Northeastern University Department of Chemistry & Chemical Biology
Nuclear Magnetic Resonance Facility
Varian 400 MHz & Varian 500 MHz Spectrometers

Basic VnmrJ4.2 Operation

1. Log in to workstation computer using your login info
2. Open VnmrJ from Desktop icon
3. *There should be a sample in the NMR at all times.* Eject the current sample and insert your own using the on screen "Eject" and "Insert" buttons.
4. Select an experiment type by dragging or double clicking an experiment from the Standards folder or Experiment Selector Tree on screen Under the Start tab, in the Sample Info menu, enter a sample name *(creates a directory with that name)* and select the solvent
5. Under the Shims menu, select "Read Default Shims" *(For samples in organic solvents only, aqueous samples use a different shim file).*
6. Under the Lock menu, select "Find Z0". Wait until the Active Window shows "Idle" again.
7. Under the Shim menu, in the "Auto Shim" controls, select "Z-Gradient" in the drop down menu (for most samples). Select "Start Shim" and wait for the NMR to complete the shimming operations. *(n.b. If after auto shimming, the Lock level is at 100.0, decrease either lock gain or power by single digits until the Lock level is less than 100.0)* [Manual shimming is possible by adjusting the Z1C & Z2C levels on the Shim menu with left & right mouse clicks to optimize lock level]
8. Under the Acquire tab, in the Acquisitions menu, you can change the spectral width, the number of scans, the observed pulse and relaxation delay *(45 degree with 1 second delay or 90 degree with 10 second delay are our recommendations)*. We also recommend you select "Auto" next to "Receiver Gain" to enable the NMR to adjust the receiver gain for your sample.
9. Under the Future Actions menu, ensure "Process/Save" is selected for "When experiment finishes" to ensure your data is saved automatically after acquisition.
10. Clicking "Show Time" will tell you how long your selected acquisition will take.
11. Press "Go" and the acquisition will proceed using your parameters.
12. If "Process/Plot" was the selected "Future Actions" the spectrum will be processed on screen and saved to your data directory. You may quickly process using VnmrJ, or transfer the data to the NMR Processing computer (accounts requested through Brian D'Amico) or onto your own computer via SSH/SFTP transfer for processing in Bruker Topspin or other NMR processing software.
13. Before leaving, eject your sample and reinsert the reference standard *(typically a $CDCl_3$ blank in a sealed NMR tube).* Close the VnmrJ software and log off (icon to log out on desktop).

Updated 03/15/18