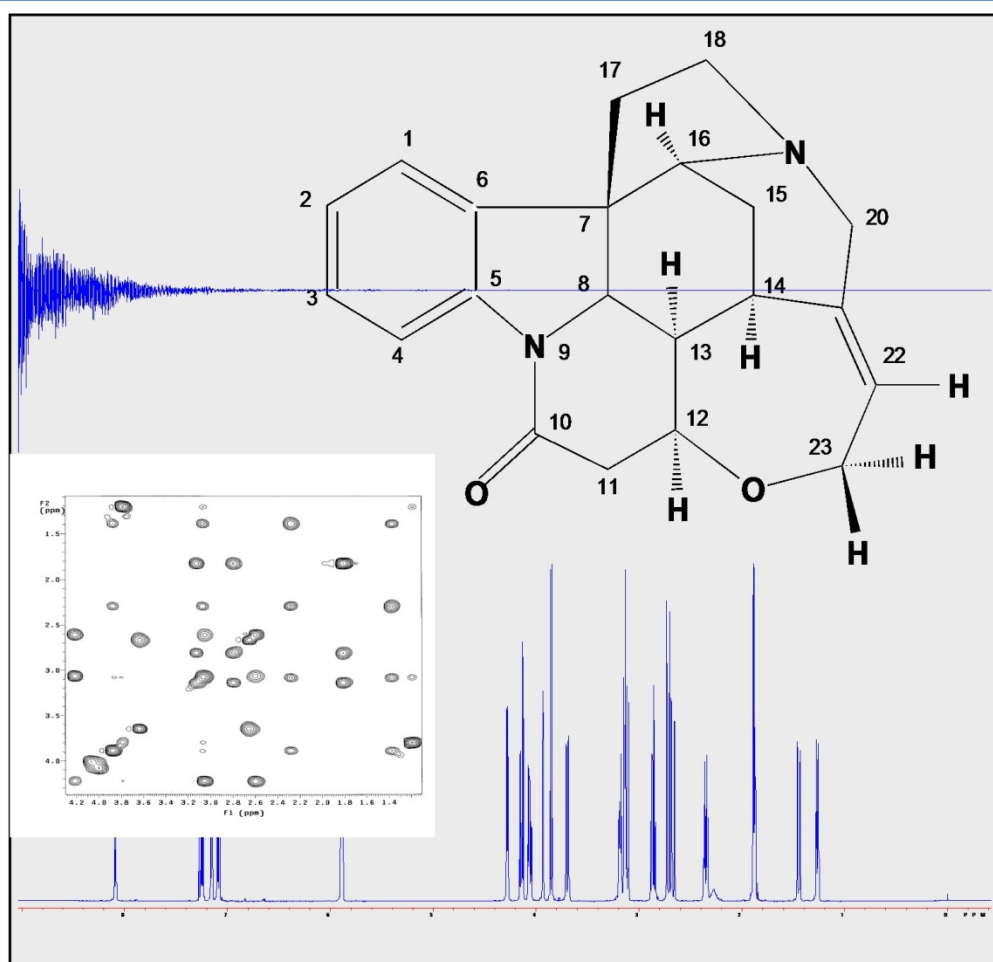


2013

NMR Experiment Procedure



COSY TOCSY NOESY

NMR Center

Emory University

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Experiment Guide for Varian NMR Spectrometers

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Introduction: NMR Experiment Procedures

Step 1. Login

Varian NMR spectrometers are controlled by a host Sun computer or PC. For security and administration reasons, all research groups at Emory University are issued their group usernames and passwords for the host computers. All authorized NMR users must use their group usernames and passwords to login to the host computers.

Step 2. Change Sample

A sealed CDCl_3 standard is always placed in the magnet to keep the instrument in working condition when not in use. Every user needs to replace the standard sample with your own sample at the beginning of each experiment and change back at the end of the experiment.

Step 3. Lock and Shim the Magnet

Locking the magnet keeps its field constant and stable during the data acquisition. Shimming the magnet makes it uniform and homogenous for a sample to get a reasonable resolution and line shape.

Step 4. Setup Parameters and Acquire Data

Retrieve default parameters that are setup and updated for you by the NMR Center so that you may collect your data efficiently. Change some parameters accordingly to meet your own experiment needs.

Step 5. Process Data, Plot Spectrum and Save the Spectrum

This step converts data into NMR spectra. After proper processing, you could plot it on paper for your record. Also you should save the spectrum for your future review.

Step 6. Logout

Your mission is completed and you need to do a few things for the next user or leaving the instrument.

Step 1, 2, 3, and 6 are the same for all experiments. We will describe them in detail in Experiment One. Step 4 and 5 differ from experiment to experiment.

Note on NMR Operating Software:

Varian INOVA600, INOVA400, UNITY Plus 600, UNITY400:
Solaris 8 and VNMR 6.1C on SUN Workstations

Varian Mercury 300, Mercury Vx 300 (at WW) VNMRS400 and Rollins V400:
RedHat Linux 4.0WS and VNMRJ 1.1D or VNMRJ2.1B on Dell 380N PC

Bruker Avance 600WB: IRIS 6.5 (SIG O2) and Xwin-NMR 3.5

Off-line data processing by PC or Mac.
NUTS from Acornnmr, Inc. www.acornnmr.com
MestReNova 7.01 from www.mestrec.com.

Experiment 1: 1D Proton and Basic Operations

Standard Sample to be used: 10% Strychnine in CDCl₃

Step 1. Login

1.1 Sign in NMR logbook.

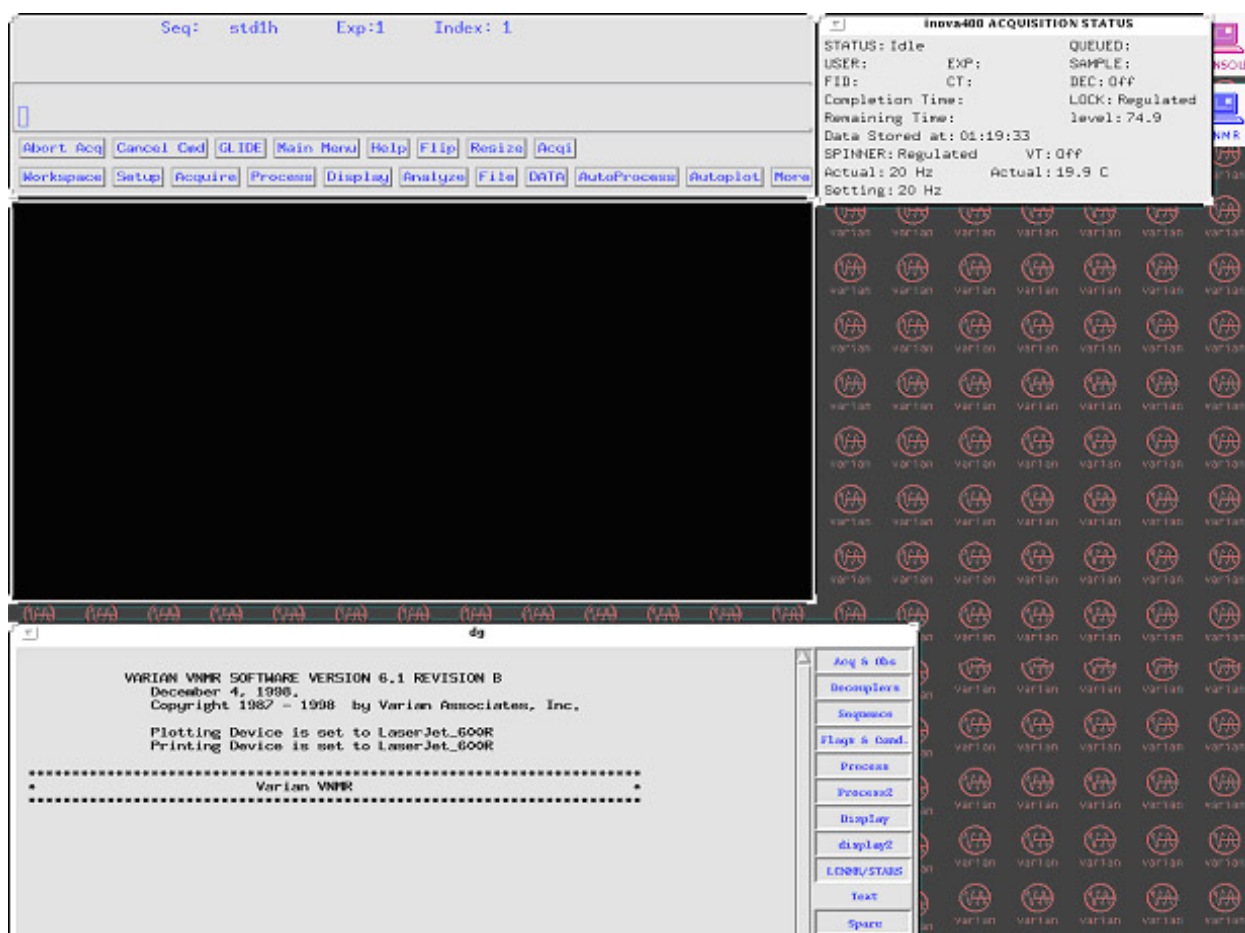
Type in your username at login prompt on the screen.

Type in your account password as the screen prompts.

Please note both the username and password are case sensitive.

If you could not login, contact Dr. Wu.

The VNMR software will be loaded in several seconds with the display of four windows. The upper left window is used for entering commands and selecting menu buttons; the middle left for displaying NMR spectra and the lower left for displaying NMR parameters and other text messages. The upper right window is called “ACQUISITION STATUS” window, indicating the working status of the instrument, such as lock level, spin rate, temperature and acquisition time, etc.

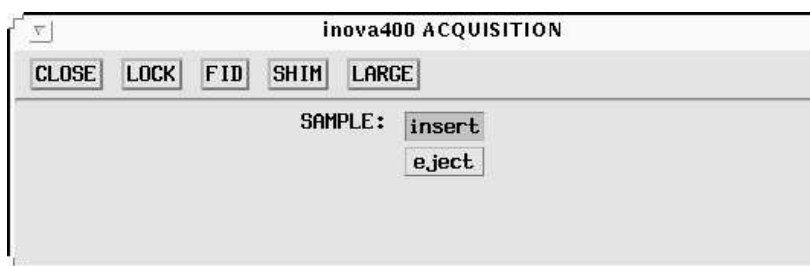


Step 2. Load Standard Parameters and Change Sample

After VNMR software loaded as above, Type **h1** to load the standard parameter for 1D proton experiment with a default CDCl₃ solvent. If your solvent is not CDCl₃, you may simply type **h1('solvent')**, where the solvent may be one among acetone, DMSO, D₂O,

etc. You may also type *h1* and then type *solvent='DMSO'* etc. In this case, you may have to check the reference peak, then reset the correct chemical shift for your spectrum.

- 2.1 Click on **Acqi** or type **acqi** in the command line to display the fifth window at lower right, which is called “**ACQUISITION**” window. All the operations hereafter in **Step 2** and **Step 3** will be operated in this window. There are **CLOSE**, **LOCK**, **FID**, **SHIM** and **LARGE** popup menu buttons, and Sample **eject** and Sample **insert** buttons. We will be focusing on the **LOCK** and the **SHIM** buttons first.



- 2.2 Click on **LOCK** button to display lock sub-window then click SPIN: **off** button to turn off sample spinning; click LOCK: **off** to turn off the lock.
- 2.3 After a few seconds, the spin rate displays zero, then click on the SAMPLE: **eject** button to eject the standard sample to the top of the magnet; remove the spinner, replace the sample with your own, use sample depth gauge to measure the correct tube position, use kimwipes to clean the spinner and your sample, then put the spinner back onto the top of the magnet again. **Caution: place the spinner with a sample on top of the magnet only when ejecting air is on.**
- 2.4 Click on the SAMPLE: **insert** button to put the spinner back down inside the probe. Wait for 3 to 5 seconds, then click on the SPIN: **on** button to make the sample spin.

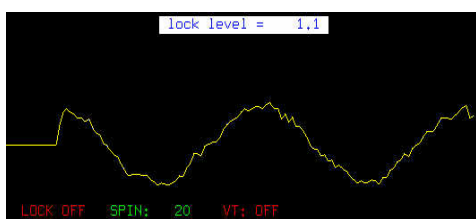


Lock sub-window

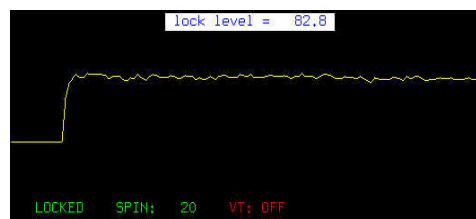
Step 3. How to Lock and Shim the Magnet

In this step, you need to adjust lock and shim parameters by using the mouse. Each parameter can be increased or decreased by 1, 4, 16 and 64 units as shown by corresponding -1+, -4+, -16+ and -64+ buttons. For example, when you place the cursor on a button, say -4+, if you click the left mouse button once, the corresponding parameter is decreased by 4 units; if you click the right mouse button twice, the parameter is increased by 8 units.

- 3.1 If you are using CDCl_3 solvent, the magnet could be locked almost instantly most of the time. This is indicated by the display of lock signal plateau and a green **LOCKED** message below it. Then you directly go to step 3.3.
- 3.2 If you don't see a plateau signal with a **LOCKED** message or you are using solvent other than CDCl_3 , click on LOCK: **off** button, adjust Z0 to make wave-like lock signal into plateau-like resonance, then click LOCK: **on** button. A green LOCKED should be shown. Then adjust the lock phase to make the lock level as high as possible. You need to reduce both the lock power and lock gain several units if the lock level exceeds 100. You may also check our record sheets on the desk. There are Z0, Lock power, Lock gain, and Lock phase values for different solvents recorded by previous users.



