MRI Harmonisation Manual
RIN – Neuroimaging Network

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The document was drafted by the WP2 working group

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Section 1 – MRI Technologists Instructions

1.1 – General Introduction to MRI Procedures

1 Prior to starting to scan subjects for the study, you must submit a 'Dummy' or test scan with pdf/txt files of each sequence to the **WP2 working group** for evaluation and acceptance (Section 2.2). Moreover, send back the present SOP to reteimaging@istituto-besta.it adding the changes specific of your site in the "**Notes – changes**" column of each sequence and the required information about multi-band/compressed sensing options. **The SOP must be renamed adding the name of your site after the version number.** Example: ReteNeuroimaging_SOP_WP2_2020_v3_Besta.

2 Perform the MRI scan using the agreed upon parameters for your scanner (Section 2.3 and 2.4). These parameters should be used for all study scans.

3 Anonymize dicom files as explained in Section 3.1. Dicom files must be saved, when it is possible, as **STANDARD DICOM** instead of enhanced dicom. If dicom files cannot be save in the standard format, please inform the **WP2 working group** sending a mail to reteimaging@istituto-besta.it. The image headers must include all scan parameters e.g.: TE, TR, FOV, image matrix. The information recorded should be consistent with the information provided to you by the WP2 working group.

Important resume:

- save DICOM as **STANDARD DICOM,**
- when you anonymize the data before loading onto the platform, leave intact all the header fields that refer to the image acquisition,
- upload only DICOM files (.dcm/.IMA); delete all other files (example: DICOM/DIR, .sr files, PS/XX files, DWI reconstructions as FA, MD maps).

4 Make a second copy of the MRI scan to be retained at your site for possible future data access (e.g. Regulatory Authority Inspection or routine study monitoring).

Section 2 – MRI scanning procedures

2.1 – General processes

Subject comfort during the scan is important. Please, take care of adequate padding and neck support to reduce head motion, in according to the standard practice at your institution.

Minimizing motion artefact is important for study scan quality. Use of standard Velcro head straps and foam wedges is recommended to immobilize the head. However, other methods of stabilizing the head which are used routinely at your institution are acceptable.

For brain scanning, the subject must be positioned appropriately so that the mid-line of the brain falls in the middle of the initial sagittal localizing sequence. Follow the routine procedures at your institution for your type of scanner for placing subject in the machine and general positioning.

Attention: Please refer back to the previous time point study scans, for study for each subject to enable exact repositioning between scans. This step is essential for the production of comparable scans.

The 32/64 channel coil should be used if available. The same coils should be used for all patients throughout the study. The information of MRI scanner and coil are the same provided in the initial Survey of the IRCCS advanced imaging Network (see Section 4).

Attention: In case of software or hardware updates of your scanner, send a communication with the module in Section 5 to Rete Imaging (reteimaging@istituto-besta.it).

2.2 – Dummy scan

Before each MRI center is accepted into the study, a test scan needs to be performed. This is referred to as the "Dummy Scan". This procedure enables the WP2 Working group to determine the following:

- scanner performance is within specification for entry into study
- the MRI site is able to produce and upload the electronic data required for the study.

When your dummy (or test) scan has been approved, you will be strongly advised that you store/save the approved scan protocol for the study on your scanner to avoid any mistakes being made when performing 'on study' MRI examinations.

2.3 – MRI scan protocol

2.3.1 – Sequences

Table 1

#	Sequence	Alignment	Notes
1	**Localiser**		Align the transverse slice to run parallel to the anterior-posterior line of the corpus callosum
2	**sT1W_3D**	Sagittal	Align the slices parallel to the median line (Fig. 3a,4a,5a) covering the entire brain (from top of the scalp to cervical vertebra C3)
3	**FLAIR_3D**	Sagittal	As above
4	**DWI_3b0_AP**	Axial (bicallosal) *	Align the slices parallel to the bicallosal line (Fig. 3b,4b,5b) covering the entire brain (from top of the scalp to the cerebellum) *
5	**DWI_2shell_7b0_PA**	Axial (bicallosal)	As above
6	**QSM**	Pure Axial	Align the slice package using a **pure axial** (0 degree) orientation covering the entire brain (from top of the scalp to the cerebellum, included)
7	**RS_fMRI_SE_AP**	Axial (bicallosal)	As sequence **DWI_3b0_AP**
8	**RS_fMRI_SE_PA**	Axial (bicallosal)	As above
9	**RS_fMRI_GE_AP**	Axial (bicallosal)	As above
10	**RS_fMRI_200vol_vox3_PA**	Axial (bicallosal)	As above; **INSTRUCTION: Talk to the subject** and ask to relax with **open eyes** during resting state

(*) Attention! Put the subject inside the scanner so that bicallosal alignment and pure axial alignment correspond.
Bicallosal plane: place the plane parallel to the anterior-posterior line of the corpus callosum (Figure 1).

Attention: **on the same subject** acquire the accelerated protocol with multiband and compressed sensing, if these options are available on the scanner of the site.

2.3.2 – Sequence details

The implementation of the sequences was carried out in the WP2 working group.
A scheme has been defined for the different vendors.
The sequence parameters suggested for the study are summarized in the following tables.

Structural protocol

We will acquire a T1 3D and a FLAIR 3D scans as structural data. These images will have a resolution of 1x1x1 mm^3 with a number of slices between 175 and 180, sagittally oriented. The total acquisition time should be ≈12 minutes.

