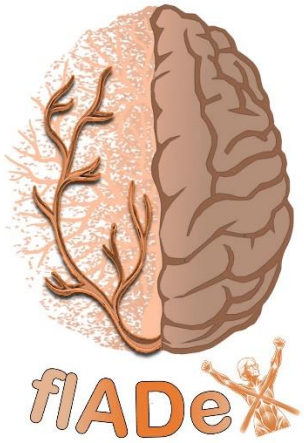


Manual of Procedures FLADEX project

Annex 7.3: MRI quality control

Promoting Fitness & Health through Physical Activity

UNIVERSIDAD DE GRANADA

Annex 7.3. MRI quality control

Index

1. **General MR images quality control**

Check that in the folder ***MRI_data_raw*** we find the folder ***corresponding to each participant and each visit/session (i.e, 101_visit1, 101_visit2, 101_visit3)*** in which there is the folder belonging to fladex_Protocol. This folder includes a folder of each of the acquired sequences. It is very important that each acquired sequence folder contains **the correct number of DCM files** that appears in **Table 1.**

Table 1. Mri_data_raw folder structure

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	20
			tof_fl3d_tra_p3_2slab_T0_MIP_COR	1
			tof_fl3d_tra_p3_2slab_T0_MIP_SAG	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	20
			tgse_pcasl_T2	20
			tgse_pcasl_T3	20
			tof_fl3d_tra_p3_2slab_T1_MIP_COR	1
			tof_fl3d_tra_p3_2slab_T1_MIP_SAG	1
			tof_fl3d_tra_p3_2slab_T1	59

It is **very important** that the names of this folders are as they are in the image and that **there are no numbers at the end because otherwise the script will not run correctly.**

2. Once it has been verified that the folders are correctly named and contain the corresponding items in the mri_data_raw folder, the following steps are:

2.1. To manually copy the files from MRI_data_raw and paste them into MRI_data folder in **(path: /profith/fladex/MRI_data) in the profith server** (smb://ziri.ugr.es/profith; user name: xxxx) **as in this way we are not spending memory space in the MAC.** Then, we would run dicom.sh (path: /profith/fladex/dicom.sh) script through Neurodesktop to copy data from MRI_data folder to DICOM folder (path: /Volumes/agueda/neurodesktop-storage/Fladex/DICOM), and remove the folder level corresponding to fladex_Protocol (same to **Table 1 but without the "Run folder" level**).

2.2. To review again that **everything is set according to the protocol** (images name, folders name, folders flow, etc). If it is not, then **modified it.**

2.3. To **call to the MRI technician the next day of evaluation** (Jose – xxxx – 8:00 am – 02:00pm) in case of **something is missing** (i.e., participant folder, acquisition folder) **or any other doubt** that could arise and it is of important to talk out.

3. Once we have completed the previous steps and all the folders corresponding to each participant are in DICOM folder, we can run the script "qc.sh" located in the server (/Volumes/agueda/neurodesktop-storage/Fladex/BIDS/derivatives/QC/scripts/qc.sh) in Neurodesktop. This will transform the DICOM files to NIFTI with the corresponding MRI sequence folders (as shown in Table 2), which would be stored in the BIDS folder.

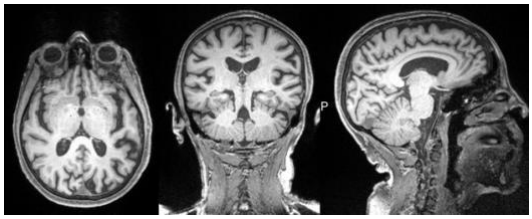
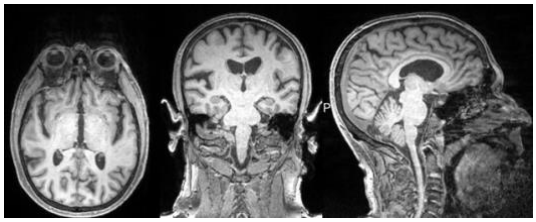
Table 2. MRI BIDS folders structure

