PCASL PREPROCESSING PIPELINE WITH MOTION SCRUBBING
Complete Documentation and Verification Guide

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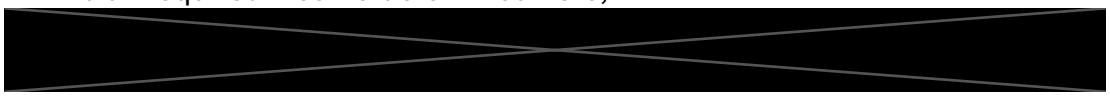
Find all required files/ folders linked here,



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1. PIPELINE OVERVIEW

PURPOSE:
Process pseudo-continuous arterial spin labeling (pCASL) data with motion correction and volume removal (SCRUB) to improve cerebral blood flow (CBF) quantification accuracy.

PIPELINE STAGES:
Stage 1: DICOM → NIfTI conversion (MASTER_SETUP_CORRECTED.sh)
Stage 2: Realignment and initial preprocessing (batch_run_PART1_clean.m)
Stage 3: Motion-corrupted volume removal and file modifications for r_ASL.nii,mean_ASL.nii and rp_ASL.txt(removing volumes from subjects that exceed threshold frame displacement 5mm, and rotation 3 degree; using matlab_step3_removal_AUTO_NO_BACKUPS.m)
Stage 4: Coregistration, smoothing, CBF quantification, normalization (batch_run_PART2_clean.m)

This approach allows identification of motion-corrupted volumes AFTER realignment, when motion parameters are most accurate, then removes those volumes before coregistration and CBF quantification.

EXPECTED OUTCOME:
Improved CBF estimates by eliminating motion-corrupted label-control pairs that would otherwise contaminate the mean image and reduce CBF values.

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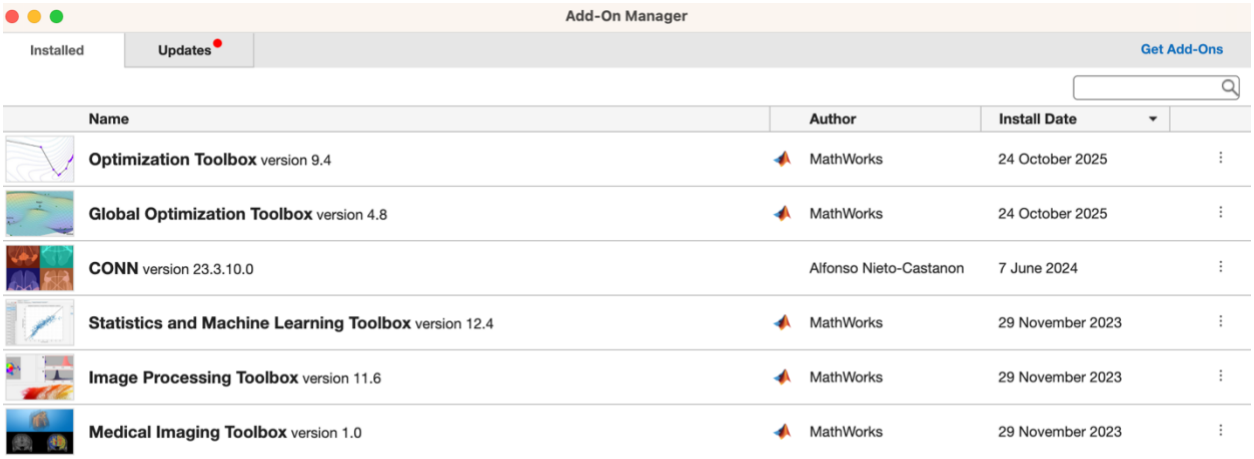
2. SOFTWARE REQUIREMENTS

- **SPM12**: https://www.fil.ion.ucl.ac.uk/spm/doc/
- **MATLAB** (tested with R2021b or later), https://www.mathworks.com/downloads/
- **FSL**: https://fsl.fmrib.ox.ac.uk/fsl/fslwiki/
- **dcm2niix**: https://www.nitrc.org/plugins/mwiki/index.php/dcm2nii:MainPage#Introduction

- Python 3.x with nibabel and numpy (for bash scripts, optional)

MATLAB TOOLBOXES:



PATH SETUP:
SPM12 should be in MATLAB path
FSL should be properly configured in shell

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3. DIRECTORY STRUCTURE TO REMEMBER AND APPLY

PROJECT ROOT here for me: /Users/vaidehipatel/Downloads/

Downloads

```
├── data_dicom_archived/       # Original DICOM archives downloaded from Lab Dropbox link below
│   ├── p033.tar.gz          # Example: sub86
│   ├── p061.tar.gz          # Example: sub135
│
├── nifti_converted/          # Intermediate NIfTI files (generated from stage1, don't worry)
│   ├── sub86/
│   │   ├── ASL.nii.gz
│   │   └── T1.nii.gz
│
├── batch_scripts_pcasl/       # Main working directory (links for downloading batchscripts and par.m as per lab on lab Dropbox linked below)
│   ├── par.m              # Configuration file (linked below)
│   ├── batch_run_PART1_clean.m (linked below)
│   ├── batch_run_PART2_clean.m (linked below)
│   ├── matlab_step3_removal_AUTO_NO_BACKUPS.m (linked below)
│
│   ├── qc_outputs/          # Quality control outputs
│   │   └── Master_Exclusion_List.txt     # file that was created for deleting volume pairs from outlier subjects linked below ;
                YOU HAVE TO SET PATH TO WHEREVER THIS FILE IS FOR YOU in the stage3 matlab script that removes volumes
│   │
│   ├── sub86/              # Subject data (files are generated here)
│   │   ├── FUNC/
│   │   │   ├── ASL.nii       # Original 90 volumes
│   │   │   ├── rASL.nii      # Realigned, then cleaned to 62 vols
│   │   │   ├── rp_ASL.txt     # Motion parameters, 62 rows
│   │   │   ├── meanASL.nii    # Mean image for coregistration
│   │   │   └── ...
│   │   └── STRUC/
│   │       └── T1.nii
│   └── [other subjects...]
└── MASTER_SETUP_CORRECTED.sh    # Stage 1 script, linked below
```

