MBME ASL/BOLD fMRI
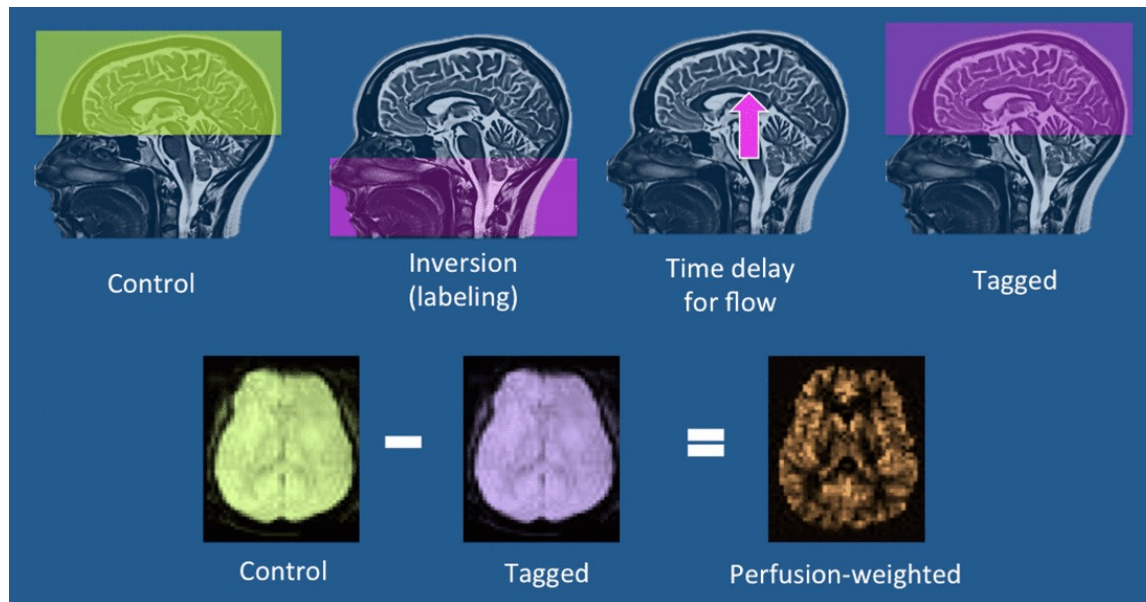
Sequence and processsing @ MRI UZ Brussel

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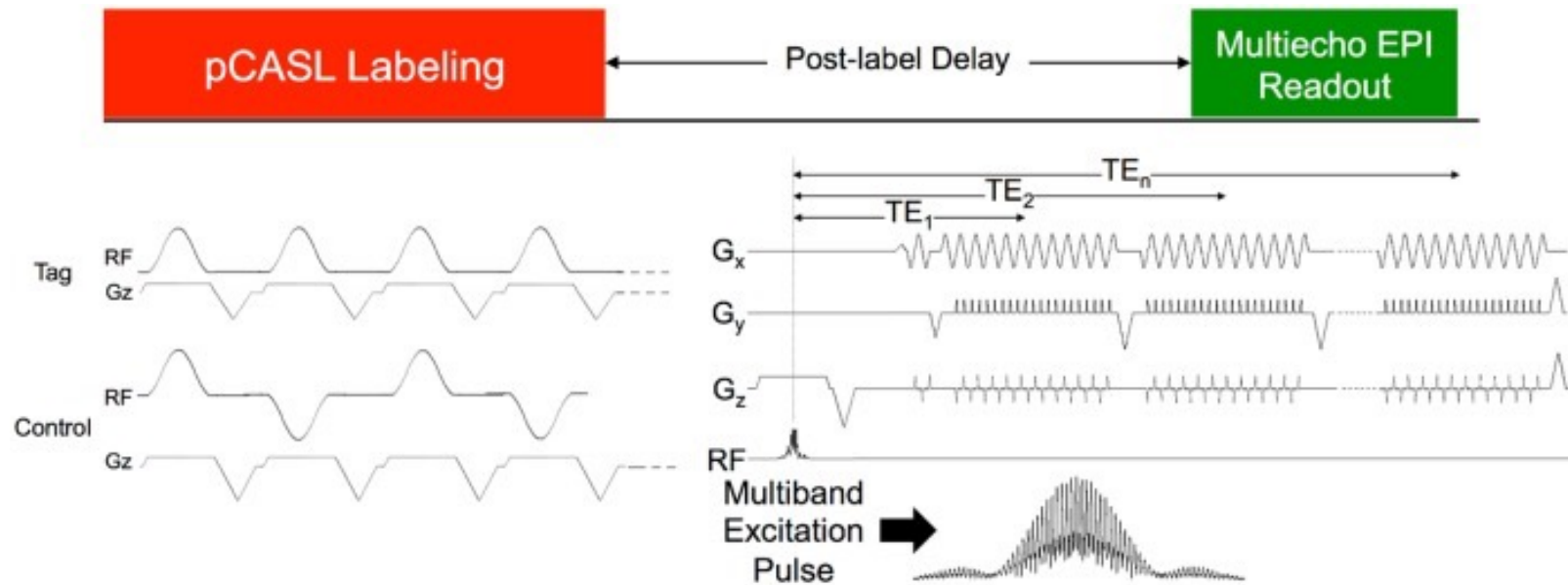
Pseudo Continuous ASL
(PCASL)