Save the T1 3D as "**sT1W_3D**" and the FLAIR 3D as "**FLAIR_3D**".

Table 2

Parameters	**sT1W_3D**			
Vendors	Philips	Siemens	GE	**NOTES - changes**
Sequence type	3D FFE	MP-RAGE	3D BRAVO	
Slice orientation	sagittal	sagittal	sagittal	
FOV [mm]	240 × 240	256 × 256	256 × 256	
Resolution [mm^3]	1 × 1 × 1	1 × 1 × 1	1 × 1 × 1	
Matrix (Base Resolution)	240 × 240	256 × 256	256 × 256	
Slice thickness	1	1	1	
Slice gap (mm)	-	-	-	
n. slices	175 – 180 (**)	175 – 180 (**)	175 – 180 (**)	
Phase Encoding direction	AP	AP	PA (non modif)	
Slice order	Interleaved	Interleaved	Interleaved	
NSA/Averages/NEX	1	1	1	
TR [ms]	shortest	2300	non modif	
TE [ms]	shortest	2.96	3.2	
TI [ms]	non modif (855)	900	900	
Flip angle	8°	9°	9°	
Fat Suppression	No	No	No	
k-space coverage (Halfscan/Partial Fourier)	No	No	No	
Acceleration factor	SENSE≤ 2.3	GRAPPA=2	ARC=2	
Filter	CLEAR on	Prescan Normalize on	PURE on	
Bandwidth	191 Hz	240 Hz/Px	31.25 kHz	
Duration [min]	**≈ 5.30**	**≈ 5.30**	**≈ 5.30**	
Compressed sensing (CS)				
yes/no				
model				
CS factor				
TR				
TE				
Duration				
Other settings				

(**) If 180 slices are not permitted, use the maximum value in the range 175-180 slices. Use the same number of slices for sT1w_3D and FLAIR_3D.

Table 3

Parameters	FLAIR_3D			
Vendors	Philips	Siemens	GE	**NOTES - changes**
Sequence type	T2-FLAIR TSE	TSE VFL	CUBE T2-FLAIR	
Slice orientation	sagittal	sagittal	sagittal	
FOV [mm]	240 × 240	256 × 256	256 × 256	
Resolution [mm^3]	1 × 1 × 1	1 × 1 × 1	1 × 1 × 1	
Matrix (Base Resolution)	240 × 240	256 × 256	256 × 256	
Slice thickness	1	1	1	
Slice gap (mm)	-	-	-	
n. slices	175 – 180 (**)	175 – 180 (**)	175 – 180 (**)	
Phase Encoding direction	AP	AP	PA (non modif)	
NSA/Averages/NEX	1-2	1	1-2	
TR [ms]	5000	4500	5000	
TE [ms]	300	383	Max (119)	
TI [ms]	1700	~~**1800**~~ **1480**	Auto (1575)	Modify from 1800 to 1480
Fat Suppression	SPIR	Fat sat (strong)	classic	
k-space coverage (Halfscan/Partial Fourier)	No	Allowed (grey)	ZIP 2	
Slice k-space coverage (Halfscan/Partial Fourier)	-	7/8	-	
Acceleration factor	SENSE=1.4	GRAPPA=2	ARC=2	
Filter	CLEAR on	Prescan Normalize on	PURE on	
Bandwidth	1157.4 Hz (WFS=0.375 pix)	781 Hz/Px	41.67 kHz	
Duration [min]	**≈ 5-7**	**≈ 6.00**	**≈ 5-7**	
Compressed sensing (CS)				
yes/no				
model				
CS factor				
TR				
TE				
Duration				
Other settings				

(**) If 180 slices are not permitted, use the maximum value in the range 175-180 slices. Use the same number of slices for sT1w_3D and FLAIR_3D.

NOTE FLAIR (change June 2020):

Modificare TI da 1800 ms a 1480ms per una migliore soppressione del segnale in CSF.

DWI protocol

For the DWI data, we will use a standard single shot echo planar imaging sequence (EPI) sequence with a resolution of 2.5×2.5×2.5 mm^3, 30/32 (depending on the vendor) isotropically distributed diffusion weighted directions and two diffusion weightings of 1000 and 2000 s/mm^2, with number of non-diffusion weighted (b = 0 s/mm^2) images as shown in table 4, in addition to a b = 0 reversed blip acquisition. Use **same sequence preparation** between DWI_3b0_AP and DWI_2shell_7b0_PA. The total acquisition time is ≈10 minutes.

Save them as "**DWI_3b0_AP**" and "**DWI_2shell_7b0_PA**".

