Siemens MRI Console Operation Manual for Level 1 Operators

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Document History

Version	Comments	Author(s)	Date
0.1	Draft	R Devlin	May 2017
0.2	Draft	D Coggan, J Hazell	September 2017

Referenced Documents

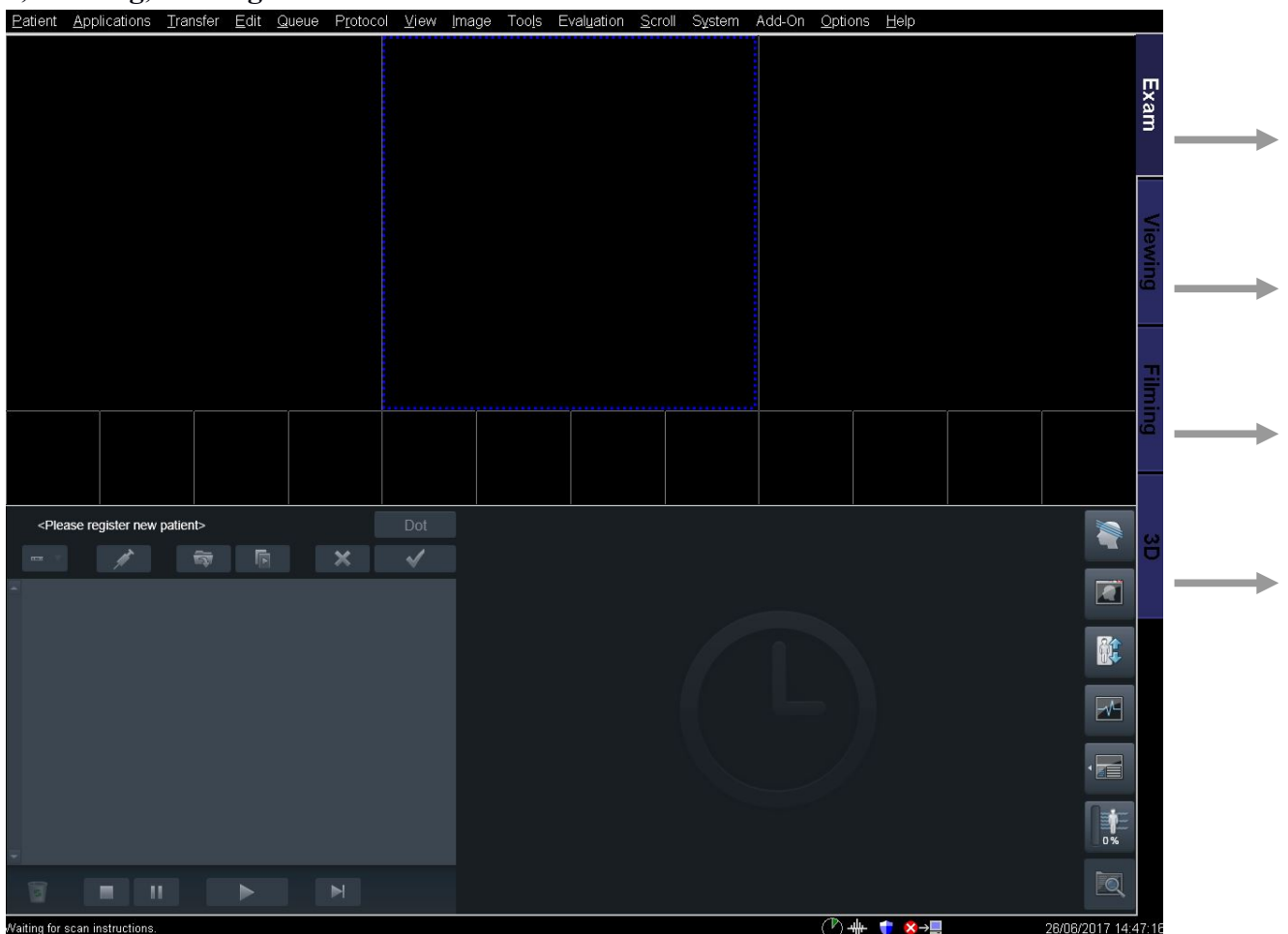| Title	Type
Siemens Operator Manual	External Document (Siemens)

Table of Contents

1. Introduction

This document is designed as a summary of the relevant parts of the Siemens MRI Scanner Console. If, as a level 1 operator, you have any doubts about the right procedure, contact a level 2 or level 3 operator. Throughout the guide, there are tips, warnings and other helpful points shown in boxes.

1.1 Getting around the Siemens System

The underlying operating system of the Siemens scanner is a windows variant. The 'home' screen you will normally see is shown below.

