



OHBA 3T MRI Scanning Procedure OxBAC-BIRAX Healthy Ageing (OHBA 3T)

Study Information

Study Title: Healthy controls for the Oxford Health Centre: harmonising with UK Biobank

Study Group: Brain Health Centre / Neurology and Psychiatry

PI: [REDACTED]

Calpendo ID: 2021_112

Ethics Number: [REDACTED]

Introduction: Acquisition protocol for the studies: Oxford UK Biobank Aligned Controls (OxBAC) and British Israel Research Academic Exchange (BIRAX) study on Microstructural MRI in Healthy Ageing. The protocol includes sequences matched to the UK Biobank imaging study as well as a specific sequence to study the brain microstructure. The UK Biobank-matched sequences are the same as those acquired in memory clinic patients of the Oxford Brain Health Clinic on the same scanner (protocol referenced below), to provide a matched healthy control group

General Info: Healthy participants aged 21 and over

Scanner: OHBA 3T Prisma

Category: Category 1a - Healthy Subjects

Staffing levels: 1x scanner operator and 1x researcher

Session Time: 90 minutes

Incidental Findings Procedure: WIN SOP Dealing with Research Neuroimaging Incidental Findings (OHBA_014_V1, FMRIB_002_V5, Neuro_002_V5)

Researchers and their contact details

[REDACTED]

Equipment Required

Standard

32 Channel Head Coil
Regular mirror
Ear plugs
Immobilization sponges
Buzzer

Lighting and stimulus

Bore lights on
Room lights on
BOLD LCD screen on (pictures and fixation cross)

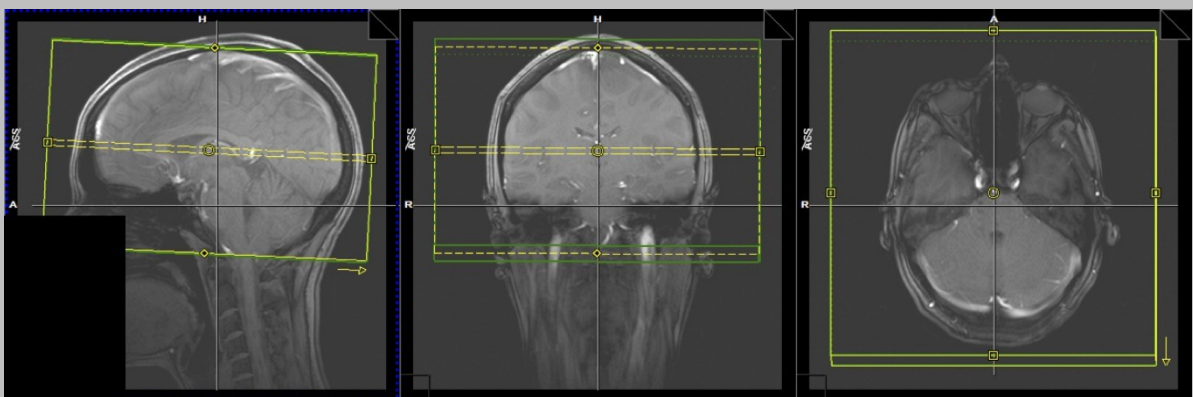
Ancillary

None

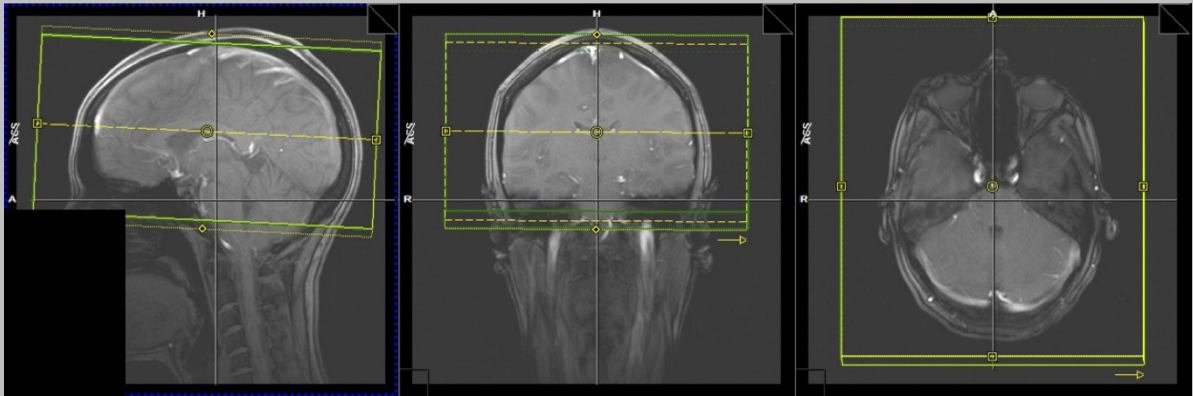
Protocol Sequences

USER >> OHBA Projects VE11C >> 2021_112 bhcHC-BIRAX >> Protocol v3

- 1. localiser_3plane_32ch** **00:14**
 - Auto-runs, no adjustment required
- 2. ep2d_diff_3scan_trace_p2_130** **00:43**
 - Axial orientation, angle to ACPC, straighten on coronal if required
 - Cover whole brain



