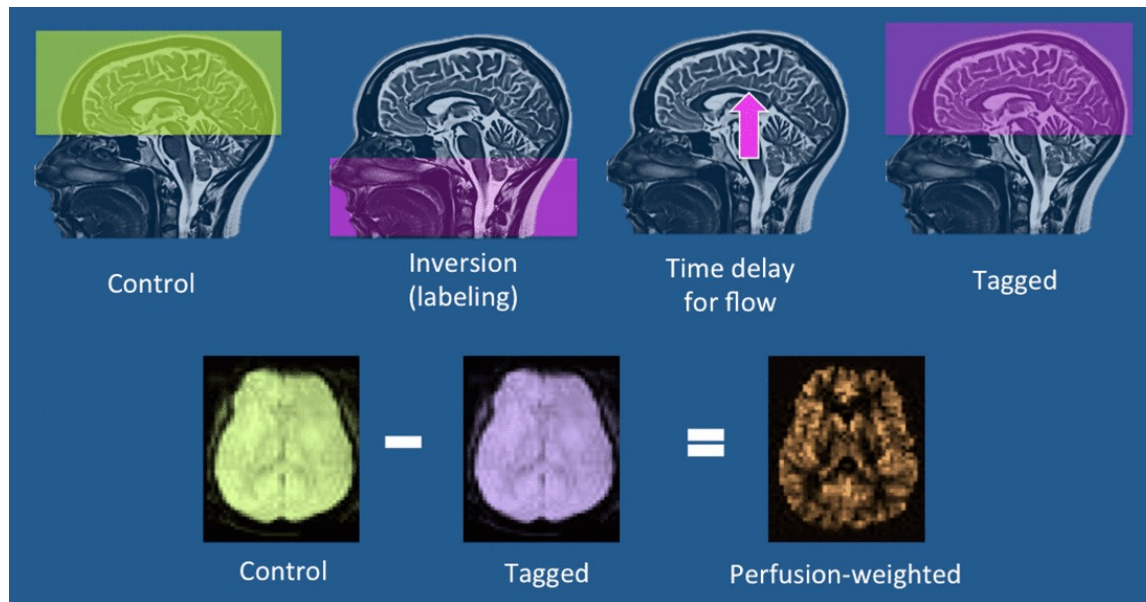


MBME ASL/BOLD fMRI

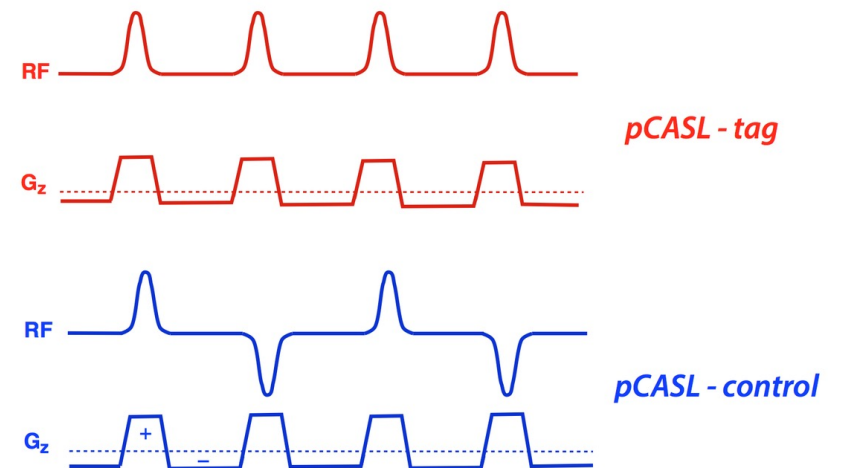
Sequence and processing @ MRI UZ Brussel