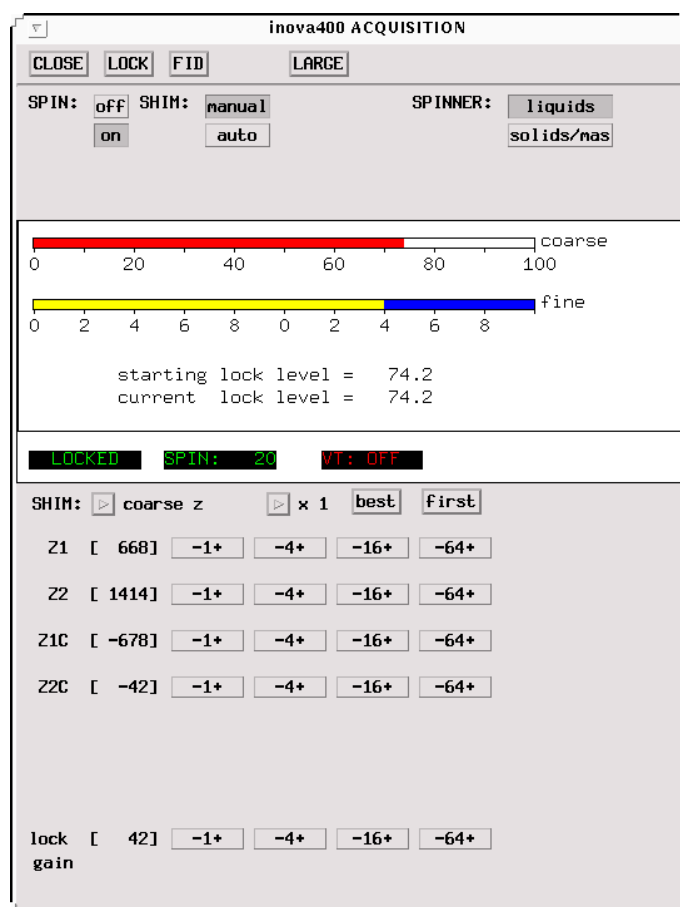
Not Locked



Locked

How to lock a sample having mixed solvents: Always select the strongest signal for your lock. For example, CD_3OD , you have two lock frequencies, Use the CD_3 resonance signal. If solvent is 10% D_2O + 90% DMSO, then you use DMSO-D as lock.

- 3.3 Now it is shimming time. There are as many ways to shim the magnet. We suggest you shim it this way:
 - 3.2.1 Click **SHIM** button to display shim sub-window. The lock level is shown in this window as two color bars and exact lock level is shown underneath the bars. In the middle of the window, there is one triangular button after '**SHIM:**' which let you switch from shim sub-windows and lock sub-window by just click on it. Now it should show **coarse z** by the button.



- 3.2.2 Adjust Z1C (Z1 coarse) and Z2C(Z2 coarse) by alternatively changing 1 or 4 units to increase the lock level as high as you can. If the lock level increases to 100, decrease lock gain on the bottom of the window and then continue to adjust Z1C and Z2C. Higher lock level indicates better homogeneity of the magnetic field.
- 3.2.3 Click on the triangular button to switch to **fine z** sub-window. Adjust Z1, Z2 and Z3 one after another to make the lock level as high as possible, then adjust Z3, Z2, Z1 as such back and forth a couple of times. We do not suggest you to adjust Z4 and Z5 at this stage. If you really want to adjust them, it is better write them down before you change them, so that you are able to go back in the case you get a worse shimming.
- 3.3 Finally click the **CLOSE** button to end the shimming procedure.

Tip 1. Retrieve our default standard shimming file.

If you have a very bad shim, type “**loadshim**” in the command window to reinstall our default shim file for the standard sample.

If you would like to save your good shims, type `svs('shim_name')`. The file will be saved in: **/export/home/nmruser/your_ID/vnmrsys/shims**.

You could reload your shims by changing to the above file folder, select the shim file, then click **main** → **file** → **data** → (high light the shim file) then click **load shim**, then type **su** to use the new shim file.

Step 4. Setup Parameters and Run 1D Proton Experiment

- 4.1 Type *dg* to check the standard parameter for 1D proton experiment with a default CDCl₃ solvent. If your solvent is not CDCl₃, you may simply type *h1('solvent')*, where the solvent may be one among acetone, DMSO, D₂O, etc. You may also type *h1* and then type *solvent='DMSO'* etc. In this case, you may have to check the reference peak, then reset the correct chemical shift for your spectrum.

ACQUISITION	SAMPLE	PROCESSING	FLAGS
sfrq 399,941	date May 30 2000	lb 0.20	il n
tn H1	solvent cdc13	sb not used	in n
at 2.499	file exp	gf not used	dp y
np 25384	DECOUPLING	awc not used	hs nn
sw 5199.2	dn H1	lsfid not used	SPECIAL
fb 3000	dof 0	phfid not used	temp not used
bs 16	d1m nnn	wtfile	
ss 0	d1m c	proc	ft
tpwr 60	d1m 200	fn 32768	
pw 6.0	dpwr 30	math	f
p1 0			
d1 1.000		werr react	
d2 0		wexp procp1ot	
tof 199.6		ubs	
nt 1		wnt	
ct 0			

Proton standard parameters.

The standard parameters will be shown in the left lower window.

Tip 2. Check Current Parameters

Type *dg* to display the current parameters for the loaded experiment. If you have to change parameters, make sure you know what it is for. Type *su* to set it up and type *dg* to look at them.

- 4.2 Type *nt=8, 16* or *32*, according to sample concentration (or use a multiple of 8 for nt).
- 4.3 Type *ga* (submit to acquisition) to begin acquisition.
- 4.4 After acquisition is completed, a proton spectrum should be displayed on the screen now. If not, type *wft* (Weight and Fourier transform) to display the spectrum, then enter *aph* (automatic phasing) to phase the spectrum. Type *vsadj* (vertical scale adjustment) to adjust the vertical scale of the spectrum automatically. Type *dscale* or click on **Dscale** button to display chemical shift scale under the spectrum.

Tip 3. Manual Phasing

If you need to improve the phasing, you may manually phase the spectrum by first clicking on the **Phase** button, clicking on the region of interest, and moving the mouse up or down while pressing the LMB to adjust its phase. You may continue to click the cursor on the next region and adjust the phase same way. Clicking on the **Box** or **Cursor** button will exit the manual phase routine or type *ds*.

Tip 4. Manual Vertical Scale Adjusting

Place the cursor above the base line and click middle mouse button to increase the vertical scale. Place the cursor below the base line and click middle mouse button to decrease the vertical scale.

Step 5. Data Processing

5.1 Zoom operation

Click the LMB on the left side and click the RMB on the right side of a peak. Two vertical red cursors will appear at the click points, then click the **Expand** button on the menu bar. The region between the red cursors will be expanded. Click on **Full** button to return to the full spectrum after expanding, or type **f** then press enter. You may do this zooming operation as many times as you like.

5.2 Set reference

After zooming the region containing the reference peak, click the LMB near the top of the peak, then type **nl** to place the cursor exactly on the top of the peak. Then type **rl(x.xxp)** to set its chemical shift. For example, **rl(4.80p)** will set a peak frequency to 4.80ppm.

5.3 Integral operation

Enter **vp=12 or larger**. Type **ds cz** to clear all the previous integral values in the buffer. Click on the **Part Integral** button for the full spectrum or its expanded region to display an integral curve, then click on the **Resets** button. Now click the LMB at both sides of each peak or integral region to get separated integral lines of the spectrum.

If you know the number of protons, a specific peak represents, you may set the value for that integral as follows: place the cursor on the integral and then click on **Set Int**. The computer will then ask what value to assign that integral. After you input the value for a particular integral, the computer will recalculate the value of every other integral relatively. You are able to see these values by typing **dpir**.

Tip 5. Redo integral operation

If you made a mistake during the integral operation, you can redo the integral operation by typing **cz**. Or you could click RMB, to correct the last setting of the integral curve.

5.4 Peak picking operation

Type **ds** and click on **Th** to display a yellow horizontal threshold line. Every peak above this line will be assigned its chemical shift in ppm (axis='p') or hz (axis='h'). Press and hold the LMB to move the yellow cursor to the position you desire, then click on the **Th** button again. Type **dpf** to display peak frequencies above spectrum peaks.

Tip 6. Returning to interactive adjustment

During the above operations, if you are not able to find the button you need or you are unable to use the red cursor, simply click on **Main menu** > **Display** > **Interactive**

5.5 Label your experiment data
Type *ctext* to clear any text label for the present experimental data. Type *text('Your sample name date||solvent')* to label the present experimental data. Command *dtext* will display the text on the top left corner of your spectrum.

5.6 Print and plot spectrum and related information
All printing procedure starts with *pl* and ends with *page*. You can put other printing commands selectively between these two commands.

ppa--- to print select parameters with text labels.
pl--- to print the present spectrum;
pap--- to print all the parameters including the text labels, if any.
ptext--- to print text labels without other parameters.
p scale--- to print the spectrum scale in ppm or hz by *axis="p"* or *axis="h"*.
ppf--- to print all the peak frequencies over the respective peaks.
pll--- to print a list of the frequencies and intensities.
pirn--- to print normalized integral values below the respective peaks.
pir--- to print proton numbers below the respective peaks.
page --- to expel the paper from printer.

If you want to print integrals, set *vp =12* first, or it wouldn't print.

5.7 Save your experimental data and reload your experimental data

You may save your spectrum data.

The directory path is /export/home/nmrusr/Login_ID/ when you login. It is your group directory. You should make a directory for your own files.

Type *mkdir('yourname')* to make a directory of your own. Type *pwd* to check the current directory. If it does not, click on **Main menu** > **File** then highlight your directory name and click on **Set directory**. Remember you can go back to your group directory at any time by typing *cd*. To check the current directory, type *pwd*. Type *svf('file_name')* to save your data in the form of FID.

5.8. To reload your file, go to your directory first as described above, then click on **Main menu** > **File** > highlight your file > click on **load**. Then type *wft*.

Step 6. Logout

6.1 Retrieve standard file and replace your sample with the standard.
Type *h1* to set up standard proton file. This is especially important after you have done a carbon-13 experiment. It will turn off the decoupling channel automatically.

Then see **Step 2** for details about replacing NMR sample tubes.

6.2 Lock and shim the magnet

See **Step 3** for details. You are required to shim the magnet to the required level:

'loadshim' will reload the current shims for the standard.

6.3 Exit the VNMR program

Type *exit* to close the VNMR program. Now you will see a full screen of Varian's logo.

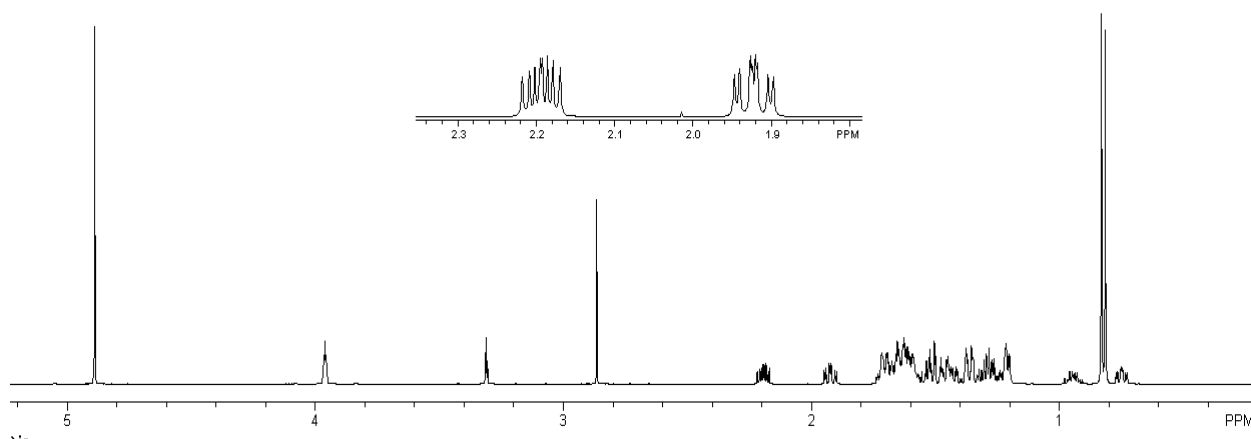
6.4 Exit UNIX system

Press the RMB to select Exit item in the popped up menu, release RMB. You will be prompted to select one of two choices: **Exit** or **Cancel**. Click on **Exit** to exit UNIX system. The screen will become blank and a prompt appears.

Caution: It is important to logout completely, otherwise your account will be still charged!

Tip:

Insert a part of your spectrum on the top of your full spectrum:



1. After the processing completed, type **pl pscale** no page command, that will save the full spectrum in plotter queue;
2. Use both red cursors to select the area you want to inserted, then type **inset**, The part of the spectrum will be displayed in the middle of the spectrum. Use mouse to adjust the size and location. Then type **pl pscale page**.
3. After printing is completed, type: **ds full f and vs=0**, you will get the original spectrum back.
4. You could repeat these steps for few times and insert several spectra in the same plot before you type the **page** command.
5. If you want to print the spectrum in particular range: type **cr=XX.Xp delta=XXp**, two red cursors will be in the positions as you specified, left cursor at XX.X ppm and the right cursor at XX ppm away from the left cursor. Then click expend and print the spectrum.

You can use the same way to plot two or more spectra together to compare the difference of these spectra by select the same region (use **cr** and **delta** command).