Down the right hand side of this screen are 4 tabs entitled:

Exam, Viewing, Filming and 3D

You will probably only ever use the Exam and view tabs.
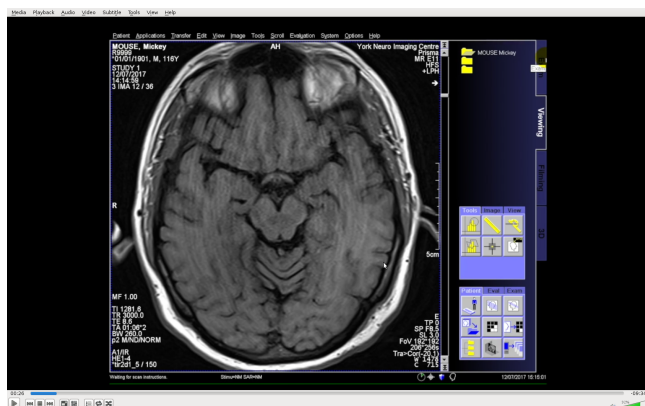
Across the top of the screen are 15 tabs entitled:

Patient, Applications, Transfer, Edit, Queue, Protocol, View, Image, Tools, Evaluation, Scroll, System, Add-On, Options and Help
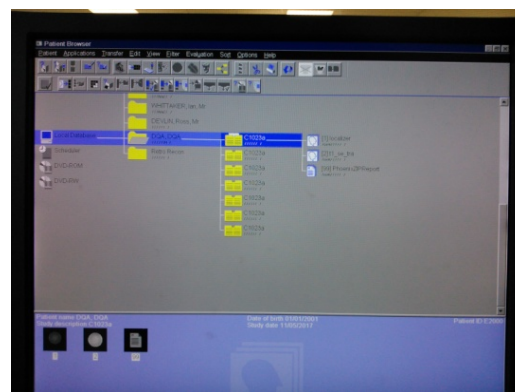
Typically you will only ever use the **Patient** tab.

The first screen you will come to will be the exam screen. If someone has been using the scanner before you

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they may have left the scanner in the 'Viewing' window or patient browser in which case you will see one of the follow two screens.

Screen 1

Screen 2

If you are on screen 1 (where an image is being displayed) you can simply select the Exam tab on the right of the screen. If you are on screen 2 (where the patient browser window is being displayed) you will first need to close the browser by clicking on the **x** in the top right hand corner of the screen. Then if the viewing window is also open you will need to select the Exam tab on the right of the screen.

2. Setting up a participant / patient acquisition

In the exam page select patient (top left of the screen) and register from the drop down menu

Enter the participant details as follows

Surname: ALL CAPITALS

Forename:	First letter CAPITALISED, the rest in lower case
Title:	Mr / Mrs /Miss /Ms as appropriate
Patient ID:	Participant's R no. – e.g. R1234 (This **must** be accurate for correct data transferral)
Date of Birth:	dd/mm/yyyy
Sex:	M/F/Other as appropriate
Age:	Will be calculated from the Date of Birth
Height:	Can be entered either in cm or feet and inches, and is **mandatory** for SAR calculations. Metric can be deselected to allow you to enter in imperial.
Weight:	Can be entered either in Kg or Lbs and is **mandatory** for SAR calculations. Likewise metric can be deselected to allow you to enter this in imperial.

The participant's height and weight must be input accurately to ensure that they are not exposed to an inappropriate amount of RF energy (which may cause tissue damage).
If the participant weighs more than 125 kg, contact a level 2 or level 3 operator before proceeding with scanning.
The maximum weight for safe operation of the MRI bed is 139 kg. Under no circumstances should this be exceeded.

Patient Position:	From the drop down select appropriate patient position (this will usually be 'Head First – Supine').
Operator:	Enter your initials in this field

Do not enter any information in any of the other fields on this page.

