelines.

For several files, you can guess their resolution if they have `res` entity in their filename:

- `res-bold` means that the image is resampled at the resolution of the BOLD timeseries
- `res-r1pt0` means that the image is resampled at a resolution of 1.00 mm isometric

```
sub-01
├── anat
│   ├── sub-01_space-individual_desc-biascor_T1w.nii                    # native res
│   ├── sub-01_space-individual_desc-skullstripped_T1w.nii              # native res
│   ├── sub-01_space-individual_label-brain_mask.nii                    # native res
│   ├── sub-01_space-individual_label-CSF_probseg.nii
│   ├── sub-01_space-individual_label-GM_probseg.nii
│   ├── sub-01_space-individual_label-WM_probseg.nii
│   ├── sub-01_space-individual_res-r1pt0_desc-preproc_T1w.nii          # 1.0 mm
│   ├── sub-01_space-IXI549Space_res-bold_label-CSF_probseg.nii         # bold res
│   ├── sub-01_space-IXI549Space_res-bold_label-GM_probseg.nii          # bold res
│   ├── sub-01_space-IXI549Space_res-bold_label-WM_probseg.nii          # bold res
│   └── sub-01_space-IXI549Space_res-r1pt0_T1w.nii                      # 1.0 mm
└── func
    ├── sub-01_task-auditory_space-individual_desc-mean_bold.nii        # native res
    ├── sub-01_task-auditory_space-individual_desc-preproc_bold.nii     # native res
    ├── sub-01_task-auditory_space-individual_desc-std_bold.nii         # native res
    ├── sub-01_task-auditory_space-IXI549Space_desc-mean_bold.nii       # native res
    └── sub-01_task-auditory_space-IXI549Space_desc-preproc_bold.nii    # native res
```

See those slides for some pointers on how to make choices for the resolution to choose for your analysis.

12.3 Results

12.3.1 How can I change which slices are shown in a montage?

> In the `bidsResults.m` I get an image with the overlay of different slices. | How can I change which slices are shown?

When you define your options the range of slices that are to be shown can be changed like this (see `bidsResults` help section for more information):

```
% slices position in mm [a scalar or a vector]
opt.results(1).montage.slices = -12:4:60;

% slices orientation: can be 'axial' 'sagittal' or 'coronal'
% axial is default
opt.results(1).montage.orientation = 'axial';
```

CHAPTER

THIRTEEN

METHODS SECTION

13.1 Dataset description

Use the `reportBIDS` function to description of your dataset that can be used for your methods section

`src.reports.`**`reportBIDS`**(*opt*)

Prints out a human readable description of a BIDS data set for every subject in `opt.subjects`.

The output is a markdown file save in the directory:

`opt.dir.output, ['sub-' subLabel], 'reports'`

USAGE:

```
reportBIDS(opt)
```

Parameters **`opt`** (*`structure`*) – Options chosen for the analysis. See `checkOptions()`.

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13.2 Preprocessing & GLM

This can be generated with the `boilerplate` function.

`src.reports.`**`boilerplate`**(*varargin*)

USAGE:

```
outputFile = boilerplate(opt, ...
                         'outputPath', outputPath, ...
                         'pipelineType', pipelineType, ...
                         'partialsPath', partialsPath, ...
                         'verbosity', 2)
```

Parameters

- **`opt`** (*`structure`*) – Options chosen for the analysis. See `checkOptions()`.
- **`outputPath`** (*`char`*) –
- **`pipelineType`** (*`char`*) – `'spatial_preproc'` or `'stats`
- **`partialsPath`** (*`path`*) –
- **`verbose`** (*`boolean`*) –