Dr. Peter Van Schuerbeek

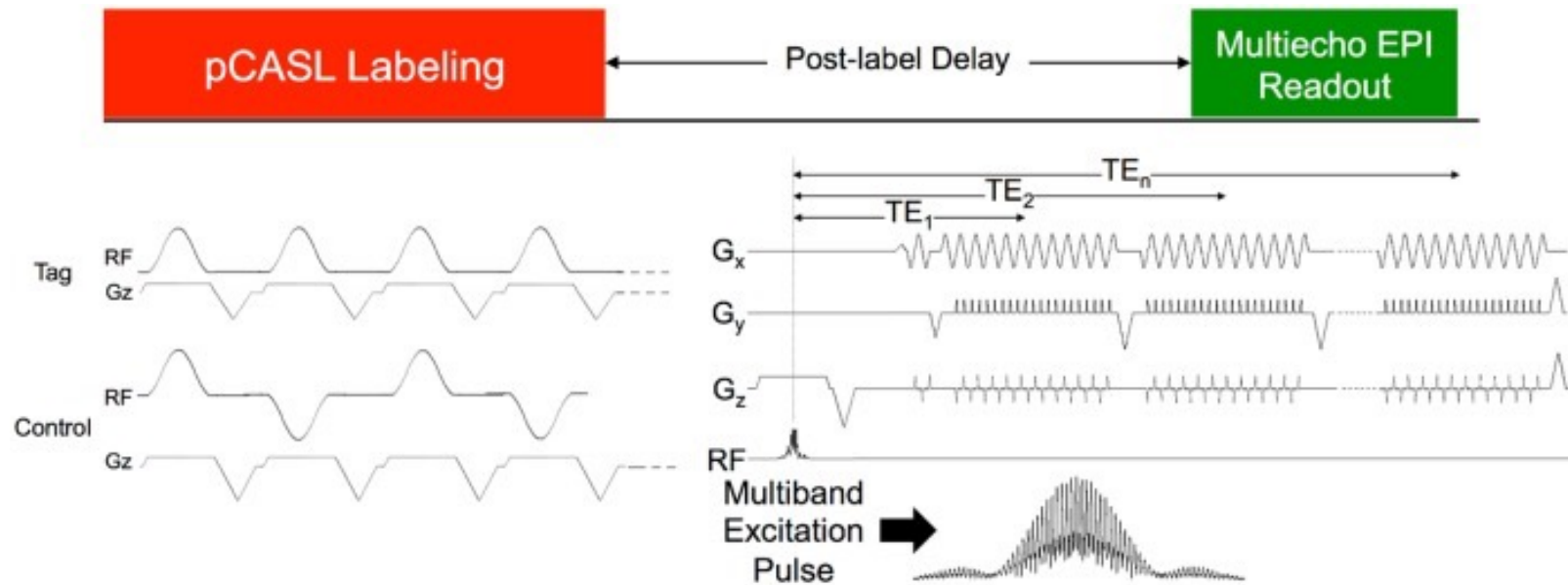
Pseudo Continuous ASL (PCASL)



<https://mriquestions.com/what-is-asl.html>
<https://mriquestions.com/pcasl.html>



Sequence from Cohen et al. 2018. Multiband multi-echo simultaneous ASL/BOLD for task-induced functional MRI. PLoS One 13(2): e0190427 (doi: 10.1371/journal.pone.0190427)



MBME ASL/BOLD pulse sequence design. The sequence consists of an unbalanced pCASL labeling train, followed by a PLD, and finally an ME EPI readout. The first echo train was acquired after the acquisition of navigator echoes through the center of k-space. The phase was then rewound to the start of k-space, and the next echo train was acquired. This was repeated three times for a total of four echoes. MB imaging was implemented by replacing the single-band excitation pulse with a MB excitation pulse. Finally, blipped-CAIPI was utilized to shift the FOV of aliased slices and reduce g-factor penalties associated with MB imaging.

Organisation of the data (BIDS standard)

