3T MRI Scanning Procedure
Study: CNS-COVID

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Document History

Version	Initials	Date	Comment
1	JC	04/01/21	

Related Documents and Location

PIS and Consent Form (electronic, study docs folder)

Study Information

Study Title: multi-modal magnetic resonance imaging (MRI) protocols at 3 Tesla for use in multi-site COVID-19 research

Ethics Number: Cambridge: HBREC.2020.44

Scanner: 3T

Session Time: 60min

Equipment Required

Standard

32 Channel Head Coil
Regular mirror
Ear plugs
Immobilization sponges
Buzzer

Lighting and stimulus

Bore lights on
Room lights on
LCD on (Biobank fixation cross)

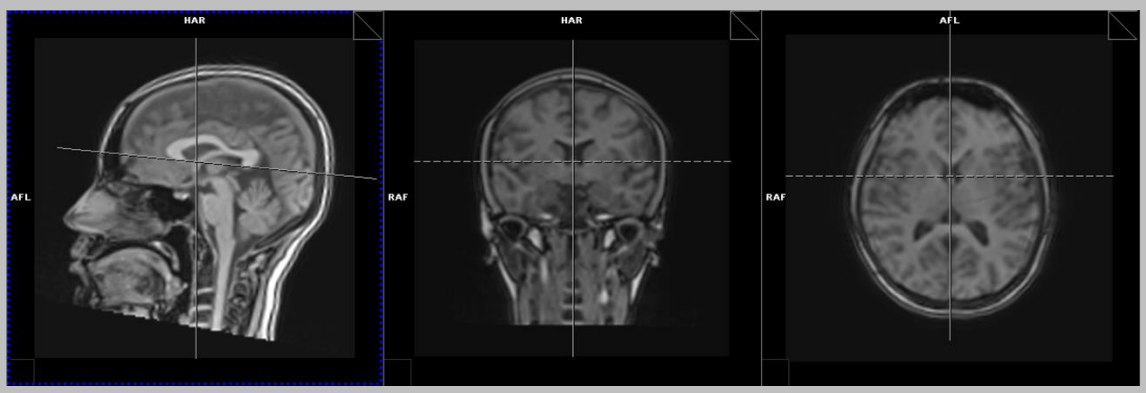
Ancillary

Siemens Respiratory bellows (connects to the ECG unit)
Siemens Pulse meter
[These should be used if available, but are not mandatory – if used the physiological information during the DTI and fMRI scans is saved to the DICOM files]

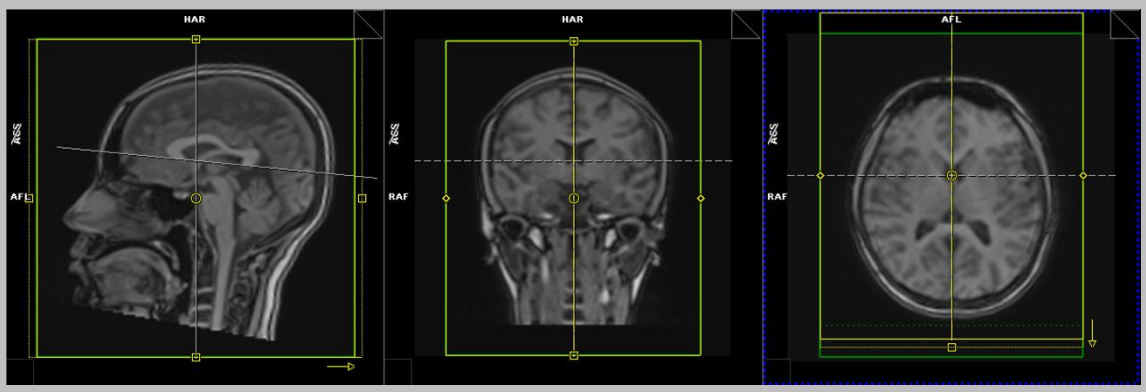
Protocol Sequences

1. ***-- Centre to the coil centre-mark --***
Note that all sequences are set to REF or FIX with a 0mm offset, such that the table does not move between scans (to avoid re-shimming).