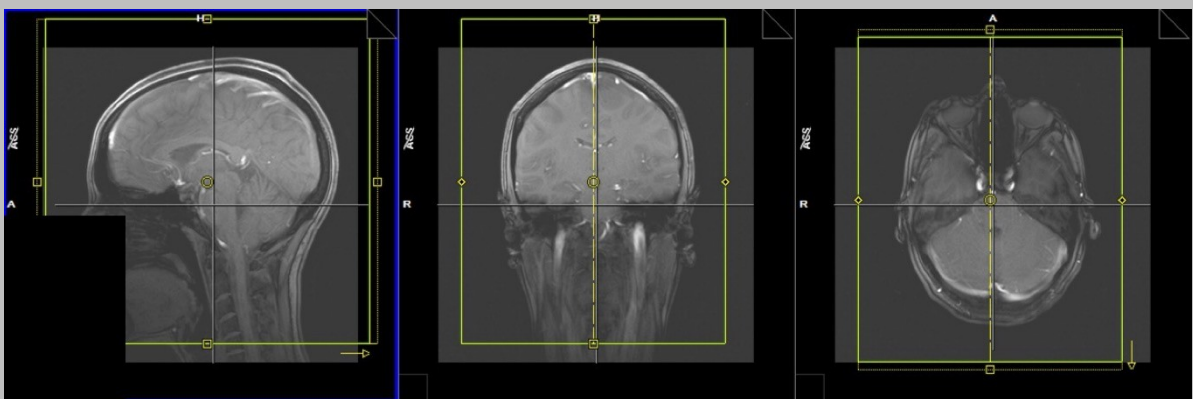
- 3. TE_10_TE_20_TR30_...._PF78** **04:46**
 - Axial orientation, straighten on coronal if required
 - Copy COSG&SR from **ep2d_diff....**
 - Cover whole brain (move slice slab if necessary)



4. T1_p2_1mm_fov256_sag_TI_880 (biobank)

04:54

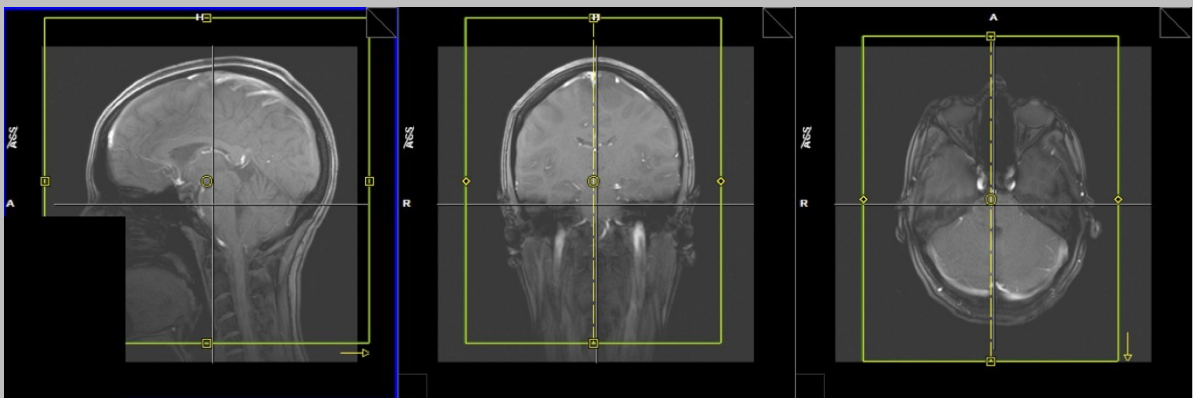
- Sagittal orientation, straighten on coronal & axial if required
- Cover whole brain, position to reduce phase wrap



5. t2_flair_sag_p2_1mm_FS_ellip_pf78

05:52

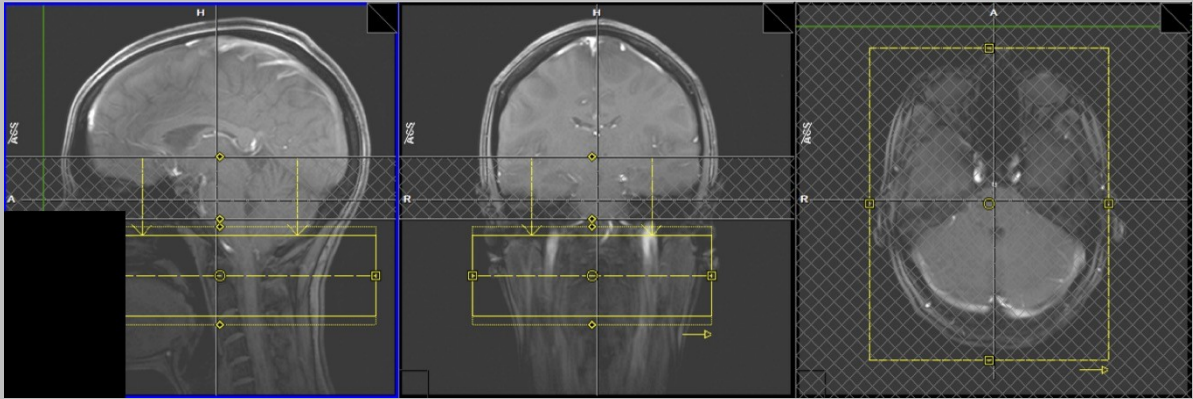
- Auto-copies COSG&SR from T1_p2_1mm.... (same FoV as T1)