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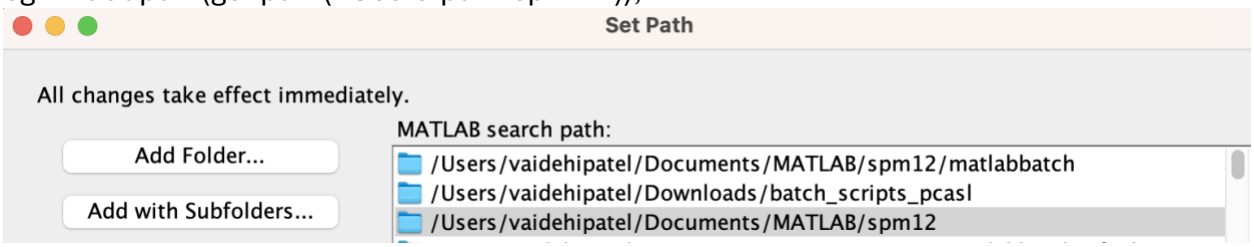
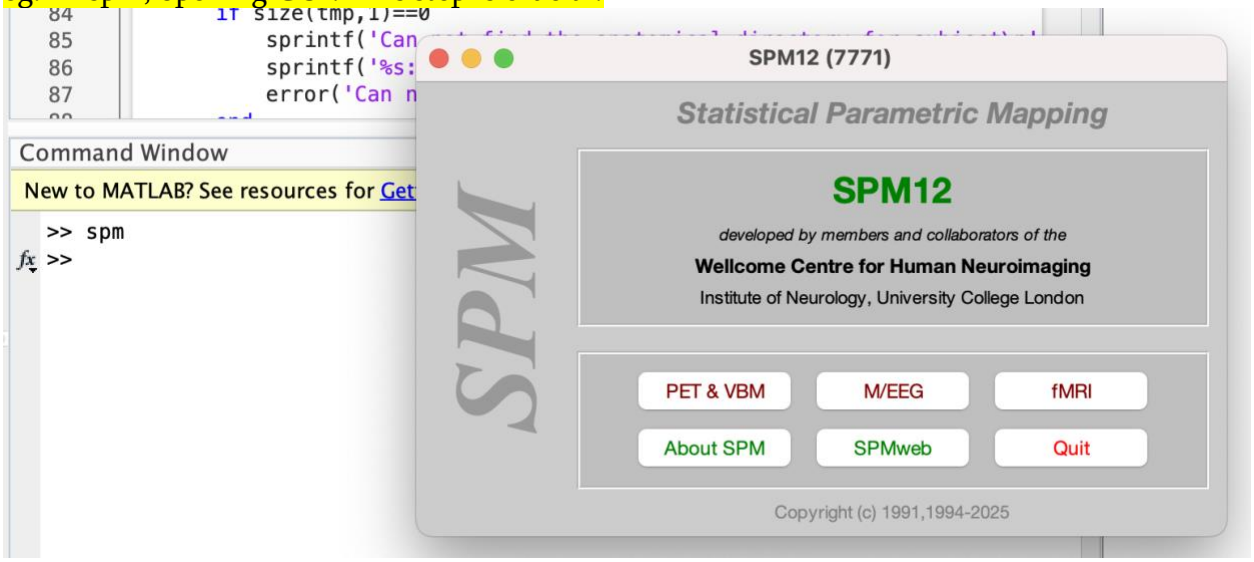
STEPS BEFORE WE MOVE TO STAGE 1,2: INITIAL PREPROCESSING

Steps to initialize Matlab-SPM if not already before downloading batch_scripts_pcasl folder:

1. Open Matlab command window, Add path or set path to SPM12,
   eg. >>addpath(genpath('/Users/path/spm12')),



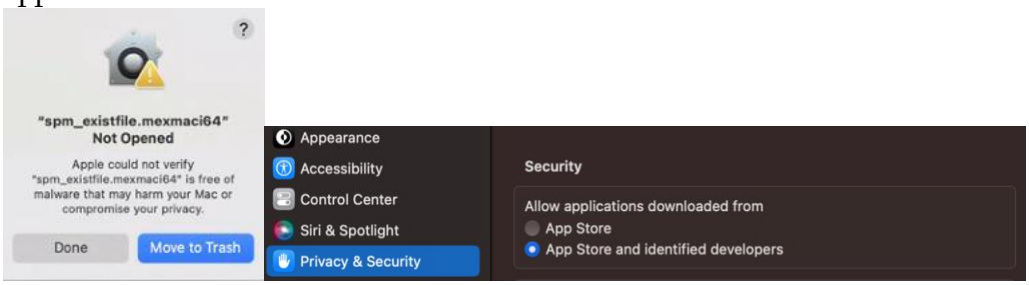
2. Initialise and run SPM.
   eg. >> spm, opening GUI. This step is crucial.



Make sure there's no multiple versions of SPM or Matlab that can cause confusion to you or the system. (Refer Error 1 below for problems in Mac for this step), then click quit spm, but don't exit Matlab.

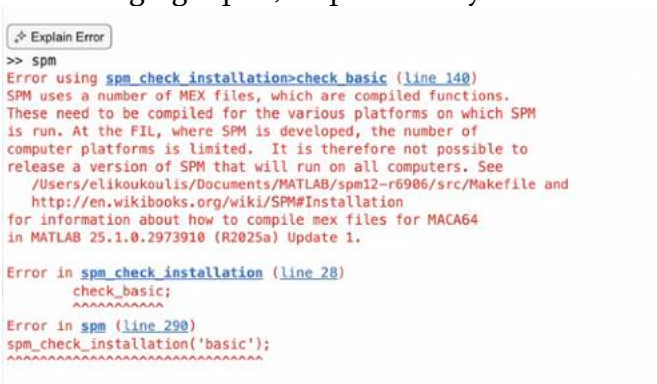
Errors usually encountered in the process of initializing SPM (Mac):

1) If while running par, an error relating to MEX files appears, you probably have one version of SPM/Matlab accessing or trying to compile using another older/newer version of the application present on your computer. If the error is relating to Mex files plus an apple pop up like below, it means you might need to goto Settings and enable downloading software/applications from sources besides AppStore.