2. **AAHead_Scout** **14s**
   - Auto-runs, no setup required
   - Once finished sagittal, coronal and axial reconstructions will automatically load into the graphic segments (as below)



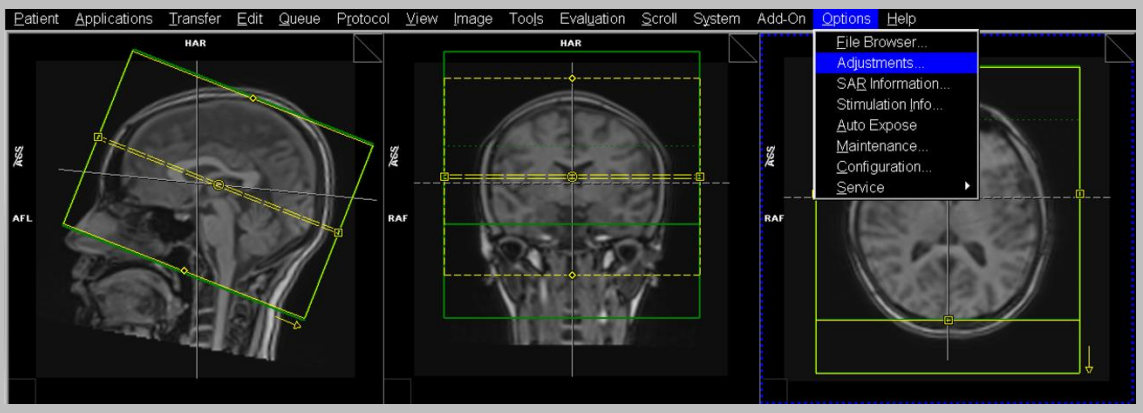
3. **T1_p2_1mm_fov256_sag_TI_880** **4m54s**



   - Open scan, allow auto-align to position scan, click close and run scan
   - NB scan will automatically shim