Table 4

Parameters	DWI_3b0_AP			DWI_2shell_7b0_PA			
Vendors	Philips	Siemens	GE	Philips	Siemens	GE**	**NOTES - changes**
Sequence type	Single shot SE EPI	EPI SE 2D	2D SE EPI	Single shot SE EPI	EPI SE 2D	2D SE EPI	
Slice orientation	transversal	transversal	oblique	transversal	transversal	oblique	
FOV [mm]	240 × 240	240 × 240	240 × 240	240 × 240	240 × 240	240 × 240	
Resolution [mm^3]	2.5×2.5×2.5	2.5×2.5× 2.5	2.5×2.5×2.5	2.5× 2.5×2.5	2.5×2.5×2.5	2.5×2.5×2.5	
Matrix (Base Resolution)	96 × 96	96 × 96	96 × 96 * (rhimsize=96 rhrcxres=96 rhrcyres = 96)	96 × 96	96 × 96	96 × 96 * (rhimsize=96 rhrcxres =96 rhrcyres = 96)	
Slice thickness	2.5	2.5	2.5	2.5	2.5	2.5	
Slice gap [mm]	0	0	0	0	0	0	
n. slices	60	60	60	60	60	60	
Phase Encoding direction	AP	AP***	AP * (pepolar = 1)	PA	PA***	PA	
Slice order	interleaved	interleaved	interleaved	interleaved	interleaved	interleaved	
TR [ms]	8400	8400	8400	8400	8400	8400	
TE [ms]	85	85	85	85	85	85	
Flip angle	90°	90°	90°	90°	90°	90°	
Fat suppression	yes	yes	yes	yes	yes	yes	
k-space coverage (Halfscan/Partial Fourier)	0.75	6/8	-	0.75	6/8	-	
Acceleration factor	SENSE≤ 2.3	GRAPPA=2	ASSET=2	SENSE≤ 2.3	GRAPPA=2	ASSET=2	
Filter	CLEAR on	Prescan Normalize on	PURE on	CLEAR on	Prescan Normalize on	PURE on	
n. directions/ b0	3 b0	3 b0	3 b0	32 dir/7 b0	30 dir/7 b0	32 dir/ 4 b0	
b [s/mm^2]	0	0	10 ****	1000/2000	1000/2000	1000/2000	
Bandwidth	1040 Hz (WFS=26)	1108 Hz/px	250kHz	1040 Hz (WFS=26)	1108 Hz/px	250 kHz	
EPI factor	47	96		47	96		
Specific settings	-	**Coil mode:** Adaptive Combine	**Option on** : EDR e Real time field adj	-	**Coil mode:** Adaptive Combine	**Option on** : EDR e Real time field adj	
Note				use same sequence preparation as DWI_3b0_AP			

Duration [min]	**≈ 1**	**≈ 1**	**≈ 1**	**≈ 10**	**≈ 10**	**≈ 10**	
Multiband (MB)							
yes/no							
model							
MB factor							
TR							
TE							
Duration							
Other settings							

(*) Acquisition in **research mode,** asterisk indicates CV that must be manually changed for GE scanner (highlighted in red).
(**) Two separate sequences are acquired. All parameters are the same except for b-value that is b=1000 (first) and b=2000 (second), use **manual prescan**.
(***) Siemens: each time the protocol is loaded, before starting the sequence, check that the **phase encoding direction** is correct **along the AP axis** (i.e. PA in DWI_2shell_7b0_PA and AP in DWI_3b0_AP). Even if the initial protocol has been correctly set and saved, upon reopening the coding is reset along the RL axis and must be modified.
(****) GE: to acquire 3b0, it is necessary to set here an additional b=10 s/mm^2.

Quantitative susceptibility mapping (QSM) protocol

For the QSM data, we will use a multi-echo gradient echo (GE) sequence with a resolution of $1\times1\times1mm^3$. Using different sequences on different vendors, standardizing echo-train and TE values is quite difficult. We aim to have uniform TE1 and average TE on all sites. The total acquisition time is ≈8'-9' minutes. **Please, make sure to save both the magnitude and the phase of the signal, for each echo**. For **GE** site, we suggest to save, for each echo, magnitude, real part and imagery part of the signal. The sequence should generate n° of echoes × n° of slices × 2 images (n° of echoes × n° of slices × 3 images for GE).

Save it as "**QSM**".

Table 5

Parameters	QSM			
Vendors	Philips	Siemens	GE	**Notes - changes**
Sequence type	3D GR MULTIECHO FFE-3D	3D GRE (swi3d8r)	3D SWAN	
Slice orientation	transversal	transversal	axial	
FOV [mm]	224 × 224	224 × 224	224 × 224	
Resolution [mm³]	1 × 1 × 1	1 × 1 × 1	1 × 1 × 1	
Matrix (Base Resolution)	224 × 224	224 × 224	224 × 224 * (rhimsize = 224 rhrcxres = 224 rhrcyres = 224)	
Slice thickness	1	1	1	
Slice gap	0	0	0	
n. slices	140	144	140-150	
Phase Encoding direction	RL	RL	RL	
NSA/Averages/NEX	1	1	1	
TR [ms]	40	51	51	
TE medio [ms]	Close 26.2	25.2	28	
First TE [ms]	5.4	5.6	5.6	
n. echo [n]	7	8	7	
Δ TE [ms]	5.2	= first TE (5.6)	~ first TE (not modif)	
Flip angle	18	18	18	
Flow compensation	yes	yes	yes	
k-space coverage (Halfscan/Partial Fourier)	no **	6/8	0.85	
Slice k-space coverage (Halfscan/Partial Fourier)	-	6/8	-	
Acceleration factor	SENSE =2	GRAPPA =2	ASSET =2	
Filter	CLEAR on	Prescan Normalize on	none	
Bandwidth	271 Hz (WFS=1.6)	340 Hz/px	31.25 kHz	
Specific Settings	Flyback=yes; To save Magnitude/Phase: MIP/MPR=M, P	To save Magn/Phase: SWI off, Coil Combine Mode=Adapt Combine	To save all echoes: rhfiesta = 0 * To save Magn/Real/Image part: rhrcctrl=13*	
Duration [min]	**≈ 8:11**	**≈ 8:45**	**≈ 8:01**	
Compressed sensing (CS)				
yes/no				
model				

CS factor				
TR				
TE				
Duration				
Other settings				

(*) Acquisition in research mode, indicates CV that must be manually changed for GE scanner (highlighted in red).
(**) Philips does not allow to enable the halfscan parameter and to save the images of Magnitude/Phase or Real/Imaginary parts.