Experiment 2: 1D Carbon-13 and Basic Operations

Sample to be used: 30% Strychnine in CDCl₃

Step 1. Login

(See Experiment One)

Step 2. Change Sample

(See Experiment One)

Step 3. Lock and Shim The Magnet

(See Experiment One)

Step 4. Setup Parameters Carbon Experiment

- 4.1 For Standard C-13 spectrum (Fully decoupled with NOE enhancement): Type ***c13*** or ***c13('solvent')*** to call up the standard carbon-13 experiment parameters with CDCl₃ solvent or different solvent.
- 4.2 Enter ***nt=128, 256***, or more according to the nature of your sample. Type ***time*** to check the total time of the experiment.
- 4.3 Type ***ga*** to begin acquisition.
- 4.5 After acquisition is done, a carbon spectrum should be displayed. If not, enter ***wft***. Type ***aph*** for automatic phasing. Manual phasing is often necessary for a carbon-13 spectrum.

Tip 7. Use large values for ***nt*** and ***aa*** Commands

¹³C sensitivity is very low. A common practice is to set a very large number for ***nt*** (ex. ***nt=5000*** etc.) to start the experiment. You can check the spectrum by typing ***wft aph*** and stop the experiment at any time by typing the ***aa*** command to abort acquisition. The ***time*** command can be used to estimate the total experiment time with a given ***nt***.

If you want to observe some longer relaxation carbons, such as N-C=O's, you may set the ***d1*** to 5 seconds or longer.

Step 5. Data Processing

5.1 Zoom operation

Click the LMB on the left side of a peak and the RMB on the right side. Two vertical red cursors will appear at the click points, then click the **Expand** button on the menu bar and the region between the red cursors will be expanded. You may do this zooming operation as many times as you like.

5.2 Set spectrum reference

After zooming the region containing the reference peak, click the LMB near the top of the peak, then type ***nl*** to place the cursor exactly on the top of the peak. Next, type ***rl(x.xxp)*** to set its chemical shift. For example, ***rl(77p)*** will set a peak frequency to 77.0 ppm.

5.3 Peak picking operation

Type ***ds*** and click the **next** and **th** buttons to display the horizontal threshold line. Press and hold the LMB to move the yellow cursor to the position you desire, then click on the **th** button again. Type ***dpf*** to display peak frequencies above spectrum peaks.

5.4 Label your experiment data

Type *ctext* to clear any text label for the present experimental data.
Type *text*("Your sample name, date\\solvent, etc") to label the present experimental data.
Type *dtext* to display the text label of present data on the upper left of the spectrum.

5.5 Print and plot spectrum and related information

pl----to begin print the present spectrum;
pap---to print all the parameters including the text labels, if any.
ppa---to print some parameters and text labels.
pscale---to print the spectrum scale in the unit of ppm or hz by *axis="p"* or *axis="h"*.
pltext--- to print the label.
ppf---to print all the peak frequencies over the respective peaks.
page ---to expel the paper from printer.

5.6 Save your experiment data

You have to save your data in /export/home/nmrusr/Login_ID/yourname/
Type *svf('file_name')* to save your data in the form of FID.

Step 6. Logout (You MUST type h1 before you logout)

- 6.1 Retrieve the standard file and replace your sample with the standard sample.
Type *h1* to set up the standard proton file. This will also turn off the decoupler power.
Next, see **Step 2** for details about replacing NMR sample tubes.
- 6.2 Lock and shim the magnet
See **Step 3** for details. Before exiting, you are required to shim the magnet to the required level.
- 6.3 Exit the VNMR program
Type *exit* to close the VNMR program. Now you will see a full screen of Varian's logo.
- 6.4 Exit UNIX system
Press the RMB to select the Exit item in the popped up menu, then release the RMB. You will be prompted to select one of two choices: Exit or Cancel. Click on Exit to exit UNIX system. The screen will become blank and a prompt appears.
- 6.5 Logout
Type *logout*. Sign off the logbook for the instrument.

Congratulations!!! You have finished a complete 1D carbon-13 experiment. Make sure you type the h1 command before you logout.

Experiment 3: Proton 90° Pulse Width Calibration

Sample to be used: 10% Strychnine in CDCl₃

Warning: You are not allowed to tune the probe without Dr. Wu's permission! If your experiment requires probe tuning, please contact our service instructors in advance.

Step 1. Login

Step 2. Change Sample and type *h1 su* to load proton parameters before doing lock and shimming. Then call up an NMR staff to check the probe. Tuning the probe may be necessary for different solvents.

Step 3. Lock and Shim the Magnet

Step 4. Setup Parameters and Run Experiment

Run a 1D proton spectrum, set the cursor to a peak near the center of the spectrum, then type **movetof** to set the peak on-resonance for calibration.

4.1 *nt=1* and *d1=10* or a value which is long enough to enable protons to relax back to thermal equilibrium status. (the default transmitter power: *tpwr=56 the max is 60*)

4.2 Type *array* and input the following parameter and numbers as the computer requests:

parameter to be arrayed: *pw*.

enter number of steps in array: 20

enter starting value: 2

enter array increment: 2

You are able to see the whole array parameters in the Text Window on the bottom by typing *da* to list array parameters.

4.3 After the acquisition is completed, save the data.

Step 5. Data Processing

5.1 Display arrayed spectrum

When the acquisition is finished, enter *ds(1)* for displaying the first spectrum of the array. Type *aph* for autophasing. Move the spectrum up a little bit by typing *vp=50*. Choose a singlet or a doublet peak to expand and then enter *ai dssh* for displaying peaks at the same chemical shift range in all of the individual spectra horizontally.



5.2 Null point and 90° pulse width

From the arrayed spectrum, identify the first null point (where the peak intensity is 0), then check the pw value corresponding to it. This pw value is the 180 degree pulse width. The 90° pulse width is this pw value divided by 2 at given power (*tpwr*). In this case *tpwr=56*. Type *pw90=xx* to set up this parameter, where xx was obtained as above. Record this number for your future application. The 90 degree pulse for an NMR standard was calibrated by NMR center and it is recorded in the logbook, your 90 degree pulse should not vary far from this number.

5.3 Label your experiment data

See Experiment One.

5.4 Print and plot spectrum and related information

Type *plww pap page* to print spectra in white wash mode (after the first spectrum, each spectrum is blanked out in regions in which it is behind an earlier spectrum).

5.6 Save your experimental data

See Experiment One

Step 6. Exit and Logout

See Experiment One

Congratulations!!! You have finished a complete Proton 90° Pulse Width Calibration experiment.

Experiment 4: 90° Pulse Width Calibration for Carbon Channel

Sample to be used: 40% p-dioxane in benzene-d⁶ (ASTM)

Warning: You are not allowed to tune the probe without Dr. Wu's permission!

Step 1. Login

Step 2. Change Sample as routine.

Type *c13* ('Benzene') *su* to load C13 parameters. Type *dm='nnn'* to turn off the decoupler.

Then call up a NMR staff person to check the probe. Probe tuning may be necessary for different solvents.

Step 3. Lock and Shim the Magnet

Step 4. Setup Parameters

4.1 Type *dm='yyy'* *su* to turn the decoupler back on.

tpwr=xx (maximum 60), *nt=1*, then enter *ga* to begin acquisition.

4.2 After the acquisition is finished, phase the spectrum.

4.3 Set *d1=20* or a value which enables the carbon to relax back to thermal equilibrium status. (If you have added Cr(AcAc), then *d1* can be set to 1 second).

4.4 Type *array* and input the following parameter and numbers as computer requests:

parameter to be arrayed: *pw*.

enter number of steps in array: 20

enter starting value: 2

enter array increment: 2

You are able to see the whole array parameters in the Text Window on the bottom by typing *da* to list array parameters.

4.5 Type *ai ga* to begin acquisition. The *ai* means absolute intensity mode.

Step 5. Data Processing

5.1 Display arrayed spectrum

When the acquisition is finished, enter *ds(1)* for displaying the first spectrum of the array. Type *aph* for autophasing, then type *vp=50* to move the spectrum up. Choose a singlet peak to expand and then enter *dssh* for displaying peaks at the same chemical shift range in all of the individual spectra horizontally.

5.2 Null point spectrum and 90° pulse width

From the arrayed spectrum, identify the first null point (where the peak intensity is 0), then check the *pw* value corresponding to it. The 90° pulse width is this *pw* value divided by 2 at given power (*tpwr*). In this case, *tpwr=60*.

Type *pw90=xx* to set up this parameter, where *xx* was obtained as above.

5.3 Label your experiment data

5.4 Print the spectrum and related information

Type *plww pap page* to print spectra in white wash mode (after the first spectrum, each spectrum is blanked out in regions in which it is behind an earlier spectrum).

5.5 Save your experiment data

Step 6. Exit and Logout (You must type h1 before you logout)

Experiment 5: APT

Sample to be used: 30% Menthol in CDCl₃ with 2% Cr(AcAc)₃

Step 1. Login The Computer System

See Experiment One.

Step 2. Change Sample

See Experiment One.

Step 3. Lock And Shim The Magnet

See Experiment One.

Step 4. Setup Parameters and Run Experiment

- 4.1 type *c13* to load standard carbon experiment parameters.
- 4.2 Set *nt=8*. Type *ga* to begin acquisition for a common 1D-carbon spectrum.
- 4.3 After acquisition, type *aph* for automatic phasing and /or manual phasing and then set the sw if needed. Remember, APT will show all carbon signals, including the solvent peaks.
- 4.4 Type *apt* to load standard APT parameters. Double check following parameters:
 - pw*----- Use 90 degree pulse or less for ¹³C
 - p1*-----180° ¹³C pulse width. (It is the double value of the 90° pulse width. Check the last page of the log book for 90° pulse width).
 - tpwr*-----transmitter power. It must be paired with 90° pulse width. (Check the last of the log book for 90° pulse width and transmitter power *tpwr*)
 - d2*-----the tau delay time. *d2=0.007* (7ms) will make CH, CH₃ peaks down and C, CH₂ peak up. We assume the ¹J_{CH}=140 Hz 1/140Hz = 7.14 ms.
 - d1*-----the pulse delay. It is set to around 10 seconds.
 - dm*-----decouple mode. It is set as *dm='yny'* for APT.
 - nt*-----scan numbers depends on sample concentration (minimum 16 scans).
- 4.5 Type *ga* to acquire data.

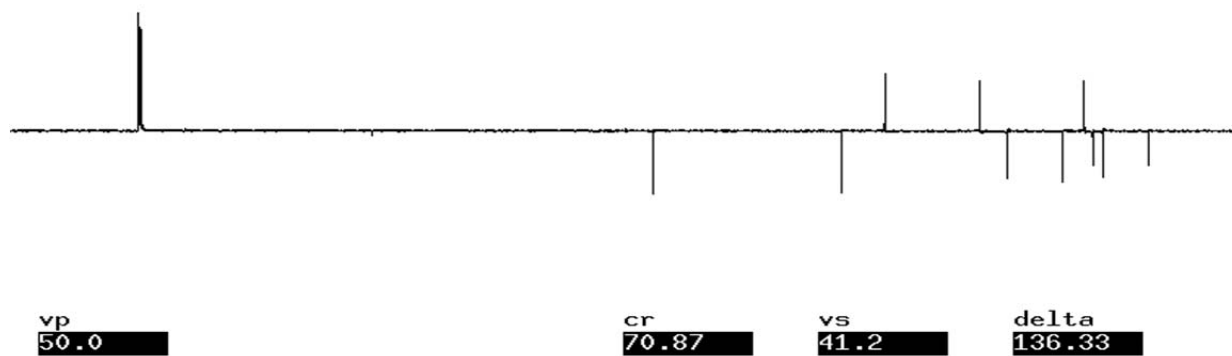
Step 5. Data Processing

When the acquisition is finished, type *aptaph* macro to phase APT automatically. Or manually phase the spectrum.

Type *pl pscale pap page* to plot the spectrum.

Step 6. Exit and Logout

See Experiment One



APT spectrum of Menthol in CDCl₃ on INOVA600. *pw=11*, *p1 =22* *tpwr=60*, *d2=0.007*, *d3=0.001* *dm='yny'* *dpwr=35* (Maximum 40) *dmf=8000* decoupling modulation frequency (1/*pw*90 at power 35 dB).

