

**OSIPI ASL Challenge**

**LOFT ASL Quantification Toolbox**

*Documentation*

Challenge participant: Chenyang Zhao (zhao361@usc.edu)

Mentor: Kay Jann, and Danny JJ Wang (jwang71@gmail.com)

Institute: Laboratory of Functional MRI Technology (LOFT), Mark and Mary Stevens Neuroimaging and Informatics Institute, University of Southern California



# Brief Overview

LOFT ASL toolbox is a MATLAB-based post-processing pipeline for CBF quantification of single-delay PASL and CASL (pCASL) data. The pipeline includes segmentation of T1w data, coregistration of T1w data and segmentation masks to M0 data, motion correction of ASL data based on M0 data, CBF quantification, and partial volume correction. The toolbox runs automatically based on a configuration file and input data that conform to the file structure introduced in [1,2]. Output files, including a mean CBF image, partial volume corrected CBF images for white (WM) and gray matter (GM), GM and WM binary masks, and GM and WM partial volume masks, will be saved.

# Detailed Analysis Pipeline

## Operating system

The toolbox has been tested on Win10, MacOS 11.4, and Ubuntu 18.04.6. Partial volume correction is not supported on Win10.

## Software

MATLAB with Image processing toolbox. (R2020a).

SPM12 (<https://www.fil.ion.ucl.ac.uk/spm/software/spm12/>)

FSL 6.0 (required for partial volume correction) (https://fsl.fmrib.ox.ac.uk/fsl/fslwiki/)

LOFT ASL tool (https://github.com/chenyang9526/LOFT\_ASL\_toolbox)

## Brain Extraction

A brain mask is generated as the sum of GM, WM, and CSF masks segmented using SPM12. For partial volume masks, BET (included in FSL) with default parameters was used to perform brain extraction.

## Segmentation

SPM12 was used to generate GM, WM, and CSF masks. If partial volume correction is performed, FAST (included in FSL) with default parameters will generate GM, WM, and CSF partial volume masks.

## Motion Correction

SPM12 was used to perform motion correction for label/control pairs with respect to the M0 image with the function of realign (estimate).

## Function-structure Coregistration

SPM12 was used to perform function-structure coregistration (estimate & reslice). T1w image and segmentation images were coregistered to the M0 image.

## CBF quantification

Perfusion maps were obtained using simple subtraction between control and label images. CBF quantification was performed with single compartment model for QUIPSS II PASL [Quantitative imaging of perfusion using a single subtraction (QUIPSS and QUIPSS II).] and pCASL [A general kinetic model for quantitative perfusion imaging with arterial spin labeling.]. Except for post labeling delay and labeling duration, which dependent on a specific sequence and can be read from the subject-specified json file, perfusion parameters were set as: brain/blood coefficient=0.9, T1 [blood=1.35s@1.5T](mailto:blood=1.35s@1.5T), [1.65s@3T](mailto:1.65s@3T), [2.1s@7T](mailto:2.1s@7T), labeling efficiency of [pCASL=0.85@1.5T](mailto:pCASL=0.85@1.5T), [0.85@3T](mailto:0.85@3T), [0.7@7T](mailto:0.7@7T), labeling efficiency of PASL=0.98 in all cases.

# Usage

## Folder structure

Diagram

Description automatically generated

Fig. 1 Folder structure. A BIDS compliant folder structure is required as the input data for the toolbox, where “Synthetic” could be a project folder (folder name can be changed for a different project), “rawdata” (folder name cannot be changed) is a folder storing data awaiting processing, “sub-DRO1” to “sub-DRO9” are subject folders (folder names can be changed for different subjects). In each subject folder, an “anat” folder contains a T1w image, and a “perf” folder contains M0 and a 4D control/label image (folder names cannot be changed).

## Configuration File

Text

Description automatically generated

Fig. 2 Configuration file for LOFT ASL toolbox. Users must prepare a json file to configure the toolbox. Several installation paths, the path to the project folder, and subject IDs have to be given correctly. Several flags can be defined as 0 or 1 according to users’ need. T1w\_flag: whether a T1w image is given. Frame\_flag: whether results of repetitions are needed. Perfusion\_flag: whether subtraction images between control and label images are needed. BOLD\_flag: whether BOLD images are needed. CBF\_flag: whether CBF quantification is performed. Mean\_flag: whether a mean CBF/perfusion/BOLD image is needed. PVC\_flag: whether partial volume correction is performed (set to 0 for Win10). Note: for Win10, use “\\” instead of “/”.

## Subject header information file

Text

Description automatically generated

Fig 3. A json file (file name: subject\_ID\_asl.json) for subject header information. This file must be stored in the perf folder under each subject folder. The toolbox will automatically read parameters from this file, such as SliceTiming, ArterialSpinLabelingType, PostLabelingDelay, BackgroundSuppression, TotalAcquiredPairs, BackgroundSuppressionNumberPulses, BackgroundSuppressionPulseTime, and LabelingDuration. A correct CBF quantification relies on the correct entries of these parameters.

## Usage

Step 1: Arrange folder structure to be consistent with that in section 2.8;

Step 2: Prepare a config json file and copy the path of the config file (see section 2.9);

Step 3: Prepare a subject json file and store it in the perf folder of each subject folder (see section 2.10);

Step 4: Add LOFT\_ASL\_toolbox into your MATLAB paths;

Step 5: In MATLAB command window, type:

LOFT\_ASLquantify('/Users/czhao/Desktop/Population\_based/config.json');

## Output

A “result” folder containing the results of subjects will be generated under the project folder. Following files are saved: CBF.nii.gz (mean CBF ml/min/100g), GM/WM\_mask\_lowres.nii.gz (binary tissue masks), CBF\_GM/WM\_pv.nii.gz (partial volume corrected CBF), GM/WM\_pv.nii.gz (partial volume masks), and txt files recording the mean and std CBF values in GM and WM.