13.2.1 Output example - Preprocessing

```
The fMRI data were pre-processed with CPP SPM (v1.1.5dev;
https://github.com/cpp-lln-lab/CPP_SPM; DOI:
https://doi.org/10.5281/zenodo.3554331) using statistical parametric mapping
(SPM12 - 7771; Wellcome Center for Neuroimaging, London, UK;
https://www.fil.ion.ucl.ac.uk/spm; RRID:SCR_007037) using MATLAB 9.2.0.538062 (R2017a)
on a unix computer (Ubuntu 18.04.6 LTS).

The preprocessing of the functional images was performed in the following order:

-   removing of dummy scans
-   slice timing correction
-   realignment and unwarping
-   segmentation and skullstripping
-   normalization MNI space
-   smoothing

4 dummy scans were removed to allow signal stabilization.

Slice timing correction was performed taking the 16^th slice as a reference
(interpolation: sinc interpolation).

Functional scans from each participant were realigned and unwarped using the
mean image as a reference (SPM single pass; number of degrees of freedom: 6 ;
cost function: least square) (Friston et al, 1995).

The anatomical image was bias field corrected. The bias field corrected image
was segmented and normalized to MNI space (target space: IXI549Space; target
resolution: 1 mm; interpolation: 4th degree b-spline) using a unified
segmentation.

The tissue propability maps generated by the segmentation were used to
skullstripp the bias corrected image removing any voxel with p(gray matter) +
p(white matter) + p(CSF) > 0.75.

The mean functional image obtained from realignement was co-registered to the
bias corrected anatomical image (number of degrees of freedom: 6 ; cost
function: normalized mutual information) (Friston et al, 1995). The
transformation matrix from this coregistration was applied to all the functional
images.

The deformation field obtained from the segmentation was applied to all the
functional images (target space: IXI549Space; target resolution: equal to that
used at acquisition; interpolation: 4th degree b-spline).

Preprocessed functional images were spatially smoothed using a 3D gaussian
kernel (FWHM = 6 mm).

This method section was automatically generated using CPP SPM (v1.1.5dev;
https://github.com/cpp-lln-lab/CPP_SPM; DOI:
https://doi.org/10.5281/zenodo.3554331) and octache
(https://github.com/Remi-Gau/Octache).
```

13.2.2 Output example - GLM subject level

```
The fMRI data were analysed with CPP SPM (v1.1.5dev;
https://github.com/cpp-lln-lab/CPP_SPM; DOI:
https://doi.org/10.5281/zenodo.3554331) using statistical parametric mapping
(SPM12 - 7771; Wellcome Center for Neuroimaging, London, UK;
https://www.fil.ion.ucl.ac.uk/spm; RRID:SCR_007037) using MATLAB 9.2.0.538062 (R2017a)
on a unix computer (Ubuntu 18.04.6 LTS).

The input data were the preprocessed BOLD images in individual IXI549Space space
for the task "facerepetition".

At the subject level, we performed a mass univariate analysis with a linear
regression at each voxel of the brain, using generalized least squares with a
global AR(1) model to account for temporal auto-correlation and a drift fit with
discrete cosine transform basis (128.2051 seconds cut-off).

Image intensity scaling was done run-wide before statistical modeling such that
the mean image would have a mean intracerebral intensity of 100.

We modeled the fMRI experiment in a block design with regressors entered into
the run-specific design matrix. The the onsets
were convolved with a canonical hemodynamic response function (HRF) and its
temporal and dispersion derivatives for the conditions: famous_1, famous_2,
unfamiliar_1, unfamiliar_2.

Nuisance covariates included the 6 realignment parameters to account for
residual motion artefacts.

This method section was automatically generated using CPP SPM (v1.1.5dev;
https://github.com/cpp-lln-lab/CPP_SPM; DOI:
https://doi.org/10.5281/zenodo.3554331) and octache
(https://github.com/Remi-Gau/Octache).
```

13.2.3 Output example - GLM Group level

WIP

13.3 References

```
@software{CPP_SPM,
  author  = {Gau, Rémi and Barilari, Marco and Battal, Ceren and Rezk, Mohamed and␣
↪Collignon, Olivier and Gurtubay, Ane and Falagiarda, Federica and MacLean, Michèle␣
↪and Cerpelloni, Filippo},
  license = {GPL-3.0},
  title   = {CPP SPM},
  url     = {https://github.com/cpp-lln-lab/CPP_SPM},
  version = {1.1.5dev},
  doi     = {https://doi.org/10.5281/zenodo.3554331},
}

@article{Corbin2018,
author = {Corbin, Nadège and Todd, Nick and Friston, Karl J. and Callaghan, Martina F.
↪},
```