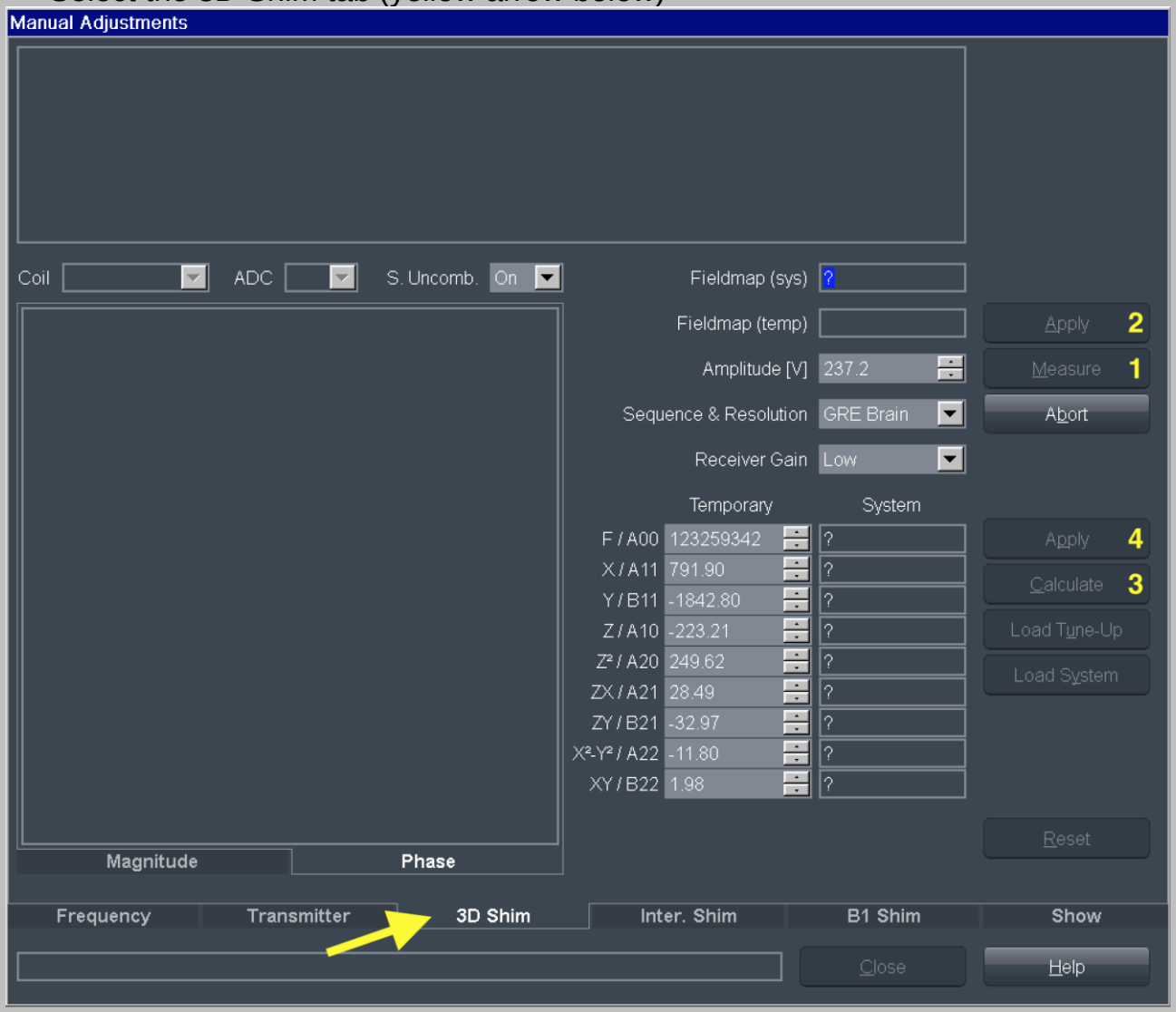
4. ***-- fixation cross --***
[Display the Biobank fixation cross during the resting state fMRI scan and ask the subject to try not to think about anything specific, to stay awake with eyes open, and to fixate on the cross. The fixation cross can be downloaded from: https://www.fmrib.ox.ac.uk/ukbiobank/protocol/Crosshair.png]

5. ***-- Shim x3 --***
[Perform a manual scan three times to obtain a good starting shim over the brain. To do this, open the MB8_FMRI_fov210_2.4mm_resting sequence and click on 'Options -> Adjustments' to bring up the manual shimming interface



- Now click on ‘Options’ - > ‘Adjustments’ to bring up the manual shimming interface

- Select the 3D Shim tab (yellow arrow below)



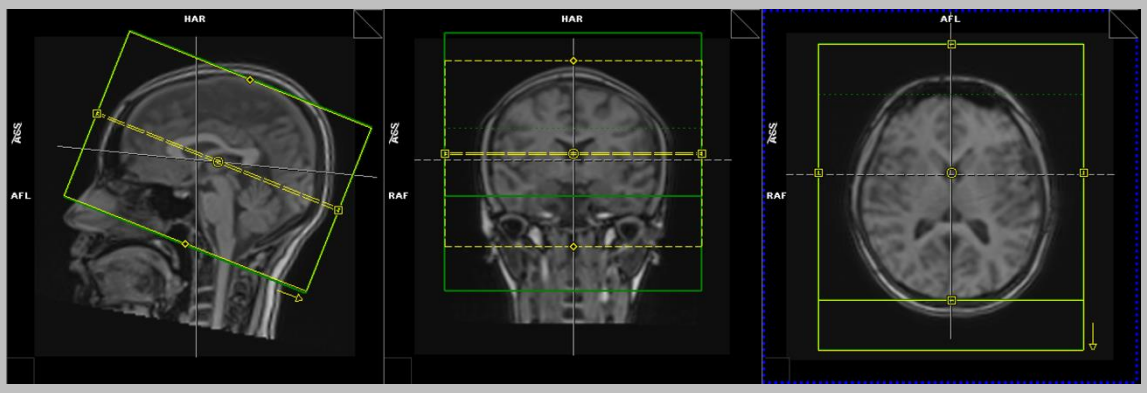
- Shim by clicking on 1) Measure, 2) Apply, 3) Calculate and 4) Apply (as indicated above).
- Repeat this 2 more times and you should see 6 rows of text in the light grey shim box, along the lines of:

