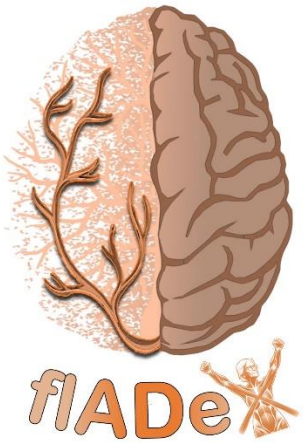

Manual of Procedures FLADEX Project

Annex 7.1.: Instructions for MRI acquisition

Annex 7.1. Instructions for MRI acquisition

Instructions during the MRI scan

The following document provides a brief description of the events that occur while the participant is in the MRI exam. This includes both the prompts that are given to the participant, as well as the screens that should appear at the same time as the sequence is being performed. See Chapter7.MRI_session for MRI parameters of each sequence.
The MRI session will have **¡THREE DIFFERENT SCENARIOS!** depending on the pre- / post- condition runs and the number of visit /session (1, 2, 3).
Scenario 1: Pre-condition 1st visit. MPRAGE T1-weigthed images, TOF-T0 and pCASL-T0.
Scenario 2: Pre-condition 2nd & 3rd visit. TOF-T0 and pCASL-T0.
Scenario 3: Post-condition 1st, 2nd & 3rd visits. TOF, pCASL-T1, pCASL-T2, pCASL-T3
Please **look carefully the following visual acquisition protocol images** to further understand how to overcome each pre- / post-condition run and each visit / session (Figure 1).

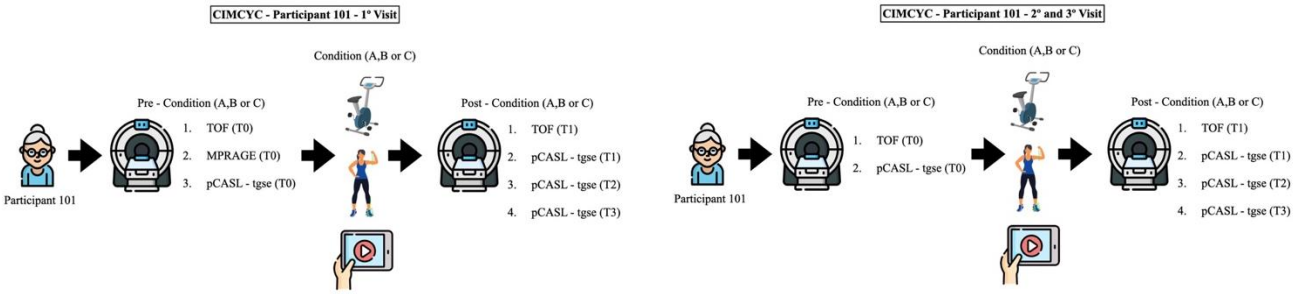

Figure 1. Protocol for each session/visit.

Before acquiring each of the sequences:
The evaluator will open the file "Cruz_MRI.jpeg" from the path fladex_project/ or on the computer desktop itself and place it on the MRI screen in full screen mode.
The technician will tell participants to be **as relaxed and still as possible** for the next few minutes, to keep his eyes open and **look at the crosshairs** on the screen and that they will hear a loud noise and thus, should not panic.

1. MPRAGE sequence (7min) → Acquired once in the 1st MRI session

This sequence acquires a 3D structural image of the participant's whole brain.
The technician
At the end of the acquisition: Check that the acquired image has been taken correctly. This can be done quickly by following the steps below:

- Step 1. Check that the participant has maintained a correct position throughout the scan (e.g., no misaligned body parts, no tilt of the head, etc.).
- Step 2. Check that the image has good resolution, and that there is no extraneous brightness or overlapping.

- Step 3. If the acquisition had to be repeated, save only one acquisition per sequence.

2. **Time-Of-Flight (TOF) sequence (46 seconds) → Acquired twice per visit (TOF-T0 pre-condition; TOF-T1 post-condition)**

This sequence allows us to identify the carotid arteries. It highlights the flowing blood while suppressing signals from stationary tissues.

The technician

It is crucial to follow the following steps for a successful acquisition:

- Step 1. Open ASL scan and position the frame of view (FOV) to cover brain and cerebellum if possible. FOV should be perpendicular to internal carotid arteries.

Write down H value from Position (In Sequence > Routine tab) → H_{ASL}

Clue: H = positive (Head direction)

Clue: H = negative (FOOT direction)

- Step 2. Open TOF scan and position FOV close to the circle of Willis (**Figure 1**) (4 images are created by TOF)