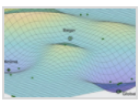
Online refer: https://www.mathworks.com/matlabcentral/answers/2154500-spm12-problem-in-macos

2) If there's an error while intialising spm like below, you might have to check if you followed all instructions for installation properly. Here's a video channel many beginners prefer while installing SPM, it's a good resource channel for neuroimaging topics, https://www.youtube.com/watch?v=qbcBLXJhzZg



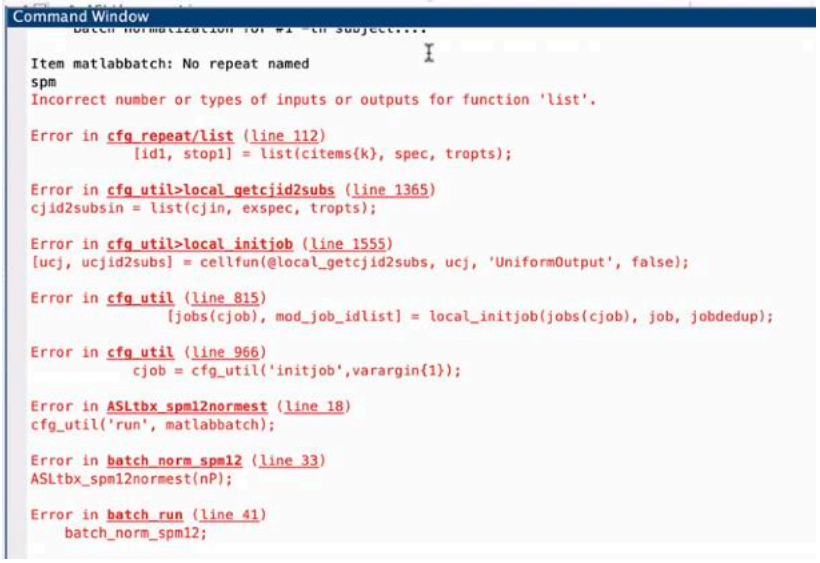
https://www.fil.ion.ucl.ac.uk/spm/docs/installation/#macos

3) Other error is about installing some toolboxes, this step needs to be done if and only if the errors indicate some function in batch_run needs one of three toolboxes. Click one of the toolboxes like below and sign in your Matlab account when prompted, download and intall the toolbox like below and when Matlab terminates and restarts follow steps 4,5,6,7 from the steps to execute again.



Global Optimization Toolbox version 4.8

4) If there's an error like below it simply is indirectly indicating that spm wasn't initialized properly after installation. Refer Error 2) solution and execute steps 4,5,6,7 from steps to execute again after initializing spm.



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BEFORE WE MOVE TO STAGE 1,2: INITIAL PREPROCESSING (PART1)

Steps to organize ASLtbx2

1. Download a version of approved **batch_scripts_pcasl.zip** available on our lab Dropbox link .

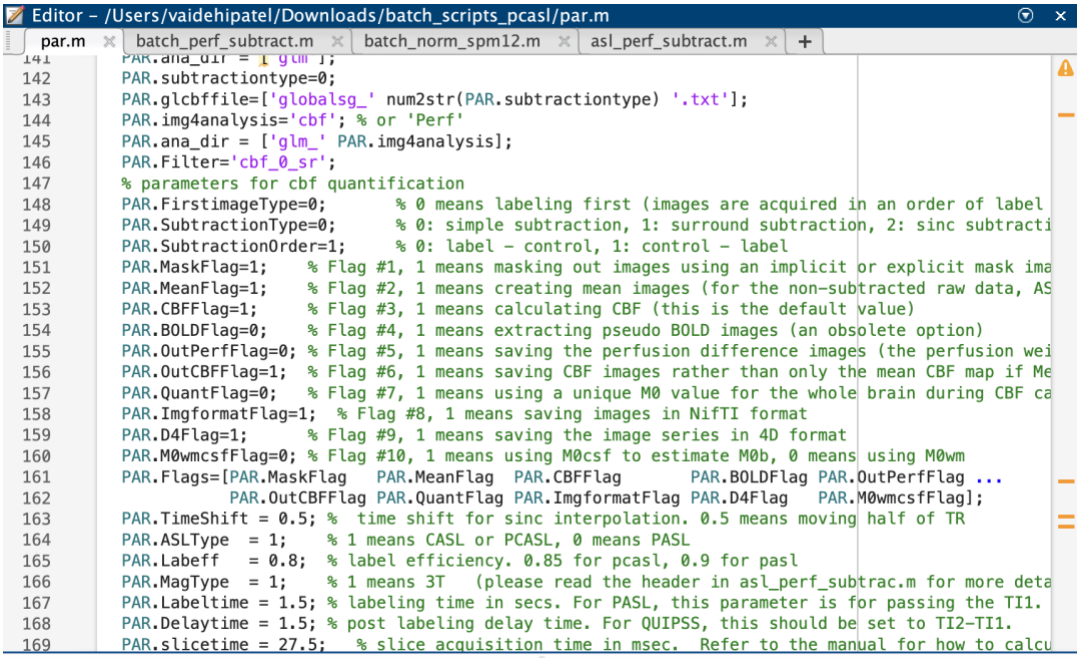
[redacted]

You have to confirm if the par.m on dropbox match your requirements first, depending on the dataset you're working on, we are working on MOSS dataset here.

Alternatively, you can download Batch_scripts folder named as **ASLtbx2** from Upenn website, link, https://www.cfn.upenn.edu/zewang/download.php

But two scripts folders linked above, have scripts, namely par.m and batch_norm_spm12.m and batch_perf_subtract.m different in bounding box size and accepting PAR global parameters instead of local parameters. So its preferable to have atleast par.m from lab version and make minute change regardless of where you get batch_scripts_pcasl folder from. Differences explained in point 3.

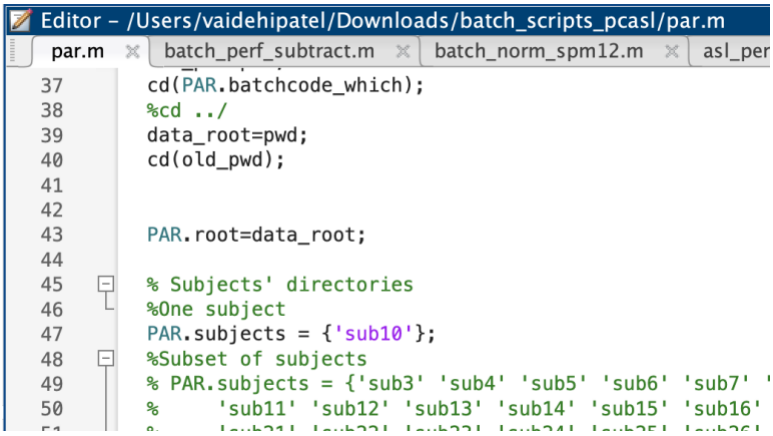
2. There is **lab-specific version of script par.m** that we have to replace in batch_scripts_pcasl folder (refer to Hoon for more details). Linked here, **par.m()**