Manual Adjustments

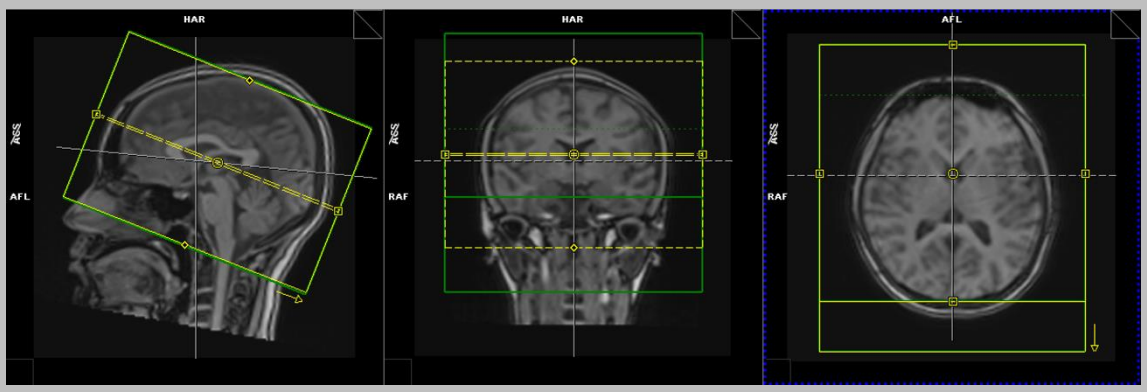
No	X [µT/m]	Y [µT/m]	Z [µT/m]	A20 [µT/m²]	A21 [µT/m²]	B21 [µT/m²]	A22 [µT/m²]	B22 [µT/m²]	Converged
1	-	-	-	-	-	-	-	-	Yes
2	792.69	-1,847.40	-216.32	286.25	41.43	6.92	-36.98	4.08	Yes
3	-	-	-	-	-	-	-	-	Yes
4	792.32	-1,847.79	-215.85	292.68	40.52	11.45	-37.98	1.48	Yes
5	-	-	-	-	-	-	-	-	Yes
6	792.56	-1,847.52	-215.88	291.16	42.38	13.65	-38.44	3.74	Yes

- Close and apply to start the scan
- Remind researcher to display the fixation cross
- Resting state instructions: "Look at the cross for the next scan, blink normally and try not to fall asleep"