6. TOF_3D_neck

00:42

- True axial, don't angle or straighten
- Position to cover from C2/C3 to lower cerebellum
- Once completed load into the viewer and find the best slice between vertebral loops

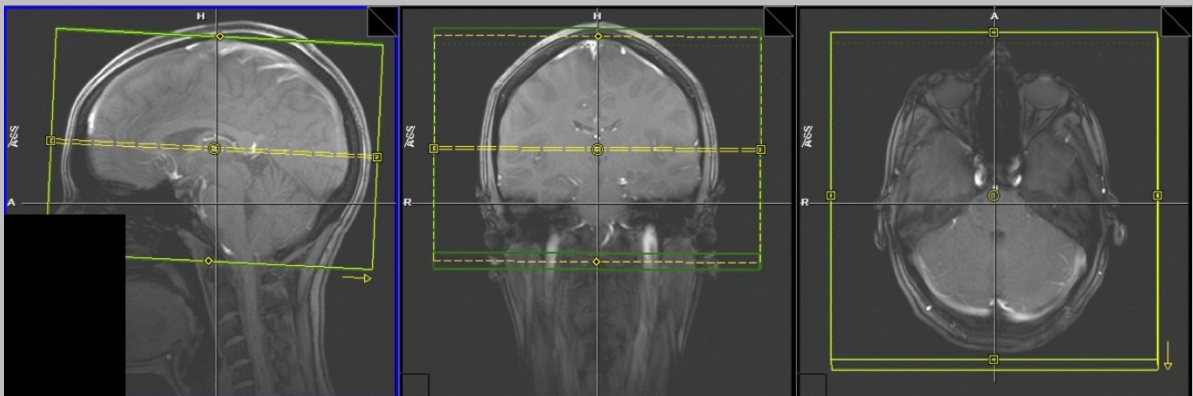


7. -- Manual shim x3 –

8. diff_PA_MPopt_MB3_3b0_lowflip

00:36

- Axial orientation, angle to ACPC, straighten on coronal if required
- Cover whole brain
- Open adjustments, click the 3D Shim tab and do 3x manual shims (ie Measure, Apply (top), Calculate, Apply (bottom))
- NB do not need to swap phase direction (already set in seq – special)
- Warn patient this scan, and the next, are very noisy and they may feel the table vibrate



9. diff_AP_MPopt_MB3_50b1000_50b2000_8b0_lowflip

06:32

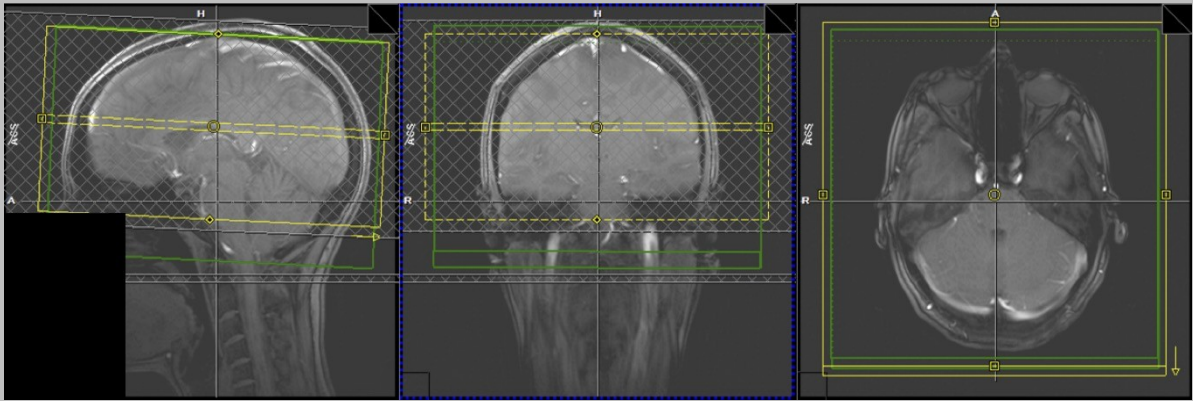
- Auto-copies COSG&SR from diff_PA...
- NB do not need to swap phase direction (set in seq – special)

10. -- Copy diff Adj Vol –

11. to_ep2d_PCASL

07:17

- Axial orientation, angle to ACPC and adjust Sat region 1 to match
- Copy adj vol from diff_PA...
- Go to the Geometry Tab, select the Saturation Sub-Tab, choose Sat. region 1 and centre and angle to cover the scan volume
- Select Sat. region 2 and click the ... button, input the height chosen above, eg F76.8 and click enter in the centre of XX box
- Ensure the orientation is set to “transverse” If not, click on the three dots next to the orientation and reset it to “transverse”
- NB do not angle Sat region 2
- ASL instructions: “Look at the cross for the next scan, blink normally and try not to fall asleep.” Ensure researcher is using red BHC/Biobank cross

