Getting Started on the Varian INOVA 500 running VNMRJ (ver. 1.2)

1. Logging in and Starting VNMRJ

1.1. Everyone uses the *chem* account.

1.2. If not logged in already, enter the username, *chem* and password *mehc11*.

1.3. Start VNMRJ by clicking the *VNMRJ* icon. You should see something like the following:
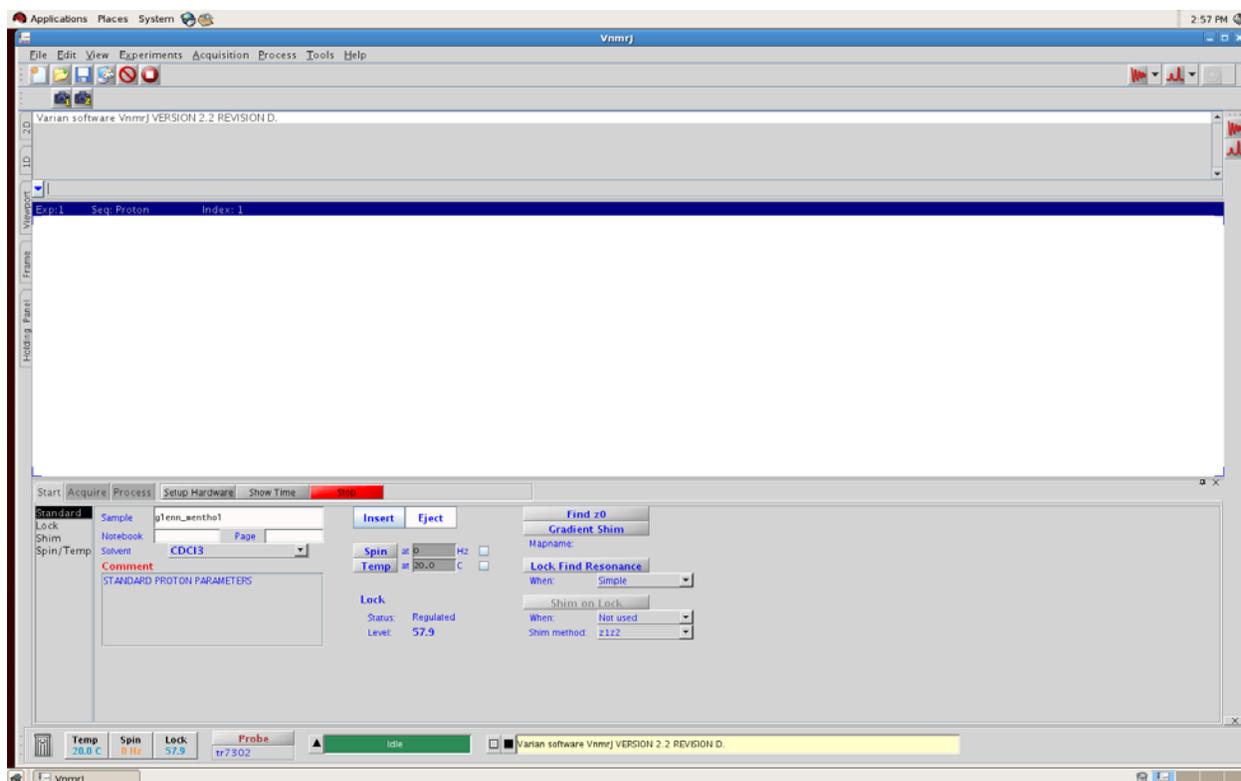
2. Collecting a proton NMR spectrum