6. MB8_FMRI_fov210_2.4mm_resting 6m10s

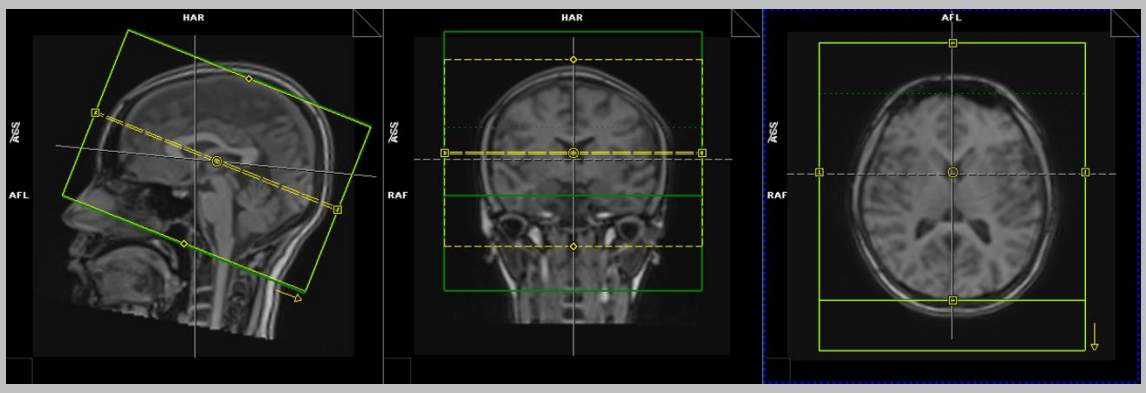


7. diff_PA_MPopt_MB3_3b0_lowflip 36s



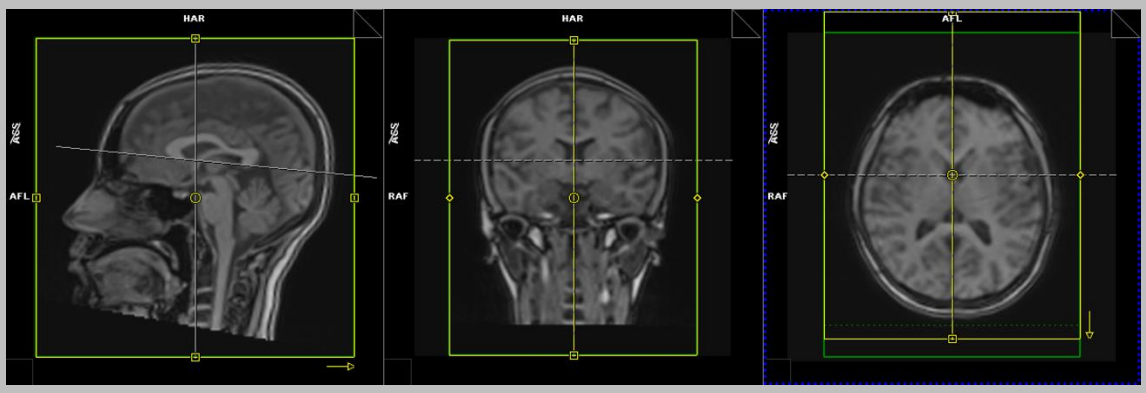
- Open scan, allow auto-align to position scan, click close and run scan
- NB do not change phase encoding direction

8. diff_AP_MPopt_MB3_50b1000_50b2000_8b0_lowflip **6m32s**



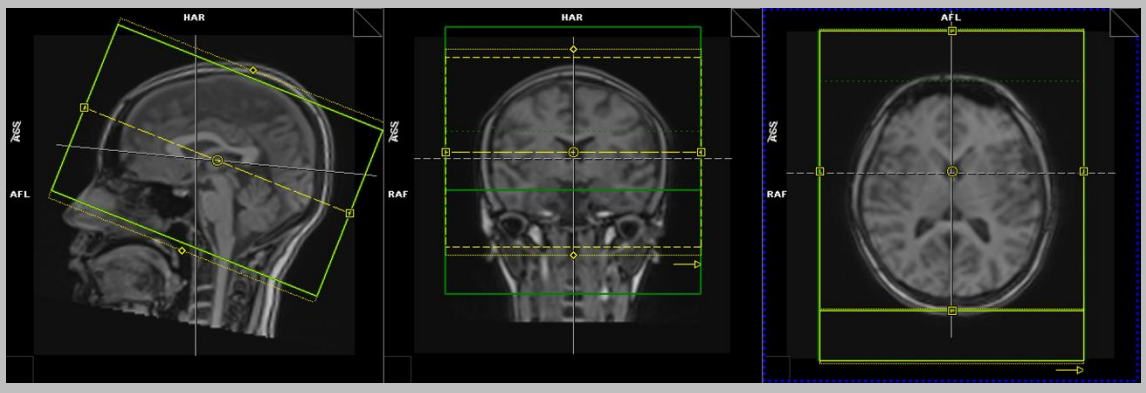
- Open scan, allow auto-align to position scan, click close and run scan
- NB do not change phase encoding direction