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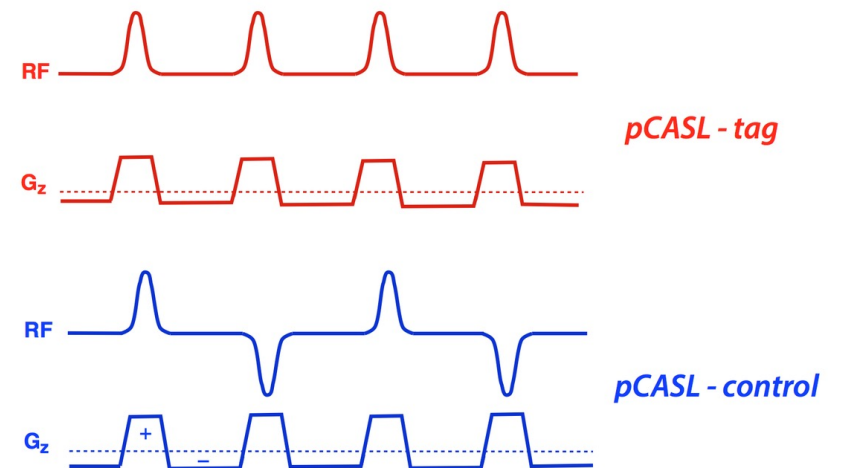
Sequence from Cohen et al. 2018. Multiband multi-echo simultaneous ASL/BOLD for task-induced functional MRI. PLoS One 13(2): e0190427 (doi: 10.1371/journal.pone.0190427)