NOTE QSM: Siemens scanner (change June 2020)

It has been observed that recent software package **N4_VE11C_LATEST_20170704_P26** on MAGNETOM Prisma scanners might prevent acquisition due to predicted PNS threshold exceeding. If this happens, please allow the system software to automatically recalculate the gradient rise times and re-save the updated protocol.

Resting state functional imaging (rs-fMRI) protocol

For the rs-fMRI data, we will use a standard gradient echo (GE) echo planar imaging sequence (EPI) sequence with a resolution of 3×3×3 mm^3, repetition time of 2400 ms and echo time of 30 ms, in addition to a GE-EPI reversed blip acquisition. Two spin echo (SE) EPI images with reversed blip acquisitions will be acquired. The total acquisition time is ≈10 minutes. **Please, talk to the subject** and ask to relax with **open eyes** during resting state RS_fMRI_200vol_vox3_PA. Use **same sequence preparation** between RS_fMRI_GE_AP and RS_fMRI_200vol_vox3_PA.

Save the Spin Echo sequences as "**RS_fMRI_SE_P**A" and "**RS_fMRI_SE_AP**".

Table 6

Parameters	**RS_fMRI_SE_AP**			**RS_fMRI_SE_PA**			
Vendors	Philips	Siemens	GE	Philips	Siemens	GE	**NOTES - changes**
Sequence type	Single shot SE EPI	EPI SE 2D	2D SE EPI	Single shot SE EPI	EPI SE 2D	2D SE EPI	
Slice orientation	transversal	transversal	oblique	transversal	transversal	oblique	
FOV [mm]	240 × 240	240 × 240	240 × 240	240 × 240	240 × 240	240 × 240	
Resolution [mm^3]	3.0×3.0×3.0	3.0×3.0×3.0	3.0×3.0×3.0	3.0×3.0×3.0	3.0×3.0×3.0	3.0×3.0×3.0	
Matrix (Base Resolution)	80 × 80	80 × 80	80 × 80 * (rhimsize= 80 rhrcxres = 80 rhrcyres = 80)	80 × 80	80 × 80	80 × 80 * (rhimsize= 80 rhrcxres = 80 rhrcyres = 80)	
Slice thickness	3.0	3.0	3.0	3.0	3.0	3.0	
Slice gap [mm]	0.5	0.5	0.5	0.5	0.5	0.5	
n. slices	40	40	40	40	40	40	
Phase Encoding direction	AP	AP**	AP * (pepolar = 1)	PA	PA **	PA	
Slice order	default	interleaved	interleaved	default	interleaved	interleaved	
TR [ms]	2400	2400	2400	2400	2400	2400	
TE [ms]	30	32	30	30	32	30	
Flip angle	80°	80°	not modif	80°	80°	not modif	
Fat suppression	yes	yes	yes	yes	yes	yes	
k-space coverage (Halfscan/Partial Fourier)	No	No	No	No	No	No	
Acceleration factor	SENSE= 2	GRAPPA=2	ASSET=2	SENSE=2	GRAPPA=2	ASSET=2	
Filter	CLEAR on	Prescan Normalize on	PURE on	CLEAR on	Prescan Normalize on	PURE on	
Dynamic scans	1	1	1	1	1	1	
Dummies scans	0	0	0	0	0	0	
Bandwidth	3114.5 Hz (WFS=10.47)	2404 Hz/px	250 kHz	3114.5 Hz (WFS=10.47)	2404 Hz/px	250kHz	
Specific settings		**Coil mode:** Adaptive Combine			**Coil mode:** Adaptive Combine		
Duration [min]	**≈ 0:15**	**≈ 0:15**	**≈ 0:15**	**≈ 0:15**	**≈ 0:15**	**≈ 0:15**	
Multiband (MB)							
yes/no							
model							
MB factor							
TR							
TE							

Duration							
Other settings							

(*) Acquisition in **research mode,** indicates CV that must be manually changed for GE scanner (highlighted in red).
(**) Siemens: each time the protocol is loaded, before starting the sequence, check that the **phase encoding direction** is correct **along the AP axis** (i.e. PA in RS_fMRI_SE_PA and AP in RS_fMRI_SE_AP). Even if the initial protocol has been correctly set and saved, upon reopening the coding is reset along the RL axis and must be modified.

Save the Gradient Echo sequences as "**RS_fMRI_GE_AP**" and "**RS_fMRI_200vol_vox3_PA**".