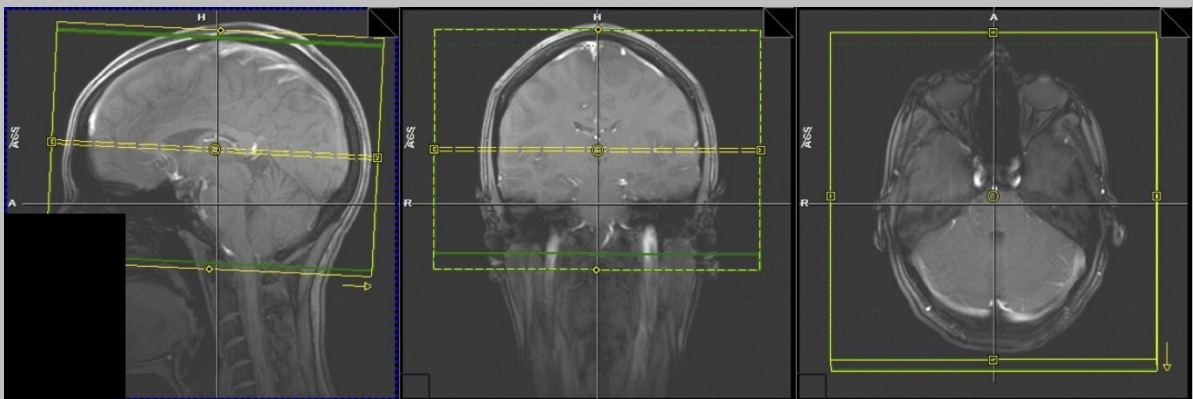


12. -- Copy diff Adj Vol --

13. MB8_FMRI_fov210_2.4mm_resting

06:10

- Copy COSG&SR from #9 diff_PA_MPopt_MB3_3b)_lowflip...
- Copy Adj Vol from diff_PA...
- Cover whole brain
- Resting state instructions: **“Look at the cross for the next scan, blink normally and try not to fall asleep.”** Ensure researcher is using red BHC/Biobank cross

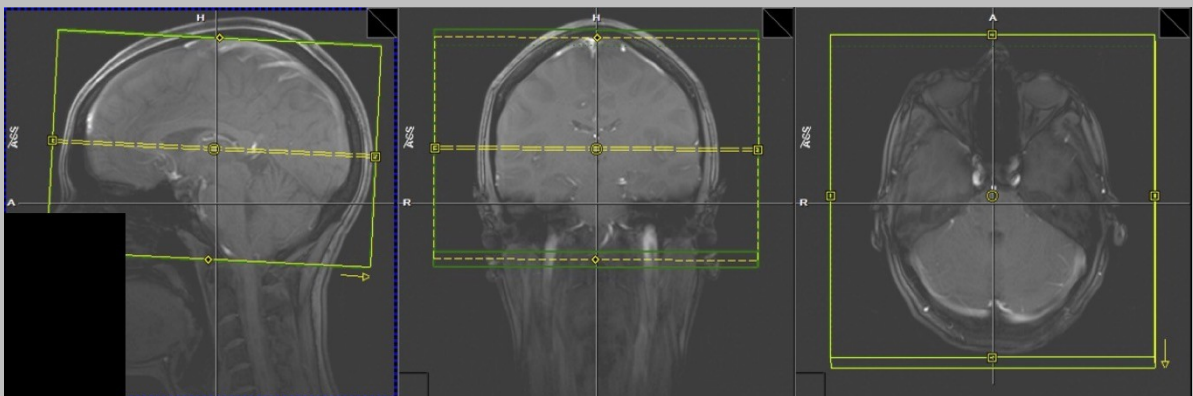


14. -- BIRAX --

15. dMRI_MB4_185dirs_d15D45_AP

11:10

- Axial orientation, angle to ACPC, straighten on coronal if required
- Copy COSG&SR from **diff_PA...**
- Cover cortex at expense of cerebellum



16. dMRI_MB4_6dirs_d15D45_Aprev

00:44

- Auto copies COSG&SR from dMRI_MB4_185dirs_d15D45_AP

- Do not need to swap AP/PA

17. -- Do retro-recon of SWI --

Post Scan

- Do retro-recon of SWI scan (see Appendix)
 - Researcher must confirm that the SWI retro-recon has been done before leaving
 - Researcher to return stimulus equipment to default state
-