2.1. Near the bottom left portion of the screen click the *Start* tab and under the start tab click *Standard*.
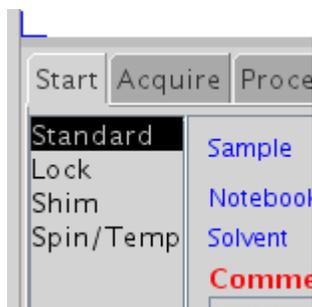
2.2. Click the *Eject* button.
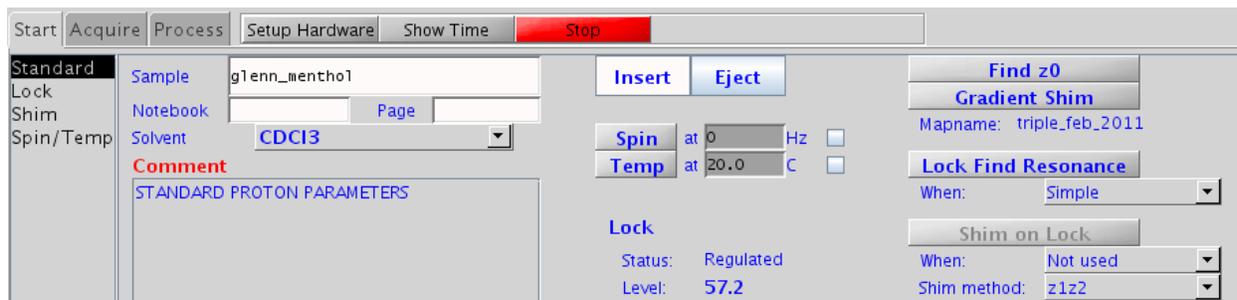
When you hear the flow of air, remove any sample that was in the magnet. Put your sample in the spinner and set the correct depth with the depth gauge. Put your sample at the top of the magnet. It should float on the top from the flowing air. Push the *Insert* button to lower the sample into the probe.

2.3. On the top menu bar…..
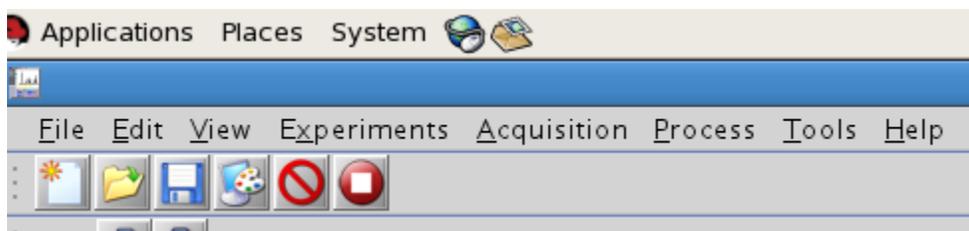
Click the *Experiments* menu and *Proton* in the sub-menu.

2.4. Click the *Setup Hardware* button.
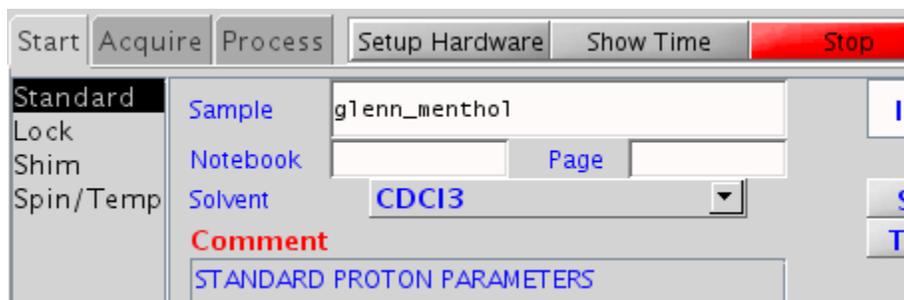
2.5. Input a name for your data set in the *Sample* field. This will be used to name you data set. **DO NOT USE ANY SPACES OR SPECIAL CHARACTERS OTHER THAN THE " – " or " _ " CHARACTERS.** Leave the *Notebook* and *Page* fields blank.

2.6. Select the *Solvent* from the pull-down menu.

2.7. Tune the probe.   Probes are tuned by disconnecting the rf cable for the nucleus you want to observe from the preamplifier and reconnecting it to the tuning bridge, located in the center of the preamplifier assembly. Once the rf cable is connected to the tuning bridge set the appropriate tuning channel number using the **CHAN** button on the bridge (when observing protons, this should be set to "1") . Ensure that the value of the adjacent **ATTN** (attenuator) setting is set to "9". Use the tuning and matching controls on the probe to minimize the reflected power reading. When finished tuning the probe set the channel selector to the zero position and reconnect the rf cable to the preamplifier.

