VNMRJ ^{13}C Operating Instructions

Check the cable with Dr. Bao if the instrument is set for carbon experiment

Follow the VNMRJ ^{1}H instructions to login to vnmrj and insert, shim, and lock your sample.

Acquiring your ^{13}C spectrum

1. Choose to run a ^{13}C experiment by dragging the carbon icon on the left of the screen to the black area.
2. Check the current acquisition parameters by clicking on the process tag, then by typing **dg** in the input box above the black box.
3. To change any parameters, click the acquire tag and make adjustments as necessary by typing in the input box. Use the format **"parameter = value"** to make changes.
4. Alternatively, you may use the default parameters and simply change the number of scans by typing in the command input box (i.e., type **nt = 16** for 16 scans).
5. After typing in the number of scans, type **time** to find out how long the experiment will take. If you run an excess number of scans and would like to stop early, type **aa** to abort the experiment.
6. Start the experiment by typing **ga**.

Processing your spectrum

1. Apply the same commands as used on the other instruments to process the spectrum (i.e., type **wft aph** in the input box for fourier transform and autophasing, respectively).
2. ***Displaying the scale***: As in the case for a ^{1}H experiment, note the set of processing icons to the left of the spectrum. Display the scale by clicking on the white ruler icon.
3. ***Expanding the spectrum***: To expand the spectrum, select the top icon containing 2 red lines. Place the cursors where desired, then expand the region by choosing the zoom in/out (magnifying glass) icon. Use this icon to expand the spectrum and also to return to normal size.
4. ***Setting the solvent reference peak***: As in the case with the other instruments, place the red cursor on your solvent peak, then type **rl(xx.xxp)** in the input box to place the cursor directly on the peak and set the reference value (i.e., **rl(77.23p)** for $CDCl_3$).

Follow the VNMRJ ^{1}H instructions to plot and print the spectrum, save the data, and replace your sample with the standard sample. **Before exiting the system, make sure to drag the proton icon to the black window to turn of the decoupler.**