

# ParaVision Short Manual

## ***Disclaimer***

This manual is intended to be a *brief*, easily digestible introduction to using the Bruker MRI spectrometers running ParaVision at the UC Davis NMR Facility. It is not intended to be comprehensive or exhaustive. For complete information about the ParaVision software or running experiments, consult the various on-line forms of documentation that Bruker provides under “Help” in the ParaVision program.

## ***Conventions***

Keyboard input is shown as **boldface** type in this manual. Note that both in ParaVision and in unix the “enter” key must be used after the command is typed; this is assumed through-out this manual and “enter” key strokes are not given explicitly. Commands in ParaVision are typed in various fields of the various ParaVision windows; again this is assumed and will not generally be stated explicitly herein. LMB, MMB, and RMB are used to indicate actions of the left, middle, and right mouse button respectively.

## ***Login***

ParaVision software runs under RedHat Linux and the “guest” account for the NMR Facility has the user name nmrfac. Enter **nmrfac** as the user, then enter the password you will be issued. The computer will then start up and present various icons to you.

Open a Unix shell by clicking RMB with the cursor anywhere over the desktop and choose Konsole.

Type: **S116**. This command tells ParaVision that you will use the S116 (big) gradient set. The equivalent command for the microgradient set is G060. IF YOU GET ANY SORT OF ERROR MESSAGE CALL ME IMMEDIATELY.

Double click with the LMB on the ParaVision icon on the desktop. This will start the Bruker ParaVision software which is what allows you to communicate with the spectrometer. An alternative is to open a unix shell (See above) and type **ParaVision** or **pv**. During start up, the will be disclaimer window. You must click okay before ParaVision will continue booting.

## ***Coil insertion***

MRI coils of various sizes are available. **Warning!**: In general MRI volume coils have glass components which can be broken with mishandling. **Be Careful!** A dropped coil is a several thousand dollar mistake.

**Note:** When returning the coil to the box, please remember to put the tuning wands up so as not to put side ways stress on them. **Also**, do not put the larger coils on top of the smaller mouse coil as this will put an undue strain on the mouse coil tuning wands.

Coil goes in from BACK OF MAGNET (side with the aluminum box).

Connect BNC cable from “H1” to BNC Port on coil (the one that is axially symmetric)

Put in the right distance measuring with the T square

Lock coil in place with thumb screws

Correct distances are taped to the magnet

## Sample insertion

There are several ways to put the sample in. The easiest is to mount it in the coil with something like Styrofoam. For best results the sample should be centered and not placed near the edge (wall or bottom) of the coil. There are various plastic coil holders which mount to the table. Care should be taken that the sample holder does not contact the coil or magnet. Please note that the first method can produce motion artifacts in some experiments which is why you should avoid contact in the second method.

## Data Set Up

There are usually several ways to issue instructions to the spectrometer. The top bar of each ParaVision window presents pull down menus (much like any Windows program). Commands are usually issued from buttons or the pull down menus that launch you into GUIs or macros, which constitute still further routes for issuing instructions to the spectrometer.

The first thing that must be done is define a new patient. If there is no patient defined acquisition commands will not work.

Click once with left mouse button on “**New Patient**”

Enter **Patient Name**

Enter **Registration** – (this is the Unix file name) → Hit <Return>

Click: “**Accept**”

Enter **Study**

Click on “**Location**” and choose “**Class\_2006**”. (Location is where your protocols reside.)

Click: “**Accept**”

Click on “**SINGLEPULSE**”

Click: “**Accept**”

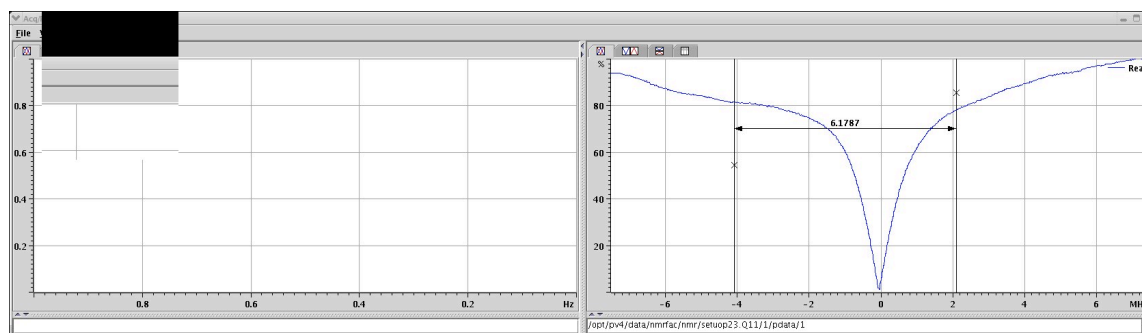
**\*NOTE\***: In the **Scan Overview** portion of the **Scan Control** menu, **Your Patient** should appear and it should say “**Ready**”. If it says new, you didn’t load a protocol.

## Probe Tuning

Click on the icon with a picture of **two tools**; this brings up the “**Spectrometer Control Tool**”

Click on “**Acq Menu**” and choose “**Wobb**”

The window “**Acq/Reco Display**” is launched:



Go to back of magnet and tune the coil.

Start with **Match**. Vary **Match** until only green LED's are lit vertically

Vary **Tune** until only green LED's are lit horizontally

Iterate until only green LED's are lit in both directions

(Arrow LED's indicate which way you are going!!)