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```
title = {Accurate modeling of temporal correlations in rapidly sampled fMRI time␣
↪series},
journal = {Human Brain Mapping},
volume = {39},
number = {10},
pages = {3884-3897},
keywords = {accelerated acquisitions, functional MRI, functional sensitivity,␣
↪prewhitening, temporal correlation},
doi = {https://doi.org/10.1002/hbm.24218},
url = {https://onlinelibrary.wiley.com/doi/abs/10.1002/hbm.24218},
eprint = {https://onlinelibrary.wiley.com/doi/pdf/10.1002/hbm.24218},
abstract = {Abstract Rapid imaging techniques are increasingly used in functional MRI␣
↪studies because they allow a greater number of samples to be acquired per unit time,
↪ thereby increasing statistical power. However, temporal correlations limit the␣
↪increase in functional sensitivity and must be accurately accounted for to control␣
↪the false-positive rate. A common approach to accounting for temporal correlations␣
↪is to whiten the data prior to estimating fMRI model parameters. Models of white␣
↪noise plus a first-order autoregressive process have proven sufficient for␣
↪conventional imaging studies, but more elaborate models are required for rapidly␣
↪sampled data. Here we show that when the "FAST" model implemented in SPM is used␣
↪with a well-controlled number of parameters, it can successfully prewhiten 80\% of␣
↪grey matter voxels even with volume repetition times as short as 0.35 s. We further␣
↪show that the temporal signal-to-noise ratio (tSNR), which has conventionally been␣
↪used to assess the relative functional sensitivity of competing imaging approaches,␣
↪can be augmented to account for the temporal correlations in the time series. This␣
↪amounts to computing the t-score testing for the mean signal. We show in a visual␣
↪perception task that unlike the tSNR weighted by the number of samples, the t-score␣
↪measure is directly related to the t-score testing for activation when the temporal␣
↪correlations are correctly modeled. This score affords a more accurate means of␣
↪evaluating the functional sensitivity of different data acquisition options.},
year = {2018}
}

@article{Friston1995,
  author   = {Friston, Karl. J. and Ashburner, J. and Frith, C. D. and Poline, J.-B.␣
↪and Heather, J. D. and Frackowiak, R. S. J.},
  title    = {Spatial registration and normalization of images},
  journal  = {Human Brain Mapping},
  volume   = {3},
  number   = {3},
  pages    = {165-189},
  keywords = {realignment, registration, anatomy, imaging, stereotaxy, morphometrics,␣
↪basis functions, spatial normalization, PET, MRI, functional mapping},
  doi      = {https://doi.org/10.1002/hbm.460030303},
  url      = {https://onlinelibrary.wiley.com/doi/abs/10.1002/hbm.460030303},
  eprint   = {https://onlinelibrary.wiley.com/doi/pdf/10.1002/hbm.460030303},
  abstract = {Abstract This paper concerns the spatial and intensity transformations␣
↪that map one image onto another. We present a general technique that facilitates␣
↪nonlinear spatial (stereotactic) normalization and image realignment. This␣
↪technique minimizes the sum of squares between two images following nonlinear␣
↪spatial deformations and transformations of the voxel (intensity) values. The␣
↪spatial and intensity transformations are obtained simultaneously, and explicitly,␣
↪using a least squares solution and a series of linearising devices. The approach is␣
↪completely noninteractive (automatic), nonlinear, and noniterative. It can be␣
↪applied in any number of dimensions. Various applications are considered, including␣
↪the realignment of functional magnetic resonance imaging (MRI) time-series, the␣
↪linear (affine) and nonlinear spatial normalization of positron emission tomography␣
↪(PET) and structural MRI images, the coregistration of PET to structural MRI, and,␣
↪implicitly, the conjoining of PET and MRI to obtain high resolution functional␣
↪images. © 1995 Wiley-Liss, Inc.},
```

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(continued from previous page)