/your_folder

/sub-01

/ses-001

/anat

sub-01_T1w.nii

sub-01_T1w.json

/fmat

sub-01_ses-001_dir-AP_echo-1_epi.nii

... sub-01_ses-001_dir-AP_echo-*n*_epi.nii

sub-01_ses-001_dir-AP_echo-1_epi.json

... sub-01_ses-001_dir-AP_echo-*n*_epi.json

/func

sub-01_ses-001_task-**your_task**_run-1_dir-PA_echo-1_**aslbold**.nii

... sub-01_ses-001_task-**your_task**_run-1_dir-PA_echo-*n*_aslbold.nii

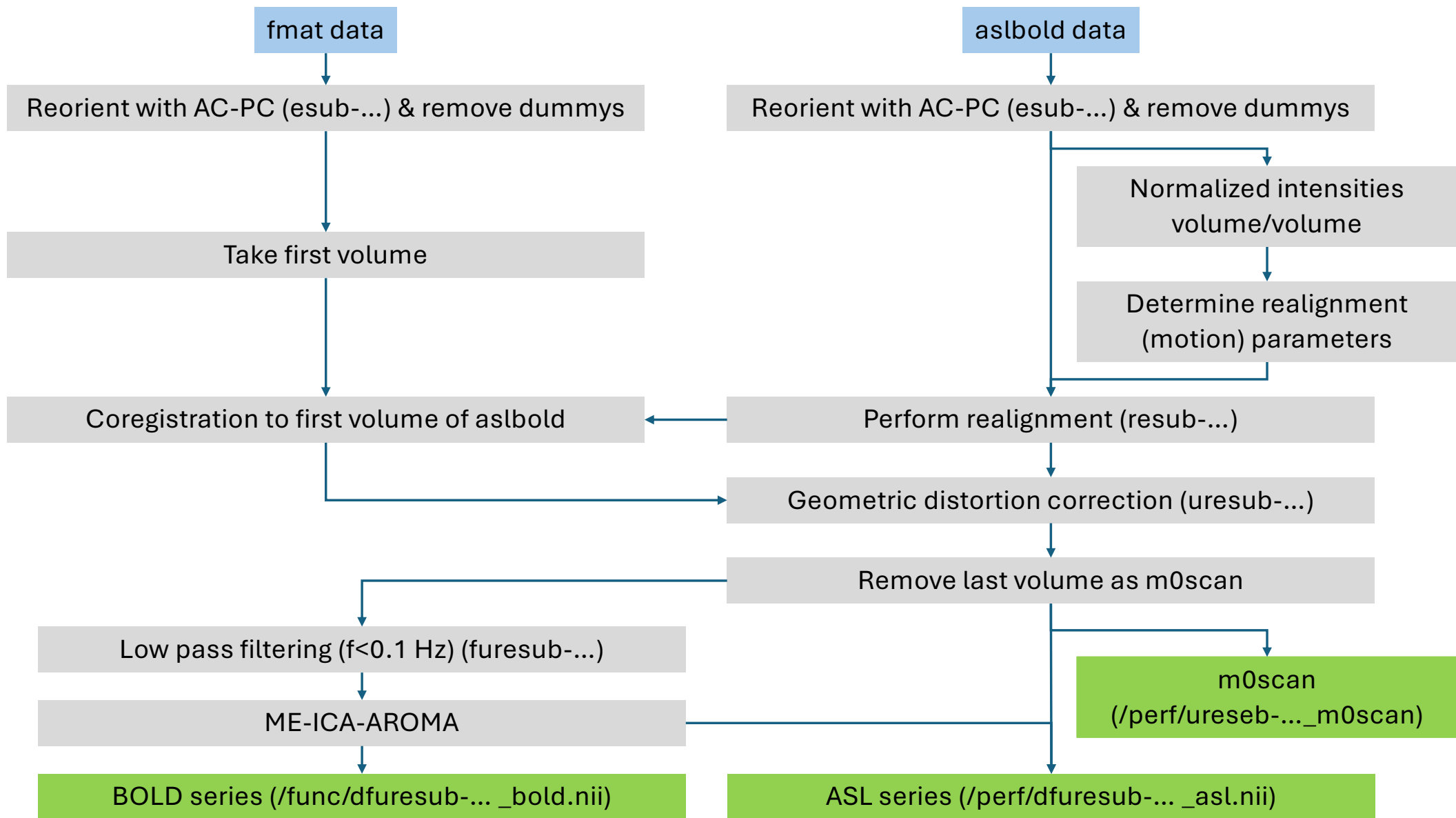
sub-01_ses-001_task-**your_task**_run-1_dir-PA_echo-1_**aslbold**.json