Once these fields are completed the 'Exam' tab at the bottom of this window will be active. Click on the 'Exam' tab and you will be presented with the patient confirmation screen:
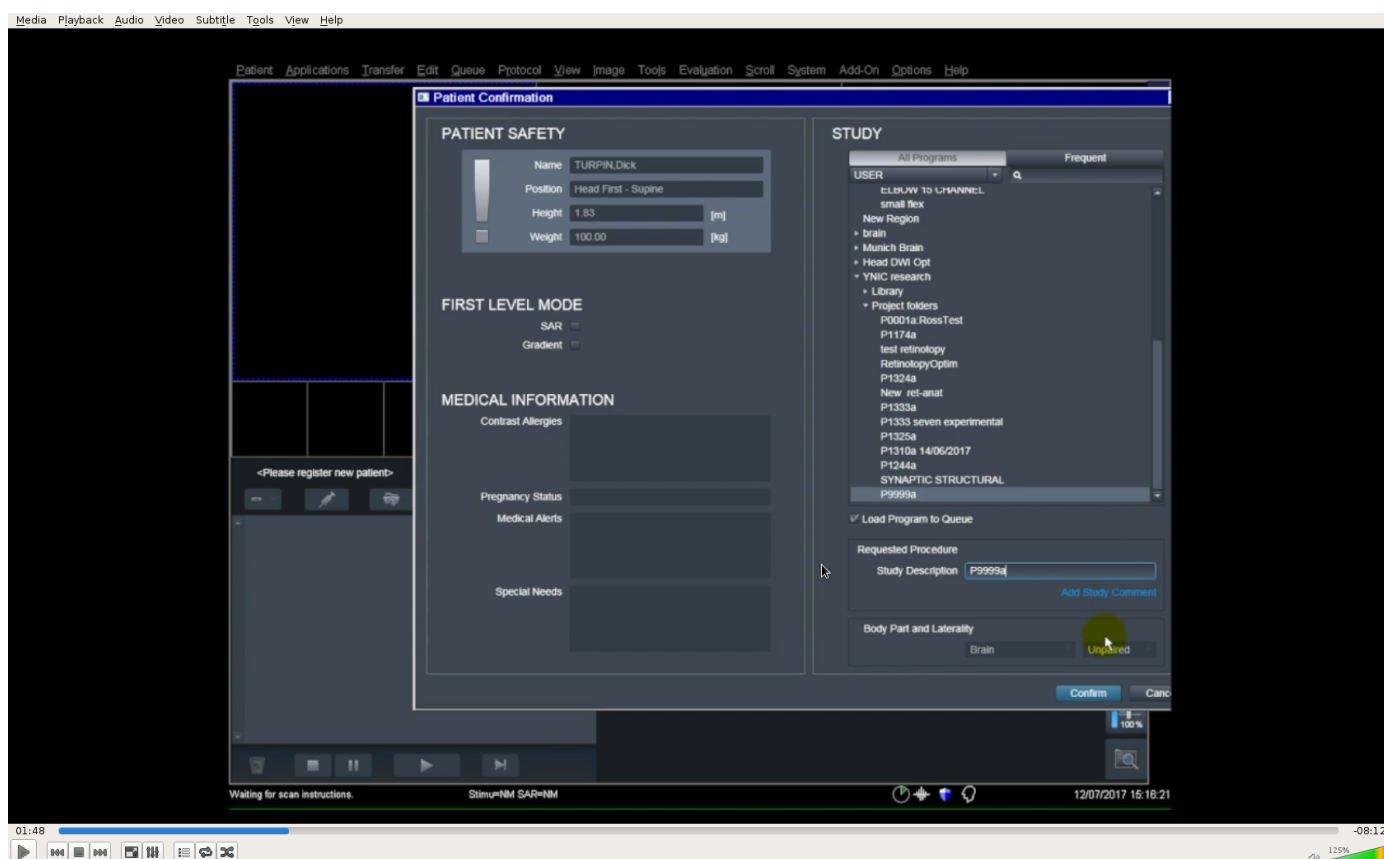
The left hand side of the screen presents the participant details you have entered. Check that they are correct. If they are not click Cancel at the bottom right of the screen and you will returned to the registration page so

you can make any corrections. The first level SAR and Gradient check-boxes should be unselected.

The right hand side of the screen shows a list of all available protocols.

3. Selecting a protocol

If you click the arrow next to YNIC research you will be presented with a drop down menu. Select the relevant project number from the list. Edit the field entitled 'Study description' to contain your project ID this should be in the format P1234a (capital 'P', followed by four numbers, followed by lower case 'a') This is used for the majority of Project scanning, and ensures that the data is sent to the folders of the correct project group, and is anonymised before processing.

From the drop down menu entitled 'Body Part and Laterally' select Brain.

> *Note that failing to use the right format for the study name will delay or prevent data being transferred to the main server.*
>
> *Do not proceed with setup if you do not understand the implications of these settings or think you have accidentally clicked the wrong button. End the exam and start over, or contact a level 2 or level 3 operator.*
>
> *Note that if you make a mistake at any time, your can restart the process of adding a participant by selecting **Patient**/**Close patient** from the Patient tab at the top left of the screen.*

Click on 'Confirm'. You will now be returned to the 'Exam' page and your protocol with all its associated series will be automatically loaded.

At this point, you can remove scans from your protocol list if you know that you will not run them (e.g.

patient has a pre-existing MPRAGE). Select a scan, right-click and select delete or cut.

You are now ready to start scanning.

4. Running a Protocol

4.1 Introduction

Before running the structural and functional brain scans, we need to acquire a structural localiser scan. This scan allows us to localise where we have placed our participant's head relative to the centre of the scanner. It gives us a few slices in the x, y and z direction at the centre of the scanner, and allows us to confirm that the participant is appropriately positioned. The images the Localiser scan provides are the background images we use to position the slices we want to acquire through the head in our structural and functional data. In some cases (the functional and field mapping scans) it is not necessary to manually apply the prescription as this is performed automatically.

4.2   3 plane localiser

The structural 3 plane localiser will always be the first scan in your scan list and requires no modification. Double click (L mouse) on the localiser in the scan list or click on the man with the spade. Then click the green 'play' button to start the localiser.

