Your First Experiment

This Document

This document is a bare bones guide to acquiring an anatomical image, T1 and T2 weighted images and T1 and T2 maps on the Bruker 7T MRI scanner. More help is available in the Paravision 5.1 Manual which you can find by clicking on the "?" icon in ParaVision. Hardcopy of an older manual (PV4.0) is stored in the closet near the entrance to the console room.

Contents

Log into the Console and Start ParaVision 5.1

1. Log in the to the Bruker console as fmriuser
2. Double the PV5.1 (Paravision) icon on the desktop
3. Click OK in the window titled "Welcome to Paravision"
4. When PV5.1 is loaded three windows fill the screen.
    a. "*Image Display & Processing*" where you will see your images
    b. "*System Control,*" is where you can open the other main windows if you accidentally close them.
    c. "*Scan Control,*" which allows you to set up and direct the scan

Match and Tune the Coil

To match and tune properly your sample should be centered in the coil and the coil centered in the magnet. You can use the LEDs on the pre-amp (on the floor behind the magnet) to help you match/tune. The *Acq/Reco* window on the computer displays a curve with similar information.

1. Connect the coil wiring in the tuning configuration (instructions posted in the filter box). For quadrature coils, each channel needs to be tuned and matched separately.
2. Start the matching/tuning
    a. Open the *Spectrometer Control* window by clicking the tools icon (hammer and screwdriver) in the *Scan Control* window
    b. Click *Acq->Wobble* in the *Spectrometer Control* window
    c. The wobble (reflectance) curve will display in the *Acq/Reco* window
    d. The goal is to see a curve with a minimum at 0% on the vertical axis and 0 MHz on the horizontal axis
3. Adjust match and tune capacitors on the coil
    a. Adjust the matching rod until the minimum number of LED lights are illuminated
    b. Adjust the tuning rod until the minimum number of LED lights are illuminated
    c. Iterate from match to tune to match to optimize. When you are finished you should only see green LEDs illuminated.
    d. Check the console computer. The *Acq/Reco* window should show a central minimum with steep, symmetric sides with a minimum at 0 % and 0 MHz.
4. If you are using a quadrature coil, connect the other channel for matching/tuning and continue through until step 4
5. Once you have successfully calibrated the coil, close the rear door and hit the *Stop* button in the *Acq/Reco* window.

Run a Localizer and Pre-Scan

A localizer scan will help you position your sample appropriately. For your first scan, hold down the shift key when you start the scan to launch the pre-scans.

1. Create a new patient
    a. Click "*New Patient*" in the "*Scan Control*" window
    b. The *patient name* and *registration* fields must begin with your initials followed by characters of your choice that you will remember
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 be "B_ANATOMY" or your choice
    e. Set the coil appropriately.
        i. Transceiver: If the coil is for both transmit and receive
        ii. Quad: If the coil is a quadrature coil
        iii. H1: If the coil detects the signal from protons
        iv. Coil array: For multi-coil arrays
        v. Cross coil: One coil for transmit and different coil for receive
        vi. 1000 W or 300 W – this differs from coil to coil
    f. Click *Accept* when you are finished and the *Protocols* window will open
3. Choose a protocol in the *Protocols* window
    a. 1-TriPilot (in B_ANANTOMY) – as a localizer
    b. Run the pre-scan[1] and the scan
    c. Hold down Shift and hit the traffic signal button.
    d. Wait for the tripilot scan to finish (no more than 30 seconds)
4. Adjust position
    a. Return to the *Scan Control* window and select and drag your scan to the image view window with the middle button to inspect the images
    b. Adjust the sample as necessary to bring the sample into field center
    c. Run the scan again to check the new positioning

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[1] Note on pre-scan: On subsequent scans where the sample positioning is identical, you may choose to not do the pre-scan. To start a scan without pre-scan, click the traffic light button without holding down the shift key.

Acquire Anatomical and T1/T2 Weighted Images

1. Load an anatomical protocol
    a. Click *New Scan* from the *Scan Control* window.
    b. Location: B_ANATOMY
    c. Use RARE-T1 or TurboRARE-T2 for either T1 or T2 weighted images
    d. Set the coil mode appropriately
2. Click the traffic light to run the scan and view your images

Acquire T1 and T2 Maps

1. Load a relaxometry protocol
    a. Click *New Scan* from the *Scan Control* window.
    b. Location: B_RELAXOMETRY
    c. Select one of the following protocols
        i. FISP-T1+T2-map (to measure T1 and T2 maps)
        ii. MGE-T2star-map (T2* map)
        iii. MSME-T2-map (T2 map)
        iv. RARE-T1+T2-map   protocols (T1 and T2 maps)
    d. Set coil mode appropriately
    e. Click the traffic light to scan

Transfer Raw Data to Another Computer

Data in the native, Bruker format is stored under /opt/PV5.1/data/fmriuser/nmr/

1. Open a terminal

2. Issuing the following command in the terminal will show you the raw (Bruker ParaVision format) data directories on the disk:

udata; ls

3. Your data directory should be in the list above. It helps to know that Bruker creates directory name in the following way:

*<Registration>_<PatientName>_*E*<StudyNumber>_*P*<ScanNumber>_*<other stuff>

4. Use scopy (scp) to send your data to a remote server. The model below will help you construct a command to issue in the terminal:

scp -r <beginning> <username on server>@<servername>:~*

Example: scp –r rgbTest_rgbPatient2* rbussell@cfmri.ucsd.edu:~

Transfer Bruker DICOM Data to Another Computer

Data is stored under /opt/PV5.1/data/fmriuser/dicomfiles/

1. Open the Data Manager window

2. Right click the scan you want to save or the whole study and select "Transfer Immediately"

3. Wait until the transfer above finishes

4. Open a terminal

5. Issue the following command in the terminal:

vdata; ls

6. Identify your data directories. Note: The directory name of a DICOM series has the following format: *<Registration>_<SubjectLast-Name>_<StudyId>_*E*<Expno>_*P*<Procno>_<other_stuff>*

7. Continue at step 4 of "Transfer Raw Data to Another Computer," above

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

Image Files

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

registration.xyz /4/pdata/1/2dseq for scan 4

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

Basic Scan Parameters

registration.xyz /n/method for scan n

Base Level Acquisition Parameters

registration.xyz /n/acqp for scan n

Alternate Processing

You may have processed your data more than one way. If so, your processed images are saved under different directories under pdata.

Image from first post-processing method: registration.xyz/12/pdata/1/2dseq

Image from second post-processing method: registration.xyz/12/pdata/2/2dseq

Image from n[th] post-process method: registration.xyz/12/pdata/n/2dseq