Researcher Acknowledgement

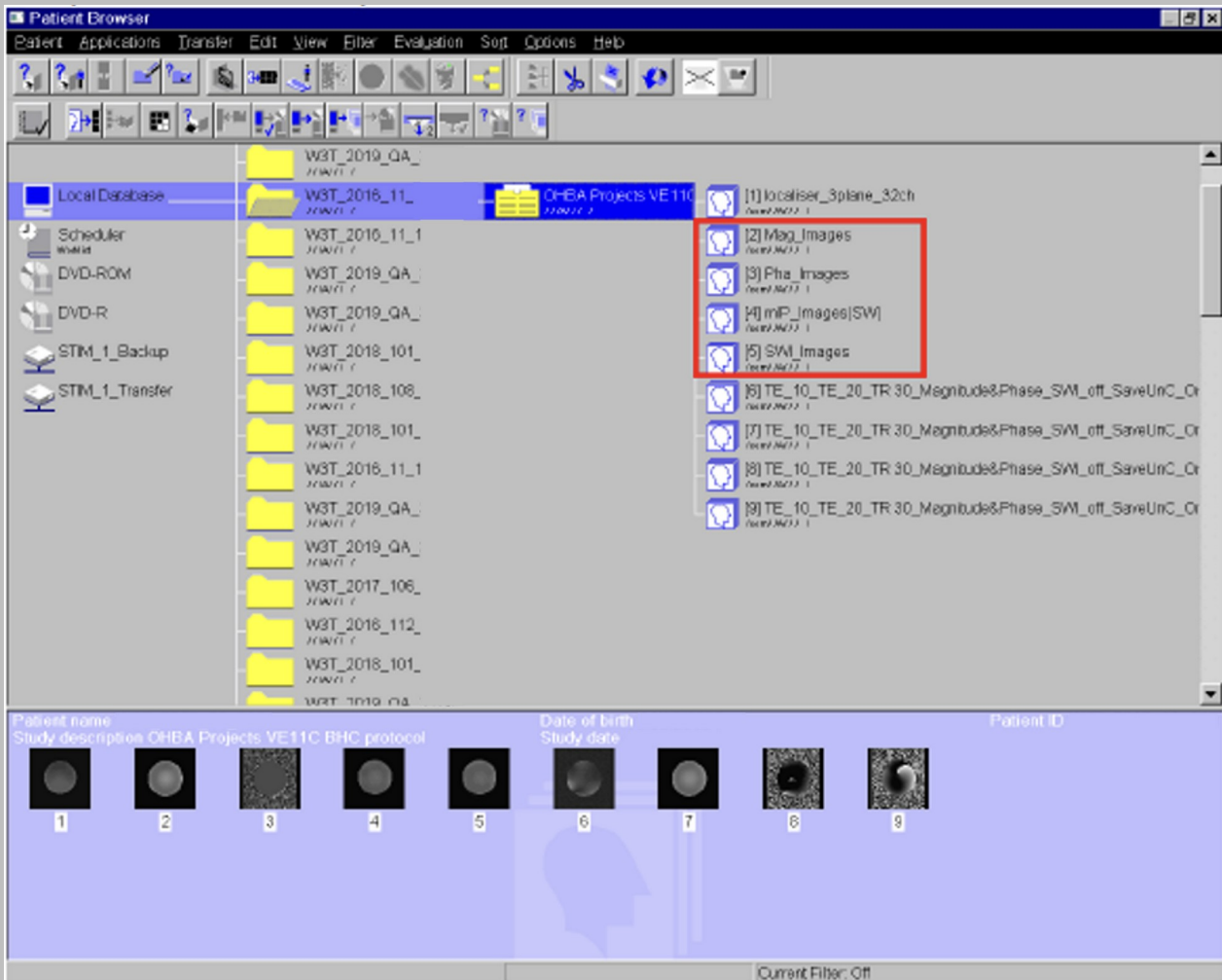
Use of limited release sequences


The use of limited release sequences entails a risk that they will crash or otherwise slow down a session.

It is important to note that in the case where there is a delay caused by these sequences you may be required to cut other scans in order to finish within your allocated time.

Appendix – Retrospective Recon of SWI Data

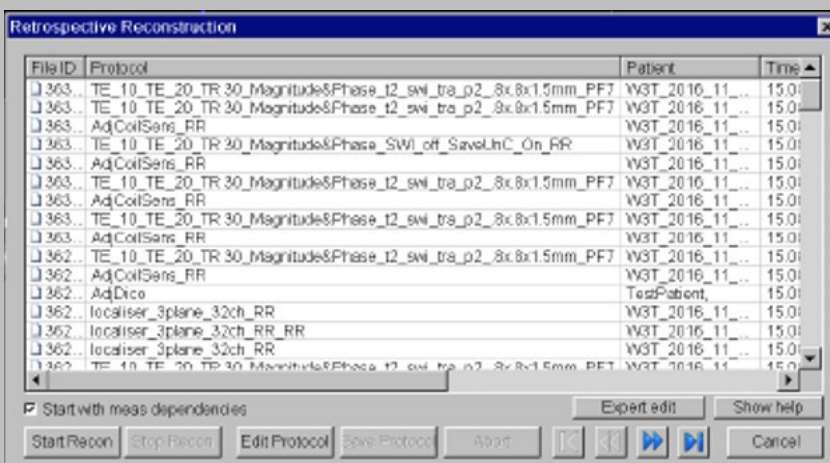
1. The patient browser only shows the online recon scans