Table 7

Parameters	**RS_fMRI_GE_AP**			**RS_fMRI_200vol_vox3_PA**			
Vendors	Philips	Siemens	GE	Philips	Siemens	GE	**Notes - changes**
Sequence type	GE EPI	EPI FID 2D	GE EPI Multi-Phase	GE EPI	EPI FID 2D	GE EPI Multi-Phase	
Slice orientation	transversal	transversal	oblique	transversal	transversal	oblique	
FOV [mm]	240 × 240	240 × 240	240 × 240	240 × 240	240 × 240	240 × 240	
Resolution [mm^3]	3.0×3.0×3.0	3.0×3.0×3.0	3.0×3.0×3.0	3.0×3.0×3.0	3.0×3.0×3.0	3.0×3.0×3.0	
Matrix (Base Resolution)	80 × 80	80 × 80	80 × 80 * (rhimsize= 80 rhrcxres = 80 rhrcyres = 80)	80 × 80	80 × 80	80 × 80 * (rhimsize= 80 rhrcxres = 80 rhrcyres = 80)	
Slice thickness	3.0	3.0	3.0	3.0	3.0	3.0	
Slice gap [mm]	0.5	0.5	0.5	0.5	0.5	0.5	
n. slices	40	40	40	40	40	40	
Phase Encoding direction	AP	AP**	AP * (pepolar = 1)	PA	PA**	PA	
Slice order	default	interleaved descending	interleaved	default	interleaved descending	interleaved	
TR [ms]	2400	2400	2400	2400	2400	2400	
TE [ms]	30	30	30	30	30	30	
Flip angle	80°	80°	80°	80°	80°	80°	
Fat suppression	yes	yes	yes	yes	yes	yes	
k-space coverage (Halfscan/Partial Fourier)	No	No	No	No	No	No	
Acceleration factor	SENSE= 2	GRAPPA=2	ASSET=2	SENSE= 2	GRAPPA=2	ASSET=2	
Filter	CLEAR on	Prescan Normalize on	PURE on	CLEAR on	Prescan Normalize on	PURE on	
Dynamic scans (phases)	3	3	3	200	200	203 (multi-phase)	
Dummies scans	0	0	0	3	-	-	
Bandwidth	2556 Hz (WFS=14.07)	2404 Hz/px	250 kHz	2556 Hz (WFS=14.07)	2404 Hz/px	250 kHz	
EPI factor	39	80		39	80		
Specific settings		**Coil mode:** Adaptive Combine			**Coil mode:** Adaptive Combine		
Note				use same sequence preparation as RS_fMRI_GE_AP			
Duration [min]	**≈ 0:15**	**≈ 0:15**	**≈ 0:15**	**≈ 8**	**≈ 8**	**≈ 8**	
Multiband (MB)							
yes/no							
model							

MB factor							
TR							
TE							
dynamic scans							
Duration							
Other settings							

(*) Acquisition in **research mode,** indicates CV that must be manually changed for GE scanner (highlighted in red).

(**) Siemens: each time the protocol is loaded, before starting the sequence, check that the **phase encoding direction** is correct **along the AP axis** (i.e. PA in RS_fMRI_200vol_vox3_PA and AP in RS_fMRI_GE_AP). Even if the initial protocol has been correctly set and saved, upon reopening the coding is reset along the RL axis and must be modified.

2.4 – Positioning of sequences packages

Plan your scans as follow, in order to standardize the positioning of the sequence packages between the different centers and to avoid introducing confounding effects.

Localiser

Position the subject and perform 'localiser' scans in order to align the transverse slices for all scans to run parallel to the inferior points of the corpus callosum (bicallosal plane).

Attention: Put attention to place the subject inside the scanner so that **bicallosal alignment** and pure axial alignment correspond. (see **Figure 1**).

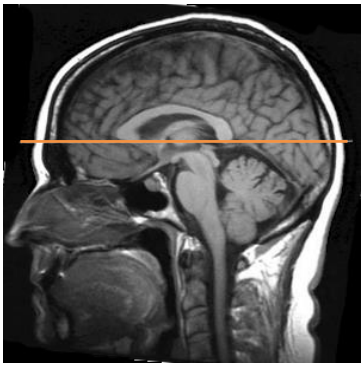


Figure 1

We recommend that you use axial, coronal and sagittal planning scans to optimally position the subject (example image showing positioning in all three planes given below).

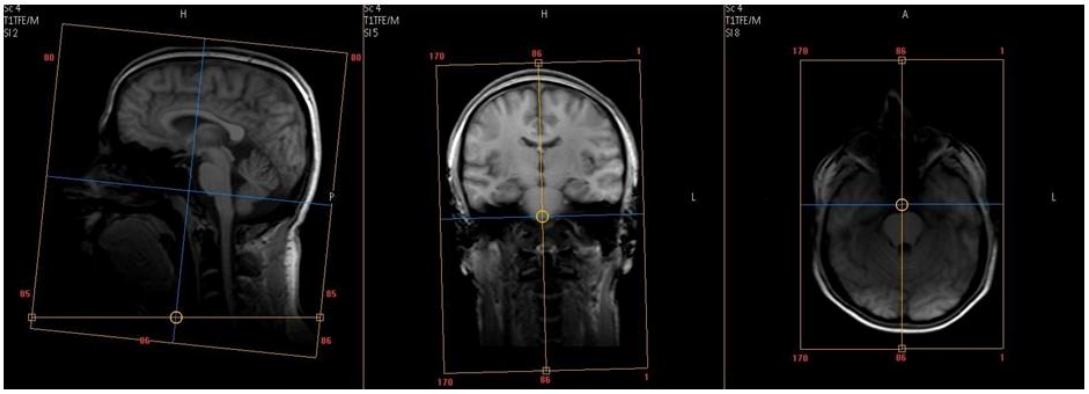


Figure 2

Structural protocol (sT1W_3D and FLAIR_3D)

For the 3DT1w and FLAIR protocols, plan the scan to achieve adequate coverage of the entire brain, and also include the brainstem, and down to cervical cord level C3 if possible.