```
  year      = {1995}
}
```

CHAPTER

FOURTEEN

MANUAL COREGISTRATION

Manual coregistration tools

---

lib.mancoreg.**mancoreg**(*varargin*)

This function displays 2 SPM ortho-views of a `targetimage` and a `sourceimage` image that can be manually coregistered.

USAGE:

```
mancoreg('targetimage', [], 'sourceimage', [], 'stepsize', 0.01)
```

Parameters

- **targetimage** (*string*) – Filename or fullpath of the target image. If none is provided you will be asked by SPM to select one.
- **sourceimage** (*string*) – Filename or fullpath of the source image. If none is provided you will be asked by SPM to select one.
- **stepsize** (*positive float*) – step size for each rotation and translation

Manual coregistration tool

The source image (bottom graph) can be manually rotated and translated with 6 slider controls. In the source graph the source image can be exchanged with the target image using a radio button toggle. This is helpful for visual fine control of the coregistration. The transformation matrix can be applied to a selected set of volumes with the `apply transformation` button. If the transformation is to be applied to the original source file that file will also need to be selected. If the sourceimage or targetimage are not passed the user will be prompted with a file browser.

The code is loosely based on `spm_image()` and `spm_orthoviews()` It requires the m-file with the callback functions for the user controls (`mancoregCallbacks()`).

lib.mancoreg.**mancoregCallbacks**(*operation*)

Callback routines for `mancoreg()`: defines the different actions for the different buttons.

USAGE:

```
mancoreg_callbacks(operation)
```

Parameters **operation** (*string*) – Can be any of the following: `move`, `toggle_off`, `toggle_on`, `reset`, `apply`, `plotmat`

CHAPTER

FIFTEEN

DOCKER

15.1 Build docker image locally

If you want to build the docker image locally and not pull it from the docker hub:

```
docker build . -f docker/Dockerfile -t cpplab/cpp_spm:stable
```

This will create an image with the tag name `cpp_spm:stable`

Running `make docker_img` will also build the `stable` version and a `latest` version.

15.2 Run docker image

The following command would pull from our docker hub and start the docker image:

```
docker run -it --rm cpplab/cpp_spm:latest
```

The image is set up to start Octave in the `/code` folder.

The following command would do do the same, but it would also map 2 folders from your computer to the `output` and `code` folder inside the container image:

```
code_folder=fullpath_to_your_code
output_folder=fullpath_to_your_output_folder

docker run -it --rm \
    -v $output_folder:/output \
    -v $code_folder:/code \
    cpplab/cpp_spm:latest
```

For example, you could run the demos by doing this:

