Your First Experiment

This Document

This document describes the most essential points you need to begin scanning on the 7T Pharmascan MRI system using ParaVision 6.0.1. You can find more detailed information in the Operating Manual from the Help menu in PV 6.0.1.

Contents

Log in to the Console and Start Paravision 6.0.1

1. Log into the Bruker console using your groups' login and password
2. Double-click the PV6.0.1 icon on the desktop

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. Select *New* and *Study* option in the *File* menu. A window called *Study Registration* opens.
   b. Fill in the fields on the left. Note that by our convention, the *Animal ID* must have the following structure:
   group name_initials of person scanning_animal code, while the *Animal Name* must be *YYMMDD_initials of person scanning_animalcode.*
   It is very important to follow this structure for MIC personnel to be able to find your data later.
2. Create a study: fill in the fields on the right in the *Study Registration* window.
   a. Choose a descriptive study name and write it in *Study Name.*
   b. *Location* should correspond to either an appropriate *MIC* folder, such as *MIC_Rat/Head/Tumor*, or your own location.
   c. 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.
   d. Click *Create* and *Exam* when you are finished and the *Study Registration* window will close and the *Examination Card* (tab) will open.
3. Choose a protocol in the *Palette Explorer* (select *Scan Programs & Protocols* to see the available protocols).
   a. Select the 1-Localizer (for either mouse or rats) as the first scan by dragging it down to the *Instructions* panel. This is your localizer scan and will help you position the subject in the middle of the field-of-view.
   b. Press the *Continue* button to run the scan
   c. Pay attention to the initial adjustments (setting reference frequency, iterative shimming, reference power) and wait for the TriPilot scan to finish (no more than 30 sec).
4. Adjust position
   a. The recorded images are automatically displayed in the Geometry Editor in the Examination Card.
   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. Right click the 1-Localizer scan and select *Duplicate Scan* 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. Select *Scan Programs & Protocols* in the *Palette Explorer.*
    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/Abdominal/Fatimaging*, etc.
    c. Select a relevant protocol (such as 02_T2_RARE) and drag it into the instruction list (where the 01_Localizer (Ex) is located).
    d. Click the *Continue* to run the scan.
    e. View the images by selecting *Datasets* in the *Palette Explorer* and double-clicking the scan you would like to view.

Transfer Raw Data and DICOM Data to Another Computer

The **raw data** is stored in the following folder:
- /opt/PV6.0.1/data/<user>/nmr/
- Data directories are named by the *Animal ID* field (see paragraph on Image Files below).

RAW data is usually very big so an external hard drive or a memory stick is the easiest transferring method. You can also transfer data via network, but the transfer might take a while.

To export ParaVision datasets to DICOM:
1. Select Subjects, Studies, Examinations, Image Series to be exported to DICOM
    a. in the *Workspace Explorer* below the *Datasets* node
    b. in the *Palette Explorer* (only Image Series)
    c. or in the *Dataset Browser* in the different dataset views
2. Export the datasets to DICOM by
    a. clicking Export to DICOM... in the context menu of the selected datasets in the *Workspace Explorer* or *Palette Explorer* (right click)
    b. or clicking the Export to DICOM... button in the action row below one of the dataset views
3. If the DICOM export is done to a directory a directory selection dialog appears that requests the base directory to store the DICOM files.
4. The actual export operation starts. A progress may appear. Depending on the number of exported datasets and their size the export may be very time consuming.
5. After the export is finished a dialog is displayed which shows in its details which image series have been correctly converted to DICOM files and which have not been.

The **DICOM data** are now stored in the folder **/opt/DICOM/.**
- Data directories are named using the following format:
<Registration>_<other stuff>

To **transfer** either **raw** or **DICOM data**:
- Open a terminal window by clicking on the terminal icon on the desktop.

- In the terminal window, type: scp –r *<beginning>* <username>@<login.uib.no>*:

where *beginning* is the beginning of the file/folder you would like to transfer, and *username* is your university user name. An example would be: scp –r StromaData* tpa082@login.uib.no:

> NB: remember to put a space between the file/folder name and your username, and a colon at the end of the command.
>
> The file/folder will be transferred to the disk called "W: Archive".

After the transfer of DICOM files:

✓ Delete your DICOM files from the /opt/DICOM folder.

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 located under /root/opt/PV6.0.1/data/<group username>. The folder names always start with the scanning date and time, followed by the Animal ID and two numbers, the last one indicating the study number (1 for the first study for this Animal ID, 2 for the second etc). 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).

date_time_registration_x_y/1/pdata/1/2dseq for scan 1
date_time_registration_x_y/2/pdata/1/2dseq for scan 2
date_time_registration_x_y/n/pdata/1/2dseq for scan n

Basic Scan Parameters

The basic scan parameters for the nth scan are stored in the following file:

date_time_registration_x_y/n/method

Base Level Acquisition Parameters

The base level acquisition parameters for the nth scan are stored in the following file:

date_time_registration_x_y/n/acqp

The fid file (the unprocessed raw data file)

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

date_time_registration_x_y/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: date_time_registration_x_y/n/pdata/1/2dseq
Image from 2nd post-processing method: date_time_registration_x_y/n/pdata/2/2dseq
Image from n^{th} post-processing method: date_time_registration_x_y/n/pdata/n/2dseq