DWI and rs-fMRI protocols

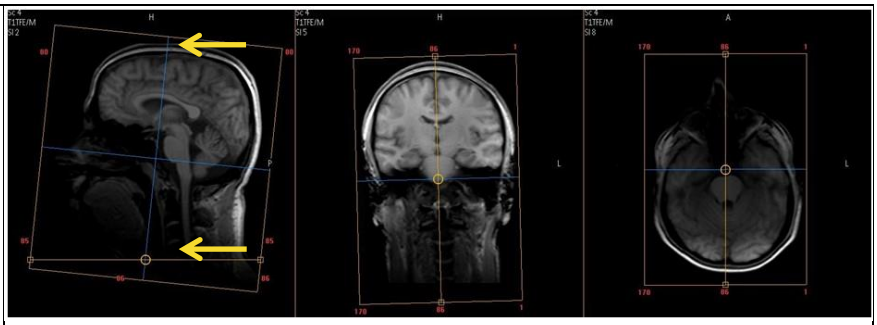
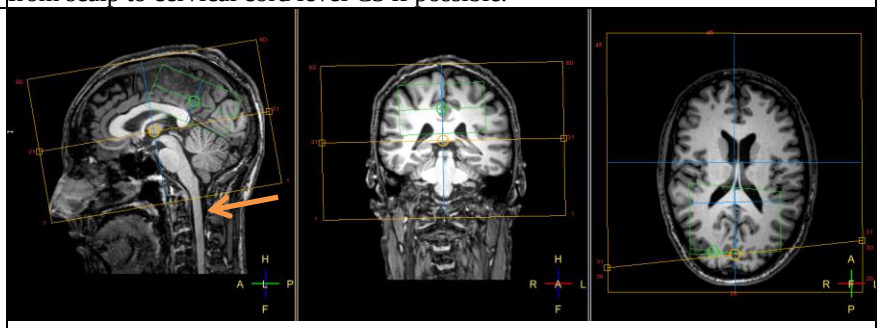
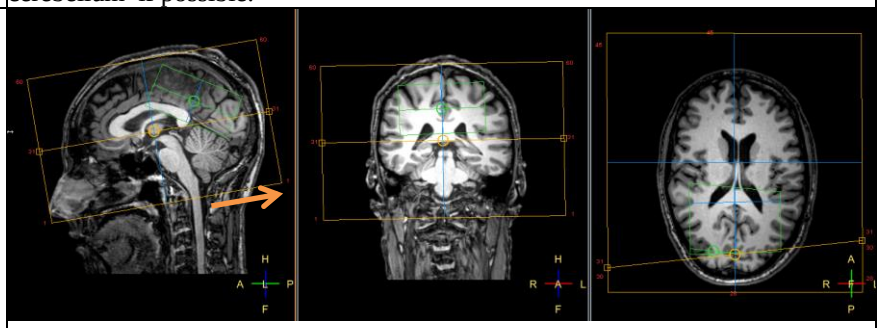
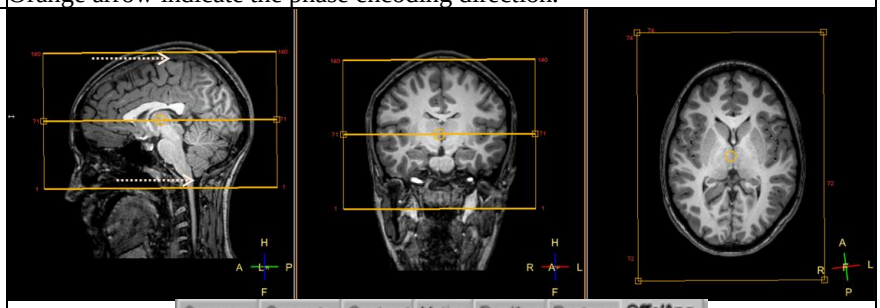
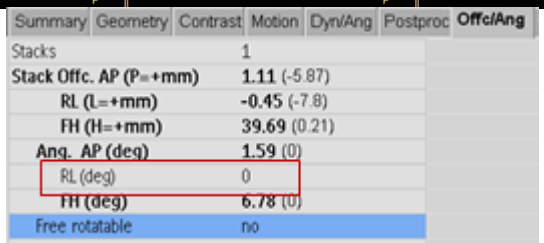
For the axial DWI and fMRI acquisitions, plan the scan to achieve adequate coverage of the whole brain, including the scalp and cerebellum, using the anterior-posterior line of the corpus callosum (bicallosal plane) as reference. Try to put the subject inside the scanner so that this alignment correspond to the pure axial alignment (0 degree).