Experiment 6: DEPT

Sample to be used: 30% Menthol in CDCl₃

Step 1. Login The Computer System

See Experiment One

Step 2. Change Sample

See Experiment One

Step 3. Lock And Shim The Magnet

See Experiment One

Step 4. Setup Parameters And Run Experiment

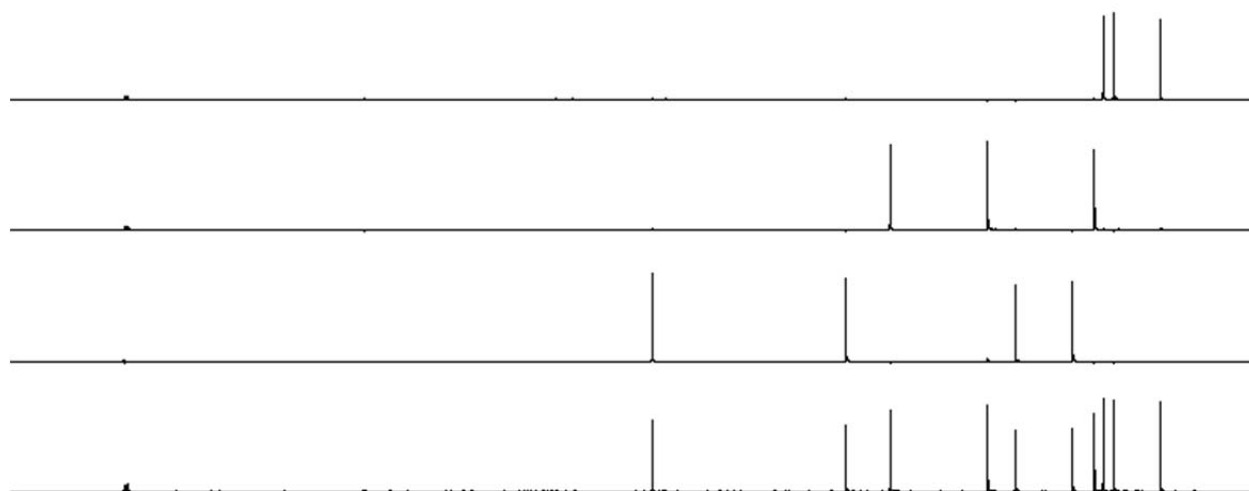
- 4.1 Type command *c13* to setup standard parameters for 1D carbon spectrum.
- 4.2 Set *nt=4* or 8 to acquire an 1D carbon spectrum, and set the chemical shift reference and spectral width, remember all carbons without proton attached, including the solvent peak will not show on the DEPT spectrum.
- 4.3 Type *dept* to setup standard parameters for DEPT experiment.
- 4.4 Check and/or change the following important parameters:
 - ss=4* steady-state pulse or dummy scans
 - pw*=the value of 90° pulse width for C13 channel; Check the last page of the log book.
 - tpwr*=the value transmitter power of C13 for 90° pulse width; Check the last page of the log book.
 - pp*=the value of proton 90°-pulse width from decoupler channel; Check the last page of the log book.
 - pplvl*=the value of proton 90°-pulse transmitter power from decoupler channel; Check the last page of the log book.
 - d1=5* relaxation time
 - j=140* average C-H coupling constant;
 - nt=32* or more number of scans, A multiple of 16 is suggested.
- 4.5 Type command *ga* to acquire data.

Step 5. Data Processing

- 5.1 After the acquisition, type *ds(1)* to display the first spectrum.
- 5.2 Phase the spectrum and select a proper threshold by using menu button of **th**. Then type **fp**.
- 5.3 Enter *autodept* to analyze and display arrayed spectra of CH_x, CH, CH₂ and CH₃ and print out DEPT spectrum. There are several ways to process the arrayed spectra. You could use *adept* and *dssa*, then *pldept* to plot the spectra.

Step 6. Exit and Logout

See Experiment One



vs	sp(ppm)	wp(ppm)	first	last	step
43.7	5.77	136.87	1	4	1

DEPT spectrum of Menthol in CDCl₃ on INOVA600. pw=12 p1=22 tpwr=60 pp=12.2 pplvl=56 J=140 dm='nny' dmm='ccw' dmf=8000 dpwr=35 mult=arrayed (0.5,1,1,1.5).

Note:

This experiment takes four times of the acquisition time of your 1D ¹³C spectrum that reaches a good enough S/N ratio. For example, your 1D carbon takes 256 scans (about 15 minutes) to get a good spectrum, then your DEPT needs about one hour (15 x 4=60 minutes).

Experiment 7: INEPT

Sample to be used: 30% Menthol in CDCl₃

Step 1. Login The Computer System

See Experiment One

Step 2. Change Sample

See Experiment One

Step 3. Lock And Shim The Magnet

See Experiment One

Step 4. Setup Parameters And Run Experiment

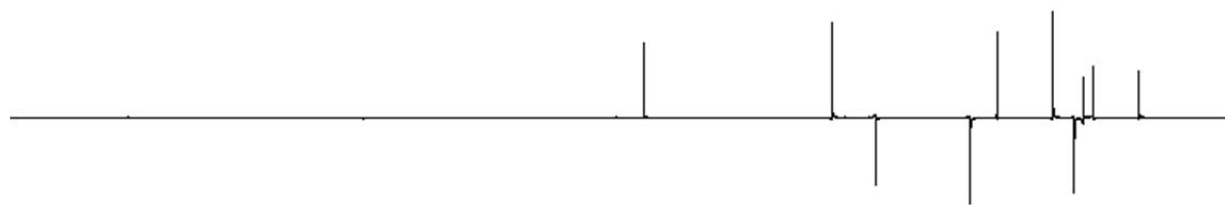
- 4.1 Type command *c13* to setup standard parameters for 1D carbon spectrum.
- 4.2 Set *nt=4* or 8 to acquire an 1D carbon spectrum, and set the chemical shift value.
- 4.3 Type *inept* to setup standard parameters for DEPT experiment.
- 4.4 Check the following important parameters:
 - ss=4* steady-state pulse or dummy scans
 - pw*= the value of 90° pulse for carbon-13; Check the last page of the log book.
 - tpwr*= the value of transmitter power of 90° pulse for C13 channel; Check the last page of the log book.
 - pp*= the value of proton 90° pulse width from decoupler channel; Check the last page of the log book.
 - pplvl*= the value of proton 90°-pulse power from decoupler channel; Check the last page of the log book.
 - d1=5* relaxation time
 - j=140* average C-H coupling constant;
 - mult=3* multiplicity to make CH, CH₃ up and CH₂ down;
 - nt=64* number of scans, A multiple of 16 is suggested.
 - dm='nny'* setting for coupled spectrum;
 - focus='y'* refocusing for coupled spectrum;
 - normal='y'* normal multiplets in coupled spectrum
- 4.5 Type command *ga* to acquire data.

Step 5. Data Processing

- 5.1 After the acquisition, the first spectrum will be displayed automatically.
- 5.2 Phase the spectrum, if necessary.
- 5.3 Type *pl pscale pap page* to plot the INEPT spectrum.

Step 6. Exit and Logout

See Experiment One



vp
50.0

cr
70.87

vs
50.0

delta

INEPT spectrum of Menthol in CDCl_3 on INOVA600. pw=11 p1=22 tpwr=60 pp=12.2 pplvl=56

Experiment 8: Presaturation and Water Suppression

Sample to be used: 10% Strychnine in CDCl_3

Step 1. Login The Computer System

See Experiment One

Step 2. Change Sample

See Experiment One

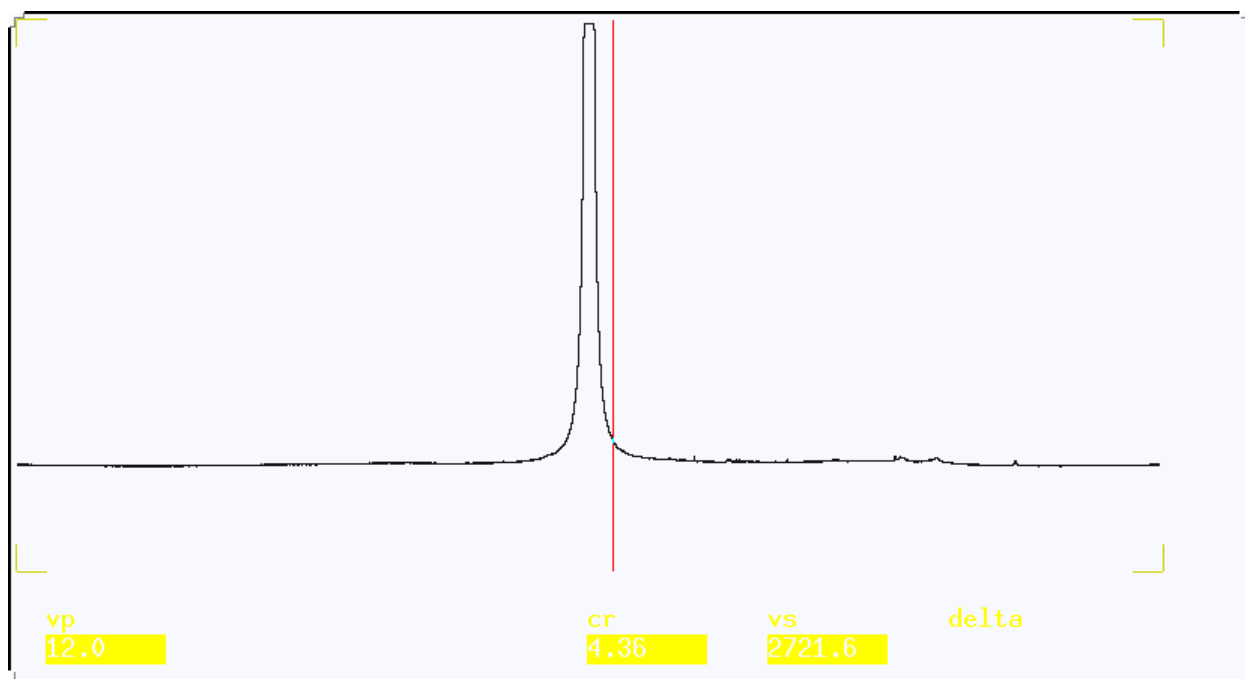
Step 3. Lock And Shim The Magnet

See Experiment One

Note: For the samples using $\text{H}_2\text{O} + \text{D}_2\text{O}$ as solvent, the water peak is huge. To be able to see other signals the water peak need to be suppressed more efficiently. There are several aspects we need to emphasize here: 1) Tune the probe on your sample. 2) Use gradient shimming to get a good shimming. 3) Put the transmitter frequency on the water peak.

Step 4. Setup Parameters and Run Experiment

- 4.1 Load your sample into the probe as usual. Type *h1('D2O')* *su* to load the proton experiment parameters. Because of the huge water signal, the receiver will be overflowed if you start to acquire the data using the default value. To avoid the receiver overflow, do as follows: Type *gain?* to check the value of the *gain*. Change the *gain* value to a smaller value. The *gain* value could be set as small as 1. When acquiring the data. If you still get an “ADC overflow” error message after you set *gain=1*, then the *pw* value needs to be set to a smaller value until no “ADC overflow” message is shown. If you have less than 2% water in the solvent, then you could use the standard proton parameters.
- 4.2 After acquisition completes, type *aph* for automatic phasing and do any necessary manual phasing. At this point spectrum is only the water peak.



Plasma sample in 90% $\text{H}_2\text{O} + 10\% \text{D}_2\text{O}$ without suppression.

- 4.3 Set the reference peak, then move the red cursor to the peak to be saturated and type the *nl* and *sd* commands to set the saturation peak.
- 4.4 Type *presat* to retrieve the standard file for the presaturation experiment. Check and change the following parameters: *ss=4*, *nt=8*, *d1=0.2*, *satdly=1*, *tof=dof*; *satfrq=dof*. *satpwr=6* (Min=1, Max=12 step by 1 unit), *spin=0* and finally, type *su* to set up the parameters. Reset the gain by typing *gain=5* or *10*, *pw=5* etc..

ACQUISITION	SAMPLE	PROCESSING	FLAGS
sfrq 599.738	date Jun 3 2005	lb 0.20	composit n
tn H1	solvent cdc13	sb not used	il n
at 1.598	temp not used	gf not used	in n
np 25570	DECOUPLING	fn not used	dp y
sw 8000.0	dn H1	math f	hs nn
fb not used	dof 534.6		
bs 16	dm nnn	werr react	sspul n
ss 4	dmm w	wexp procplot	satpwr 2
tpwr 56	dpwr 0	wbs testsn	satfrq 534.597
pw 5.0	homo n	wnt	satdly 1.000
p1 0			satmode ynn
d1 0.200			
d2 0			
tof 534.6			
nt 4			
ct 0			

Presat parameters.

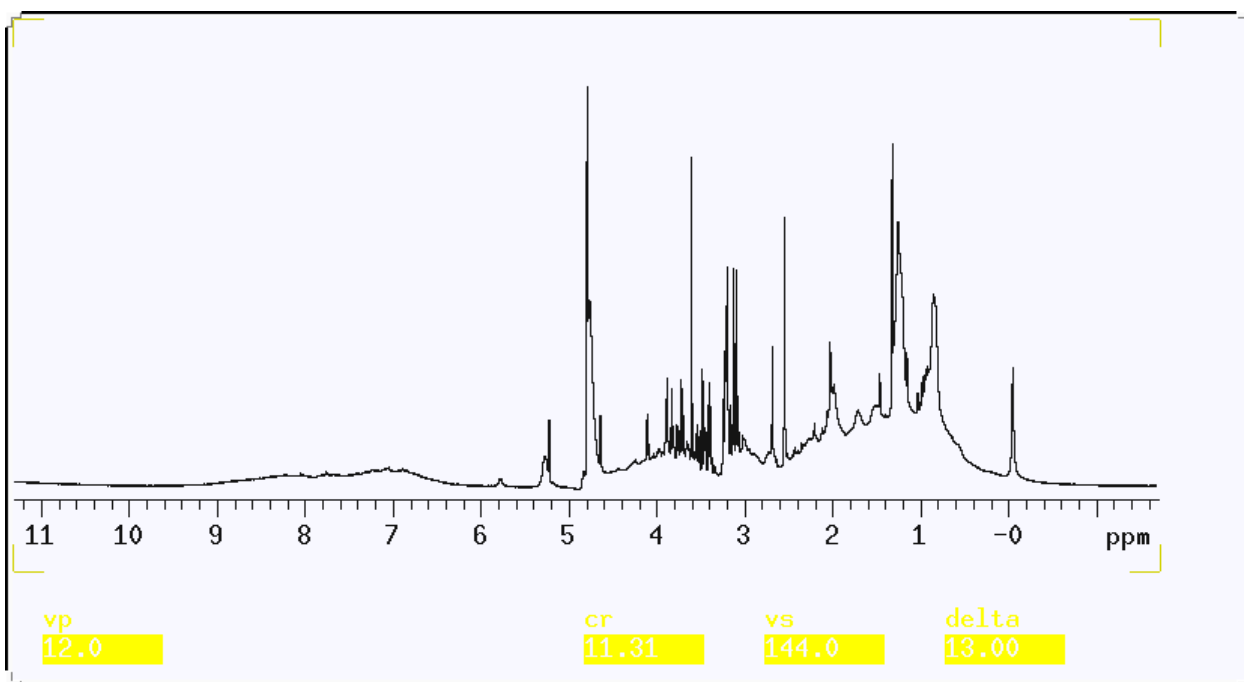
- 4.5 Type *ga* to acquire data. A spectrum will be displayed when acquisition is finished.
- 4.7 Check if the peak of interest is efficiently removed by the pulse in the resulting phased spectrum. If not, increase *satpwr* by 2 units and repeat the above experiment (The maximum *satpwr* 16). If the water peak is still unable to suppressed, please contact Dr. Wu for help. If yes, set *nt* between 64 and 128, then enter *ga* to acquire data.