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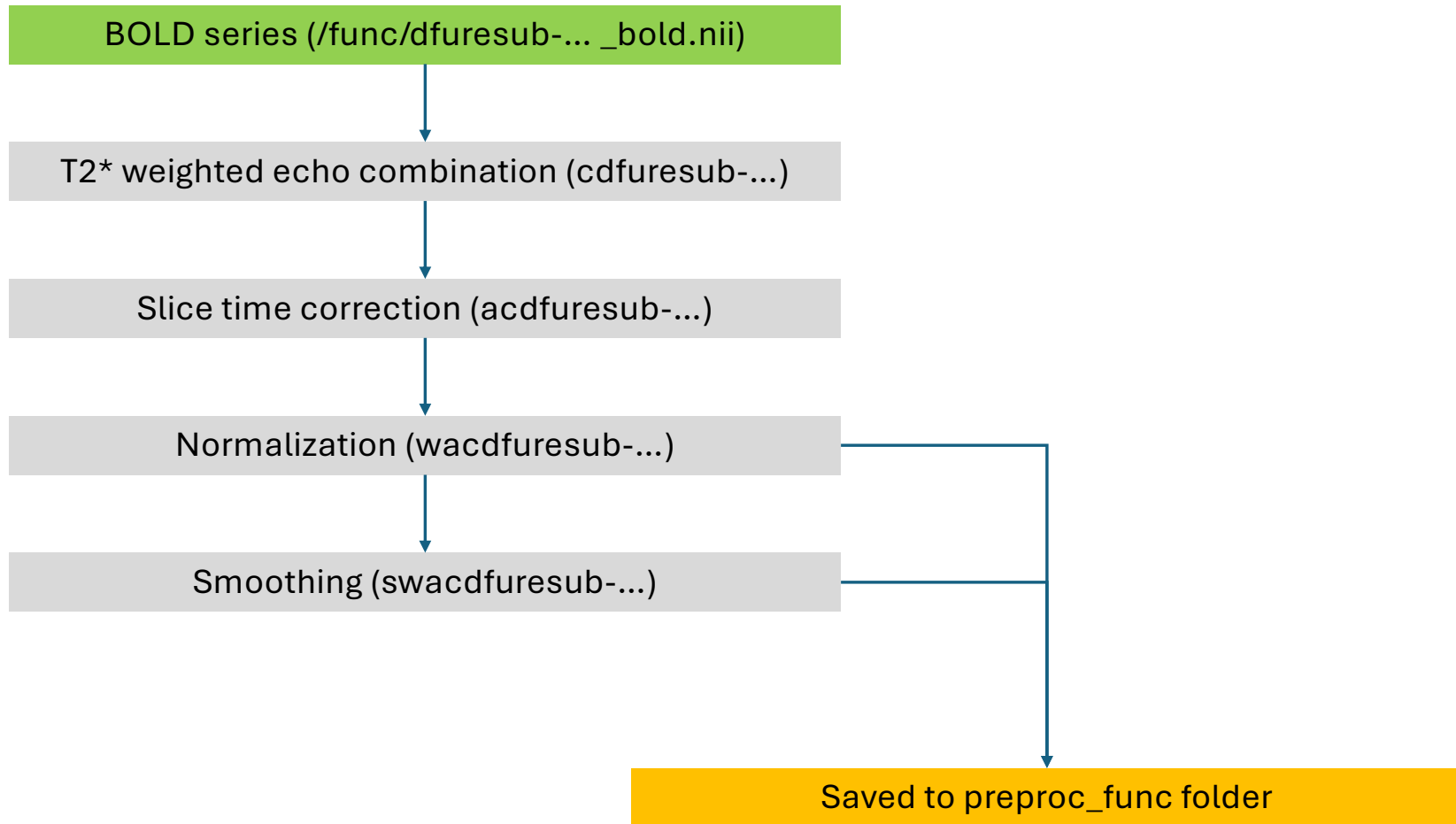
                    … sub-01_ses-001_task-**your_task**_run-1_dir-PA_echo-n**_aslbold**.json