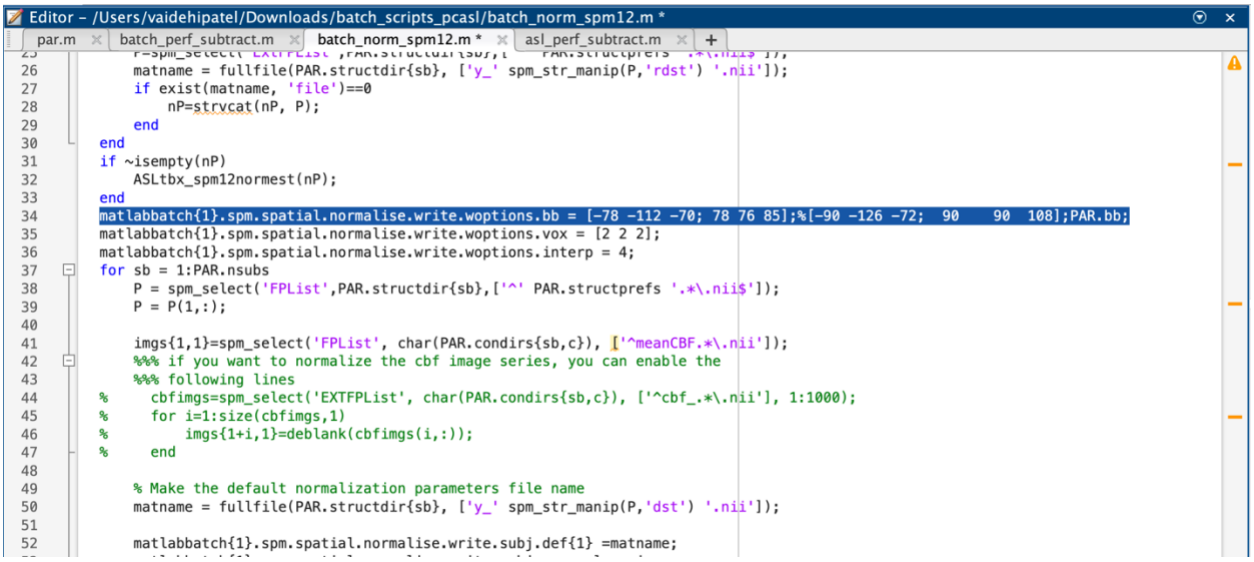
These parameters are lab-specifc in par.m()

3. Now regardless of what version of Batch_scripts_pcasl folder you have, make sure at least par.m is lab-version. And check the following lines in following scripts and re-confirm with Hoon if some or all of the changes should apply to your scripts.

a. Confirm Which subjects should be part of line PAR.subjects in par.m, mapping of subject id details in next stage.

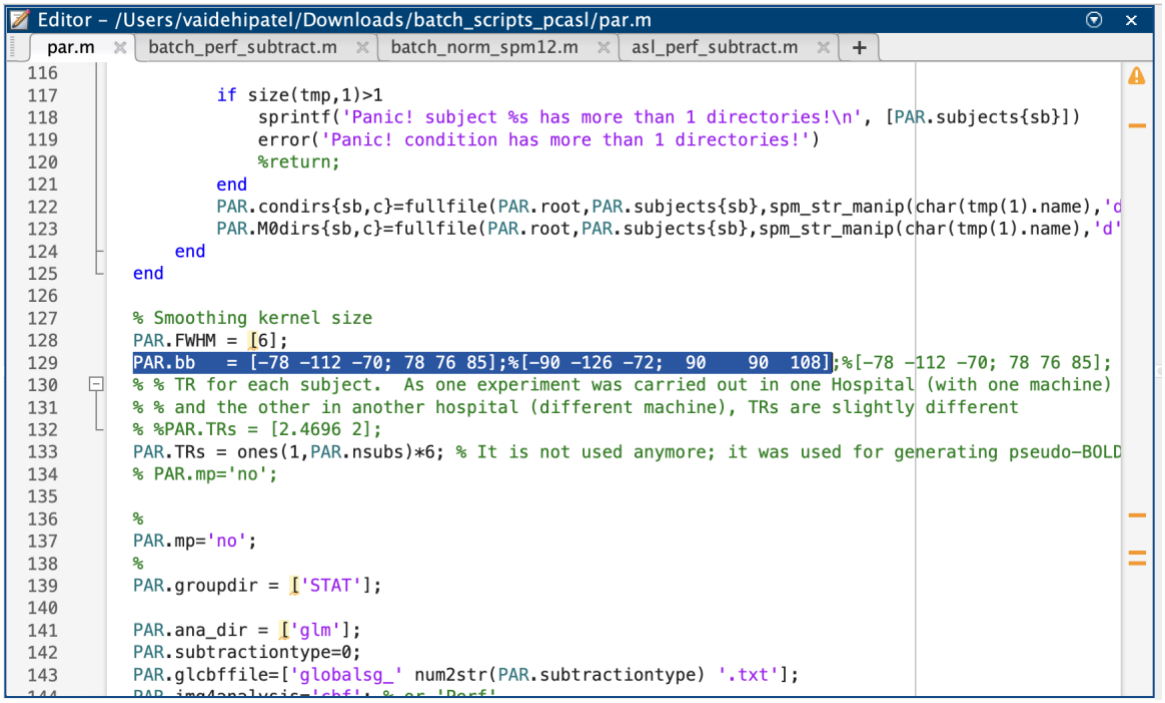


b. In batch_norm_spm_12.m check the line highlighted in screenshot below it should have bounding box smaller than [-90 -126 -72; 90 90 108]<- which we have to comment % in case its uncommented . And make sure the bounding box size is either hardcoded [-78 -112 -70; 78 76 85] or accepting PAR.bb; as input from par.m (explained below)