Step 5. Data Processing

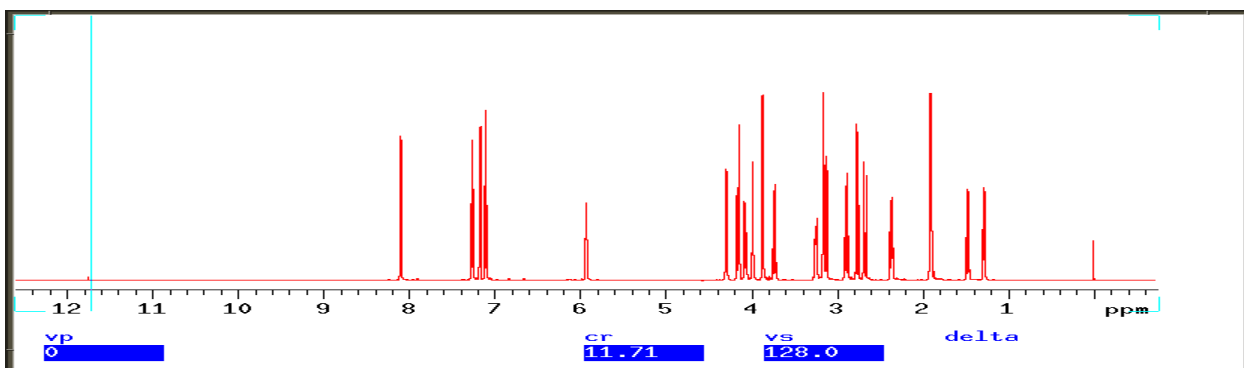
The data processing for the Presat experiment is same as that of 1D Proton experiment. See Experiment One.

Step 6. Exit And Logout

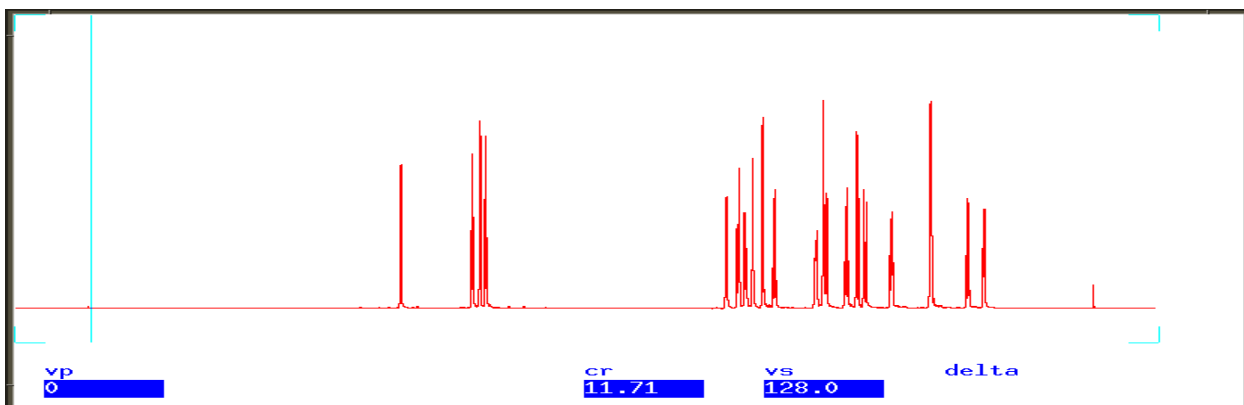
See Experiment One



Plasma sample in 90% H₂O + 10% D₂O after the water peak suppressed.



Normal 1D proton spectrum of strychnine in CDCl₃.



Same sample, but the peak at 6 ppm was suppressed.

Experiment 9: Gradient Shimming

Sample to be used: 2% H₂O in doped D₂O

Step 1. Load your sample into the probe as usual. Type *h1('d2o')* *su* to load the proton experiment parameters. Ask an NMR staff person to help you tune the probe. Lock the machine and shim manually.

Step 2. Because of the huge water signal, the receiver will be overflowed if you start to acquire the data using the default value. To avoid the receiver overflow, do as follows:

Type *gain?* to check the value of the *gain*. Change the *gain* value to a smaller value. The *gain* value could be set as small as 1. When acquiring the data. If you still get an “ADC overflow” error message after you set *gain=1*, then the *pw* value needs to be set to a smaller value until no “ADC overflow” message is shown. Save the spectrum and change to another experiment (*jexp2*) to do gradient shimming.

Step 3. Turn on the Pulsed Gradient Driver module in the console (ask an NMR staff person for help if this is the first time you do this)

Type *pfgon='nny'*

Type *gmapsys* and press return.

Click on **Set Params > Gradient, Nucleus > Pfg H1 > Return > Go, dssh**

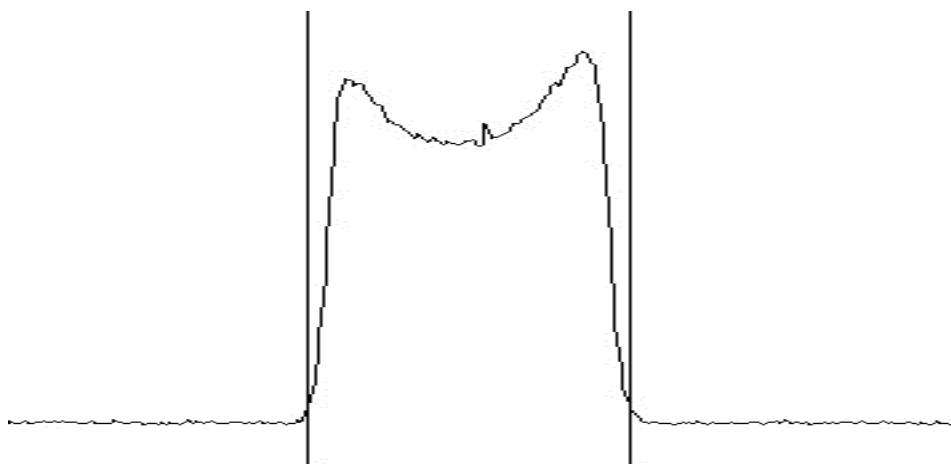
You may set the *pw*= “90 degree pulse” and *p1*= “180 degree pulse” these numbers are written on the log book of each instrument.

After acquisition completes, there are two broad peaks displayed. If the peaks do not look like as following, then there is a problem. You may have to talk to our NMR center staff.



vs	sp(ppm)	wp(ppm)	first	last	step
38880.4	-78.66	166.74	1	2	1

The click **find gzwin**, computer will find the gradient shim region.

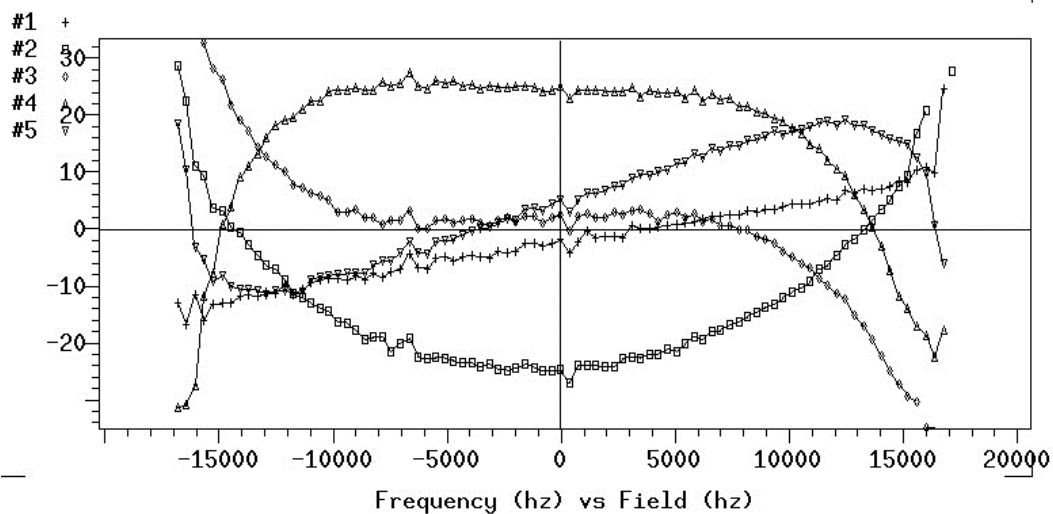


Then type `gmapsys`

(Shimming size can be changed now by typing `gsize=7`)

Click on **Shim Maps** > **Make Shimmap**, then type a file name when prompted.

(file is saved in directory `/vnmrsys/gshimlb/shimmaps`)



After you finish mapping,

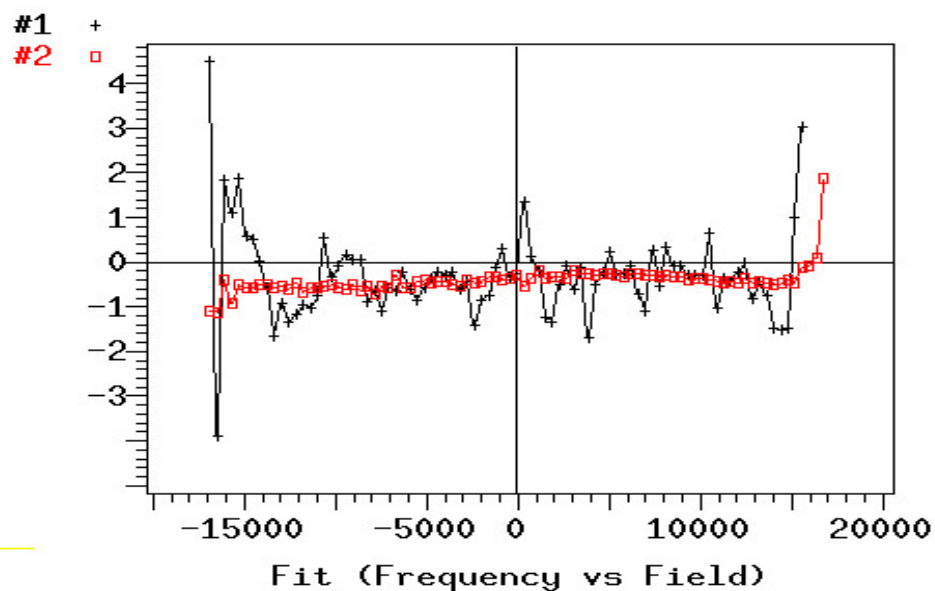
Click on **Return** > **Display** > **Display Shimmaps**

(lines should be smooth in the shimmap)

Click on **Return** > **Autoshim on Z**

The map rms err should be smaller than 1.00.

Click on **Set Shim**



Finishing:

Type **Pfgon='nnn' su**

Turn off the pfg module to standby.

Save the shim file svs('shim_021909')

Gradient Shim On VNMRS System:

Same concept, but there is a little difference. Type gmapsys, a new window will come up. Click Acquire Trial Spectrum, That is same as Go dssh icon as above. If everything is OK, then click Make Gradient map, you may have to input the map name. After completed, then click auto gradient shim on Z. Save the new shim file.

Experiment 10: COSY

Step 1. Login The Computer System

See Experiment One

Step 2. Change Sample

See Experiment One

Step 3. Lock And Shim The Magnet

See Experiment One

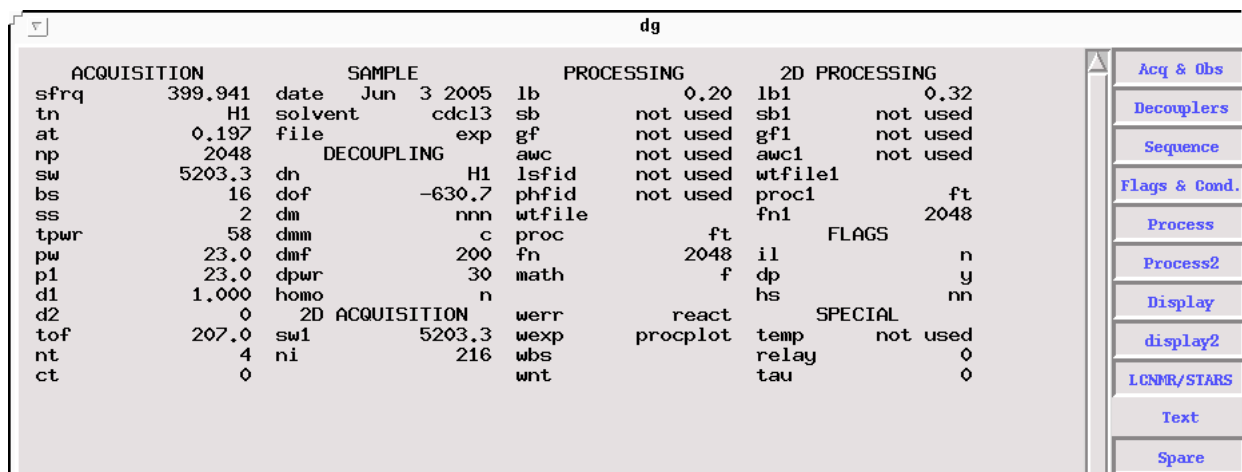
Step 4. Setup Parameters And Run Experiment

- 4.1 Run a proton 1D spectrum by using proton standard parameters. (See **Experiment One**)
- 4.2 Set the two red cursors to define the desired *sw* (spectrum width); type *movesw* then *ga*. Check the new spectrum and make sure no peak is fold in. Save this spectrum in case for later reference. Type **COSY** on the command line and type *dg* to show the parameters. Check the following parameters:

ss=4 dummy scans for COSY
d1=2 delay; set to 2 seconds.
fn1=2048 zero-fill the f1 dimension to 2K data points.
tpwr=xx transmitter power of the 90°-pulse-width of proton channel: check the last page of the log book.
pw=xx.x 90° pulse width for proton: check the last page of the log book.
nt=8 minimum *nt* is 8 (16, 32). The larger the value, the better the spectrum.
ni=128, 256 number of FIDs, (128, 256,512). The larger the value, the better.