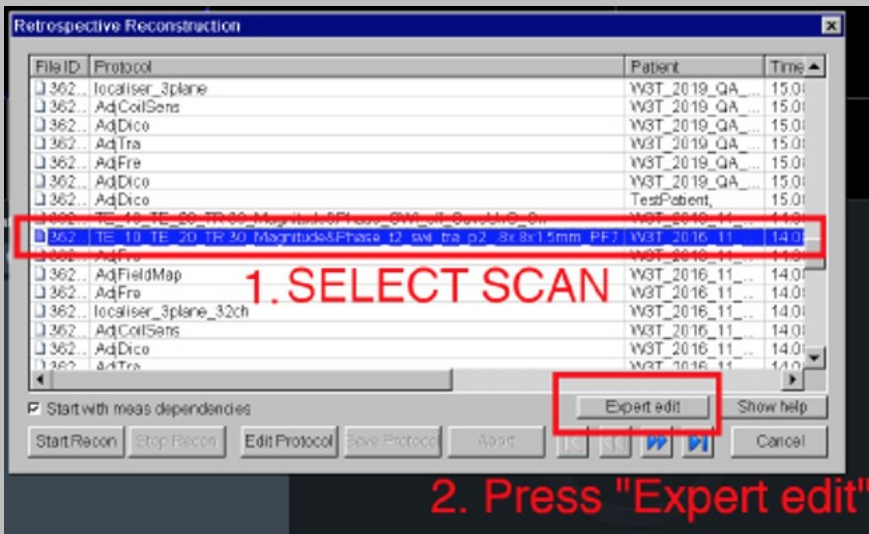
2. Shift+click the  button at the bottom of the screen to bring up the Retro Recon Window



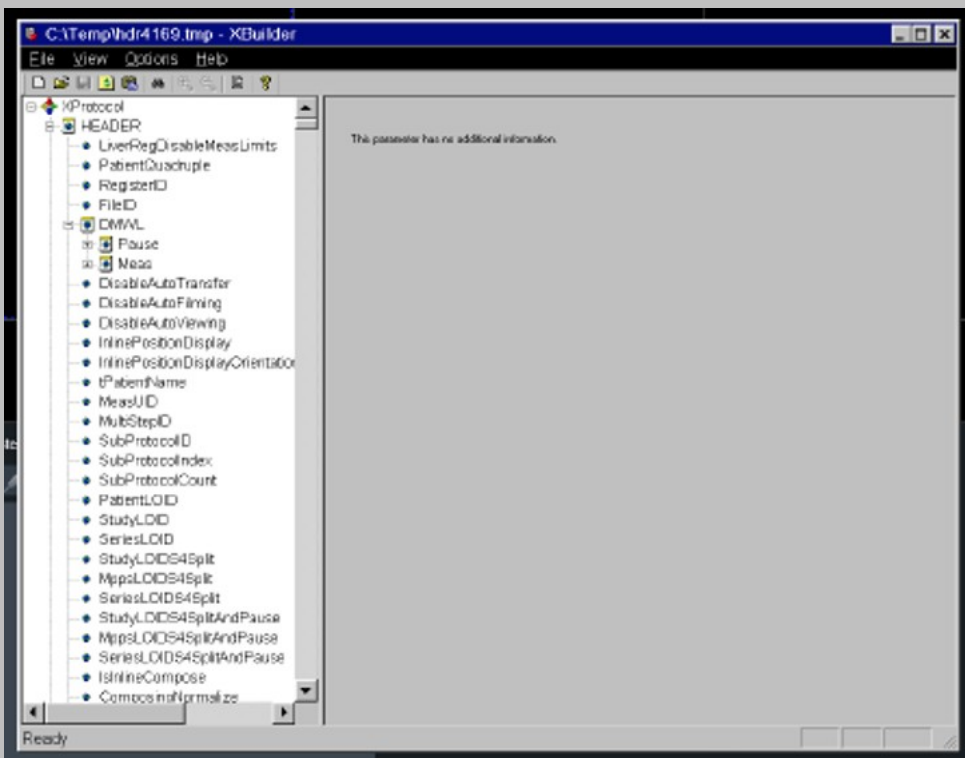
3. The Retrospective Reconstruction window should now appear



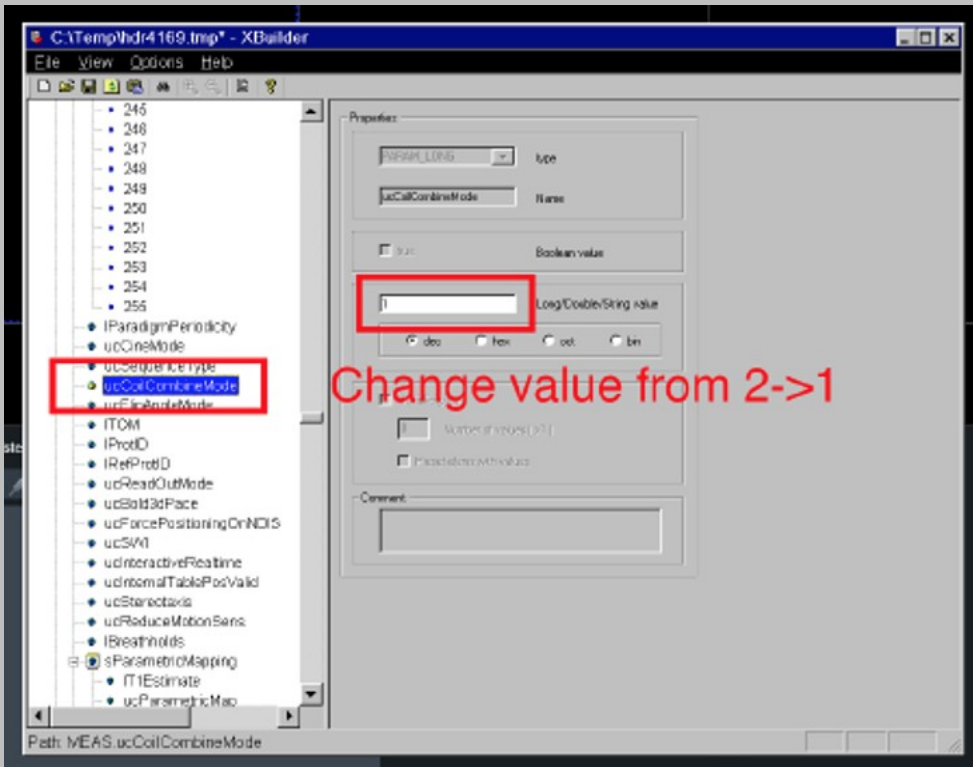
4. Select the scan you want to re-reconstruct, then press “Expert edit”