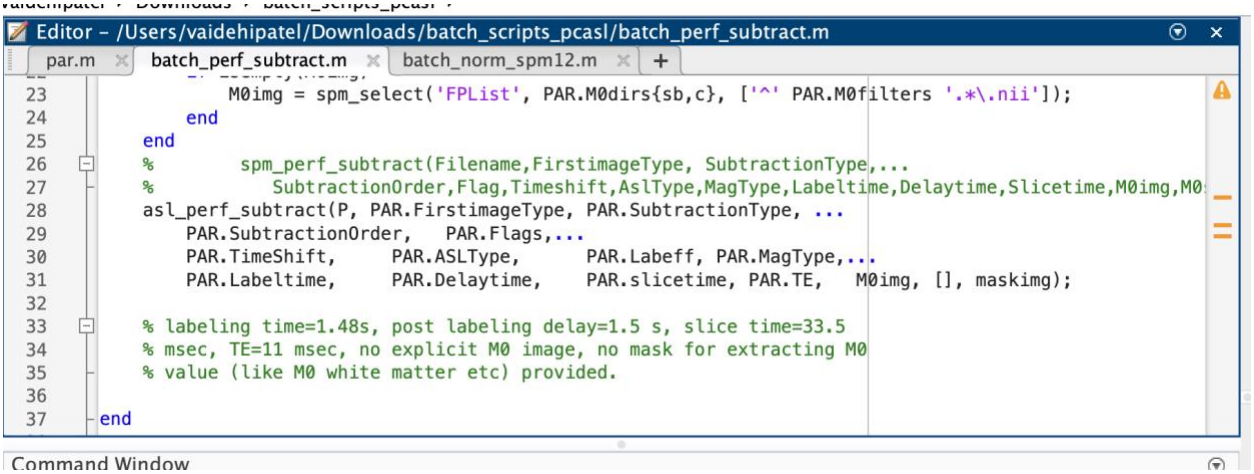
c. In par.m the bounding box size is defined in PAR.bb, in the lab version of par.m the bounding box is orginally [-90 -126 -72; 90 90 108], we have to comment it %, and specify the bounding box size to[-78 -112 -70; 78 76 85] like below, especially if using the Lab batch_scripts_pcasl.zip folder and not the scripts folder from ASLtbx2 directly.

If in case you're not accepting bounding box variables in batch_norm_spm12.m **from Par.bb;** then making change in Par.bb line hardcoding [-78 -112 -70; 78 76 85] is optional.

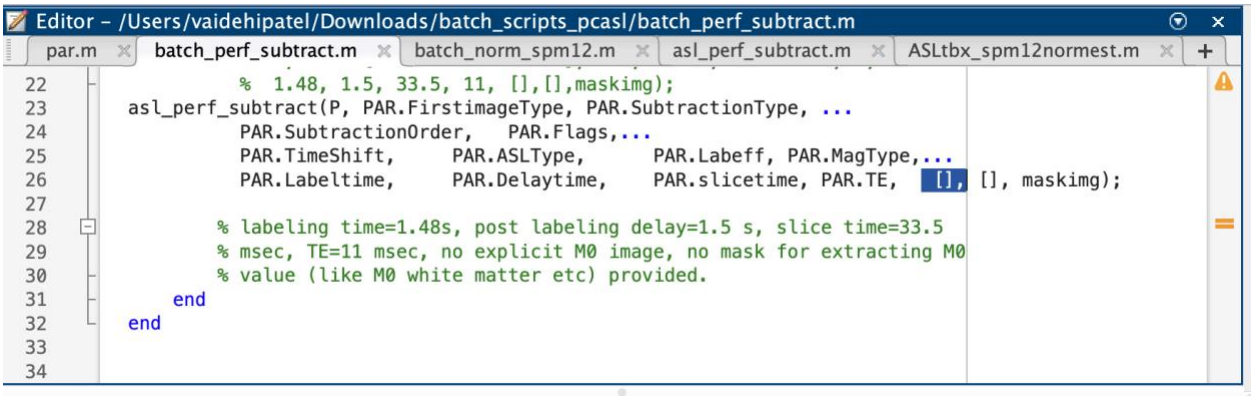


d. Lastly, especially if your're not using the Lab batch_scripts_pcasl.zip folder, and using the scripts folder from ASLtbx2 directly, then make sure the batch_perf_subtract.m calls the asl_perf_subtract.m script passing labeling and other parameters during it defined in PAR. variables in par.m. Make sure the parameters are not hardcoded in the asl_perf_subtract() call,

```
asl_perf_subtract(P, PAR.FirstimageType, PAR.SubtractionType, ...
    PAR.SubtractionOrder,   PAR.Flags,...
    PAR.TimeShift,     PAR.ASLType,     PAR.Labeff, PAR.MagType,...
    PAR.Labeltime,     PAR.Delaytime,    PAR.slicetime, PAR.TE,   [], [], maskimg);
```



M0img mostly needs be empty if in case if it gives error make it empty like highlighted line below.



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4. STAGE 1: DICOM TO NIFTI CONVERSION

SCRIPT TO USE: MASTER_SETUP_CORRECTED.sh
Download MASTER_SETUP_CORRECTED.sh at link [redacted]

INPUT FOLDER NEEDED FOR IT: Download data_dicom_archived folder that has all the Moss raw data from Lab Dropbox linked here [redacted]

The subject mapping excel sheet example, p033_s1=sub86, uploaded on Dropbox, for reference [redacted]

PURPOSE:
Extract DICOM files from archives, convert to NIfTI format, and setup directory structure for preprocessing.

BEFORE EXECUTION:
CHANGE PATH TO your ‘data_dicom_archived (input) folder’
CHANGE PATH to your ‘batch_scripts_pcasl (output)

USAGE:
In ./MASTER_SETUP_CORRECTED.sh set path to your data_dicom_archived folder. And set output folder to your specific output folder.

Execution command example(bash): ./MASTER_SETUP_CORRECTED.sh sub86

WHAT IT DOES:

1.Maps subject ID to archive name and session (if multi-session)sub86 | p033 | s1 IS NOW EXCLUDED SO MAKE SURE TO NOT PROCESS IT ANYMORE with any steps.

2. Extracts DICOM from compressed archive
3. Locates ASL (pCASL) and T1 (MPRAGE) series
4. Converts to NIfTI using dcm2niix
5. Creates batch_scripts_pcasl/[subject]/ directory structure
6. Copies ASL.nii to FUNC/ and T1.nii to STRUC/, as required as input for ASLtbx

It does OUTLIER SUBJECT MAPPING in **data_dicom_archived** folder from Dropbox:

---

sub86 → p033.tar.gz, session s1
sub135 → p061.tar.gz, session s1
sub123 → p053.tar.gz, session s3
sub122 → p053.tar.gz, session s2
[...additional subjects in script...]

OUTPUT:

---

batch_scripts_pcasl/sub86/FUNC/ASL.nii (90 volumes, 64x64x18)
batch_scripts_pcasl/sub86/STRUC/T1.nii

VERIFICATION:

Check volume count:
fslinfo batch_scripts_pcasl/sub86/FUNC/ASL.nii | grep dim4
Expected: dim4 = 90

CRITICAL DECISION MADE #1:

Multi-session subjects (e.g., p053 archive contains s1, s2, s3) require session specification. The script navigates to the correct session subfolder before searching for ASL and T1 series.