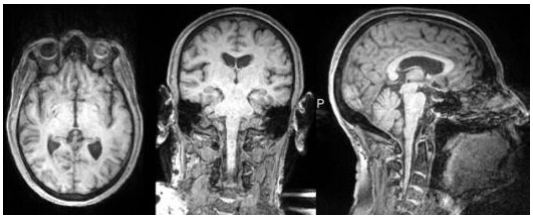
Main folder	**Participant folder**	**Session folder**	**Sequence folder**	**NIFTI files**
BIDS	sub-101	ses-1	anat	sub-101_ses-1_T1w.nii.gz
				sub-101_ses-1_T1w.json
				sub-101_ses-1_ acq-pre_run-1_angio_tra.nii.gz
				sub-101_ses-1_ acq-pre_run-1_angio-cor.nii.gz
				sub-101_ses-1_ acq-pre_run-1_angio-sag.nii.gz
				sub-101_ses-1_ acq-pre_run-1_angio.nii.gz
				sub-101_ses-1_ acq-post_run-1_angio_tra.nii.gz
				sub-101_ses-1_ acq-post_run-1_angio-cor.nii.gz
				sub-101_ses-1_ acq-post_run-1_angio-sag.nii.gz
				sub-101_ses-1_ acq-post_run-1_angio.nii.gz

			perf	sub-101_ses-1_acq-post_run-1_asl.nii.gz
				sub-101_ses-1_acq-post_run-2_asl.nii.gz
				sub-101_ses-1_acq-post_run-3_asl.nii.gz
				sub-101_ses-1_acq-pre_run-1_asl.nii.gz
				sub-101_ses-1_acq-post_run-1_asl.json
				sub-101_ses-1_acq-post_run-2_asl.json
				sub-101_ses-1_acq-post_run-3_asl.json
				sub-101_ses-1_acq-pre_run-1_asl.json
				sub-101_ses-1_acq-post_run-1_aslcontext.tsv
				sub-101_ses-1_acq-post_run-2_aslcontext.tsv
				sub-101_ses-1_acq-post_run-3_aslcontext.tsv
				sub-101_ses-1_acq-pre_run-1_aslcontext.tsv

2. MPRAGE visual inspection

1. Once the flADex project has been completed, we can go on to evaluate the quality of the images. ACP will open the Mri_qc instrument in redcap and fill it up using the following scale for the evaluation:

Rating	**Description**		
10	perfect	Good Quality	
9	excellent		
8	very good		
7	good		
6	fair to good	Doubtful Quality	
5	fair		
4	fair to poor		
3	poor	Poor Quality	
2	very poor		

1	unusable		

The score we give to each image will depend on whether:

- Gray matter and white matter are correctly identified in all slices and planes.
- Subcortical structures are correctly identified
- The image does not show movement in any slices and planes.

2. Once this is clear, we can begin to evaluate the images. In this case we will use the MPRAGE one. We will open the xxx.nii.gz file in the MRIcroGL (Figure 4) program and considering the above, we will move through the three planes (axial, coronal or frontal, sagittal) to give a final score that we will place in the Score column followed by a comment if necessary. If there is a discrepancy greater than 2 points between reviewers, a third reviewer will view the images, and an agreement will be reached between the 3 reviewers.