                …

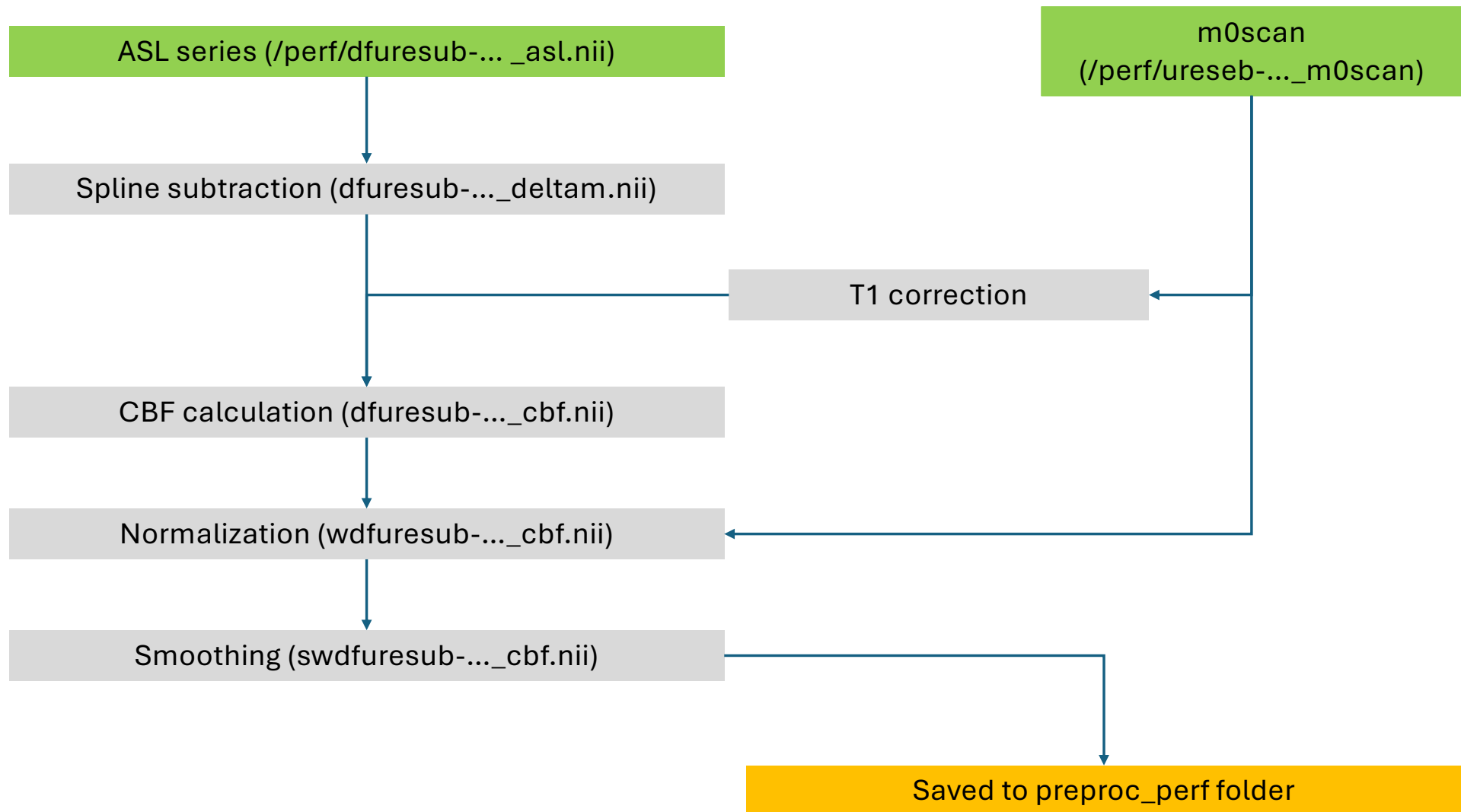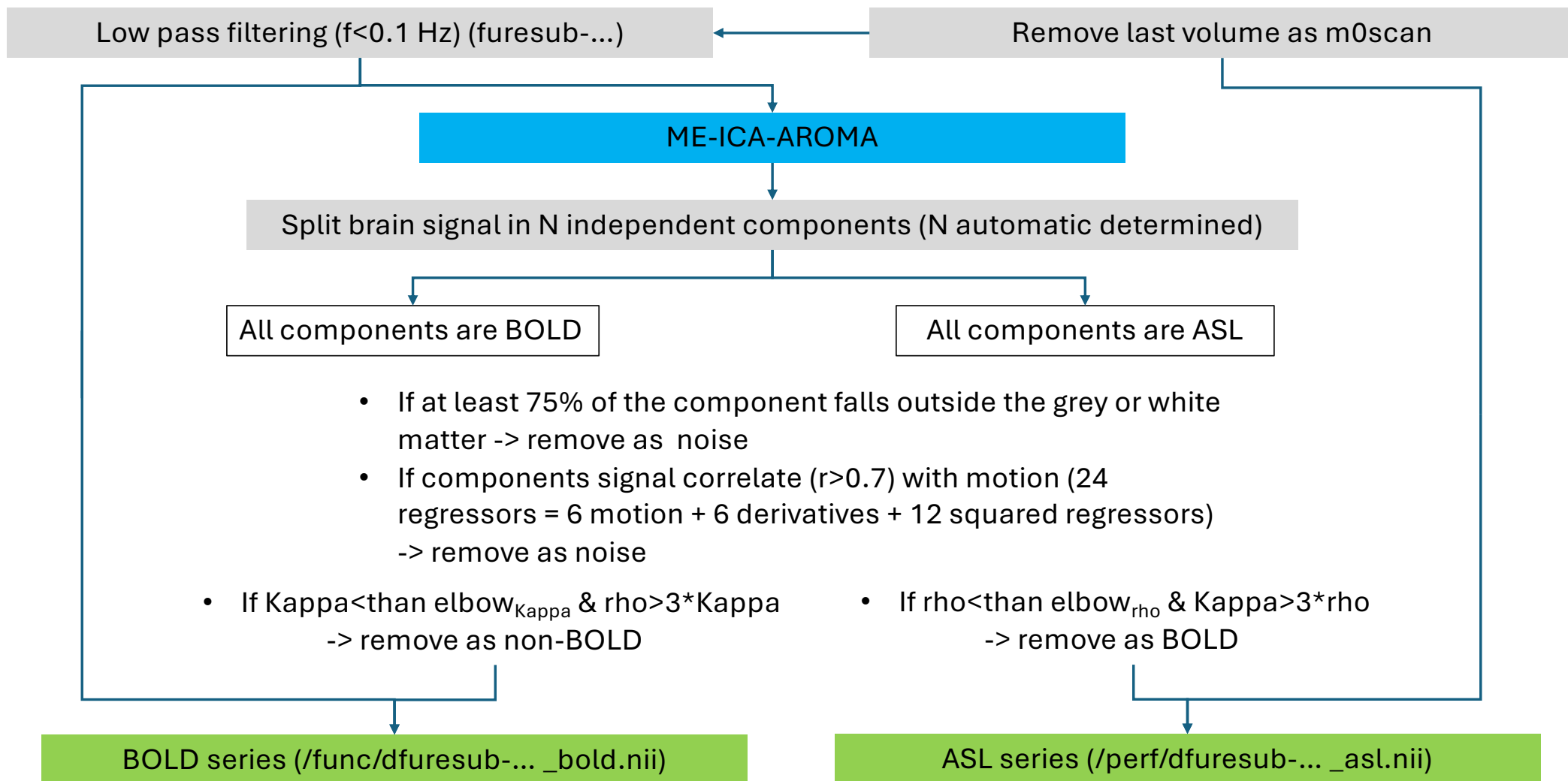   sub-01_ses-001_task-**your_task**_run-1_events.tsv