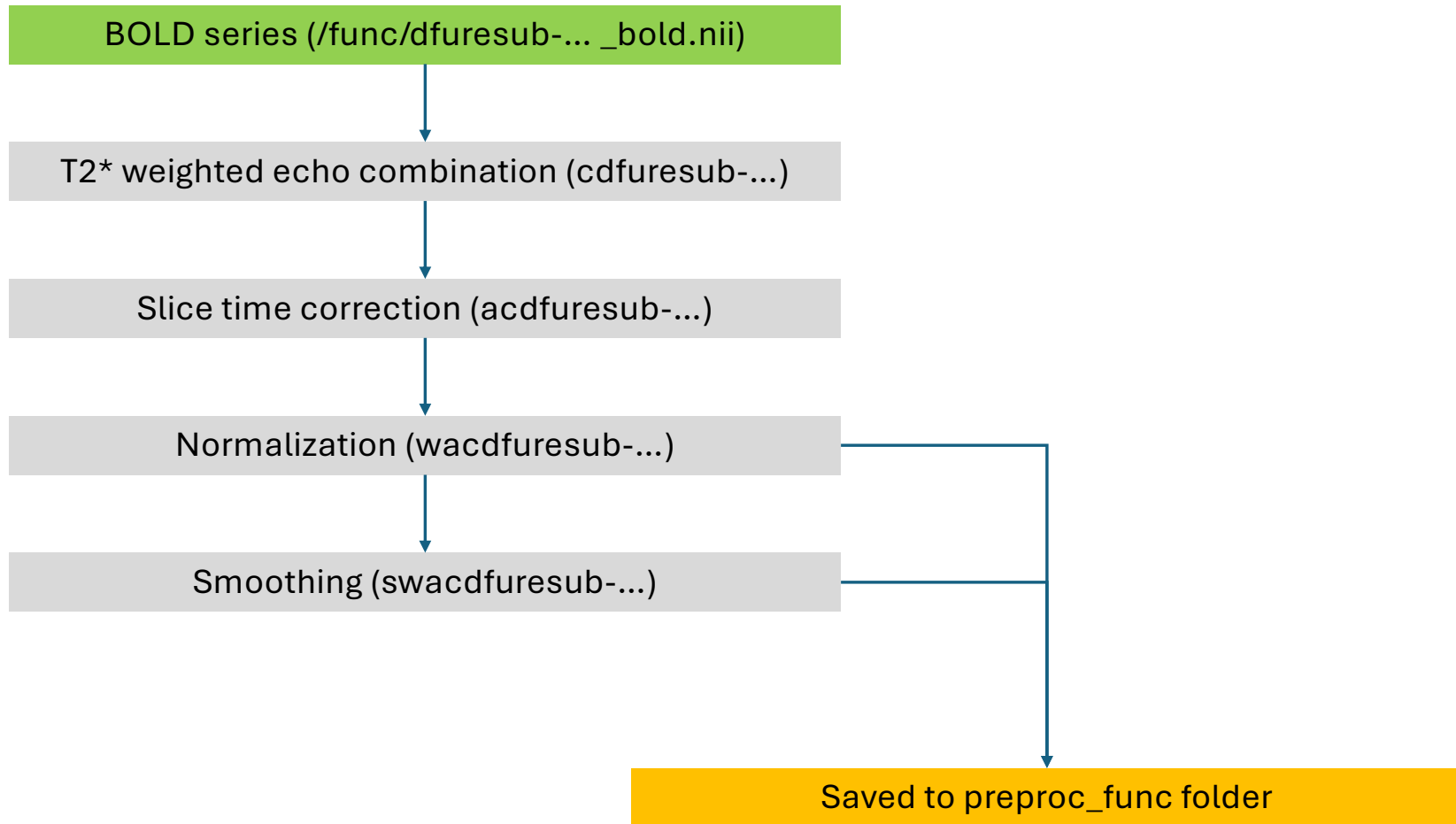
... sub-01_ses-001_task-**your_task**_run-1_dir-PA_echo-*n*_aslbold.json

...