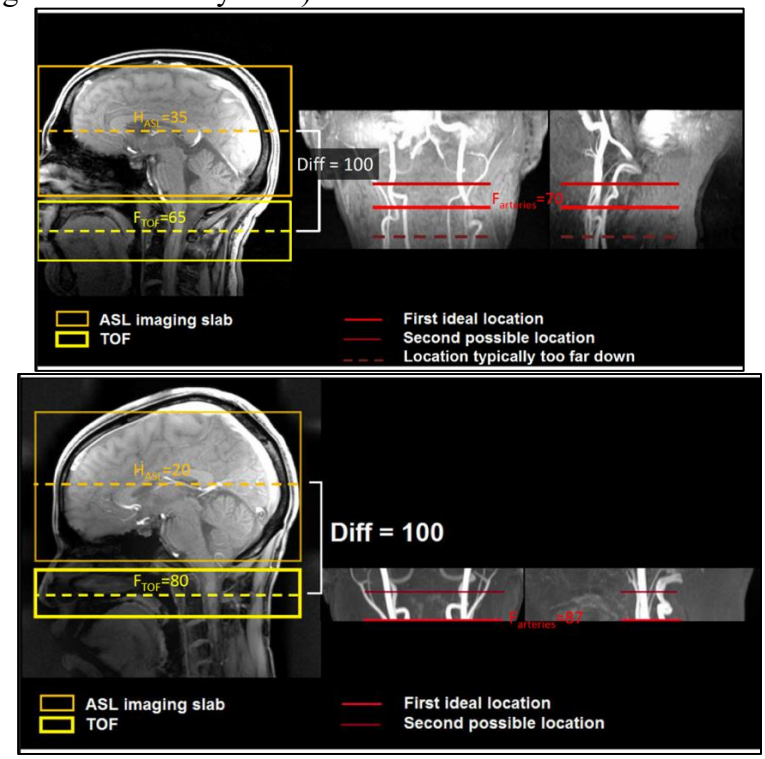

Figure 1. Position of the frame of view to identify the carotids arteries.

- Step 3. Open 2nd and 3rd TOF images in the console next to the sagittal localizer to visualize the arteries in their sagittal and coronal views.

Clue: Find the transversal location at which vertebral and internal carotid arteries are as **straight** as possible.

Clue: You can do this by opening the ASL scan again and moving the FOV box around while looking at the Position parameter. Once you are done with the calculations though remember to set back the ASL FOV to H_{ASL} (Step 1)

Clue: Remember that the labeling plane is ~1cm wide **so avoid being too close to bends**

Write down chosen **F** value → $\mathbf{F}_{arteries}$

- Step 4. Open ASL scan and go to Sequence > Special tab to locate:
  [5] Label Plane Offset parameter (by default set to 105 mm)

Set it to the correct value = $\mathbf{H}_{ASL}$ + $\mathbf{F}_{arteries}$

3. **pCASL sequence (6 min) →Acquired 4 times per visit (pCASL-T0 pre-condition; pCASL -T1,2,3 post-condition)**

This sequence is a type of MRI technique used to measure cerebral blood flow non-invasively. It is particularly focused on studying perfusion in the brain.

The technician

pCASL-tgse sequence basically requires **three types of images taken with a flip angle of 120dg**. The first will **be the calibration image (M0),** which will be followed by a dummy image, and **a pair of label-control images.** The acquisition of the M0 image, the enhanced proton density image, is necessary for the calculation of the magnetization balance of the arterial blood (individual parameter). For the acquisition of the label images, it is necessary to previously **mark a plane in the neck to mark the blood that will later pass to the brain as explained in Time-Of-Flight (TOF) (Figure 1).** In the case of control images, the blood will not be marked but the rest of the parameters will be maintained.

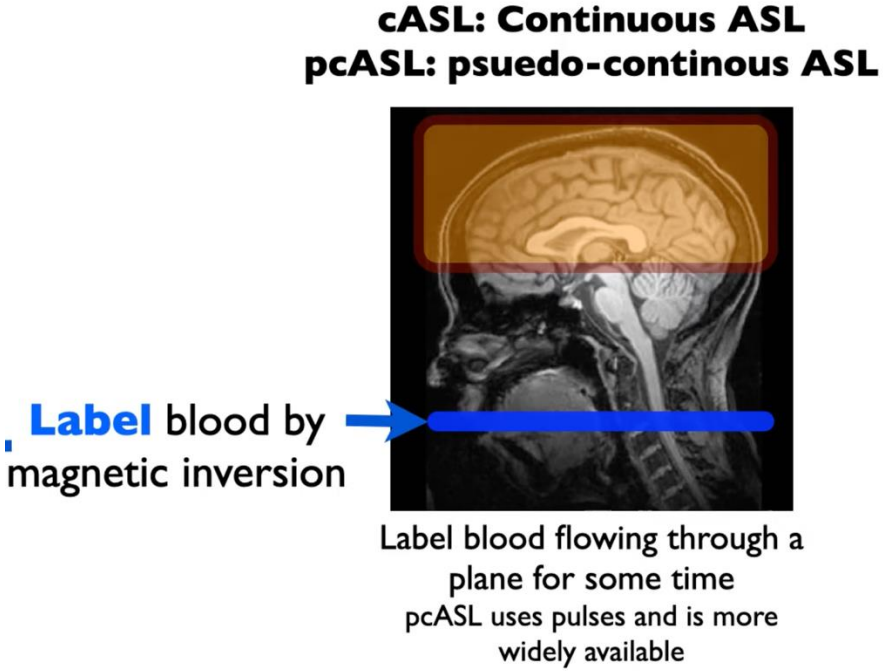

Figure 2. Blood labelling process

With the aim of keeping **the same Label Plane Offset Parameter set in the pCASL-tgse_T0** with the TOF sequence in the following pCASL-tgse acquired in the following runs/sessions/visits, the technician will always **load the pCASL-tgse_T0 in the following run tab** and copy-paste it (one time in pre-condition and three times in post-condition). The technician will change the name of the copied-pasted sequences to pCASL-tgse-T0, pCASL-tgse-T1, pCASL-tgse-T2 or pCASL-tgse-T3 depending on