Make sure *sw = sw1* and *fn = fn1*

Type *time* to check the total experiment time. You can increase or decrease the value of *nt* or *ni* to fit your allotted time. **Turn the spin off** and type *ga* to start the experiment. After acquisition, save the data.



ACQUISITION		SAMPLE		PROCESSING		2D PROCESSING	
sfrq	399.941	date	Jun 3 2005	lb	0.20	lb1	0.32
tn	H1	solvent	cdcl3	sb	not used	sb1	not used
at	0.197	file	exp	gf	not used	gf1	not used
np	2048	DECOUPLING		awc	not used	awc1	not used
sw	5203.3	dn	H1	lsfid	not used	wtfile1	
bs	16	dof	-630.7	phfid	not used	proc1	ft
ss	2	dm	nnn	wtfile		fn1	2048
tpwr	58	dmm	c	proc	ft	FLAGS	
pw	23.0	dmf	200	fn	2048	il	n
p1	23.0	dpwr	30	math	f	dp	y
d1	1.000	homo	n			hs	nn
d2	0	2D ACQUISITION		werr	react	SPECIAL	
tof	207.0	sw1	5203.3	wexp	procplot	temp	not used
nt	4	ni	216	wbs		relay	0
ct	0			wnt		tau	0

COSY parameters.

Step 5. Data Processing and Spectrum Printing

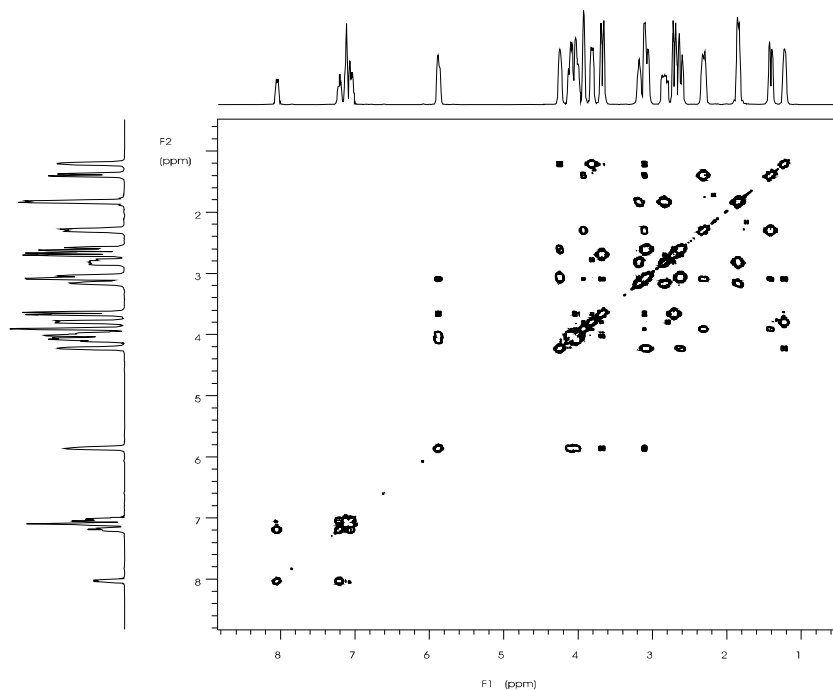
- 5.1. Reload the data:

Click on **Main Menu** and **File**, then highlight the file name and click on **Load**

- 5.2. See detailed processing instruction in **Experiment 17**. Alternately, you could type *wft2d foldt* to autoprocess the data by using default processing parameters.
- 5.3. Adjust the vertical scale of the 2-D spectrum using the **vs+20** and **vs-20** button to eliminate the unnecessary background noise.
- 5.3. Type *pcon page* to print the 2-D spectrum.
- 5.4. To print 2-D spectrum with 1-D projection spectrum:
Click on **Return**, **Size** and **Center** buttons to place the spectrum in the middle of the screen.
- 5.5. Click on **Proj**, **Hproj(max)** and **Plot** buttons to display the horizontal projection 1-D spectrum on the top of the 2-D spectrum. Use the MMB to adjust the vertical scale of the 1-D projection spectrum.
Click on **Vproj(max)** and **Plot** buttons to display vertical projection 1-D spectrum on the left of the spectrum. Use the MMB to adjust the scale of the 1-D spectrum.
- 5.6. Type *pcon page* to print the 2-D spectrum with 1-D projection spectra.
- 5.7. To expand the area you are interested in:
Press and drag left mouse button to control a pair of the cursors (looks like a red-cross) and define the left and bottom edge of the spectrum. Use the right mouse button to control another pair of cursors to define the upper and right edge of the spectrum. Then click **Expand** to expand the spectrum.

Step 6. Exit And Logout

See Experiment One



COSY Spectrum of Strychnine in CDCl₃.

Experiment 11: HETCOR

Step 1. Login The Computer System

See Experiment One

Step 2. Change Sample

See Experiment One

Step 3. Lock And Shim The Magnet

See Experiment One

Step 4. Setup Parameters And Run Experiment

- 4.1. In exp1, run a 1D proton spectrum by using standard parameters. After phasing and setting reference, use the two red cursors to narrow the spectrum of interest by 1ppm upfield and 1ppm downfield. Type *movesw* to change the spectral width.
- 4.2. Type *ga* to run the 1D proton experiment with a modified *sw*. Phase the spectrum.
- 4.3. Type *jexp2* to joint exp2. Run a 1D-carbon experiment. After phasing and setting the reference, narrow the spectrum of interest using the two red cursors. Type *movesw* to change the *sw*. Remember you will not see these carbons without proton attached on the HETCOR. So set the correct *sw* will increase your spectrum quality!
- 4.4. Type *ga* to run the 1D carbon experiment with a new *sw*. Phase the spectrum.
- 4.5. Type *hetcor* to set up a standard HETCOR experiment. Remember: your proton spectrum is in exp1.
- 4.6. Double-check the following two pairs of parameters (the correct values are listed on the last page of the log book):

tpwr transmitter power for carbon

pw 90° pulse for carbon

pp 90° pulse for proton decoupler channel

pplvl proton pulse power for decoupler channel

(*pp* and *pplvl* should be as same as the ones in DEPT experiment in Experiment 6)

After entering correct values for the above parameters, check the following parameters:

ss=4 dummy scans

sw= *sw* should equal to the *sw* value in exp2 for carbon domain

sw1= *sw1* should equal to the *sw* value in exp1 for proton domain;

dof= *dof* should equal the *tof* value in exp1 for proton;

*nt=n*16* acquisition scans of multiple of 16;

ni=256 number of increments in 1st dimension;

np=2048 number of points to record FID;

d1=3 carbon relaxation time

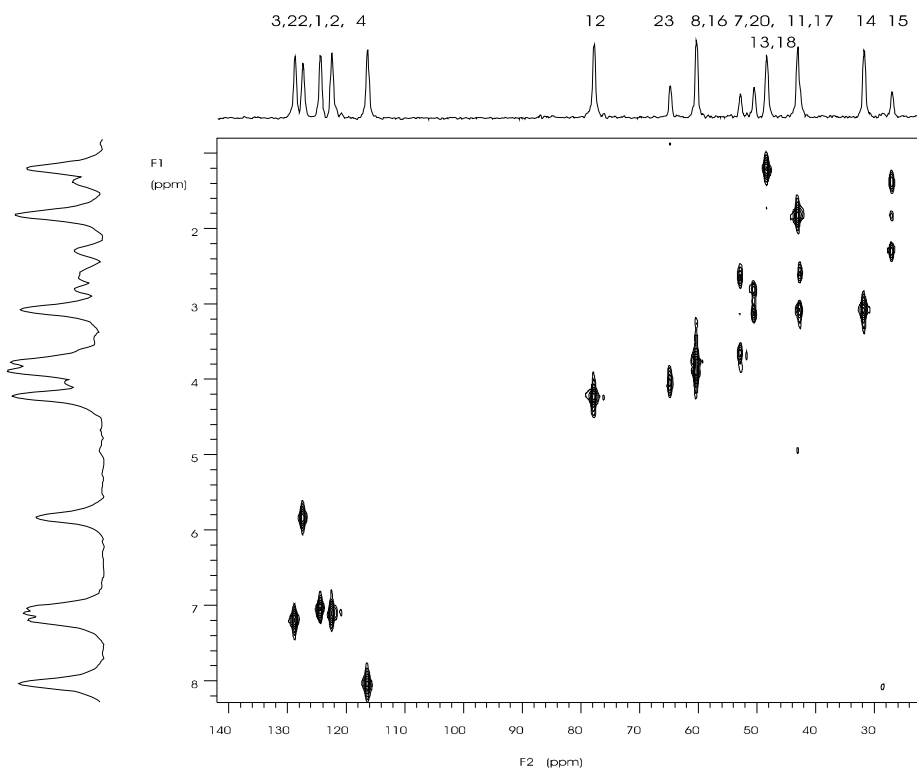
- 4.7. Type *time* to check the experiment time. *d1* can be adjusted to fill the allotted time.
- 4.8. Turn the spin off and do any needed minor shimming. Enter *ga* to acquire data.
- 4.9. Save the spectrum by typing *svf('hetcor_mydata')*

Step 5. Data Processing and Spectrum Printing

- 5.1. Recall the data "hetcor_mydata.fid"
Click on **Main Menu** and **File**, then highlight the file name and click on **Load**
- 5.2. Type *wfi2da* or follow the detailed processing method in experiment 17.
- 5.3. Click on **Return**, **Size** and **Center** buttons to place the spectrum in the middle of the screen.
- 5.4. Adjust the vertical scale of the 2-D spectrum using the **vs+20** and **vs-20** button to eliminate the unnecessary background color.
- 5.4.1. Click on **Proj**, **Hproj(max)** and **Plot** buttons to display the horizontal projection 1-D spectrum on the top of the 2-D spectrum. Use the MMB to adjust the vertical scale of the 1-D projection spectrum.
- 5.6. Click on **Vproj(max)** and **Plot** buttons to display vertical projection 1-D spectrum on the left of the spectrum. Use the MMB to adjust the scale of the 1-D spectrum.
- 5.7. Type *pcon page* to print the 2-D spectrum with 1-D projection spectra.

Step 6. Exit And Logout

See Experiment One



HETCOR Spectrum of strychnine in CDCl₃.

Experiment 12: 1D NOE-----Presat

Sample to be used: 10% Strychnine in CDCl₃

Step 1. Login The Computer System

See Experiment One

Step 2. Change Sample

See Experiment One

Step 3. Lock And Shim The Magnet

See Experiment One

Step 4. Setup Parameters And Run Experiment

4.1 Run a standard proton spectrum and save the file.

4.2 Put the cursor on the peak to be irradiated, then type *nl sd* to display the frequency, shown as *dof=xxx.xx* on the top of the screen. Write down this first *dof* value (If the peak is a multiplet, put the cursor in the middle of the multiplet and type *sd*). Next, move the cursor to a no-peak region close to the peak to be irradiated, Type *sd* to display the second *dof* value. Make sure to record this value.

4.3 Type *presat* to load standard file for the presaturation experiment. Check and change the following parameters: *ss=4, nt=8, gain=10, d1=2, satdly=1, satfrq=the first dof value written down.*

satpwr=2 (Min=1, Max=15 step by 1 unit), and type *su*. Finally, turn off the *spin*. Type *ga* to run a quick spectrum. Check if the irradiated peak has disappeared from the resulting spectrum. If not, repeatedly increase *satpwr* by 2 units and run the experiment again until the peak has disappeared.

4.4 Change the *nt* value to *128* or *256* and type *ga* to acquire data for the first spectrum. After the acquisition is finished, save the spectrum.

4.5.1 **ONLY** change the *satfrq* parameter to the second *dof* value recorded previously, then type *ga* to obtain a second spectrum. Save this new spectrum.

Step 5. Data Processing

5.1. Type *jexp5* to go to Exp5 and load the first spectrum by the following procedure (*you must use Exp5 to do this operation*): Click on **Main Menu**, **File** and highlight the first spectrum file, then click on **load**. Type *lb=5 wft* to show the spectrum.

5.2. Type *jexp1* to go to Exp1. Load and process the second spectrum by the procedure as described in step 5.1.

5.3. Type *spsub* to subtract the second spectrum (in Exp1) from the first (in Exp5) and then type *jexp5* and *ds* to show the resulting spectrum in Exp5. Type *vp=50* to move the spectrum to the middle of the screen.