Once complete the scanner will post the middle image from each slice group in the 3 viewing ports in the top half of the screen. It will also open the next scan in the scan list and place its default slices on those images ready for you to prescribe their position.
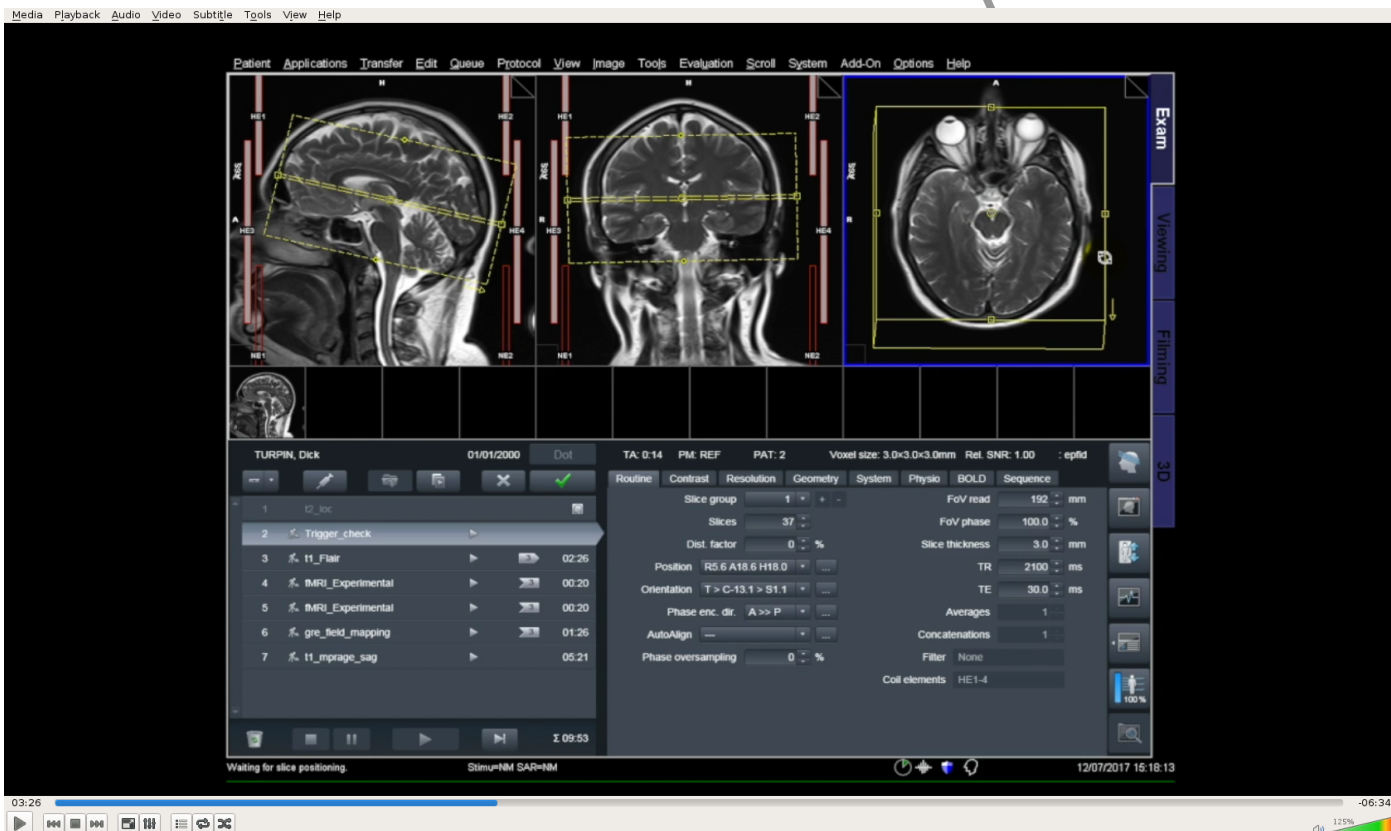
4.3   Trigger check

The next sequence in the list will be opened automatically; in this case it will be the trigger check. To prescribe the position of the slices, click on the centre circle in the yellow slice box. This will enable you to move the slices around.

If you need to angle the slices then place the cursor over the centre line away from the centre circle and a rotational icon will appear (do not drag the diamonds and squares around the edge of the prescription as this will alter the slice gap and number of slices).

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If the rotational icon does not appear try holding down control and placing the cursor over the yellow lines away from the diamonds and squares and the rotational icon should appear.

To zoom in or out first make sure that zoom/pan has been selected in the tool bar. Place the cursor outside the field of view left click and drag or draw.