- 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

```
        fmat data                                    aslbold data

Reorient with AC-PC (esub-...) & remove dummys    Reorient with AC-PC (esub-...) & remove dummys

                                                         Normalized intensities
                                                            volume/volume

        Take first volume
                                                         Determine realignment
                                                           (motion) parameters

Coregistration to first volume of aslbold  ◄────    Perform realignment (resub-...)

                                              ──►    Geometric distortion correction (uresub-...)

                                                     Remove last volume as m0scan

Low pass filtering (f<0.1 Hz) (furesub-...)
                                                                                    m0scan
                                                                              (/perf/ureseb-..._m0scan)
         ME-ICA-AROMA

BOLD series (/func/dfuresub-... _bold.nii)         ASL series (/perf/dfuresub-... _asl.nii)
```

```
BOLD series (/func/dfuresub-... _bold.nii)

        │
        ▼

T2* weighted echo combination (cdfuresub-...)

        │
        ▼

Slice time correction (acdfuresub-...)

        │
        ▼

Normalization (wacdfuresub-...)

        │
        ▼

Smoothing (swacdfuresub-...)

        │
        ▼

Saved to preproc_func folder
```

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

ASL series (/perf/dfuresub-... _asl.nii)

m0scan (/perf/ureseb-..._m0scan)

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

T1 correction

CBF calculation (dfuresub-..._cbf.nii)

Normalization (wdfuresub-..._cbf.nii)

Smoothing (swdfuresub-..._cbf.nii)

Saved to preproc_perf folder

```
Low pass filtering (f<0.1 Hz) (furesub-...)  ←  Remove last volume as m0scan
```

ME-ICA-AROMA

Split brain signal in N independent components (N automatic determined)

All components are BOLD

All components are ASL

- If at least 75% of the component falls outside the grey or white matter -> remove as noise
- If components signal correlate (r>0.7) with motion (24 regressors = 6 motion + 6 derivatives + 12 squared regressors) -> remove as noise

- If Kappa<than $elbow_{Kappa}$ & rho>3*Kappa -> remove as non-BOLD

- If rho<than $elbow_{rho}$ & Kappa>3*rho -> remove as BOLD

BOLD series (/func/dfuresub-... _bold.nii)

ASL series (/perf/dfuresub-... _asl.nii)

$S=S_0*exp(-TE/T2*)$ -> measure for the amount of signal variation explaned by variation in T2* (Kappa) and variation in S_0 due to spin inflow (rho)
$Elbow_{Kappa}$ and $elbow_{rho}$ are threshold for kappa and rho to be meaningfull

Original series (zigzag yelow 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.

Spline subtraction (dfuresub-..._deltam.nii)		m0scan (/perf/ureseb-..._m0scan)