5.4. Plot the spectrum.

Step 6. Exit And Logout

See Experiment One

Experiment 13: 1D NOE----- NOEDIF

Sample to be used: 10% Strychnine in CDCl₃

(This method is for Mercury 300. Because of the hardware configuration, two NOE methods we introduced here (Experiment 12 and 14) are not available on Mercury 300)

Step 1. Run a proton spectrum in experiment 1. then type *mp(1, 2)* to move this proton parameter to experiment 2. Type *jexp2* to go to experiment 2. Type *wft* to show the proton spectrum.

Step 2. Type *noedif* to bring up the NOEDIF parameters.

Find and expand the peak you want to irradiated. Now you need to set up some parameters:

f0 to *f5* are the irradiation points (frequencies).

For a singlet, use *f0, f1* and *f2*.

Set up *f0* value: put the red cursor on the halfway-up point of the left side of the peak and type *sd* then type *f0=dof*.

Use the same method to set up *f1* and *f2*. *f1* is for the top of the peak and *f2* is for the halfway-up point of the right side of the peak.

For a doublet, use *f0, f1, f2* and *f3*. *f0* is for left side of the first peak and *f1* is for the left side of the second peak. *f2* is for the right side of the first peak and *f3* is for the right side of the second peak.

For a triplet or higher multiplets, *f0* to *f#* (# is equal to the number of the multiplets) are used with each value is set on the top of the each peak.

dofoff is off resonance frequency. Default value is -10000 Hz. You can also set it up to by putting the red cursor to where there is no peak and type *sd* and then type *dofoff=dof*.

Check up following parameters:

Ctrl='n'

ss=16

satpwr is the irradiate power from 0 to 10.

tau=0.1

d1=4

d2=0

dm='ynn'

nt is a value of multiple of 16. Usually put a big number like 128 or more.

bs='n'

Turn off the spinner.

Type *ga* to start the acquiring the data.

Step 3. After finishing the acquisition, type *wft* to start to process the spectrum. (Note, this spectrum is already the result of the subtraction of two spectra. If you type *aph* to phase it, usually the peak irradiated is up and noe peaks are down. If you prefer the other way, phase the peaks manually.)

Experiment 14: 1D NOE----- CYCLENOE

Sample to be used: 10% Strychnine in CDCl₃

Step 1. Run a proton spectrum in experiment 1. Type *mp*(1,n) to move this proton parameter to experiment n. Type *jexpn* to go to experiment n. Type *wft* to show the proton spectrum.

Step 2. Type *cyclenoe* to bring up the cyclenoe parameters.

Find and expand the peak you want to irradiated. Now you need to set up some parameters:

satfrq is the frequency of the peak you want to irradiated. Put the red cursor on the middle of the peak, type *nl* and *sd*, and then type *satfrq=dof*.

control is the off-resonance frequency. Put the red cursor to where there is no peak (but close to the peak you want to irradiated) and type *sd*, followed by typing *control=dof*.

pattern is the pattern type (1 for singlet, 2 for doublet, etc. If it is difficult to decide what a multiplet is, just guess one. Anyway, you need to set a number for *pattern*)

spacing is the coupling constant, in Hz, for the multiplet you want to irradiate. Again, if it is difficult to measure a coupling constant, guess one.

Check up following parameters:

cycle='y'

intsub='y'

satpwr is the irradiate power from -10 to 2. -10 usually is enough.

tau=0.1

mix=0.3

nt is a value of multiple of 16. Usually put a big number like 128 or more.

Turn off the spinner.

Type *ga* to start the acquiring the data.

Step 3. After finishing the acquisition, type *wft* to start to process the spectrum. (Note, this spectrum is already the result of the subtraction of two spectra. If you type *aph* to phase it, usually the peak irradiated is up and NOE peaks are down. If you prefer the other way, phase the peaks manually.)

Experiment 15: 1D Carbon with Complete Fluorine Decoupling by Using Wave Function Generator

Sample to be used: 20% Perfluoro-2-methyl-2-pentene

Step 1. Login The Computer System

(See Experiment One)

Step 2. Change Sample

(See Experiment One)

Step 3. Lock And Shim The Magnet

(See Experiment One)

Step 4. Setup Parameters And Run Experiment

- 4.1 type *f19* to load standard fluorine parameters with CDCl_3 as solvent. Run a F19 spectrum and save the file.
- 4.2 Find the value of *tof* by typing *dg* and record this value. *tof* is the center frequency of the observe transmitter.
- 4.3 Find the transmitter frequencies for each peaks as follows:
 - 4.3.1 Put the cursor on a peak and type *movetof*. Write down the new *tof* value after typing *dg*.
 - 4.3.2 Load the original spectrum again and find the *tof* value for another peak as in step 4.3.1.
 - 4.3.3 Repeat step 4.3.1 and 4.3.2 until all the frequency values for all peaks are recorded.
- 4.4 Calculate the *offset* value.
 - 4.4.1 Subtract the transmitter frequency value of each peak recorded in step 4.3 from the *tof* value of the spectrum recorded in step 4.2. Record these values.
Remember, always subtract the frequency value of a peak from the *tof* value, so that when the frequency of a peak is higher than the *tof* value, you get a positive *offset* value and when the frequency of a peak is lower than *tof*, you get a negative *offset* value.
- 4.5 Use Waveform generator to generate a shaped decoupling sequence:
 - 4.5.1 Load the F19 spectrum and type *wft*
 - 4.5.2 Click **Pbox** button on the menu bar
Click **Het-dec**
Click **Adiabatic** and then type 300 after J in Hz on the top of the screen for C-F coupling.
Click **Options**
Click **Offset** and input the *offset* value of the first (leftmost) peak which should be decoupled.
Click **Bandwidth** and input 4000----- the area will be decoupled.
Click **Return**.
Click **WURST**, three parameters will be displayed for the decoupling on the top.
 - 4.5.3. Click **Options** and repeat the remaining steps in the step 4.5.2. until all the *offset* value are input.
Click Close.
 - 4.5.4. Click **Name** and give a file name for the shaped pulse.
Click **Close**.
The computer will ask you to
Enter reference 90 degree pulse width (μse): (F19 90 degree pulse width)

Enter reference power level: (power level when you measure the F19 90 degree)
A shaped pulse will be displayed on the screen.

Write down the following parameters:

dres=x

dmf=xxxxxx

Remember you shaped pulse file name.

4.5.5 Load the standard C13 experiment parameters by typing *c13*

Input following parameters:

dres = x

dmf = xxxxxx

dm = 'nny'

dmm = 'ccp'

dseq = 'shaped pulse file name'

dof = the *tof* of F19 spectrum

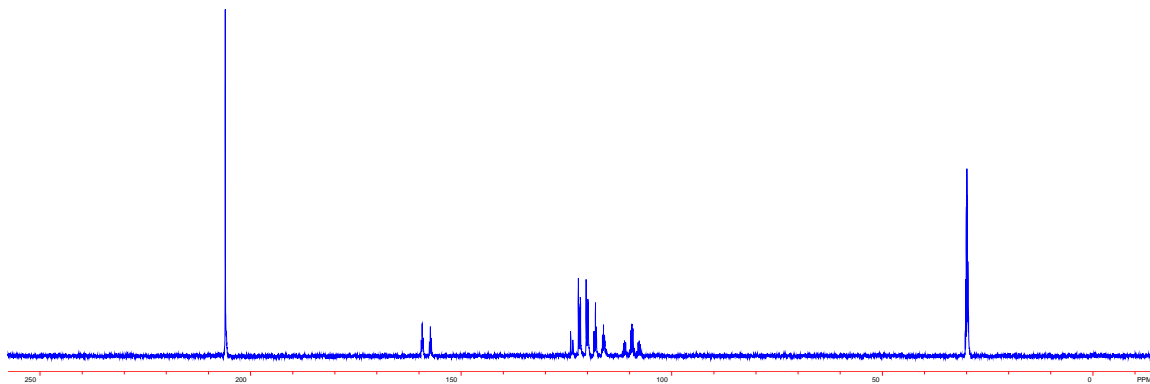
Type *ga* to acquire data.

Step 5. Data Processing

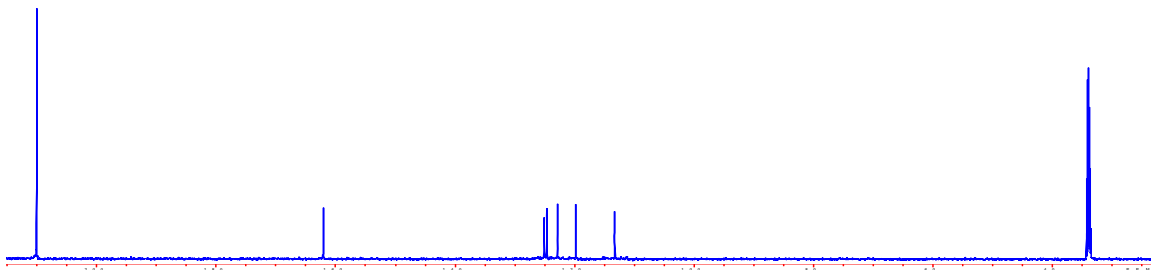
See steps in Experiment Two.

Step 6. Exit And Logout

See Experiment One.



¹³C spectrum of (CF₃)₂CCFCF₂CF₃ in Acetone_D6 was acquired on INOVA600 without ¹⁹F decoupling.



Fully ¹⁹F decoupled ¹³C spectrum of (CF₃)₂CCFCF₂CF₃ acquired on INOVA600.

Experiment 16: Variable Temperature Experiment (25 to 80 °C)

Sample to be used: 10% Strychnine in CDCl₃

Step 1. Login The Computer System

See Experiment One

Step 2. Change Sample

See Experiment One

Step 3. Lock And Shim The Magnet

See Experiment One

Note: Double check your solvent boiling point or freezing point. If you need much higher temperature or much lower temperature experiments, please let us know. We could help you. You may have to order a high pressure Liquid Nitrogen tank for Low temperature Experiments. The temperature range we have done on the Unity plus -120 °C – 120°C with a Broad Band Probe.

Step 4. Setup Parameters And Run Experiment

4.1 type *h1*('solvent') to load standard proton parameters and run a normal 1D experiment.

4.2 For a single temperature:

type *temp* to open the temperature control box. Click on and drag the temperature bar to the desired temperature. Wait until the temperature reading on the remote display reaches the desired value, then for another 5 to 10 minutes to let the sample reach the equilibrium temperature. Shim the magnet again and type *ga* to start acquiring the data.

Step 5. Data Processing

See Experiment One.

Step 6. Terminated the variable temperature function and exit

Click and drag the temperature control bar to 25°C. Wait until the temperature drops to around 25°C, and click the temperature off button. Close the temperature control window. Exit and logout.

Note: The operational temperature ranges are limited on INOVA600, INOVA400 and VNMRS400. The high temperature is set to 75°C and low temperature is set to -10°C. Beyond this range, you need to talk to Dr. Wu for help.

Experiment 17: NOESY

The procedure for NOESY experiment is quite similar to COSY experiment (see experiment 9)

Step 1 Insert your sample and tune the probe on proton channel.

Step 2 Parameters Set-up and Run Experiment

Run a proton 1D spectrum by using proton standard parameters (See **Experiment One**)

Using two cursors to define the *sw* (spectrum width) just wide enough to include all peaks and then type *movesw* and *ga* to run another proton experiment with new *sw*. Save the spectrum.

Step 3 Type *NOESY* to load NOESY parameters.

Check the parameters:

pw= 90° pulse width of proton channel.

tpwr= transmitter power of the proton channel for 90° pulse width

d1=2

nt=16, or 32

ni=128 (or 256 or 512, depends on the machine time you have)

Type *time* to check how long the experiment it will take and adjust the *nt* and *ni* to fit your time signed up.

mix (mixing time)=0.3 The value is ranging from 0.1 to 0.6(ms) depends on the molecular size of your sample. To obtain best result, it is better to do a set of experiments with different *mix* value and chose a best spectrum.

fn1=2048; *fn*=2048 *np*=2048

Turn off spin, Double check the non-spin shims.

Type *ga* to start acquisition.

After the acquisition, save the spectrum.

Step 4 Processing and Printing

Reload your NOESY spectrum file by clicking on **Main Menu** and **File** , then highlight the file name and click on **Load**.

Type *wft2da* to do automatic weighting and Fourier transformation or follow the procedure in **Experiment 17** to process the data manually.

For a good NOESY spectrum, you should deoxygenate your sample.

Experiment 18: TOCSY

Standard Sample to be used: 10% Strychnine in CDCl₃

Step 1. Login The Computer System

See Experiment One.

Step 2. Change Sample

See Experiment One.

Step 3. Lock And Shim The Magnet

See Experiment One.

Step 4. Setup Parameters and Run Experiment

- 4.1 type *h1* to load standard proton experiment parameters.
- 4.2 Set *nt=1*. Type *ga* to begin acquisition for a common 1D-proton spectrum.
- 4.3 After acquisition, type *aph* for automatic phasing and /or manual phasing and then set the *sw* if needed.
- 4.4 Type *tocsy* to load standard tocsy parameters. Double check following parameters:

PI ---- 90 degree of proton at the power of *p1lvl* (I600, *p1level*=58, *p1*=8.1)

P1lvl ---- Power level for *p1* pulse (hard pulse 90 degree)

pw----- spin lock 90 degree pulse (50us at *tpwr*=47 on INOVA600)

tpwr----- Spin lock power level for *pw*.

sw=sw1 ---- It is homo nuclear, so both scales are the same.

Np=2048

Ss=8 dummy scans

Ni = 256 or more

Mix =0.3 – 0.7 seconds ----- Spin lock time

Trim=0.003 seconds ----- trim pulse

Hs='nn'

Fn=*fn1*=2048

d1-----the pulse delay. It is set to around 1 second or longer.

nt-----scan numbers depends on sample concentration (minimum 16 scans).