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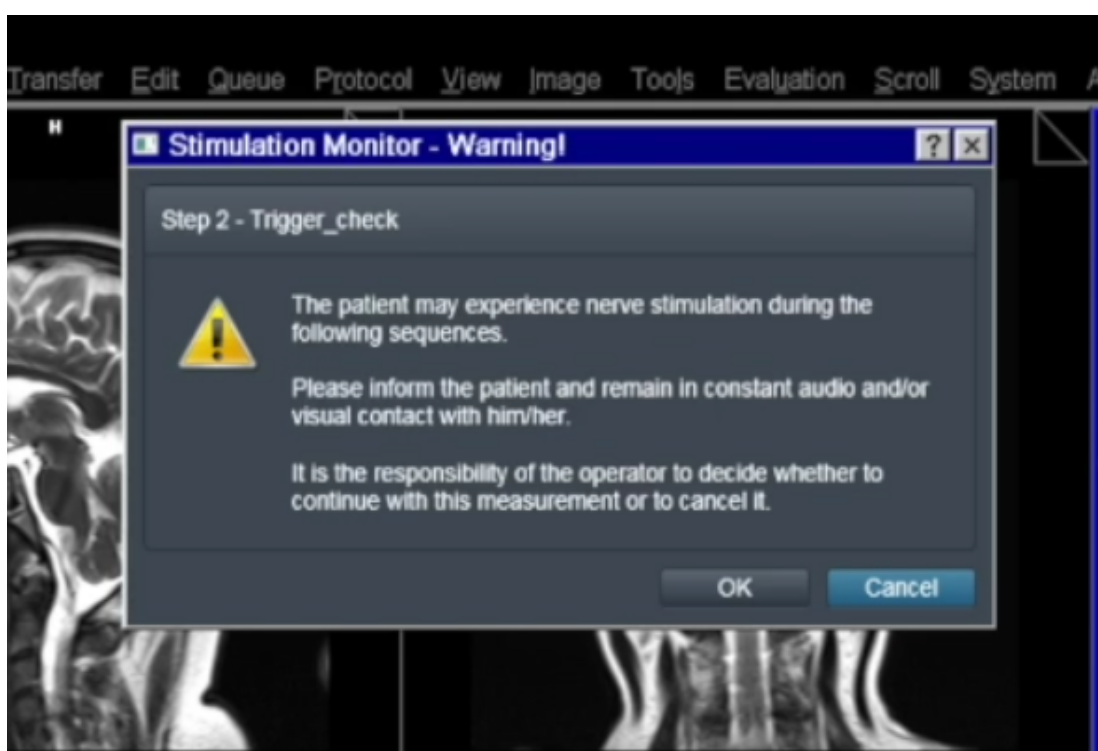To page through the slices, click on the triangles in the top right of each viewing port.