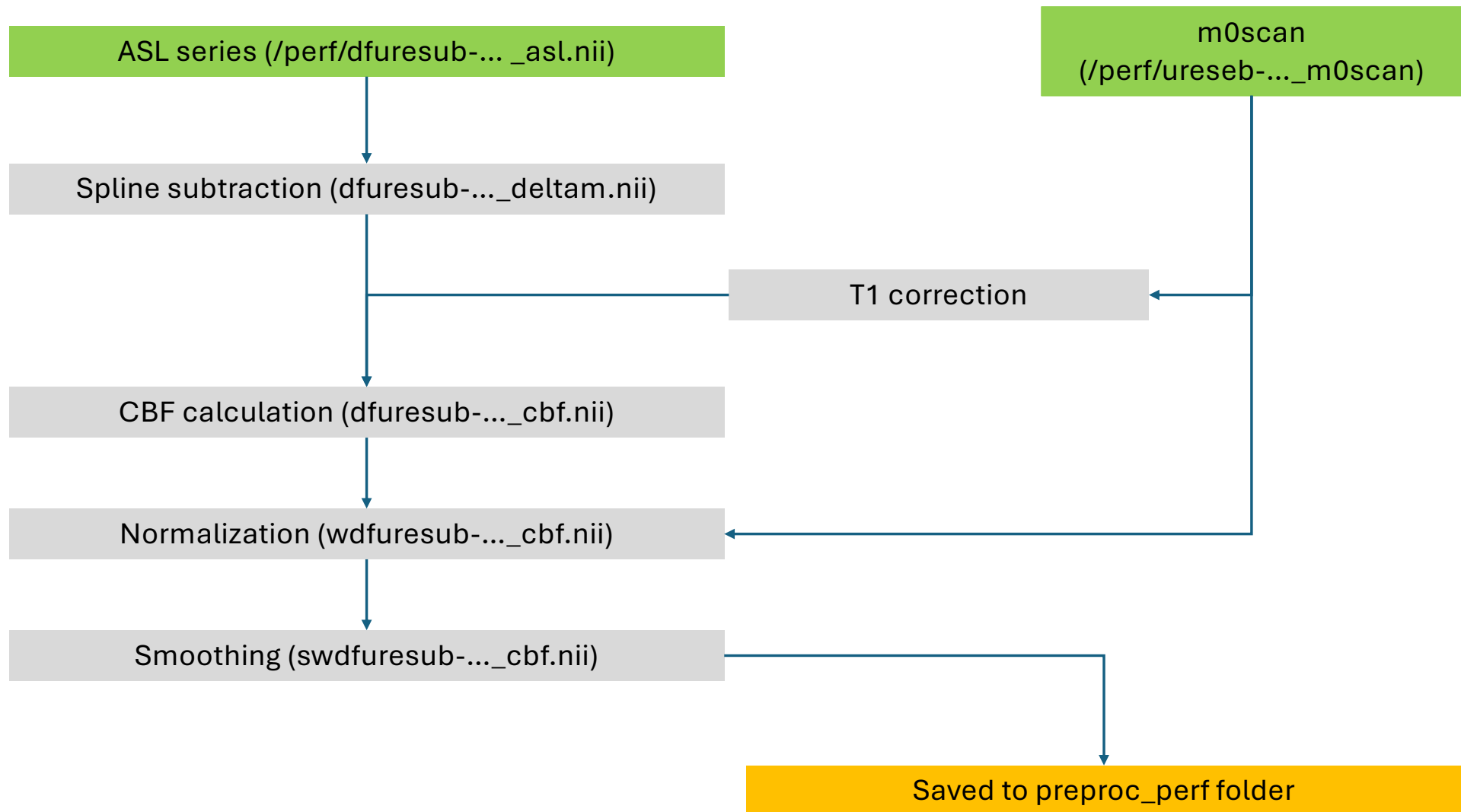
sub-01_ses-001_task-**your_task**_run-1_events.tsv

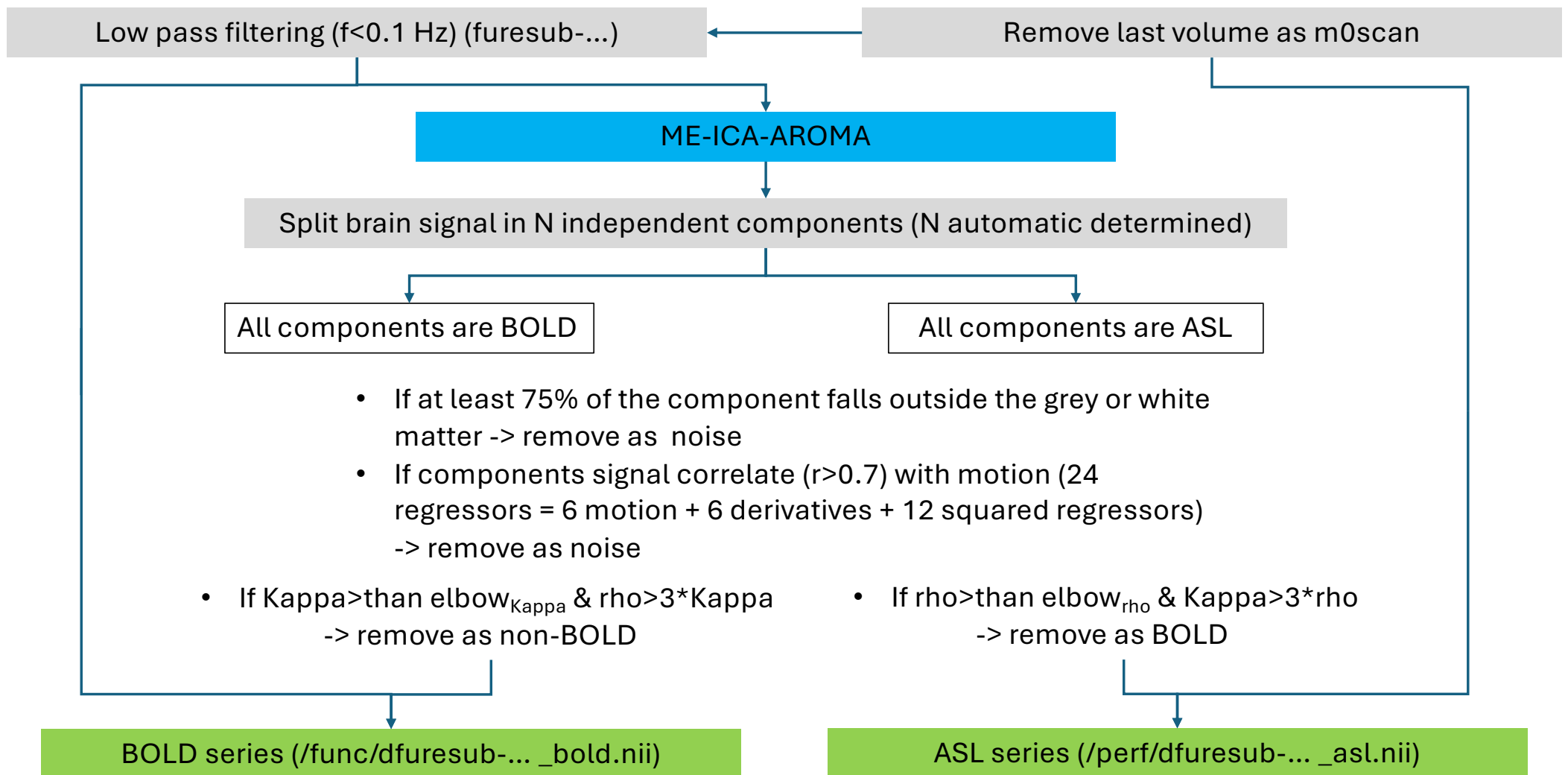
- Replace **your_task** by an identifier for the fMRI task (e.g. **fingertapping**, **rest**, **posner**, ...)
- Try to avoid spaces in folder and filenames
- **dir-PA** and **dir-AP** depends on the **pepolar** parameter