9. t2_space_dark-fluid_sag_p3 **4m32s**



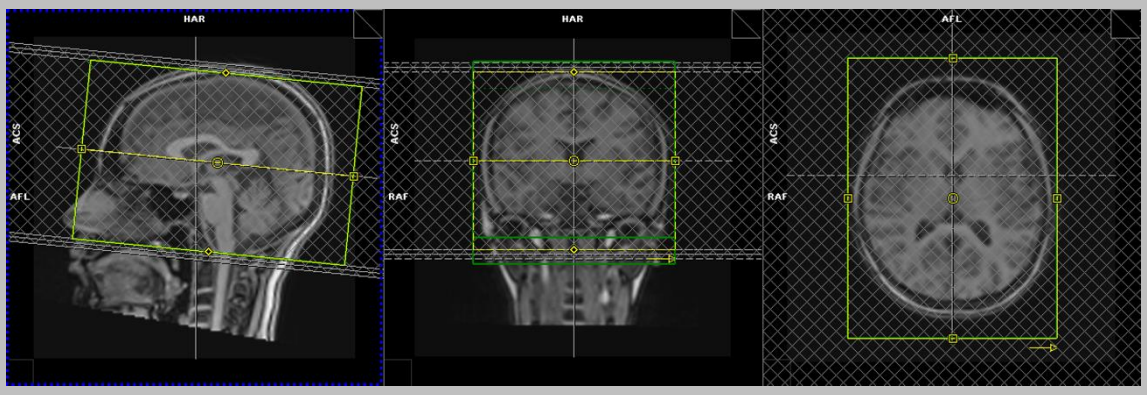
- Open scan, allow auto-align to position scan, click close and run scan

10. SWI_3mm_Updated_v1.1 **2m8s**



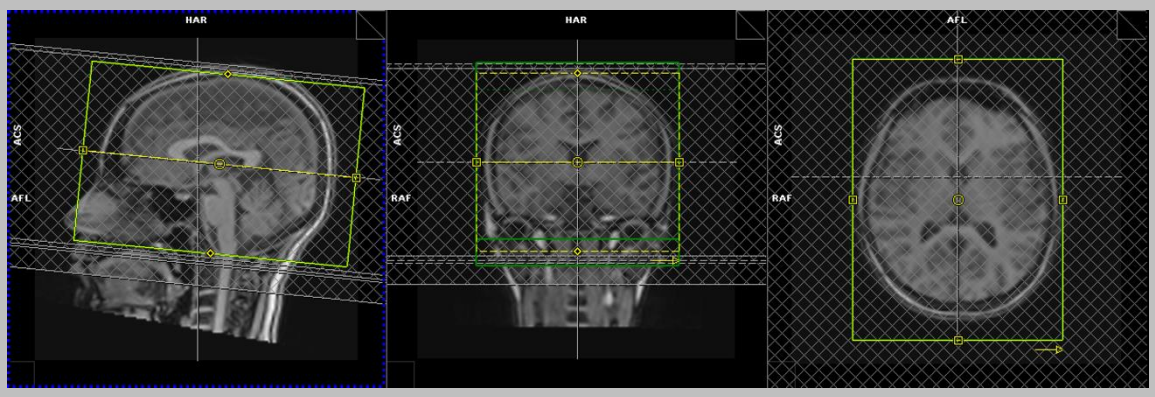
- Open scan, allow auto-align to position scan, click close and run scan