T1 correction

CBF calculation (dfuresub-..._cbf.nii)
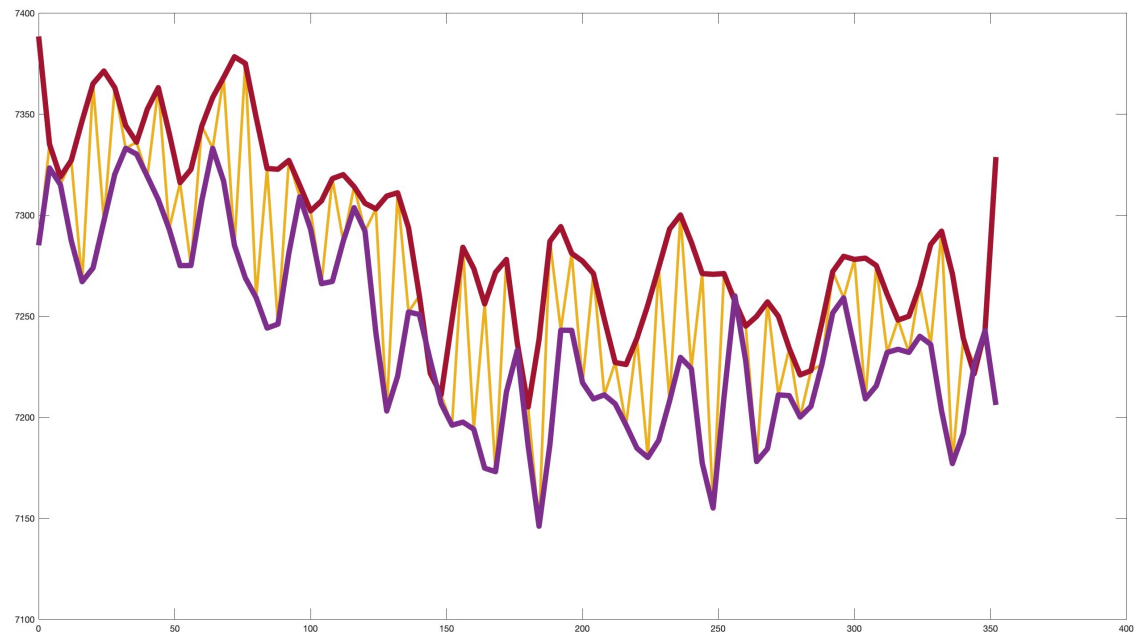
$$CBF = \frac{6000 \cdot \lambda \cdot (Control - Label) \cdot e^{PLD/T1_{blood}}}{2 \cdot \alpha \cdot T1_{blood} \cdot M0_{T1} \cdot (1 - e^{-\frac{\tau}{T1_{blood}}})}$$

In ml/100g tissue/min

With:

- PLD = Post Labeling Delay
- T1blood = 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 ($M0_{T1} = M0 \cdot \left(1 - e^{-\frac{TR}{T1}}\right)$ 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';          Set SPM and GroupICAT_path
params.GroupICAT_path = '/Users/accurad/Library/CloudStorage/OneDrive-Personal/Matlab/GroupICATv40c';

%% Give the basic input information of your data

datpath = '/Volumes/LaCie/UZ_Brussel/asl_bold/ASL_fingertapping';          Set path to your data folder (with sub-01 ... as subfolders)

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          List of subjects and sessions you want to preproccess

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          Give name for the preprocessed data output folders

task ={'bilateralfingertapping'};          Task identifier (as in aslbold filename _task-...)

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

% For ME-fMRI
params.func.meepi = true; %true if echo number is in filename (default=true)          MBME ASLBOLD is multi echo / give number of echoes
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)          For parallel processing of data (only tested on MAC)
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)          To reduce the amount of data loaded at once to avoid memory errors

params.save_intermediate_results = false; %clean up the directory by deleting unnecessary files generated during the processing (default = false)
          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 defaullt the last volume @GE (set 'last')
    params.asl.LabelingDuration = 1.450; % in seconds (parameter is ignored if LabelingDuration is in json file)    ASL parameters in the scan
    params.asl.PostLabelDelay = 1.525; % in seconds (parameter is ignored if PostLabelDelay is in json file)

    params.asl.temp_resolution = 'original'; %tempporal 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

```matlab
%% 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

    % Realignnment (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 ussing 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 multilpe echoes in 1 weighted timeseries
    %none: all echoes are preprocessed separatly
    %average: The combination is the average of the multiple echo images
    %TE_weighted: The combination is done wi=TEi or
    %T2star_weighted: dynamic T2* weighted combination (loglinear fit from tedana)
    %dyn_T2star: dynamic T2* mapping (not adviced due to the propagation of noise leading to spikes in the T2* maps)
    %see Heunis 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)
    params.func.smoothfwhm = 6; %(default=6)     smoothing
```

Settings in AutoSPMpreprocessing_ASLBOLD.m

```matlab
%% 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                                                 Use AROMA to differentiate noise from non-noise components (Van Schuerbbeek et al. 2022 The optimized
    params.denoise.do_ICA_AROMA = true; %(default=true)         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