When done, click on one of the **Stop** signs or on the word stop in the “**acqDisplay**”.

## Sample Shimming




Click on **Edit Method**.

Check pulse parameters. Pulse should be short ( $< 50 \mu\text{sec}$ ) and power low ( $> 20 \text{ dB}$  attenuation on TX0) so that the tip angle is small. Also the repetition time TR should be as small as possible. Put in **0** and it will calculate the minimum for you.



Click on **GSP** button within “**Spectrometer Control Tool**”. This starts a repetitive version of the experiment for set up purposes. Data is not saved. The window “**Acq/Reco Display**” is brought to the front (as in the wobble routine). On the left the time domain is displayed while the frequency domain is displayed on the right.



At the bottom of time domain display there are 2 arrows . Click either one to expand the text box below. The text box contains measurements for “**Digitizer Filling**” and “**Normalized Area**”. Adjust receiver gain via the slider (in the **Spectrometer Control Tool**) until “**Digitizer Filling**” is approx. 70% (i.e. greater than 50 but less than 100).

Go to **Spectrometer Control Tools** → **Tools Menu** → “**Shim Tool**”

Change the increment in **X, Y, Z and Z<sup>2</sup>** to **1.000**

Click on either side of the **Slider Button** to change the shim value. Adjust **Z-shim** until “**Normalized Area**” is a **maximum**. Repeat for **X, Y and Z<sup>2</sup>**. Run through **AT LEAST twice**.

Click: “**Z3**” → Shim **Z3**

Repeat for other shims as needed, maximizing the normalized area each time.

Click “**Okay**”. This saves shim values to hardware, not to a file.

Adjust offset frequency with slider until signal is on resonance. Click “**Set Basic Frequency**”.

Go to **Spectrometer Control Tools** and click on the button “**GOP**” This acquires a spectrum.

### ***Check Linewidth***

Click on the “Magic Hat” icon to bring up the Macro controller. Click on the macro Calc linewidth and then on the **play** button.

### ***Pulse Calibration:***

Move mouse over **Scan Overview**

Click and Hold “**RMB**” → **Load Scan Protocol**

Choose “**MSME**”

Click on “**Edit Method**” button in the **Spectrometer Control Tools** to check on parameters:

Click On “**Expand**” next to “**RF\_Pulses**”.

Check pulse shape = Sinc3,

Check pulse length = 2ms for both pulses

Click on “**Expand**” Next to “**Standardinplanegeometry**”

Check **Field Of View (FOV)** to make sure they are reasonable for your sample

Click on “**Expand**” Next to “**Standardslicegeometry**”

Check **Slice Thickness** to make sure they are reasonable for your sample

Click “**Okay**”

In **Spectrometer Control Tools**:

→ set “**TxAttn.0**” to “**25**”

→ set “**TxAttn.1**” to “**19**”

(Note that they are 6dB apart and that TxAttn.0 is larger)

Uncheck “**Independent Scale**”

Click on “**GSP**”

Click to the right of the slider in **Tx0** to change the attenuator (Note that Tx1 follows)

Go Slow: **DO NOT** click and drag the slider handle

Gradually (about once per click from magnet) decrease **Tx0**. This increases the **RF Power**

Watch the **Digitizer Filling**; it should gradually increase to a **maximum** and then go to **null** and then get large again. When the digitizer filling goes through a null, the **echo** in the **acqDisplay** should change sign. The null is the condition for a 180 and 360 degree rotation.

To obtain 90-180 add **6dB**

### ***Acquiring a Scout Image***

Put mouse over **Scan Overview**

Click and Hold “**RMB**” → **Load Scan Protocol**

Choose “**RARE\_tripilot**”

Click on **“Edit Method”** button in the **Spectrometer Control Tools**

Click on **“Expand”** Next to **“Standardinplanegeometry”**

Check **Field Of View (FOV)** to make sure they are reasonable for your sample

Click on **“Expand”** Next to **“Standardslicegeometry”**

Check **Slice Thickness** to make sure they are reasonable for your sample

Click On **“Expand”** next to **“RF\_Pulses”**.

Check pulse shape = Sinc3,

Check pulse length = 2ms for both pulses

Click **“Okay”**

For **TX0** and **TX1**, make sure the values are set to the values you determined in pulse calibration for a 90 and 180 degree pulses.

Click on **GSP** in **Spectrometer Control Tools**

Adjust **Receiver Gain** until **Digitizer Filling** is approx. **75%**

Click on **GOP**

### ***Acquiring a Spin Echo Image***

Put mouse over **Scan Overview**

Click and Hold **“RMB”** → **Load Scan Protocol**

Choose **“MSME”**

Click once with left mouse button on the Geometry Editor button.

Use various tools to steer the image area.

Click **“Okay”**

Click **GSP**

Adjust **Receiver Gain** until **Digitizer Filling** is approx **75%**

Click **“Stop”**

Click **“GOP”**



### ***Image Display***

From the system control window chose image display from the tools menu. Then, from anywhere in the scan overview section of the scan control window, hold down the shift key, and click (with the MMB) and drag to the image display. This will drag whatever data is highlighted. If you want to drag a different data set, highlight it first by clicking with the LMB. If you do not hold down the shift key before clicking with the MMB, only the center image of the data set will be displayed.

## ***Alternate Reconstruction***

Put mouse over **Scan Overview**

Click and Hold “**RMB**” → **Clone Reco**

In the **Spectrometer Control Tool**, click the button **Edit Reco**