Rationale: Some archives contain multiple scanning sessions. Without session

specification, the script would find all sessions and fail or select the wrong data.

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5. STAGE 2: INITIAL PREPROCESSING (PART1)

If you're running just batch_run.m once with the whole pipeline, you don't need to see the next steps but if you're preprocessing batchrun in two parts where first you rest orientation, realign and then remove volumes and complete rest of batch run with removed volumes , continue.

FOR SCRIPT: batch_run_PART1_clean.m , run in Matlab

I divided batch_run.m into two parts, linked here, in case you aren't running batch_run.m all at once for pre-processing, below is link for batchrun_PART1,

PATH SETTING IN par.m: adjust path between line 30-45 in case your subjects aren't being searched at the folder where you have your subjects

SUBJECT SPECIFICATION IN Line ~47 in par.m:

```
PAR.subjects = {'sub86'};
```

Change this to process different subjects as per the mapping of subjects eg p033_s1 is sub86, p033_s2 becomes sub87 and so on.

NOTE: Make sure you run clear all command on matlab console after each subject is fully processed after completion of stages, I processed all steps one subject at a time. Clear all makes sure the workspace variables for one subject does not get previous subjects workspace variable while processing new subject, as both have individual differences.

WHAT batch_run PART1 DOES:

---

1. Resets orientation matrices to standard space
2. Realigns all 90 ASL volumes using spm_realign_asl.m
3. Generates motion parameters (rp_ASL.txt, 90 rows x 12 columns)
4. Creates rASL.nii (90 realigned volumes)
5. Creates meanASL.nii (mean of all 90 volumes)

REALIGNMENT ALGORITHM:

Uses SPM's two-pass realignment with mean image as reference:
  Pass 1: Realign to first volume, create initial mean
  Pass 2: Realign to mean from Pass 1, create final mean
For a detailed flowchart of these two passes that happens automatically within realign, refer SPM_TwoPass_Flowchart.html u loaded on dro box, link

(NOTE: the key insight section at the botton isn't accurate but the Flowchart is)

Motion parameters (rp_ASL.txt) contain 12 columns:
  Columns 1-6: Translation (x,y,z) and rotation (pitch,roll,yaw)
  Columns 7-12: "zigzag pattern cleaned" motion timecourses.

INPUT FILE:
batch_scripts_pcasl/sub86/FUNC/ASL.nii (90 volumes) from stage1 program for dicom to nifti conversion

OUTPUT FILES:
---

batch_scripts_pcasl/sub86/FUNC/rASL.nii (90 volumes, realigned)
batch_scripts_pcasl/sub86/FUNC/rp_ASL.txt (90 rows, motion parameters)
batch_scripts_pcasl/sub86/FUNC/meanASL.nii (1 volume, mean of 90)

VERIFICATION:

Check files created:
  ls -lh batch_scripts_pcasl/sub86/FUNC/rASL.nii
  ls -lh batch_scripts_pcasl/sub86/FUNC/rp_ASL.txt

Check volume counts:
  fslinfo batch_scripts_pcasl/sub86/FUNC/rASL.nii | grep dim4
  Expected: dim4 = 90

  wc -l batch_scripts_pcasl/sub86/FUNC/rp_ASL.txt
  Expected: 90 rows

CRITICAL DESIGN DECISION #2:

Volume removal is performed AFTER realignment, not before.

Rationale: Motion parameters are most accurate after realignment. Attempting to identify bad volumes before realignment would require using unreliable motion estimates. Additionally, realignment itself can reveal motion through the creation of a blurry mean image when motion-corrupted volumes are included.

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6. STAGE 3: VOLUME REMOVAL AND MODIFICATIONS

INPUT: Master_Exclusion_List.txt

Masterlist for outlier subject with info on volume pairs to remove, its uploaded on Dro box link here

[redacted]

The Severe Motion report where the outlier volumes and values highlighted are uploaded here, just for reference and big picture understanding,

[redacted]

FORMAT:

Subject: sub86
Pairs to remove: 14

24-25
26-27
28-29
30-31
42-43
44-45
46-47
48-49
62-63
64-65
70-71
84-85
86-87
88-89

CRITICAL: INDEXING CONVENTION

Master_Exclusion_List.txt uses 0-BASED INDEXING (like FSL, Python)
- First volume = 0
- Last volume = 89
- Total volumes = 90 (indices 0-89)

Pair "24-25" means:
- Volume at index 24 (0-based) = 25th volume physically
- Volume at index 25 (0-based) = 26th volume physically

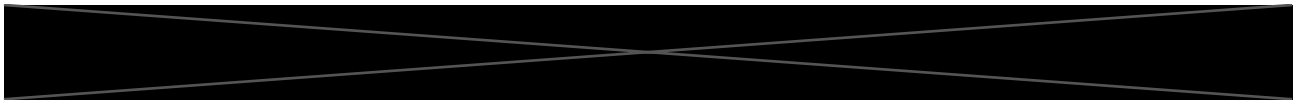
MATLAB uses 1-BASED INDEXING:
- First volume = 1
- Last volume = 90
- Total volumes = 90 (indices 1-90)

CONVERSION REQUIRED: Add 1 to all Master List indices for MATLAB. For removal program is in matlab we switch indexing, if it's a shell script we don't have to switch indexing.

Example:
Master List (0-based): 24-25
MATLAB (1-based): 25-26

SCRIPT: matlab_step3_removal_AUTO_NO_BACKUPS.m

Download matlab ste 3 removal AUTO NO BACKUPS.m sta e 3 matlab scri t link



PURPOSE:
Read Master_Exclusion_List.txt, convert indexing, remove volumes from rASL.nii and rows from rp_ASL.txt, recreate meanASL.nii from clean data.