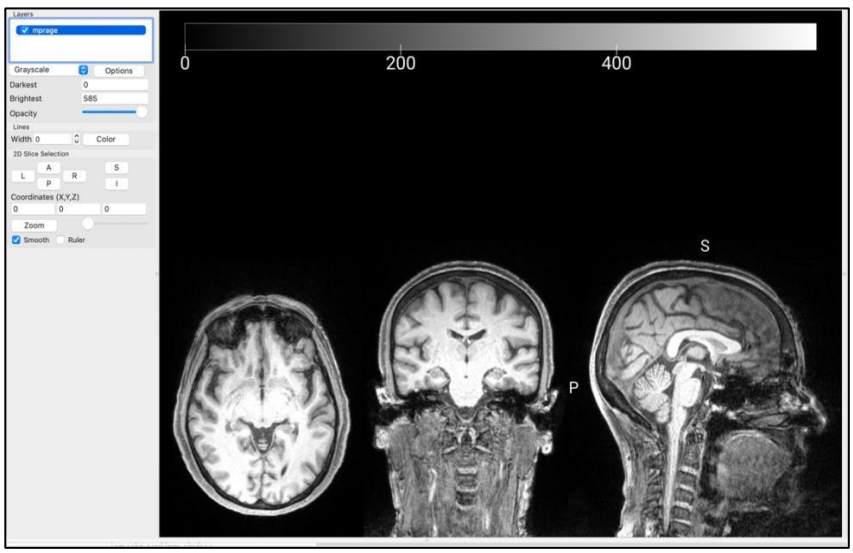


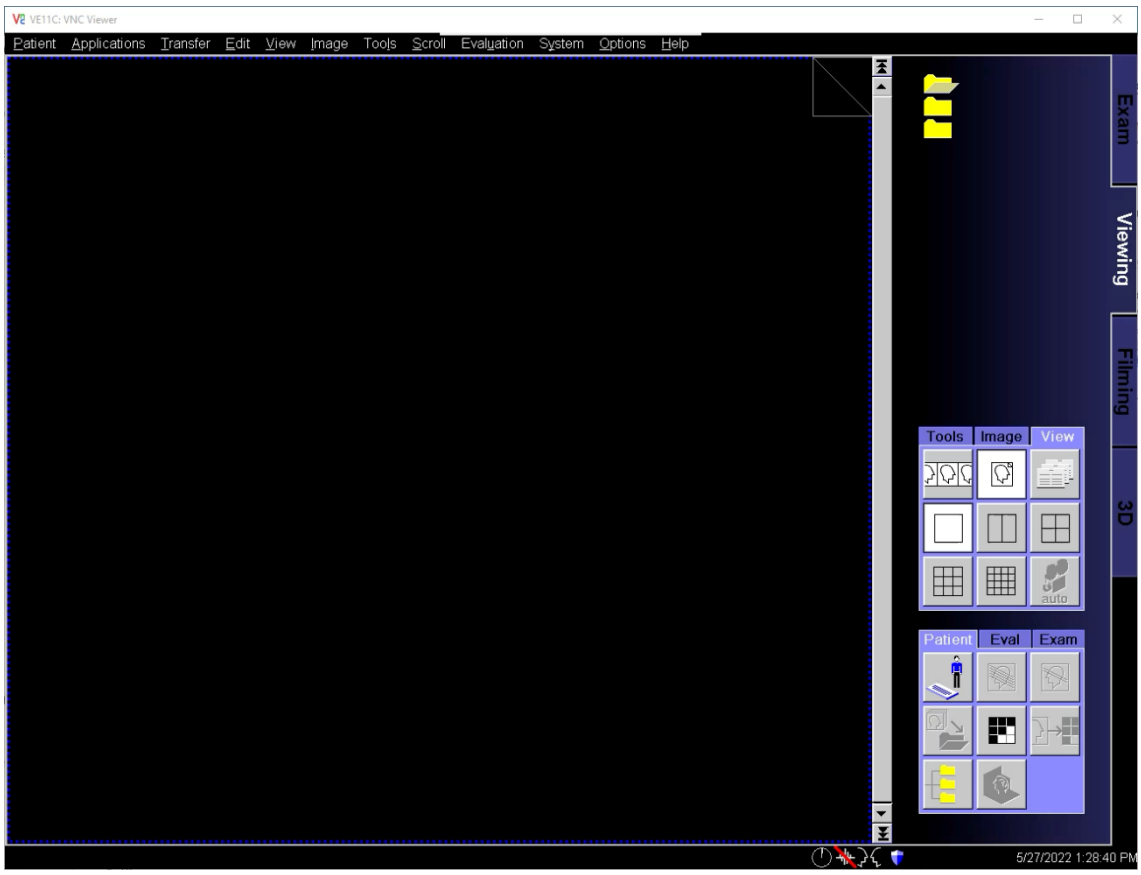
Figure 4: Visualization of the images in the MRIcroGL program.

3. PCASL visual inspection

Pcasl sequence gives us 20 images: 1st is M0 volume, 2nd is dummy image (to be discarded), then we have 9 pairs of label-control images. To test whether images were acquired properly we can follow these steps:

- Load the ASL series into the viewer.
- Set the viewer to show all images in the series at once
- With the mouse and without releasing the Ctrl key, select all the label images and take their arithmetic average (with the viewer tool)
- Repeat the process with Control images.
- Perform a subtraction (visualization tool) between the average control image – average label image

This process may allow us detecting any territorial defect during the labeling process.



Areas which appear considerably brighter could be areas of diffusion restriction (Figure 5). The three corresponding processed images below present large areas of low ASL signal (white triangles), with increased ASL signal (white arrowhead) within the communicating segment of the right internal carotid artery, which may reflect an ineffective labelling.

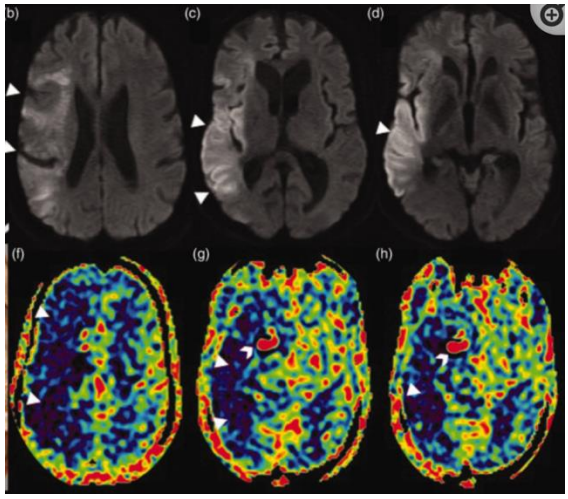


Figure 5: Examples of hypoperfusion.