QSM protocol

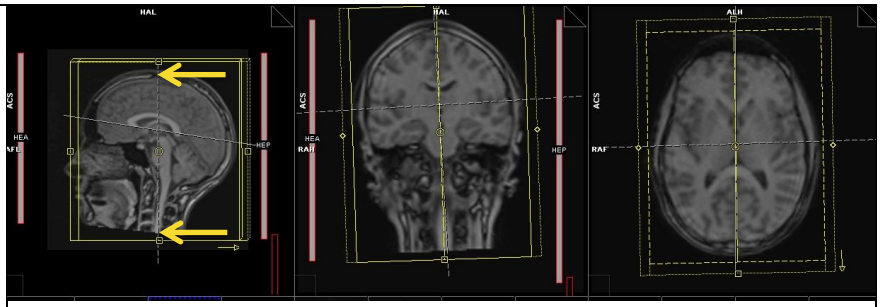
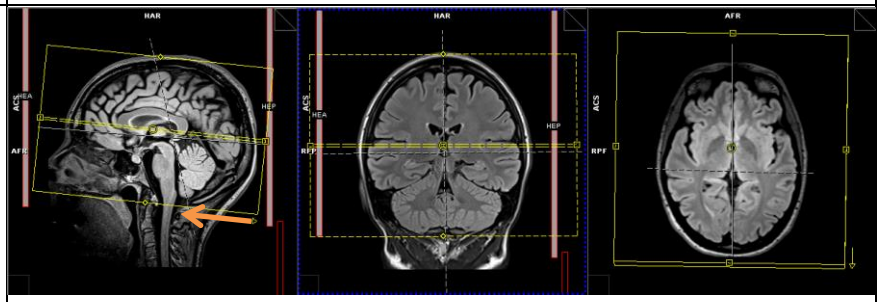
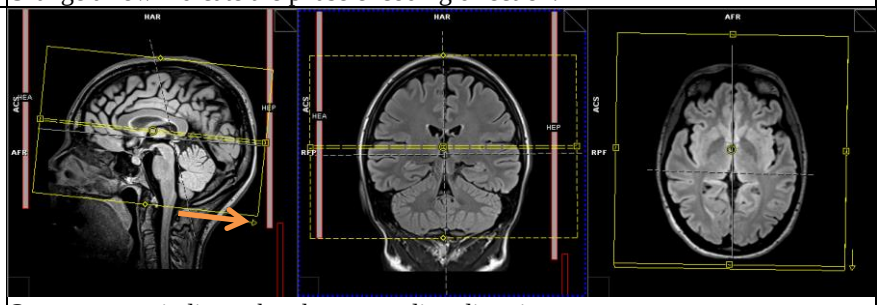
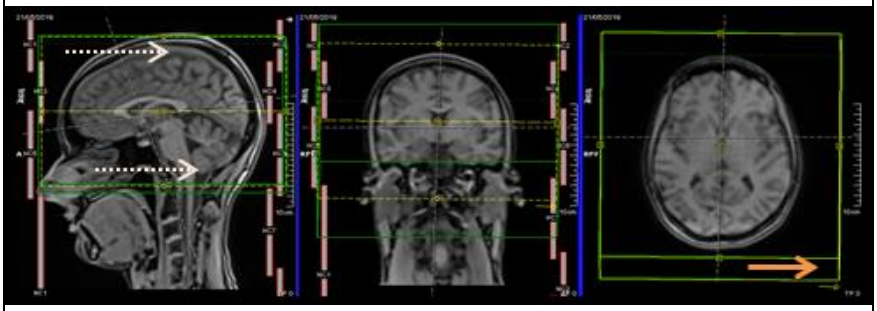
For the QSM acquisition, plan the scan to achieve adequate coverage of the whole brain, including the scalp and cerebellum, using the pure axial alignment (0 degree).

For the detailed description and visual inspection of sequence alignment follow the subsequent figures for Philips, Siemens, and GE.

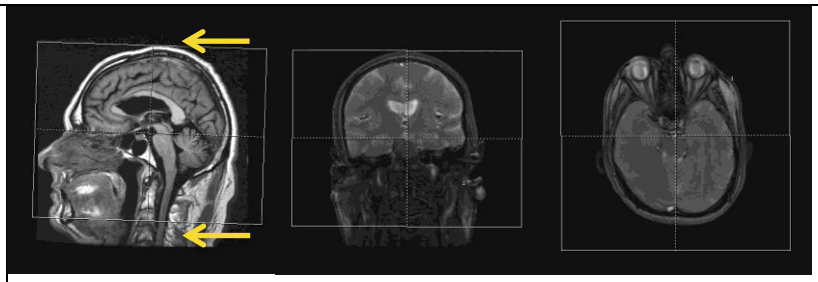
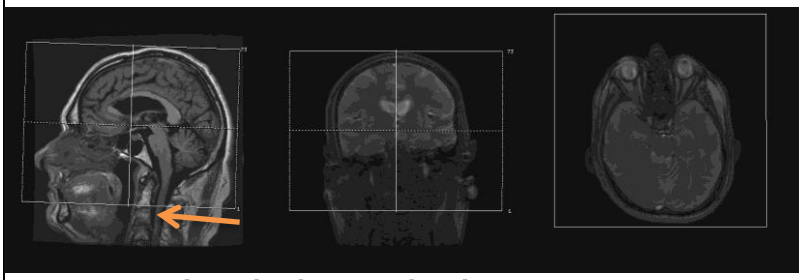
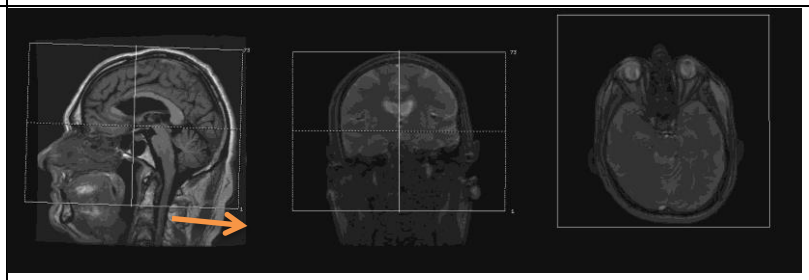
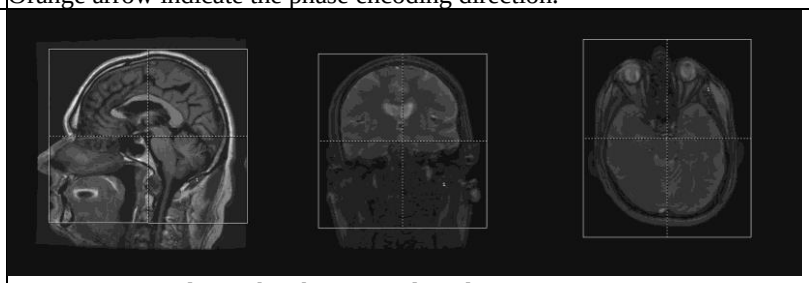
2.4.1 – Positioning using a 3T Philips Achieva scanner