USAGE:

In MATLAB:
```
>> cd /Users/vaidehipatel/Downloads/batch_scripts_pcasl
>> matlab_step3_removal_AUTO_NO_BACKUPS('sub86')
```

WHAT IT DOES:

---

1. Reads Master_Exclusion_List.txt
2. Locates subject section
3. Extracts volume pairs (0-based indices)
4. Converts to 1-based by adding 1
5. Calculates volumes to keep using setdiff()
6. Loads rASL.nii (90 volumes)
7. Extracts only good volumes
8. Overwrites rASL.nii with cleaned data (62 volumes for sub86)
9. Loads rp_ASL.txt (90 rows)
10. Extracts only good rows
11. Overwrites rp_ASL.txt with cleaned data (62 rows)
12. Deletes old meanASL.nii
13. Loads cleaned rASL.nii
14. Computes mean across cleaned volumes
15. Writes new meanASL.nii (mean of 62 clean volumes)

INDEXING CONVERSION EXAMPLE (example: sub86):

Master List pairs (0-based):
24-25, 26-27, 28-29, 30-31, 42-43, 44-45, 46-47, 48-49,
62-63, 64-65, 70-71, 84-85, 86-87, 88-89

Convert to MATLAB 1-based (add 1):
25-26, 27-28, 29-30, 31-32, 43-44, 45-46, 47-48, 49-50,
63-64, 65-66, 71-72, 85-86, 87-88, 89-90

Flatten to individual volumes to remove:
25, 26, 27, 28, 29, 30, 31, 32,
43, 44, 45, 46, 47, 48, 49, 50,
63, 64, 65, 66,
71, 72,
85, 86, 87, 88, 89, 90

Total: 28 volumes to remove

Calculate volumes to keep:
all_volumes = 1:90
volumes_to_remove = [25, 26, ..., 90]
volumes_to_keep = setdiff(all_volumes, volumes_to_remove)

Result: [1:24, 33:42, 51:62, 67:70, 73:84]
Count: 24 + 10 + 12 + 4 + 12 = 62 volumes

OUTPUT:

---

batch_scripts_pcasl/sub86/FUNC/rASL.nii (62 volumes, cleaned)
batch_scripts_pcasl/sub86/FUNC/rp_ASL.txt (62 rows, cleaned)
batch_scripts_pcasl/sub86/FUNC/meanASL.nii (1 volume, clean mean)

Note: ASL.nii (original 90 volumes) is NEVER modified.

VERIFICATION:

Check volume counts:
fslinfo batch_scripts_pcasl/sub86/FUNC/rASL.nii | grep dim4
Expected: dim4 = 62

Check row counts:
wc -l batch_scripts_pcasl/sub86/FUNC/rp_ASL.txt
Expected: 62 rows

Check meanASL quality:
fsleyes batch_scripts_pcasl/sub86/FUNC/meanASL.nii &
Expected: Sharp image, no motion blur

CRITICAL DESIGN DECISION #3:

No backup files are created during volume removal.

Rationale: SPM batch scripts fail if unexpected backup files (e.g., rASL_BEFORE_SCRUB.nii) exist in the FUNC/ directory. The original ASL.nii remains untouched and serves as the permanent backup. All modifications are done to rASL.nii, rp_ASL.txt, and meanASL.nii only.

CRITICAL DESIGN DECISION #4:

---

meanASL.nii is recreated from the cleaned volumes rather than simply removing bad volumes from the original mean.

Rationale: The mean image is used for coregistration to the structural image. A blurry mean (from 90 volumes including motion artifacts) will result in Slightly poor coregistration. Recreating the mean from only the 62 clean volumes produces a sharp reference image, improving coregistration accuracy and ultimately CBF quantification.

CRITICAL DESIGN DECISION #5:

Both rASL.nii and rp_ASL.txt must be modified to have matching counts.

Rationale: PART2 preprocessing expects rASL.nii volume count to match rp_ASL.txt row count. Mismatch causes errors. Both files must be updated to maintain 1-to-1 correspondence between volumes and motion parameters.

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7. STAGE 4: FINAL PREPROCESSING (PART2)

SCRIPT: batch_run_PART2_clean.m

Uploaded code on lab Dropbox, batch_run_PART2,

WHAT PART2 DOES:

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1. Coregisters structural T1 to functional meanASL
2. Smooths functional images with 6mm FWHM Gaussian kernel
3. Performs CBF quantification (label-control subtraction)
4. Segments structural T1 (gray matter, white matter, CSF)
5. Normalizes to MNI space

CBF QUANTIFICATION PARAMETERS (from our lab specific par.m):

PAR.FirstimageType = 0 (labeling first)
PAR.SubtractionType = 0 (simple subtraction)
PAR.SubtractionOrder = 1 (control - label)
PAR.ASLType = 1 (CASL/pCASL)
PAR.Labeff = 0.8 (label efficiency for pCASL)
PAR.MagType = 1 (3T scanner)
PAR.Labeltime = 1.5 (labeling duration, seconds)
PAR.Delaytime = 1.5 (post-label delay, seconds)
PAR.slicetime = 27.5 (slice acquisition time, msec)

OUTPUT:

globalsg.txt in later version of asl_perf_subtract.m.

filename	descriptions
ASL.nii	The 4D raw data saved in an order of label-control-label …
rASL.nii	Output of motion correction.
meanASL.nii	Output of motion correction. The average of all images.
rp_ASL.txt	Output of motion correction. Motion timecourses. There are 12 columns. The first 6 ones are the output of SPM motion correction: x,y,z translations and 3 rotations; the last 6 are the zigzag pattern cleaned motion timecourses.
ASLflt_rASL.nii	Output of temporal filtering.
sASLflt_rASL.nii	Output of smoothing.
meanCBF_0_srASLflt_rASL.nii	Output of CBF quantification. The mean CBF map. "_0_" means simple subtraction.
cmeanCBF_0….	Outlier cleaned mean CBF map.
meanPERF_0_srASLflt_rASL.nii	Output of CBF quantification. The mean perfusion difference map (nonquantitative).
wmeanCBF_0_srASLflt_rASL.nii	Mean CBF map warped into the MNI space.
cbf_0_srASLflt_rASL.nii	Output of CBF quantification. The CBF map time series. Each control/label image pair has a corresponding CBF map saved in this

	file.
brainmask.nii	A rough brain mask by hard thresholding if FSL BET is not available.
globalsg_0.txt	The first and second column are the whole brain mean of the perfusion difference image and the CBF map at each timepoint.

CONSOLE OUTPUT EXAMPLE (sub86):

CBF quantification for L/C pair: # 31 / 31: ...done
The mean CBF is 52.457554 (44.345489).

Interpretation:
  52.46 mL/100g/min = whole brain mean CBF
  44.35 mL/100g/min = likely gray matter only

VERIFICATION:

Visual inspection:
  fsleyes batch_scripts_pcasl/sub86/FUNC/Meancbf_0_sr_rASL.nii &

  Expected:
    - Higher CBF in gray matter (cortex, deep gray nuclei)
    - Lower CBF in white matter
    - Clear anatomical structure
    - No extreme outliers or artifacts

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9. DESIGN DECISIONS AND RATIONALE

DECISION 1: Split Preprocessing into PART1 (before removal) and PART2 (after)

RATIONALE:
SPM realignment generates most accurate motion parameters. Identifying motion-corrupted volumes before realignment would require unreliable motion estimates. Splitting allows:
  1. Accurate realignment of all volumes
  2. Identification of bad volumes using reliable motion parameters
  3. Removal of bad volumes
  4. Final preprocessing with clean data

ALTERNATIVE REJECTED:
Removing volumes before any preprocessing. This would require identifying bad volumes from raw, unrealigned data with inaccurate motion estimates.