Only the 1ste echo (shortest TE) series is used!





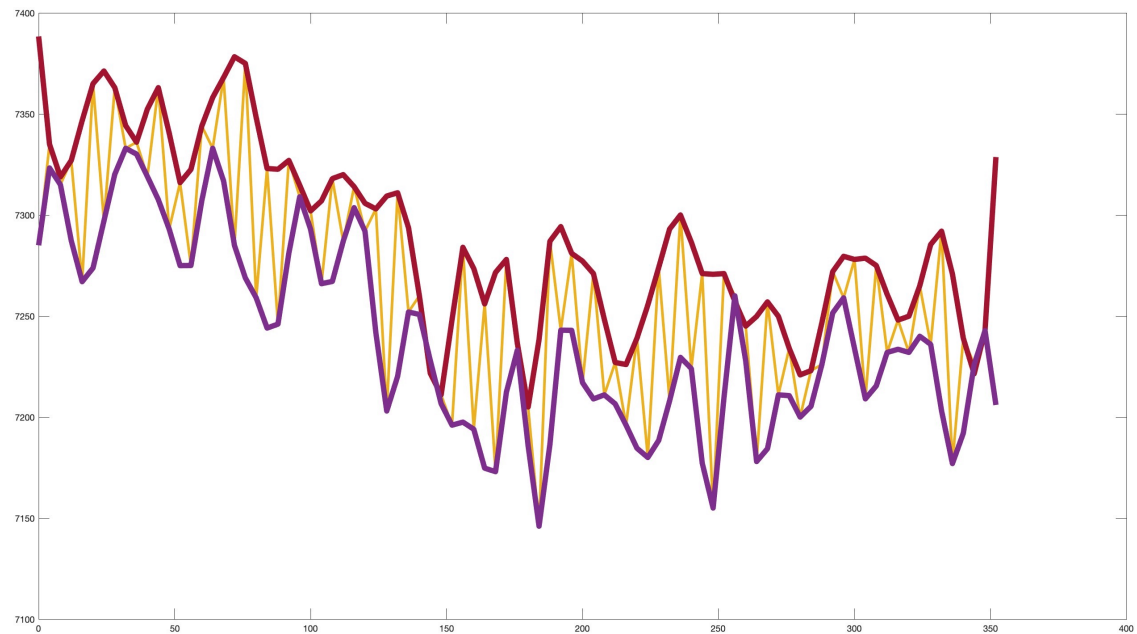
$S = S_0 \cdot \exp(-TE/T2^*)$ -> measure for the amount of signal variation explained by variation in $T2^*$ (Kappa) and variation in S_0 due to spin inflow (rho)
 $\text{Elbow}_{\text{Kappa}}$ and $\text{elbow}_{\text{rho}}$ are threshold for kappa and rho to be meaningful