```
code_folder=/home/remi/github/CPP_SPM/demos/MoAE

docker run -it --rm \
    -v $code_folder:/code \
    cpplab/cpp_spm:latest

# once inside the docker image
moae_01_preproc
```

CHAPTER

SIXTEEN

LINKS AND REFERENCES

16.1 SPM starters

If you start from zero, go through the 2 first tutorials of SPM

16.2 Andrew Jahn videos and blogs

- video playlist
- marsbar
- SPM
- SPM.mat

16.3 SPM code snippets

SPM wikibook has some very useful sections.

From John Ashburner on Tom Nichols blog

From Rik Henson

Some follow along tutorials written a long time ago, and that probably should be turned into notebooks and updated.

- Basic file / image manipulation with SPM
- HRF, convolution and GLM ("by hand")
- Design efficiency

16.4 Content of SPM.mat

This is here because SPM has the sad (and bad) Matlabic tradition of using variable names that have often attempted to replicate the notation in the papers to make engineers and the generally math enclined happy, rather then the `TypicalLongVariableNames` that many programmers and new comers would prefer to see to help with code readibility.

Adapted from: http://andysbrainblog.blogspot.com/2013/10/whats-in-spmmat-file.html

16.4.1 details on experiment

- `SPM.xY.RT` - TR length (RT =”repeat time”)
- `SPM.xY.P` - matrix of file names
- `SPM.xY.VY` - (number of runs x 1) struct array of mapped image volumes (.nii file info)
- `SPM.modality` - the data you’re using (PET, FMRI, EEG)
- `SPM.stats.[modality].UFp` - critical F-threshold for selecting voxels over which the non-sphericity is estimated (if required) [default: `0.001`]
- `SPM.stats.maxres` - maximum number of residual images for smoothness estimation
- `SPM.stats.maxmem` - maximum amount of data processed at a time (in bytes)
- `SPM.SPMid` - version of SPM used
- `SPM.swd` - directory for SPM.mat and nii files. default is `pwd`

16.4.2 basis function

- `SPM.xBF.name` - name of basis function
- `SPM.xBF.length` - length in seconds of basis
- `SPM.xBF.order` - order of basis set
- `SPM.xBF.T` - number of subdivisions of TR
- `SPM.xBF.T0` - first time bin (see slice timing)
- `SPM.xBF.UNITS` - options: `'scans'` or `'secs'` for onsets
- `SPM.xBF.Volterra` - order of convolution
- `SPM.xBF.dt` - length of time bin in seconds
- `SPM.xBF.bf` - basis set matrix

16.4.3 Session structure

Note that in SPM lingo sessions are equivalent to a runs in BIDS.

user-specified covariates/regressors

e.g. motion

- `SPM.Sess([sesssion]).C.C` - (n x c) double regressor (`c` is number of covariates, `n` is number of sessions)
- `SPM.Sess([sesssion]).C.name` - names of covariates

conditions & modulators specified

i.e. input structure array

- `SPM.Sess([sesssion]).U(condition).dt:` - time bin length (seconds)
- `SPM.Sess([sesssion]).U(condition).name` - names of conditions
- `SPM.Sess([sesssion]).U(condition).ons` - onset for condition's trials
- `SPM.Sess([sesssion]).U(condition).dur` - duration for condition's trials
- `SPM.Sess([sesssion]).U(condition).u` - (t x j) inputs or stimulus function matrix
- `SPM.Sess([sesssion]).U(condition).pst` - (1 x k) peri-stimulus times (seconds)

parameters/modulators specified

- `SPM.Sess([sesssion]).U(condition).P` - parameter structure/matrix
- `SPM.Sess([sesssion]).U(condition).P.name` - names of modulators/parameters
- `SPM.Sess([sesssion]).U(condition).P.h` - polynomial order of modulating parameter (order of polynomial expansion where 0 is none)
- `SPM.Sess([sesssion]).U(condition).P.P` - vector of modulating values
- `SPM.Sess([sesssion]).U(condition).P.P.i` - sub-indices of `U(i).u` for plotting

scan indices for sessions

- `SPM.Sess([sesssion]).row`

effect indices for sessions

- `SPM.Sess([sesssion]).col`

F Contrast information for input-specific effects

- `SPM.Sess([sesssion]).Fc`
- `SPM.Sess([sesssion]).Fc.i` - F Contrast columns for input-specific effects
- `SPM.Sess([sesssion]).Fc.name` - F Contrast names for input-specific effects