The grey bars with the red outlines in the viewing ports represent the virtual coil elements. These are set during the construction of your protocol and should cover the area of interest. Make sure you do not inadvertently change this set up, particularly by turning any from 'on' (grey fill) to 'off' (black fill). To switch these between 'on' and 'off', left click them. (see troubleshooting video #3)
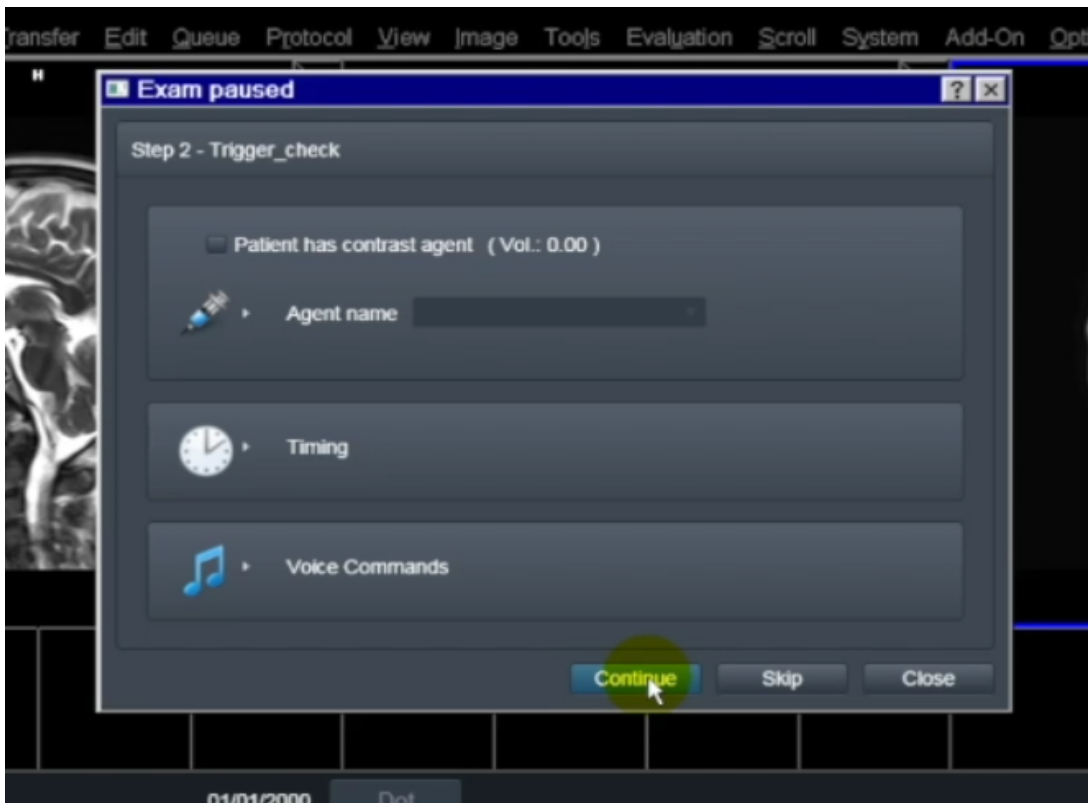
If you need to change the brightness or contrast to make it easier to prescribe your slices then click the scroll down wheel on the mouse and move the mouse left or right, up or down. When you are happy with the position of your slices, click on the green tick to apply the prescription. The scanner will then begin to prepare the sequence and a number of boxes will appear in turn. If they appear precisely as shown below, follow the instructions as stated. However, if you see any additional messages or warnings not shown in this guide, **do not proceed** without approval from a level 2 or 3 operator.
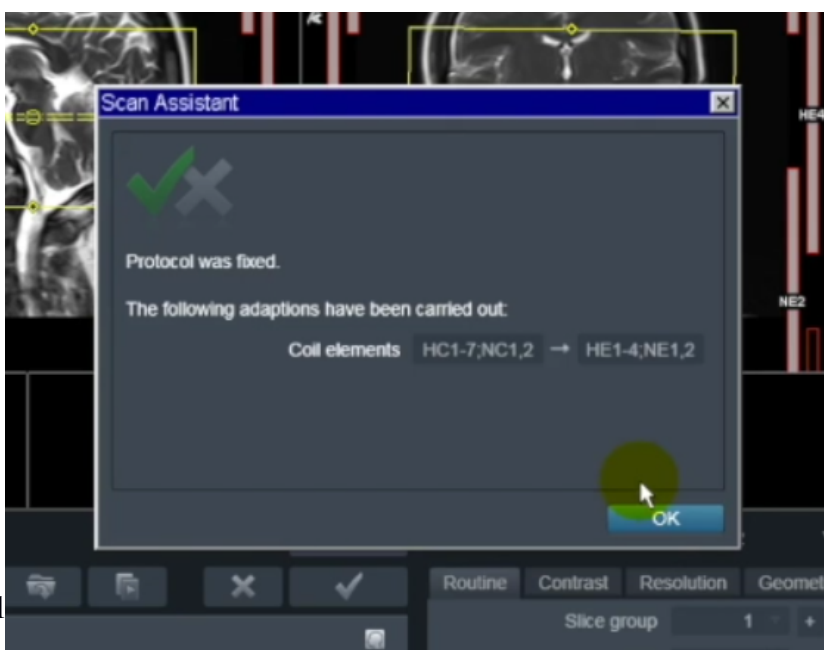
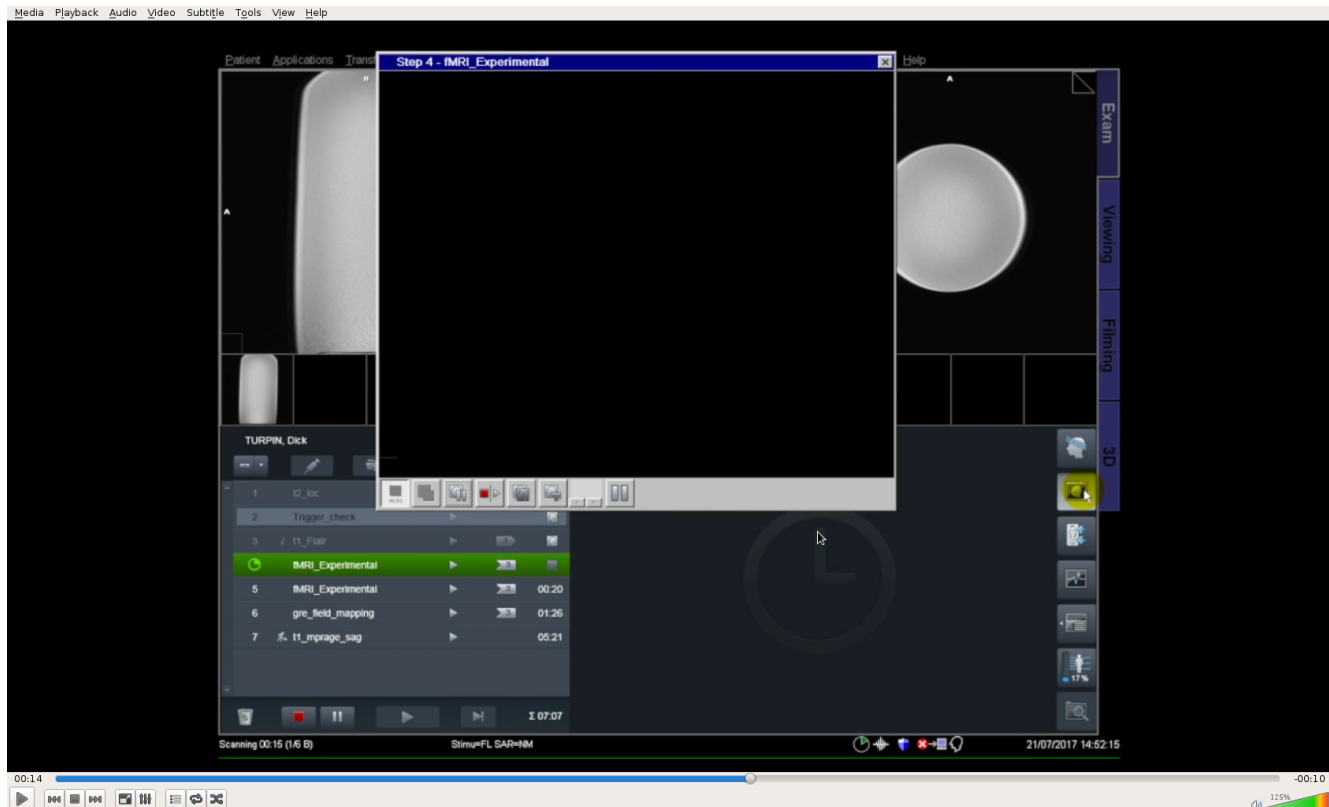1. Stimulus warning monitoring window – click ok