Spline subtraction (dfuresub-..._deltam.nii)

Original series (zigzag yellow line) is sequenc of control (high signal) and labeled (low signal) images

By using spline interpolation, series of control (red line) and labeled (purple line) images per timepoint are created

The control and labeled series are subtracted from each other per timepoint.





$$CBF = \frac{6000 \cdot \lambda \cdot (Control - Label) \cdot e^{PLD/T1_{blood}}}{2 \cdot \alpha \cdot T1_{blood} \cdot M0_{T1} \cdot (1 - e^{-\frac{\tau}{T1_{blood}}})} \quad \text{In ml/100g tissue/min}$$

With:

- PLD = Post Labeling Delay
- T1_{blood} = 1650 ms
- λ =0.9 brain/blood partition coefficient in mL/g
- α =0.85 labeling efficiency on GE
- τ =Label duration + PLD + slice time (time for T1 recovery for the labeled spins per slice)
- M0_{T1} is T1 corrected m0scan ($M0_{T1} = M0 \cdot (1 - e^{-\frac{TR}{T1}})$) with T1=1459ms for grey matter, 974ms for whitter matter and 4190ms for CSF (from Bojorquez et al. 2017. What are normal relaxation times of tissues at 3 T? Magnetic Resonance Imaging 35:69-80)

Settings in AutoSPMpreprocessing_ASLBOLD.m

%% Give path to SPM12 and GroupICA

```
params.spm_path = '/Users/accurad/Library/CloudStorage/OneDrive-Personal/Matlab/spm12';  
params.GroupICAT_path = '/Users/accurad/Library/CloudStorage/OneDrive-Personal/Matlab/GroupICATv40c';
```

Set SPM and GroupICAT_path

%% Give the basic input information of your data

```
datapath = '/Volumes/LaCie/UZ_Brussel/asl_bold/ASL_fingertapping';  
sublist = [6:10]; %list with subject id of those to preprocess separated by , (e.g. [1,2,3,4]) or alternatively use sublist = [first_sub:1:last_sub]  
nsessions = [1]; %nsessions>0  
params.func_save_folder = 'preproc_func_filter_indTE'; %name of the folder to save the preprocessed bold data  
params.perf_save_folder = 'preproc_asl_filter'; %name of the folder to save the preprocessed asl data  
task = {'bilateral_fingertapping'};  
%In case of multiple runs in the same session exist  
params.func.mruns = false; %true if run number is in filename  
params.func.runs = [1]; %the index of the runs (in filenames run-(index))  
% For ME-fMRI  
params.func.meepi = true; %true if echo number is in filename (default=true)  
params.func.echoes = [1,2,3,4]; %the index of echoes in ME-fMRI used in the analysis. If meepi=false, echoes=[1].  
params.use_parallel = false; % (default=false)  
params.maxprocesses = 2; %Best not too high to avoid memory problems % (default=2)  
params.loadmaxvols = 100; %to reduce memory load, the preprocessing can be split in smaller blocks (default = 100)  
params.keeplogs = false; % (default=false)  
params.save_intermediate_results = false; %clean up the directory by deleting unnecessary files generated during the processing (default = false)
```

Set path to your data folder (with sub-01 ... as subfolders)

List of subjects and sessions you want to preprocess

Give name for the preprocessed data output folders

Task identifier (as in aslbold filename _task-...)

If multiple runs (_run-... should be in aslbold filename)

MBME ASLBOLD is multi echo / give number of echoes

For parallel processing of data (only tested on MAC)

To reduce the amount of data loaded at once to avoid memory errors

Keep or remove the intermediate created timeseries to clean up dataspace

Settings in AutoSPMpreprocessing_ASLBOLD.m

%% Preprocessing anatomical data

```
params.preprocess_anatomical = false;    Preprocess the anatomical data

% Normalization
params.anat.do_normalization = true;      Normalization parameter
params.anat.normvox = [2.0 2.0 2.0]; %(default=[2.0 2.0 2.0]) Same as for fMRI!!

% Segmentation using CAT12
params.anat.do_segmentation = false; %(default=true)
params.anat.roi_atlas = false; %(default=false)    Do GM/WM/CSF and ROI segmentation
```