sT1W_3D ***FLAIR_3D*** **(Figure 3a)**	 Yellow arrows indicate brain structures that must be included in the scan. Include from scalp to cervical cord level C3 if possible.
DWI_2shell_7b0_PA ***RS_fMRI_3SE_PA*** ***RS_fMRI_200vol_vox3_PA*** **(Figure 3b)**	 Orange arrow indicate the phase encoding direction. Include from scalp to cerebellum if possible.
DWI_3b0_AP ***RS_fMRI_3SE_AP*** ***RS_fMRI_GE_AP*** **(Figure 3c)**	 Orange arrow indicate the phase encoding direction.
QSM **(Figure 3d)**	  Cover the entire brain (white arrows)

2.4.2 – Positioning using a 3T Siemens Skyra scanner

sT1W_3D ***FLAIR_3D*** **(Figure 4a)**	 Yellow arrows indicate brain structures that must be included in the scan.
DWI_2shell_7b0_PA ***RS_fMRI_3SE_PA*** ***RS_fMRI_200vol_vox3_PA*** **(Figure 4b)**	 Orange arrow indicate the phase encoding direction.
DWI_3b0_AP ***RS_fMRI_3SE_AP*** ***RS_fMRI_GE_AP*** **(Figure 4c)**	 Orange arrow indicate the phase encoding direction.
QSM **(Figure 4d)**	 Orange arrow indicate the phase encoding direction. Cover the entire brain (white arrows)

2.4.3 – Positioning using a 3T GE Discovery 750MR scanner

sT1W_3D ***FLAIR_3D*** **(Figure 5a)**	 Yellow arrows indicate brain structures that must be included in the scan.
DWI_1000shell ***DWI_2000shell*** ***RS_fMRI_3SE_PA*** ***RS_fMRI_200vol_vox3_PA*** **(Figure 5b)**	 Orange arrow indicate the phase encoding direction.
DWI_3b0_AP ***RS_fMRI_3SE_AP*** ***RS_fMRI_GE_AP*** **(Figure 5c)**	 Orange arrow indicate the phase encoding direction.
QSM **(Figure 5d)**	 Orange arrow indicate the phase encoding direction. Cover the entire brain with axial orientation (0 degree)

2.5 – Clinical protocols

As defined in WP1 Working group on "Dementia patients", the basic clinical protocol includes:

Sequence	Slice orientation	Phase encoding	FOV range [mm^2] or [mm^3]	ACQ Voxel range [mm^2] or [mm^3]	Slice thickness [mm]	Slice gap range [mm]
T1-3D	Sagittal	AP	FH(240-256) x AP(240-256) x RL(170-190)	1 x 1 x 1	1	-
T2-FLAIR-3D	Sagittal	AP	FH(240-256) x AP(240-256) x RL(170-190)	1 x 1 x 1	1	-
T2-2D FSE/TSE	Axial	RL	AP(220-256) x RL(220-256)	(0.5-0.7) x (0.5-0.7)	4	0-0.4
SWI-3D ^	Axial	RL	AP(220-256) x RL(220-256) x FH(120-180)	(0.5-0.7) x (0.5-0.7)	1.5	-
or						
SWI-2D ^	Axial	RL	AP(220-256) x RL(220-256)	(0.5-0.7) x (0.5-0.7)	1.5	0-0.4
or						
T2*-2D ^	Axial	RL	AP(220-256) x RL(220-256)	(0.5-0.7) x (0.5-0.7)	4	0-0.4
DWI	Axial	AP/RL	AP(240-256) x RL(240-256)	(1.5-2) x (1.5-2)	4	0-0.4

Only sequences in **red** need to be added to the harmonized protocol.

Section 3 – MRI scanner: software and hardware update

Site: _____ Site code: _____

MRI scanner information

Date of software/hardware intervention: _____

□ Hardware interventions

Describe the type of hardware intervention:

_____

_____

_____

Field Strength (T): _____

Vendor: _____

Model: _____

Year of installation: _____

Gradients Maximum Amplitude: _____

Maximum Slew Rate: _____

Coils: _____

_____

□ Software interventions

Software version: _____

Name: _____

Signature: _____

Date: _____