- `SPM.nscan([session])` - number of scans per session (or if e.g. a t-test, total number of con*.nii files)

16.4.4 global variate/normalization details

- `SPM.xGX.iGXcalc` - either `'none'` or `'scaling'`

For fMRI usually is `none` (no global normalization). If global normalization is `scaling`, see `spm_fmri_spm_ui` for parameters that will then appear under `SPM.xGX`.

16.4.5 design matrix information

- SPM.xX.X - design matrix (raw, not temporally smoothed)
- SPM.xX.name - cellstr of parameter names corresponding to columns of design matrix
- SPM.xX.I - (nScan x 4) matrix of factor level indicators. first column is the replication number. Other columns are the levels of each experimental factor.
- SPM.xX.iH - vector of H partition (indicator variables) indices
- SPM.xX.iC - vector of C partition (covariates) indices
- SPM.xX.iB - vector of B partition (block effects) indices
- SPM.xX.iG - vector of G partition (nuisance variables) indices
- SPM.xX.K - cell. low frequency confound: high-pass cutoff (seconds)
- SPM.xX.K.HParam - low frequency cutoff value
- SPM.xX.K.X0 - cosines (high-pass filter)
- SPM.xX.W - Optional whitening/weighting matrix used to give weighted least squares estimates (WLS). If not specified spm_spm will set this to whiten the data and render the OLS estimates maximum likelihood i.e. W*W' inv(xVi.V).
- SPM.xX.xKXs - space structure for K*W*X, the 'filtered and whitened' design matrix
  - SPM.xX.xKXs.X - matrix of trials and betas (columns) in each trial
  - SPM.xX.xKXs.tol - tolerance
  - SPM.xX.xKXs.ds - vectors of singular values
  - SPM.xX.xKXs.u - u as in X u*diag(ds)*v'
  - SPM.xX.xKXs.v - v as in X u*diag(ds)*v'
  - SPM.xX.xKXs.rk - rank
  - SPM.xX.xKXs.oP - orthogonal projector on X
  - SPM.xX.xKXs.oPp - orthogonal projector on X'
  - SPM.xX.xKXs.ups - space in which this one is embedded
  - SPM.xX.xKXs.sus - subspace
- SPM.xX.pKX - pseudoinverse of K*W*X, computed by spm_sp
- SPM.xX.Bcov - xX.pKX*xX.V*xX.pKX - variance-covariance matrix of parameter estimates (when multiplied by the voxel-specific hyperparameter ResMS of the parameter estimates (ResSS/xX.trRV ResMS))
- SPM.xX.trRV - trace of R*V
- SPM.xX.trRVRV - trace of RVRV
- SPM.xX.erdf - effective residual degrees of freedom (trRV^2/trRVRV)
- SPM.xX.nKX - design matrix (xX.xKXs.X) scaled for display (see spm_DesMtx('sca',... for details)
- SPM.xX.sF - cellstr of factor names (columns in SPM.xX.I, i think)
- SPM.xX.D - struct, design definition
- SPM.xX.xVi - correlation constraints (see non-sphericity below)
- SPM.xC - struct. array of covariate info

16.4.6 header info

- SPM.P - a matrix of filenames
- SPM.V - a vector of structures containing image volume information.
  - SPM.V.fname - the filename of the image.
  - SPM.V.dim - the x, y and z dimensions of the volume
  - SPM.V.dt - a (1 x 2) array. First element is datatype (see spm_type). The second is 1 or 0 depending on the endian-ness.
  - SPM.V.mat - a (4 x 4) affine transformation matrix mapping from voxel coordinates to real world coordinates.
  - SPM.V.pinfo - plane info for each plane of the volume.
  - SPM.V.pinfo(1,:) - scale for each plane
  - SPM.V.pinfo(2,:) - offset for each plane The true voxel intensities of the j:sup:*th* image are given by: val*V.pinfo(1,j) + V.pinfo(2,j)
  - SPM.V.pinfo(3,:) - offset into image (in bytes). If the size of pinfo is 3x1, then the volume is assumed to be contiguous and each plane has the same scale factor and offset.

16.4.7 structure describing intrinsic temporal non-sphericity

- SPM.xVi.I - typically the same as SPM.xX.I
- SPM.xVi.h - hyperparameters
- SPM.xVi.V xVi.h(1)*xVi.Vi{1} + ...
- SPM.xVi.Cy - spatially whitened (used by ReML to estimate h)
- SPM.xVi.CY - <(Y -)*(Y -)'> (used by spm_spm_Bayes)
- SPM.xVi.Vi - array of non-sphericity components
  - defaults to {speye(size(xX.X,1))} - i.i.d.
  - specifying a cell array of contraints ((Qi)
  - These contraints invoke spm_reml to estimate hyperparameters assuming V is constant over voxels that provide a high precise estimate of xX.V