2. Exam Paused window – click continue

3. Scan assistant window (the sequence will still run whilst this is open) – Click ok to close it.

One of the tools you can use to check your slice prescription whilst the trigger check is running (and also for checking incoming images during functional scans) is the inline display. Click on the inline display icon (2nd top on the right of the exam page) and a window will appear showing your latest images (see troubleshooting video #2)

4.4 Flair, functional and field mapping scans

The slice prescription for the trigger check will be the same used in the subsequent flair and functional scans, and therefore can be used to check your anatomical coverage. To check your coverage click on the viewing tab on the right hand side of the screen. Select the correct participant by clicking on their corresponding yellow envelope. Then to page through the sequences press the plus or minus buttons on the far right of the keyboard. Once you are happy with the coverage, this needs to be manually copied over to the flair. Left click the trigger check to highlight it, then right click and select 'copy parameters'.   In the next window, make sure 'centre of slice group and saturation regions' is selected. Then click on the green tick to apply the prescription.

The scan parameters will then automatically be applied to the subsequent functional and field mapping scans. This process is described in the box below.

This arrow is the reference to be copied
Subsequent arrows inherit that reference

The scanner will now progress through all the sequences in the list in the same way:

- Scan will automatically prepare after previous scan has finished

- 'Exam paused' window will open (coordinate with stimulus presentation if necessary, click 'continue')

- Scan will start (you may also see the scan assistant box - click 'ok')

Do not open your functional scans with the goal of adjusting your slice prescription, as any changes you make would not be copied to the other functional runs.