2.8. Click the **Lock Find Resonance** button to find the correct field value for the lock.
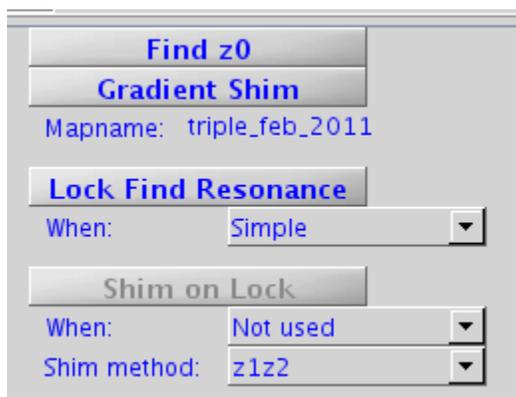
Wait for the lock to be established then click on the **Gradient Shim** button to start the shimming routine. Wait until the gradient shimming has finished. You should see something like the following near the top of the screen when the shimming has been successfully completed.
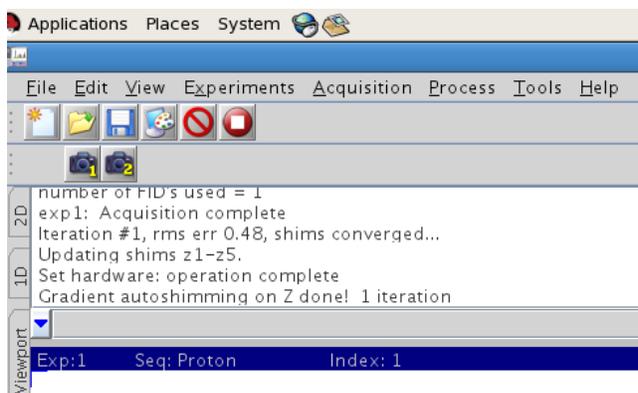
2.9. Click the *Acquire* tab and the *Default H1* option.
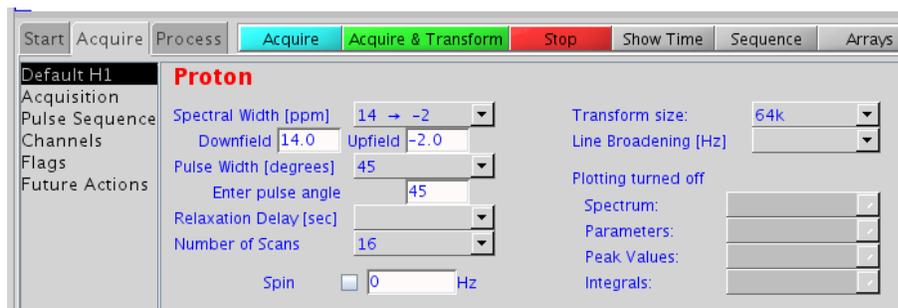
Adjust the spectral width or number of scans as needed. The click on the cyan colored *Acquire* button to collect the data. When the data collection has completed, your data will be automatically processed and displayed on the screen and then saved in the following directory:

/home/chem./vnmrsys/data

With the following name:

*Sample_Nucleus_XXX.fi*d

Where *Sample* is the name you have given to your sample, *Nucleus* is the observe nucleus, *XXX* is a number assigned to the data (e.g. 001). This number will be incremented such that your data will not be overwritten if you use the same sample name.

3. Accessing Your Data Off-Line

3.1. Using WSFTP or other FTP client from your PC, connect to IP address *137.122.43.205*.

3.2. Log in with username *chem* and password *mehc11*.

3.3. Navigate to the directory */home/chem./vnmrsys/data* and FTP your data to your computer.

All other NMR experiments are done in a similar way by selection the appropriate experiment under the *Experiments* menu.