- SPM.xVi.form - form of non-sphericity (either 'none' or 'AR(1)' or 'FAST')
- SPM.xX.V - Optional non-sphericity matrix. CCov(e)sigma^2*V. If not specified spm_spm will compute this using a 1st pass to identify signifcant voxels over which to estimate V. A 2nd pass is then used to re-estimate the parameters with WLS and save the ML estimates (unless xX.W is already specified).

16.4.8 filtering information

- `SPM.K` - filter matrix or filtered structure
  - `SPM.K(s)` - struct array containing partition-specific specifications
  - `SPM.K(s).RT` - observation interval in seconds
  - `SPM.K(s).row` - row of Y constituting block/partitions
  - `SPM.K(s).HParam` - cut-off period in seconds
  - `SPM.K(s).X0` - low frequencies to be removed (DCT)
- `SPM.Y` - filtered data matrix

16.4.9 masking information

- `SPM.xM` - Structure containing masking information, or a simple column vector of thresholds corresponding to the images in VY.
- `SPM.xM.T` - (n x 1) double - Masking index
- `SPM.xM.TH` - (nVar x nScan) matrix of analysis thresholds, one per image
- `SPM.xM.I` - Implicit masking (`0` –> none; `1` –> implicit zero/NaN mask)
- `SPM.xM.VM` - struct array of mapped explicit mask image volumes
- `SPM.xM.xs` - (1 x 1) struct ; cellstr description

16.4.10 design information

self-explanatory names, for once

- `SPM.xsDes.Basis_functions` - type of basis function
- `SPM.xsDes.Number_of_sessions`
- `SPM.xsDes.Trials_per_session`
- `SPM.xsDes.Interscan_interval`
- `SPM.xsDes.High_pass_Filter`
- `SPM.xsDes.Global_calculation`
- `SPM.xsDes.Grand_mean_scaling`
- `SPM.xsDes.Global_normalisation`

16.4.11 details on scanner data

e.g. smoothness

- `SPM.xVol` - structure containing details of volume analyzed
  - `SPM.xVol.M` - (4 x 4) voxel –> mm transformation matrix
  - `SPM.xVol.iM` - (4 x 4) mm –> voxel transformation matrix
  - `SPM.xVol.DIM` - image dimensions - column vector (in voxels)

  - `SPM.xVol.XYZ` - (3 x S) vector of in-mask voxel coordinates
  - `SPM.xVol.S` - Lebesgue measure or volume (in voxels)
  - `SPM.xVol.R` - vector of resel counts (in resels)
  - `SPM.xVol.FWHM` - Smoothness of components - FWHM, (in voxels)

16.4.12 info on beta files

- `SPM.Vbeta` - struct array of beta image handles
  - `SPM.Vbeta.fname` - beta nii file names
  - `SPM.Vbeta.descrip` - names for each beta file

16.4.13 info on variance of the error

- `SPM.VResMS` - file struct of ResMS image handle
  - `SPM.VResMS.fname` - variance of error file name

16.4.14 info on mask

- `SPM.VM` - file struct of Mask image handle
  - `SPM.VM.fname` - name of mask nii file

16.4.15 contrast details

added after running contrasts

- `SPM.xCon` - Contrast definitions structure array. See also `spm_FcUtil.m` for structure, rules & handling.
  - `SPM.xCon.name` - Contrast name
  - `SPM.xCon.STAT` - Statistic indicator character (`'T'`, `'F'` or `'P'`)
  - `SPM.xCon.c` - Contrast weights (column vector contrasts)
  - `SPM.xCon.X0` - Reduced design matrix data (spans design space under Ho)
    - Stored as coordinates in the orthogonal basis of xX.X from spm_sp (Matrix in SPM99b)
    - Extract using X0 `spm_FcUtil('X0', ...`
  - `SPM.xCon.iX0` - Indicates how contrast was specified:
    - If by columns for reduced design matrix then iX0 contains the column indices.
    - Otherwise, it's a string containing the `spm_FcUtil` 'Set' action: Usually one of `{'c','c+', 'X0'}` defines the indices of the columns that will not be tested. Can be empty.
  - `SPM.xCon.X1o` - Remaining design space data (X1o is orthogonal to X0)
    - Stored as coordinates in the orthogonal basis of xX.X from `spm_sp` (Matrix in SPM99b)
    - Extract using X1o `spm_FcUtil('X1o', ...`
  - `SPM.xCon.eidf` - Effective interest degrees of freedom (numerator df)

    * Or effect-size threshold for Posterior probability

- `SPM.xCon.Vcon` - Name of contrast (for 'T's) or ESS (for 'F's) image
- `SPM.xCon.Vspm` - Name of SPM image

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