If you have initiated the flair sequence without copying the prescription from the trigger check, your subsequent functional runs will not be in the correct position. To fix this, first stop the sequence running by pressing the stop button at the bottom of the exam page. Then hold Ctrl and select all of the runs linked by the prescription chain (typically, the flair, functional, and field mapping runs), right click and select 'cut'. Go to the 'program card' tab (3rd bottom icon on right of screen), hold Ctrl and select the scans you have just deleted. Drag and drop them below the trigger check. Then repeat the steps starting at the top of this section (see troubleshooting video #1).
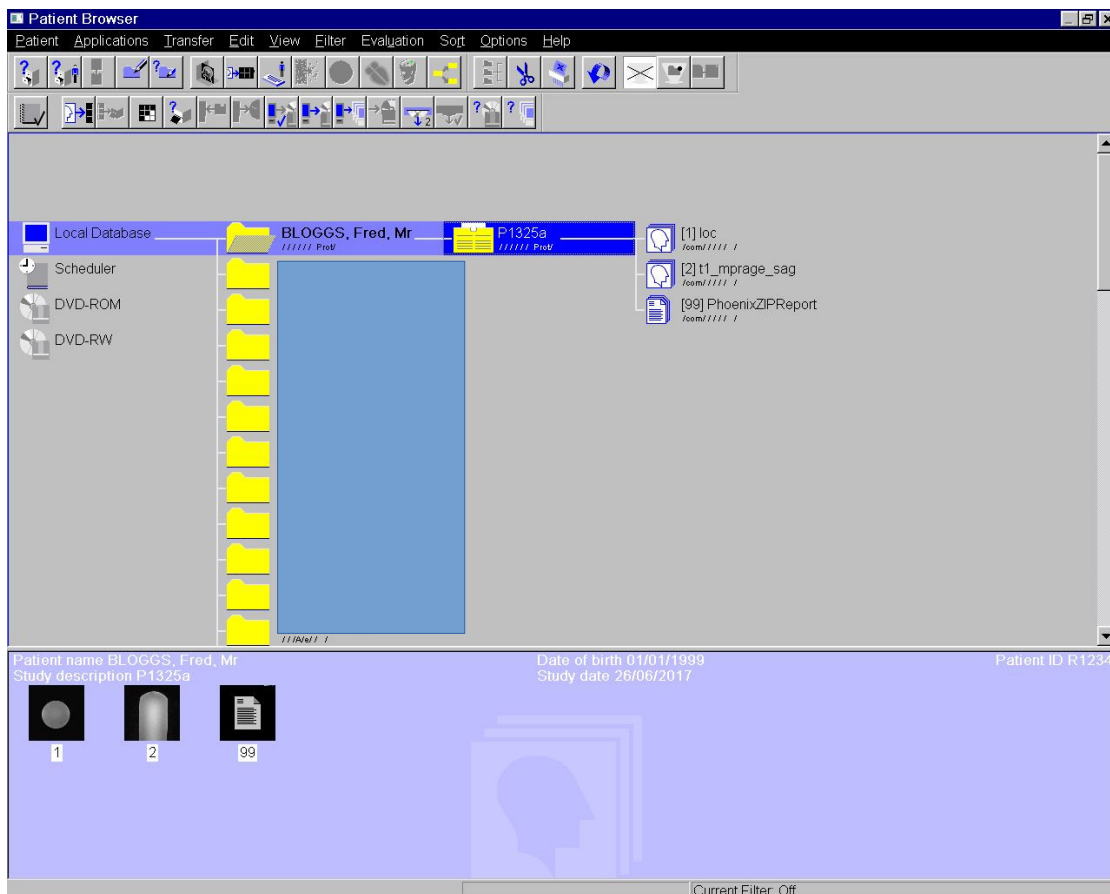
4.5 MPRAGE scan

The slices for the MPRAGE can be prescribed during or after the field mapping scan. Double click the MPRAGE scan to open it, and a slice prescription will automatically appear in the three viewing ports. You can adjust the slices in the same way as the trigger check. Only prescribe your slices in the coronal or axial orientation. Once happy with your coverage, click the green tick to apply the sequence. The 'Exam paused' window will pop up – click 'continue' to start the scan.
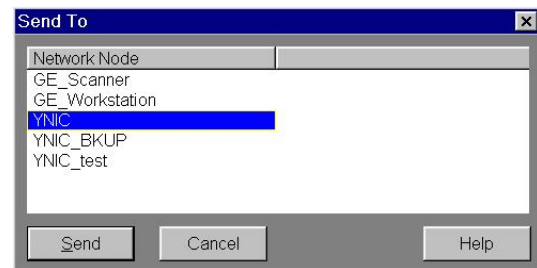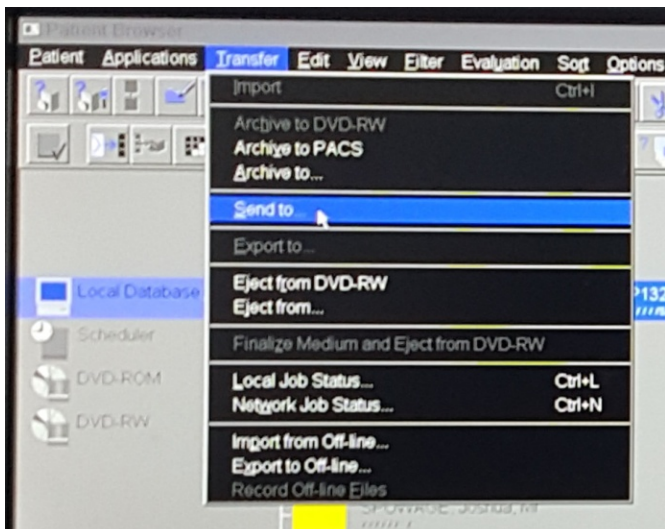

Once your protocol is finished, click **<u>Patient</u>** > **Close Patient** to end the exam.

5. Sending data to store

You can transfer the data from this session to the mnt/mridata directory **only** if the subject has had a high-resolution structural scan at YNiC (in either MRI scanner) prior to this session. Otherwise, you need to skip this step so that the data can be checked for anomalies by the radiographer. To transfer the data, open the patient browser (from **Patient** menu option at the top of the screen) and select the acquired session.

Click **Transfer** (top of screen), then select **Send to…,**
then select **YNIC** and click **Send.**

If your scan session was the last of the day, you need to shut the system down. To do this, click on 'system' on the top bar in the exam page, then click 'end session' and then 'shutdown' (see troubleshooting video #4)