EVIDENCE:
Motion parameters differ between before and after realignment by 0.2-1.4mm due to different reference frames. Only post-realignment parameters are reliable for identifying outliers.

DECISION 2: Use 0-based indexing in Master_Exclusion_List.txt

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RATIONALE:
FSL and Python (primary QC tools) use 0-based indexing. Using the same convention in the Master List avoids confusion during QC when visualizing volumes in FSLeyes or analyzing motion with Python scripts.

CONVERSION STRATEGY:
MATLAB removal script explicitly converts by adding 1, with clear documentation and verification output showing the conversion:
"0-based: 24-25 → 1-based: 25-26"

ALTERNATIVE REJECTED:
Using 1-based indexing in Master List to match MATLAB. This would cause confusion during QC in FSLeyes (0-based) and increase error risk.

DECISION 3: Remove label-control pairs, not individual volumes

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RATIONALE:
CBF is calculated by subtracting label from control images:
$CBF \propto (Control - Label)$

If only one volume of a pair is corrupted, the subtraction still produces an unreliable CBF value. Both volumes must be removed to maintain data integrity.

IMPLICATION:
If 15% of individual volumes are corrupted, removing pairs means ~30% of data is removed (each bad volume necessitates removing its pair).

For sub86: 14 corrupted pairs = 28 volumes removed.

DECISION 4: Use setdiff() to calculate volumes to keep

RATIONALE:
Manually specifying ranges (e.g., [1:24, 33:42, ...]) is error-prone and subject-specific. Using:

```
volumes_to_remove = [25, 26, 27, ..., 90];
volumes_to_keep = setdiff(1:90, volumes_to_remove);
```

...is foolproof, generalizable, and automatically handles any removal pattern.

ALTERNATIVE REJECTED:
Hard-coding volumes_to_keep ranges for each subject. This approach led to off-by-one errors in initial testing.

DECISION 5: Recreate meanASL.nii from cleaned volumes

RATIONALE:
meanASL.nii is the reference for coregistration to structural T1. A blurry mean (from 90 volumes including motion) causes poor coregistration, which propagates to CBF quantification errors.

EVIDENCE FROM sub86:
Before SCRUB: meanASL.nii appeared blurry
CBF = 38.51 mL/100g/min (underestimated)

After SCRUB: meanASL.nii sharp and clear
CBF = 52.46 mL/100g/min (+36% improvement)

The improvement demonstrates that motion-corrupted volumes were significantly contaminating the mean image and reducing CBF estimates.

DECISION 6: No backup files created during removal

RATIONALE:
SPM batch scripts in PART2 search for files matching patterns like *ASL.nii. Creating backups like rASL_BEFORE_SCRUB.nii causes SPM to find multiple matching files, leading to errors or processing wrong files.

SAFETY:
ASL.nii (original 90 volumes) is never modified and serves as permanent backup.

DECISION 7: Use explicit confirmation prompt before removal

RATIONALE:
Volume removal is irreversible (within the workflow). Showing the user exactly what will be removed and asking for confirmation prevents accidental data loss.

IMPLEMENTATION:
Script displays:

- Volumes to remove (1-based MATLAB indexing)
- Volumes to keep (ranges)
- Retention rate
- Prompt: "Continue? (y/n):"

DECISION 8: Place all subjects in batch_scripts_pcasl/ directory

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RATIONALE:
par.m uses relative path navigation (cd ../) to find data_root. To make par.m work without modification:

ORIGINAL INCORRECT:
par.m location: /Downloads/batch_scripts_pcasl/par.m
cd ../ → /Downloads/
Looks for: /Downloads/sub86/FUNC/ ← WRONG

CORRECTED:
par.m location: /Downloads/batch_scripts_pcasl/par.m
% cd ../ ← COMMENTED OUT
Looks for: /Downloads/batch_scripts_pcasl/sub86/FUNC/ ← CORRECT

This avoids modifying DICOM conversion script, removal script, and multiple paths throughout the codebase.

DECISION 9: Process subjects one at a time

RATIONALE:
While batch processing all subjects is possible, processing one at a time:
- Allows verification at each stage before proceeding
- Prevents propagation of errors to all subjects
- Facilitates troubleshooting
- Enables quality control between stages

IMPLEMENTATION:
par.m: PAR.subjects = {'sub86'}; % Single subject
Change to {'sub86', 'sub135', ...} for batch processing

DECISION 10: Verify indexing with explicit console output

RATIONALE:
Indexing errors (off-by-one) are common and catastrophic. Removal script

explicitly prints conversion for verification:

```
Converted pairs (1-based MATLAB indexing):
  0-based: 24-25 → 1-based: 25-26
  0-based: 26-27 → 1-based: 27-28
  ...
```

This allows visual verification that conversion is correct before proceeding.

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PROBLEM 8: Timeseries verification shows mismatch

SYMPTOM:
Cleaned vol 25 ≠ Original vol 33

CAUSE:
Indexing error in volume removal

FIX:
1. Verify Master List uses 0-based indexing
2. Check conversion in script output:
   0-based: 24-25 → 1-based: 25-26
3. If indexing is wrong, adjust script or Master List
4. Re-run Stage 3 after correction

APPENDIX : SUBJECT MAPPING TABLE example (refer masterlist.txt)

Subject ID	Archive	Session	Volumes	Pairs Removed	Retention	
sub86	p033	s1	90	14	68.9%	p033 IS NOW EXCLUDED SO MAKE SURE TO NOT PROCESS IT ANYMORE
sub135	p061	s1	90	TBD	TBD	
sub30	c033	s1	90	TBD	TBD	
sub10	c013	s1	90	TBD	TBD	
sub123	p053	s3	90	TBD	TBD	
sub122	p053	s2	90	TBD	TBD	
sub12	c015	s1	90	TBD	TBD	
sub66	p019	s3	90	TBD	TBD	
sub40	p006	s3	90	TBD	TBD	
sub127	p056	s1	90	TBD	TBD	
sub141	p064	s1	90	TBD	TBD	
sub20	c023	s1	90	TBD	TBD	
sub98	p039	s1	90	TBD	TBD	