%% Preprocessing ASL data

```
params.preprocess_asl = false; %(default=true)    Preprocess the ASL data

%ASL data
params.asl.isM0scan = 'last'; %The M0 image is by defaultt the last volume @GE (set 'last')
params.asl.LabelingDuration = 1.450; % in seconds (parameter is ignored if LabelingDuration is in json file)
params.asl.PostLabelDelay = 1.525; % in seconds (parameter is ignored if PostLabelDelay is in json file)

params.asl.temp_resolution = 'original'; %temporal resolution of the gennerated CBF series
% 'original' : temporal resolution of the original series
% 'only_mean' : only 1 CBF image (mean over the whole series)
% 'reduced' : the mean CBF over a few timepoints (e.g. per minute)
params.asl.dt = 40; %new temporal resolution in seconds if params.asl.temp_resolution = 'reduced'
```

The time resolution of the subtracted time series

Original -> subtraction image per timepoint

Only_mean -> mean of all subtraction images

Reduced -> subtraction images are average per dt seconds (a new timeseries at a reduced temporal resolution is created)

Settings in AutoSPMpreprocessing_ASLBOLD.m

%% Preprocessing functional (the order of the parameters represents the fixed order of the steps done)

params.preprocess_functional = true; %(default=true) Preprocess the functional (BOLD) data

% Remove the dummy scans n_dummy_scans = floor(dummytime/TR)
params.func.dummytime = 0; %time in seconds (default=2*TR) Number of dummy scans is dummytime/TR

% Realignment (motion correction)
params.func.do_realignment = true; %(default=true) realignment

% Geometric correction
params.func.pepolar = false; %(default=true) Geometric correction with fmap scan

%Denoising before echo combination and normalization using the
%parameters from params.denoise
params.func.denoise = false; %(default=false) ME-ICA-AROMA denoising

params.func.combination = 'none'; %only used for ME-EPI (default=T2star_weighted) Combining the multiple echoes in 1 weighted timeseries
%none: all echoes are preprocessed separately
%average: The combination is the average of the multiple echo images
%TE_weighted: The combination is done $w_i = TE_i$ or
%T2star_weighted: dynamic T2* weighted combination (loglinear fit from tedana)
%dyn_T2star: dynamic T2* mapping (not advised due to the propagation of noise leading to spikes in the T2* maps)
%see Heunisch et al. 2021. The effects of multi-echo fMRI combination and rapid T2*-mapping on offline and real-time BOLD sensitivity. NeuroImage 238, 118244

% Slice time correction
params.func.do_slicetime = true; %(default=true) Slice time correction

% Normalization
params.func.do_normalization = true; %(default=true) normalization
params.func.normvox = [2.0 2.0 2.0]; %(default=[2.0 2.0 2.0])

% Smoothing
params.func.do_smoothing = true; %(default=true) smoothing
params.func.smoothfwhm = 6; %(default=6)

Settings in AutoSPMpreprocessing_ASLBOLD.m

%% Denoising

%if do_denoising = true and preprocess_functional = false -> only denoising of the normalised data
%Denoising will not run if it was already done before

params.do_denoising = false; %(default=false) Apply denoising on the normalized data (only if not done before the echo combination)

% Extend motion regressors with derivatives and squared regressors Extend the motion regressors to 24
params.denoise.do_mot_derivatives = true; %derivatives+squares (24 regressors) (default=true)

% Band-pass filtering
params.denoise.do_bpfilter = true; %(default=true) Apply a bandpass filter to remove signals at non-bold frequencies
params.denoise.bpfilter = [0.008 0.1]; %no highpass filter is first 0, no lowpass filter is last Inf, default=[0.008 0.1]
params.denoise.polort = 2; %order of the polynomial function used to remove the signal trend (0: only mean, 1: linear trend, 2: quadratic trend, default=2)

% aCompCor
params.denoise.do_aCompCor = false; %(default=false) Determine noise signals in csf and non-brain areas
params.denoise.Ncomponents = 5; %if in range [0 1] then the number of aCompCor components is equal to the number of components that explain the specified per

% ICA-AROMA
params.denoise.do_ICA_AROMA = true; %(default=true) Use AROMA to differentiate noise from non-noise components (Van Schuerbbeek et al. 2022 The optimized combination of aCompCor and ICA-AROMA to reduce motion and physiologic noise in task fMRI data. Biomed Phys Eng Express. 8(5). doi: 10.1088/2057-1976/ac63f0.)

% Noise regression / remove ICA-AROMA noise components
params.denoise.do_noiseregression = true; %(default=true) Remove all noise regressors from the BOLD data

% Prepare data for DUNNET denoising in python (WIP)
params.denoise.do_DUNNET = false; %(default=false) Research in progress but not applicable yet

Run the script and wait till finished

