



Your First Experiment

This Document

This document describes the most essential points you need to begin scanning on the 7T Pharmascan MRI system using PV5.1. You can find more detailed information in the document “How to obtain your first images” and in the PV 5.1 Manuals (see the section on Manuals under *How to*).

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Log Into the Console and Start Paravision 5.1

1. Log into the Bruker console using your groups' login and password
2. Double-click the PV5.1 icon on the desktop
3. Click OK in the window titled "Welcome to Paravision"
4. When PV is loaded, three windows will fill the screen:
 - a. *Image Display and Processing* window is where you will display, inspect and analyze your images.
 - b. *System Control* is where you can open the other main windows if you accidentally close them.
 - c. *Scan Control* allows you to set up and direct scans.

Run the Localizer and Pre-Scan

A localizer scan (also called TriPilot) will help you position your subject appropriately.

1. Create a new patient
 - a. Click *New Patient* in the *Scan Control* window.
 - b. Fill out the *patient name* and *registration* fields. Note that by our convention, the patient name must have the following structure.
group name_initials of person scanning_animal code, while the registration field must be *YYMMDD_initials of person scanning_animalcode*.
2. Create a study
 - a. Click *New Study* in the *Scan Control* window.
 - b. The *Study Editor* dialog window will open on the screen.
 - c. Choose a descriptive study name and write it in *Study*.
 - d. Location should correspond to either an appropriate *MIC* folder, such as *MIC_RatBrain*, or your own location.
 - e. Double-check that the coil has been automatically detected by the hardware – compare the coil configuration to the table of possible coil configurations on the wall next to the monitor.
 - f. Click *Accept* when you are finished and the *Protocols* window will open
3. Choose a protocol in the *Protocols* Window
 - a. Select the 1-TriPilot (for either mouse or rats) as the first scan. This can be your localizer and will help you position the subject in the middle of the field-of-view.
 - b. Press the *Traffic Signal* button to run the scan
 - c. Pay attention to the initial adjustments (central frequency, shimming, transmitter gain, and the receiver gain) and wait for the TriPilot scan to finish (no more than 30 sec).
4. Adjust position
 - a. Return to the *Scan Control* window and select and drag your scan to the *Image Display and Processing* window with the middle button in order to inspect the images.
 - b. Use the *distance-measuring* tool in order to measure the offset of the subject from the middle of the field center.

- c. Move the subject by the corresponding amount either in or out of the scanner.
- d. Hold down SHIFT while pressing traffic signal button to run the TriPilot again and then check the new position.
- e. When satisfied with the position, proceed to acquire anatomical and T2/T1 weighted images.

Acquire Anatomical and T1/T2 Weighted Images

1. Load an anatomical protocol
 - a. Click *New Scan* from the *Scan Control* window.
 - b. Choose the protocol location that best fits your application. For instance, for imaging of rat head tumors, choose MIC_Rat_head_tumor; for imaging of fat in mice, choose MIC_Mouse_body_fat, etc.
 - c. Use 2-TurboRARE_T2_3500ms (with TR=3500ms) for T₂-weighted and 4-RARE_T1_1000ms (TR=1000 ms) for T₁-weighted imaging.
 - d. Click the traffic light to run the scan and view then view the images in *Image Display and Processing* window.

Transfer Raw Data and DICOM Data to Another Computer

To access **raw data**, type:

- `cd /datadisk/data/username/nmr/`
- Data directories are named by the *registration* field (see chapter on Image Files below).

To create **DICOM data**, do the following:

- Open *Data Manager* window
- Right click on the scan/study you want to save and select *Transfer Immediately*
- Wait until the transfer above finishes (when the transfer finishes, you might receive an error message saying “not all scan have been transferred”, but you can ignore this message if you had empty (i.e., ready) scan in the study.

To access **DICOM data**, type:

- `cd /opt/DICOM/`
- Data directories are named using the following format:
`<Registration>_<Patient>_<StudyId>_E<Expno>_P<Procno>_<other stuff>`

To **transfer** either **raw** or **DICOM data**, type:

- `scp -r <beginning>*<username>@<loginuib.no>:/Home/sivXX/username/MRData,`
 where *beginning* is the beginning of the file/folder you would like to transfer, *username* is your university user name, *sivXX* would be the folder containing your users *home* directory, and *MRData* would be folder in your home containing MR data. An example would be: `scp -r StromaData* tpa082@login.uib.no:/Home/siv16/tpa082/MRData`

Finding Your Data in the Bruker (not DICOM) File Hierarchy

Image Files

Raw image data (Fourier transform of the FID) can be found in 2dseq files. These files are stored in folders that are named using the *registration* field (determined when creating a new patient). Each scan has its corresponding subfolder (1, 2, ..., n). In this folder you will find several files (fid, method, acqp, etc), and also another folder (pdata) containing the processed (FT) raw data (2dseq).

registration.xyz/1/pdata/1/2dseq for scan 1
registration.xyz/2/pdata/1/2dseq for scan 2
registration.xyz/n/pdata/1/2dseq for scan n

Basic Scan Parameters

The basic scan parameters for the n^{th} scan are stored in the following file:

registration.xyz/n/method

Base Level Acquisition Parameters

The base level acquisition parameters for the n^{th} scan are stored in the following file:

registration.xyz/n/acqp

The fid file (the unprocessed raw data file)

The unprocessed raw data file is stored in the following file:

registration.xyz/n/fid

This file contains all the original information of the scan and can be useful for special applications when it is necessary to examine the original data. Note, however, that this file is very large and is the one file that you might want to delete if you are running out of space and you are absolutely sure that you will always work with the processed (2dseq) data when analyzing images.

Alternate Processing

If you have processed your data in more than one way, the processed images will be saved in different directories under pdata:

Image from 1st post-processing method: registration.xyz/n/pdata/1/2dseq
Image from 2nd post-processing method: registration.xyz/n/pdata/2/2dseq
Image from n^{th} post-processing method: registration.xyz/n/pdata/n/2dseq