Vnmr Manual

This brief manual can be used for running the Varian 300 MHz instrument in NMR facility

1. Login your account, click on Vnmr icon on the toolbar to start Vnmr.

2. Insert the spinner into the top of the sample depth Gauge and insert your NMR tube in to the spinner. Gently push your sample tube down until it touches the movable bottom of the sample depth gauge.

3. Type "**acqi**" on the command line or click the "**acqi**" button on the main menu line. A new window will pop up. Click "**eject**" button, and the air will turn on and lift the standard sample to the top of upper barrel of the magnet. Remove the standard sample and put your sample with spinner into the top of the magnet. Then click "**Insert**" button to lower the sample into the probe.

4. In **acqi** window, select "**Lock**" to "**off**". Adjust **Z0** using the left and right mouse buttons until a sine wave is seen. If no sine wave is seen, or if it is very low in amplitude, increase "**Lock Gain**" and "**Lock Power**". Then continue adjusting **Z0** until the wavelength increases and finally approximately one wavelength or less is seen. Turn the "**Lock**" "**on**", you will see a flat lock curve. Adjust "**Lock Power**" and "**Lock Gain**" until the lock signal is on scale and stable. Adjust "**Lock Phase**" to maximize the lock signal.

5. Type "**rts('shimfile') su**" on the command line (the shimfile will be updated and posted) to load shim file. In "**acqi**" window, click "**shim**" button, a bar graph will be displayed which represents the height of the lock signal. Adjust the "**Z1"** and "**Z2"** shims by using "-1+", "-4+", "-16+", or "-64+" buttons until the lock signal is at a maximum. Clicking the left button of the mouse will decrease the shim by one unit and clicking the right button of the mouse will increase it by one unit. Cycle between the "**Z1"** and "**Z2"** shims until the lock is at a maximum. When the lock signal is maximized, click "**Close**" button.

6. Type "**jexp1**" on the command line to join on to experiment number 1. On menu bar, select "**Main Menu**"-"**Setup**"-"**Nucleus"-"Solvent**" to select the nuclei and solvent. If the solvent you are using is not listed on one of the menu buttons, select "**Other**" and type in the name of your solvent on the command line. This will recall the standard parameters for acquisition. Type "dg" to check all the parameters. Change parameters as needed. You can change **nt** (number of transients) based on your sample's concentration.

7. Type "**go**" or "**ga**" on the command line, or select "**Main Menu**"-"**Acquire**"-"**Go, wft**"or "**Go**" on menu bar to start acquisition. The command "**go**" will only acquire

your spectrum; you must process it by typing "**wft**". "**ga**" is equivalent to "**Go, wft**" which will collect your spectrum and automatically processes it.

8. When the experiment is complete, the spectrum will be displayed in the graphics window or you have to type "**wft**" or "**ft**" on the command line to do Fourier transform. Type "**aph**" to do automatic phase correction. If spectrum is not well phased using autophase, you also can do manually phase. Select "**Process**"-"**Phase**", click with the left mouse button above a peak near the upfield edge of the spectrum, adjust the phase of the peaks between the cursors by clicking and dragging up or down with the left or right mouse button until the peaks look properly phased. Click with the left or right mouse button on a peak near the downfield edge of the spectrum, do it again until these peaks phased properly.

9. Place a cursor on your reference signal (TMS or solvent), type "**nl**", then type "**rl**" and input the reference chemical shift. Or click the "**Process**"-"**Ref**" button and type in the chemical shift of the solvent line in ppm.

10. Click the "**Process**"-"**Th**" button, you will see a horizontal cursor appear on the screen. Drag it with the left mouse button to an appropriate threshold level.

11. Click "**Part Integral**", The integrals will be displayed. If you want to change the reset points, type "**cz**" on the command line. Break the integrals by clicking the "**Resets**" button. Click the left button of the mouse to start or stop integrating. The values of the integrals can be calibrated by putting a cursor on the integral, clicking the "**Set Int**" button and typing in the number of protons the integral represents. When finished click on any other button.

12. Your also can type "**text('sample')**" to record your sample's information

13. Type "**pl pscale pap ppf pir page**" to print your spectrum. Based on your requirement, you can delete any options. "**pscale**": plot scale, "**pap**": plot parameters, "**ppf**" plot peak picking, "**pir**": plot integration.

14. Type "**pwd**" to print the current working directory. Change to your own directory using "**cd('/your directory/')**" command, then type "**svf('filename')** " to save the data.

15. Go to "**acqi**" window, click "**eject**" button, move your sample, put standard sample at the top of the magnet, click "**insert**" button to let the sample descend into the probe.

16. Type "**exit**" on the command line to logout VNMR, then logout your account.