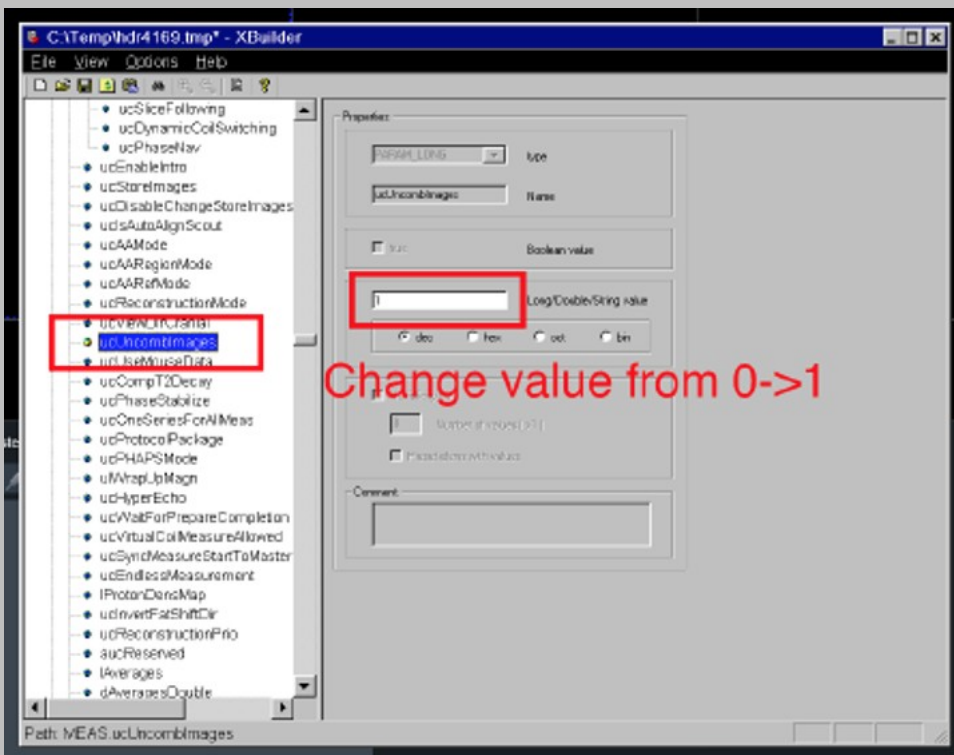
5. The XBuilder window should now appear



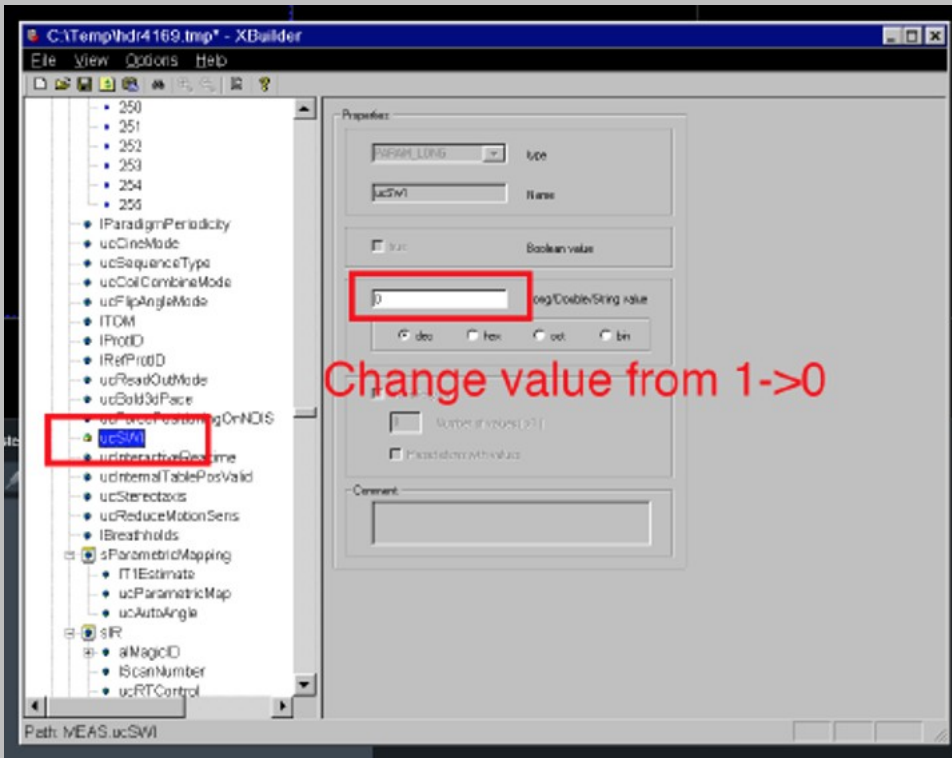
6. Find the “ucCoilCombineMode” entry under the “MEAS” node, and change its value to “1”