which scenario we are. In this way, the sequences **keep the same Label Offset Parameter** althought the H_{asl} and $F_{arteries}$ are adjusted to the new participant location in the MRI scan as the participant has left the MRI scan to go to the condition and entered again for the post – condition.

Example for a better understanding:
Visit-1

1. *The participant enters in the MRI scan in the pre-condition. After running TOF, the parameters acquired to label the blood for the pCASL-tgse_T0 are the following ones:*

***H**ASL* → *45 mm*
***F**arteries* → *75 mm*
*Label Offset (**H**ASL*+ ***F**arteries*) →*120 mm*

2. *The participant enters again in the MRI scan in the post-condition (or following pre-conditions). The technician loads the pCASL-tgse_T0 and copy-paste it three times to create the pCASL-tgse_T1, pCASL-tgse_T2, pCASL-tgse_T3. The new parameters are the following ones:*

***H**ASL* → *35 mm*
***F**arteries* → *85 mm*
*Label Offset (**H**ASL*+ ***F**arteries*) →*120 mm*
*As you can see, although the **H**ASL and **F**arteries have changed because of the new location of the participant in the MRI scan,* ***the Label Offset still sums 120mm as in the pCASL-tgse-T0, so it keeps the same value.***

4. Data exportation:

The transfer of the images acquired during the MRI session will be carried out **immediately after each visit.**
The technician logs into the server **smb://profith2.ugr.es** with the **username: xxxx.**

- The technician will have access to a folder called MRI_data_raw (/Users/heartybrain/MRI_data_raw), in where he will upload the folders with the DICOM files corresponding to each participant, session, run and sequence (Table 1)
- After the images are uploaded to the server, they would be moved from /Users/heartybrain/MRI_data_raw to /Users/agueda/neurodesktop-storage/Fladex/DICOM. Besides a copy should be stored at /Volumes/profith/fladex/MRI_data.
- The names of the sequences in the folders have a number at the end as in Table 1. ACP should then modify the names according to Table 2.

Table 1. Mri_data_raw folder structure **before** modified the names

Folder	Session folder	Run folder	Sequences folders	DCM files
MRI_data_raw	101_visit1	fladex_Protocolo - 1	Localizers_1	139
			MPRAGE_T0_9	224
			Perfusion_Weigthed_11	1
			PhoenixZIPReport_99	7
			t2_tse_tra_448_p2_3mm_5	35
			tgse_pcasl_T0_10	26
			tof_fl3d_tra_p3_2slab_MIP_COR_T0_8	1
			tof_fl3d_tra_p3_2slab_MIP_SAG_T0_7	1
			tof_fl3d_tra_p3_2slab_T0_6	59
		fladex_Protocolo - 2	Localizers_1	139
			Perfusion_Weigthed_9	1
			Perfusion_Weigthed_11	1
			Perfusion_Weigthed_13	1
			PhoenixZIPReport_99	7
			tgse_pcasl_T1_8	26
			tgse_pcasl_T2_10	26
			tgse_pcasl_T_12	26
			tof_fl3d_tra_p3_2slab_MIP_COR_T1_7	1
			tof_fl3d_tra_p3_2slab_MIP_SAG_T1_6	1
			tof_fl3d_tra_p3_2slab_T1	59

Table 2. Mri_data_raw folder structure **after** modified the names

Folder	Session folder	Run folder	Sequences folders	DCM files
MRI_data_raw	101_visit1	fladex_Protocolo - 1	Localizers_T0	139
			MPRAGE	224
			Perfusion_Weigthed_T0	1
			PhoenixZIPReport_T0	7
			t2_tse_tra_448_p2_3mm_T0	35
			tgse_pcasl_T0	26
			tof_fl3d_tra_p3_2slab_MIP_COR_T0	1
			tof_fl3d_tra_p3_2slab_MIP_SAG_T0	1
			tof_fl3d_tra_p3_2slab_T0	59
		fladex_Protocolo - 2	Localizers_T1	139
			Perfusion_Weigthed_T1	1
			Perfusion_Weigthed_T2	1
			Perfusion_Weigthed_T3	1
			PhoenixZIPReport_T1	7
			tgse_pcasl_T1	26
			tgse_pcasl_T2	26
			tgse_pcasl_T3	26
			tof_fl3d_tra_p3_2slab_MIP_COR_T1	1
			tof_fl3d_tra_p3_2slab_MIP_SAG_T1	1
			tof_fl3d_tra_p3_2slab_T1	59