PCASL-tgse sequence will be processed daily with ASLprep (v.7.2.0 or higher), through Neurodesk. For processing, we would load the pipeline (ml aslprep) and then introduce the following command in NeurodeskApp terminal:

aslprep neurodesktop-storage/Fladex/BIDS neurodesktop-storage/Fladex/BIDS/derivatives/aslprep participant –participant-label sub-101 –basil –force-bbr –fs-license-file neurodesktop-storage/Fladex/BIDS/license.txt –skip_bids_validation -w neurodesktop-storage/Fladex/BIDS

4. Situations in which repetition of image acquisition is required

Situation 1: The quality of T1 weighted images **is not good enough.**

Solution: It will be acquired again in one of the following MRI sessions of 2nd or 3rd visit as it is a structural image that is not condition – dependent.

Situation 2: The pCASL-tgse presents artifacts / looks blurred because of movement. (i.e. problem with the MRI scan or any issue with the participant)

Solution: The pCASL-tgse will be acquired again in the same session if **NO MORE** than **15 minutes** has been spent from the acquisition of the previous pCASL. If so, the whole visit will be repeated again as this sequence is condition – dependent (i.e. the main aim of the study is to examine the acute effect of a single bout of moderate aerobic exercise (A) vs. resistance exercise (B) vs. resting condition (C) on CBF).

The evaluator will note in redcap the reason for the repetition in the same session and the time delay of the acquisition regarding the previous pCASL-tgse sequence.

Situation 3: The pCASL-tgse presents artifacts / looks blurred because of movement. (i.e. problem with the MRI scan or any issue with the participant) and **MORE than 15 minutes** has been spent from the acquisition of the previous pCASL

Solution: The whole visit will be repeated again as this sequence is condition – dependent (i.e. the main aim of the study is to examine the acute effect of a single bout of moderate aerobic exercise (A) vs. resistance exercise (B) vs. resting condition (C) on CBF).

The evaluator will note in redcap the reason for doing an additional visit.

Situation 2: After processing pCASL-tgse sequence, we appreciate the following parameters could indicate a poor adquisition:

White matter cerebral blood flow is greater than gray matter cerebral blood flow.

Cerebral blood flow maps show a wide area with cerebral blood flow equal or less than 0 (Figure 6)

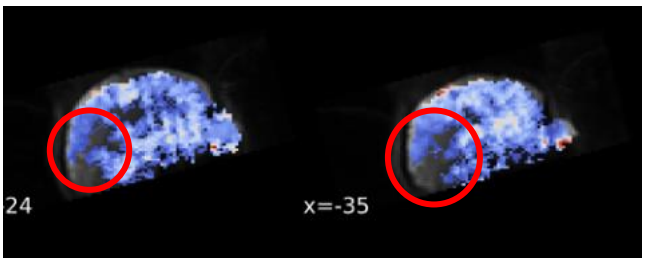


Figure 6: Dark areas on CBF ASLprep html maps showing CBF equal or less than 0

Cerebral blood flow maps show a notably difference between hemispheres (Figure 7)

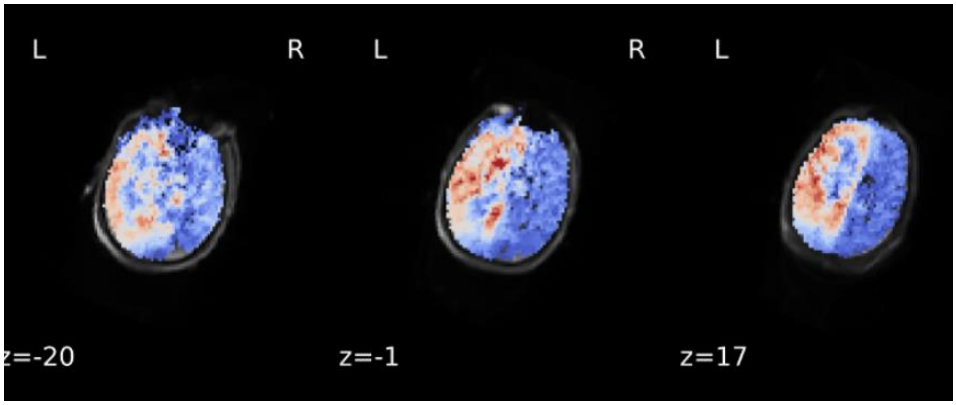


Figure 7: CBF ASLprep html maps showing a less perfused hemisphere

Solution: The whole visit will be repeated again as this sequence is condition – dependent (i.e. the main aim of the study is to examine the acute effect of a single bout of moderate aerobic exercise (A) vs. resistance exercise (B) vs. resting condition (C) on CBF). If problems persist, we would have to exclude the participant and cite another one.