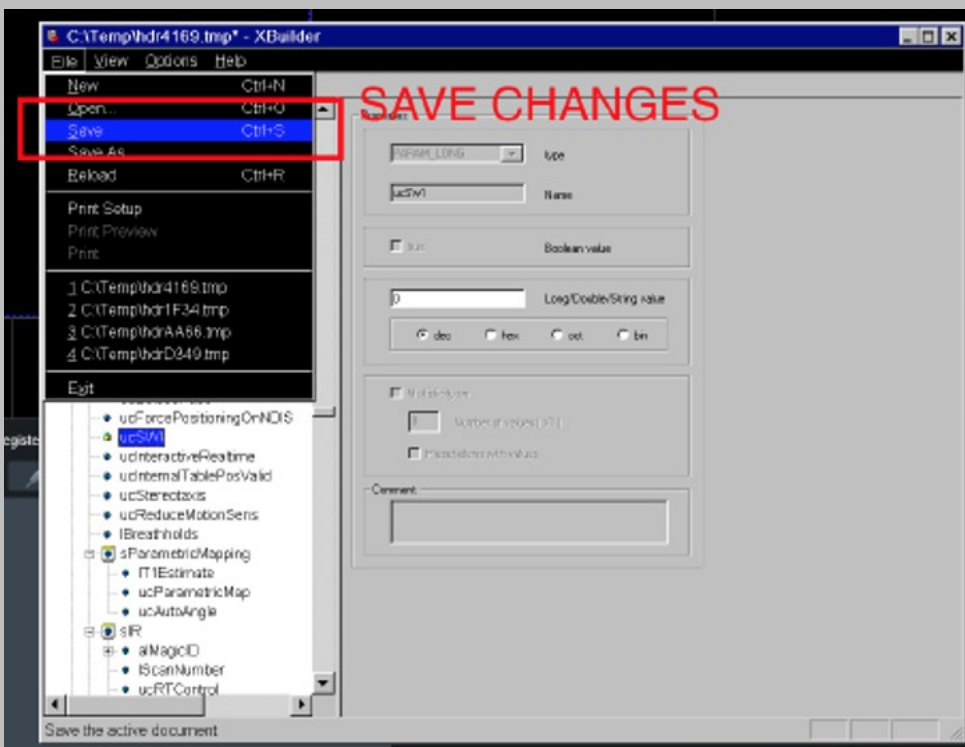
7. Find the “ucUncomblImages” entry under the “MEAS” node, and change its value to “1”



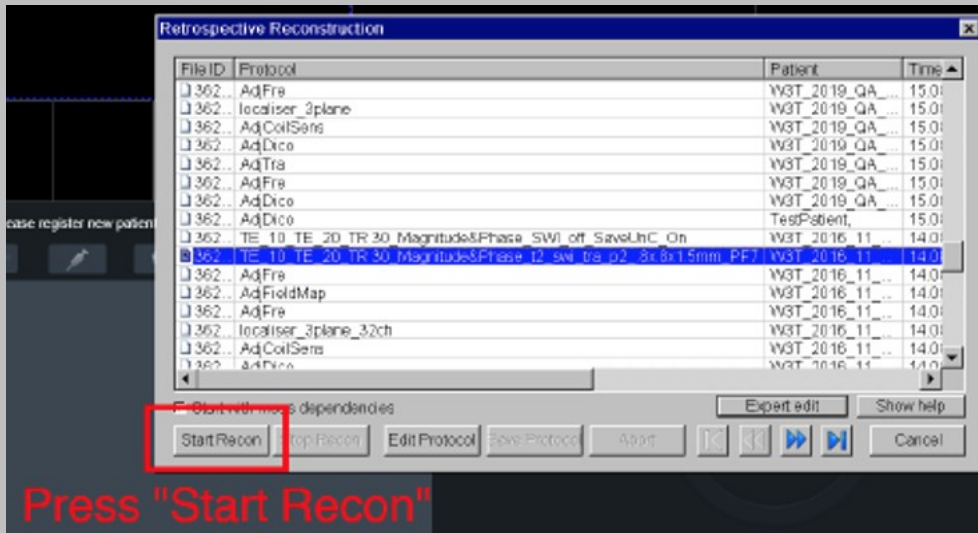
8. Find the “ucSWI” entry under the “MEAS” node, and change its value to “0”



9. Save changes in XBuilder and close the window



10. Back in the Retro Recon window, press the "Start Recon" button to start reconstruction



11. In a few minutes the new images should appear in the Patient Browser