11. fme_pCASL_M0_RL **16s**



- Open scan, allow auto-align to position scan, click close and run scan

12. fme_pCASL_BL1800_PLD400 **26s**



- Open scan, allow auto-align to position scan, click close and run scan

13. fme_pCASL_BL1800_PLD800 **30s**

- Open scan, allow auto-align to position scan, click close and run scan
- NB appearance identical to **fme_pCASL_BL1800_PLD400**

14. fme_pCASL_BL1800_PLD1200 **34s**

- Open scan, allow auto-align to position scan, click close and run scan
- NB appearance identical to **fme_pCASL_BL1800_PLD400**

15. fme_pCASL_BL1800_PLD1600 **38s**

- Open scan, allow auto-align to position scan, click close and run scan
- NB appearance identical to **fme_pCASL_BL1800_PLD400**

16. fme_pCASL_BL1800_PLD2000 **42s**

- Open scan, allow auto-align to position scan, click close and run scan
- NB appearance identical to **fme_pCASL_BL1800_PLD400**

17. -- Do not change angle --

- Reminder to not change the default angle or straighten the following 2 sequences

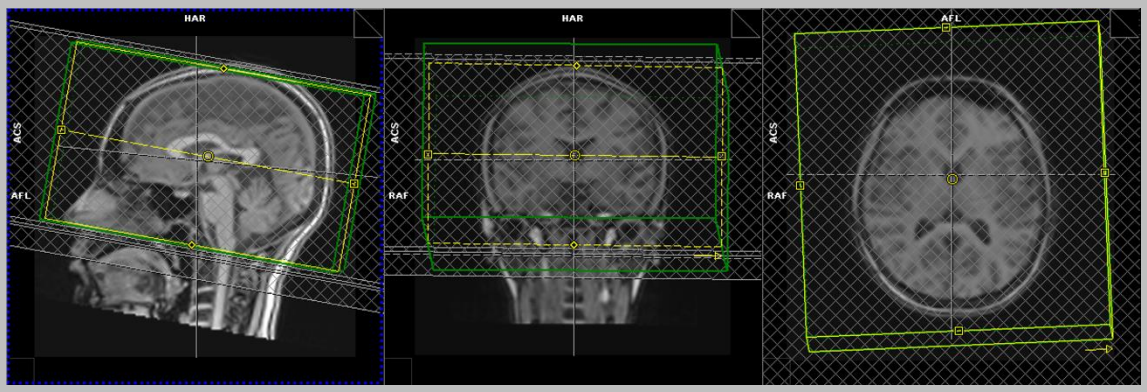
18. -- Manually position so labelling

19. plane 2cm below cerebellum --

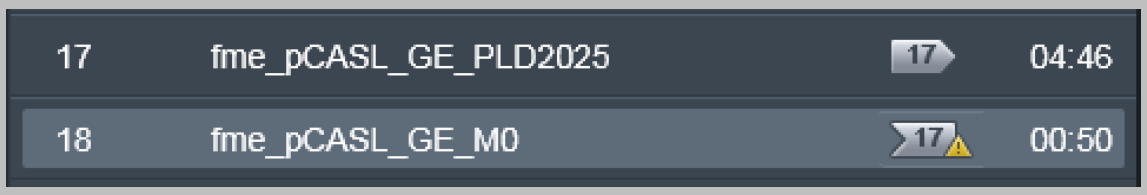
20. -- Click OK on conflict prompt --

- The **fme_pCASL_GE_M0** has a known conflict prompt which can be ok'd

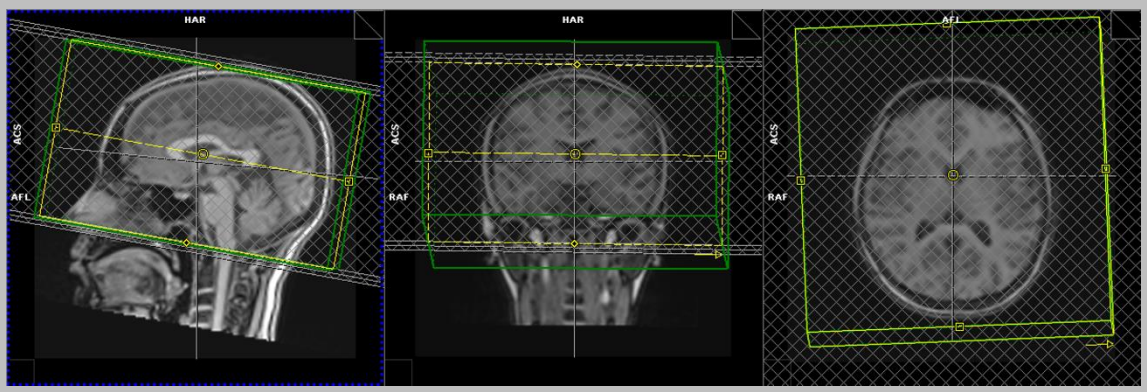
21. fme_pCASL_GE_PLD2025 4m46s



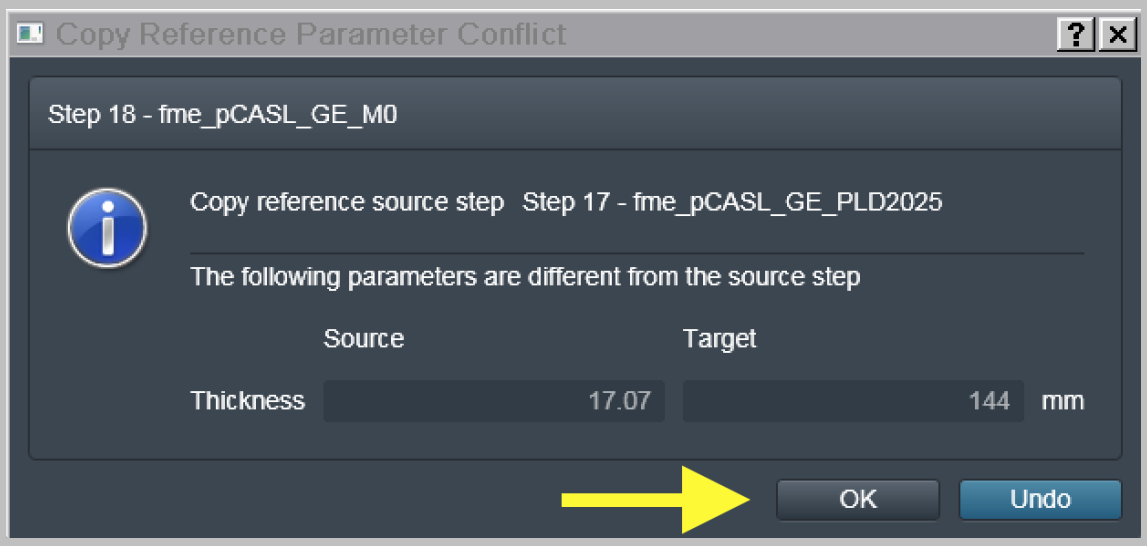
- This scan must be manually positioned
- ! Do not change angle or straighten this sequence !
- Move slice slab so that labelling plane is 2cm below the cerebellum and click apply
- NB when you click 'Apply' a yellow triangle will appear on the following sequence. This can be ignored



22. fme_pCASL_GE_M0 50s



- Auto-copies COSG&SR from sequence **fme_pCASL_ GE_PLD2025**
- Click OK on the conflict prompt when it appears


Copy Reference Parameter Conflict
Step 18 - fme_pCASL_GE_M0
Copy reference source step Step 17 - fme_pCASL_GE_PLD2025
The following parameters are different from the source step
Source
Target
Thickness
17.07
144
mm
OK
Undo