Turn spin off

- 4.5 Type *ga* to acquire data. After experiment complete, save the data.

Step 5. Data Processing

When the acquisition is finished, use the same way of COSY to process the data.

Step 6. Exit and Logout

See Experiment One

Experiment 19: HMQC/HMBC

HMQC experiment only available on INOVA600 since the default probe is an Inverse Detection probe. If it is the first time you try to do this experiment, please ask Dr. Wang or Dr. Wu to assist you to set it up to avoid hardware damage. You may have to reconfigure the hardware for proper setup.

Step 1: Sign-up your time (at least 2 hours depending on your sample concentration) and contact the NMR staff so that we can help you to tune the probes and connect a microwave filter etc.

Step 2: Run 1D proton spectrum in experiment 1. Using two red cursor to select a reasonable spectrum width (cutting off no-signal area in both high field and low field) and type **movesw**. Type **ga** to run another proton spectrum with new spectrum width. Write down the parameters **tof** and **sw**, This is for your Proton region with the correct chemical shift reference.

Step 3: Change to experiment 2 by typing **jexp2** to run 1D carbon spectrum in experiment 2. Select reasonable spectrum width and run a carbon experiment again as same as in step 2. You don't have to see all the carbon signals, the solvent peak is enough. You only need to collect one scan. Make sure the solvent peak is set to the correct chemical shift, as well as the region of the spectrum that covers all your protonated carbons. Remember, HMQC will not show the carbons without proton attached. Write down the parameters **tof** and **sw**. (remember you will only observe the protonated carbon for HMQC). This is for your Carbon region with the correct chemical shift reference.

Step 4. Return to experiment 1 (typing **jexp1**), and type **hmqc**. If presaturation is required, type **HMQC**. The computer will load the pulse sequence with default parameters. The **sw** will be the same as that in the proton spectrum. Manually change the **sw1** to the numbers of **sw** written down from the carbon experiment in step 3 and change **dof** to the number of **tof** in carbon spectrum.

Check the two pairs of 90° pulse parameters from the back of the log book:

pw is the proton 90° pulse width and **tpwr** is the power.

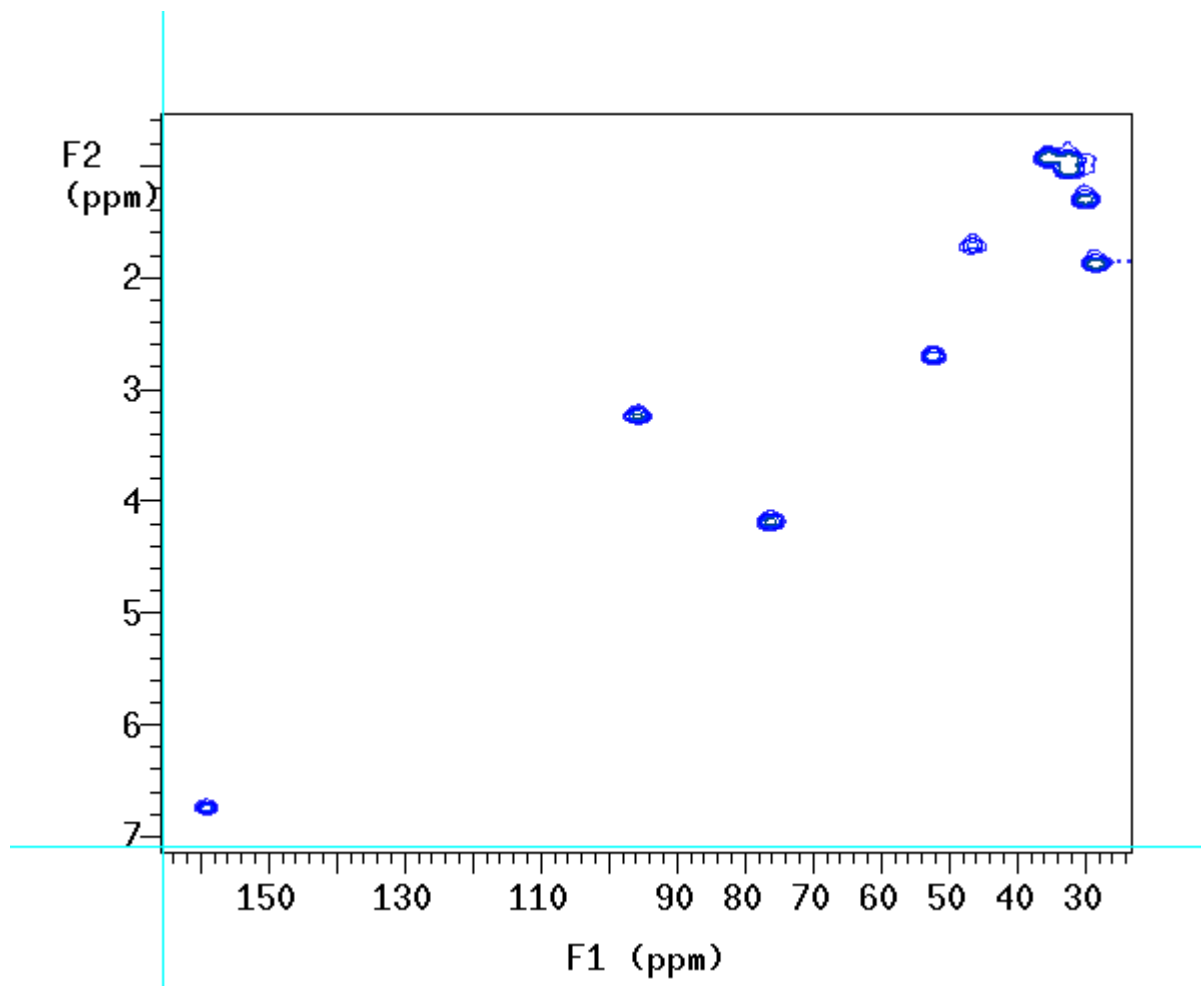
pwx is the **carbon decoupler** 90° pulse width and **pwxlvl** is the power.

ACQUISITION		SAMPLE		sw1	27285.1	2D PROCESSING	
sfrq	599.737	date	Jun 16 2004	ni	256	lb1	210.50
tn	H1	solvent	cdc13	phase	arrayed	sb1	0.002
at	0.236	file	/export/home/~	PROCESSING		sbs1	-0.002
np	2048	vnmr1/vnmrsys/ID_p~		lb	59.24	gf1	not used
sw	4341.2	robe/HMQC_yu_good.~		sb	0.035	awc1	not used
bs	not used	fid		sbs	-0.004	wtfile1	
ss	4	DECOUPLING		gf	not used	fn1	2048
tpwr	56	dn	C13	awc	not used	FLAGS	
pw	9.7	dof	105.7	wtfile		il	n
d1	0.900	dm	nny	proc	ft	dp	y
d2	0	dmm	ccg	fn	2048	hs	yy
tof	-591.5	dmf	20000	math	f	mbond	n
nt	16	dpwr	45	PRESAT		SPECIAL	
ct	0	pwx	12.0	satflg	nn	temp	not used
		pwxlvl	58	satdly	0	null	0.3
		homo	n	satpwr	0	j	140.0
		2D ACQUISITION		satfrq	0	taumb	0

Type **time** to check the total experiment time.

Finally type **ga** to start the experiment. After finish the experiment, save the data and report to the staff to help you reconnect the cable.

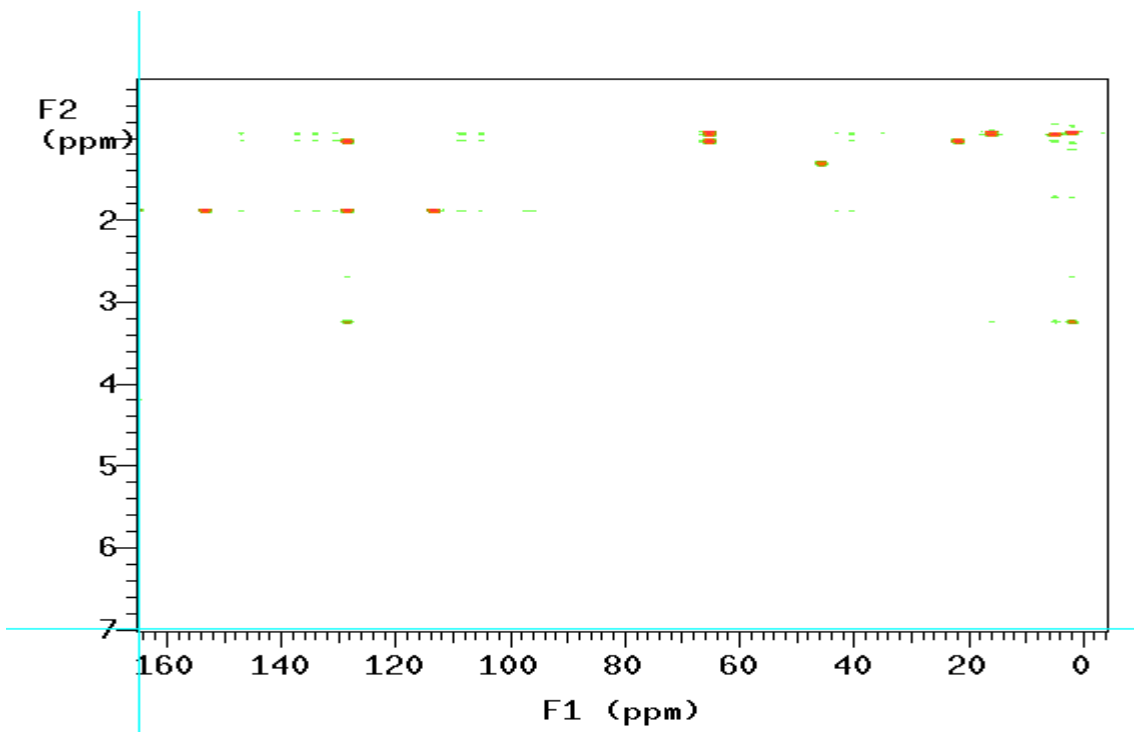
Using the same procedure for HECTOR to process the HMQC data.



HMBC experiment is the same kind of experiment, the difference is you have to input the parameter of j_{nxh} , that is the j coupling of three bond from proton to the carbon you are interested. The average number is 5 – 8 hz. Also you should double or triple of the nt scans, since HMBC is much less sensitive than the HMQC experiment. You may need little more samples.

HMBC parameters:

ACQUISITION		TRANSMITTER		HMBC		PROCESSING	
sw	4490.3	tn	H1	j1xh	137.0	sb	0.077
at	0.228	sfrq	599.737	jnxh	5.0	sbs	not used
np	2048	tof	-591.5	GRADIENTS		fn	2048
bs	16	tpwr	56	PFGflg	n	2D PROCESSING	
ss	8	pw	9.700	hsglvl	2000	sb1	0.004
d1	1.000	DECOUPLER		hsgt	0.002000	sbs1	not used
nt	32	dn	C13	SPECIAL		fn1	2048
ct	0	dof	128.0	temp	not used	SAMPLE	
2D ACQUISITION		pwxlvl	61	spin	not used	date	Jun 17 2004
sw1	27155.5	pwx	12.000	gain	2	solvent	cdcl3
ni	512	dm	nnn	pw90	8.000	sample	undefined
phase	arrayed	dmm	ccc	sspul	n		
PRESATURATION		dmf	200				
satmode	n	dpwr	0				
satfrq	0						
satdly	0						
satpwr	0						



HMBC spectrum of strychnine in CDCl₃

Experiment 20: 2D Data Processing

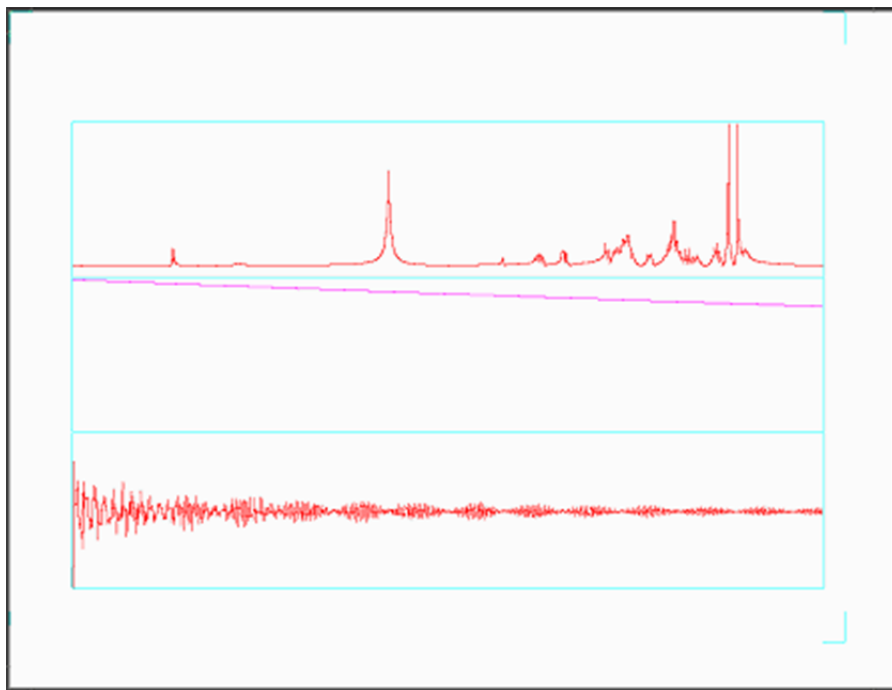
Step 1. Load the data

From the menu: **Main** → **File** → select the file you saved, then click **Load**.

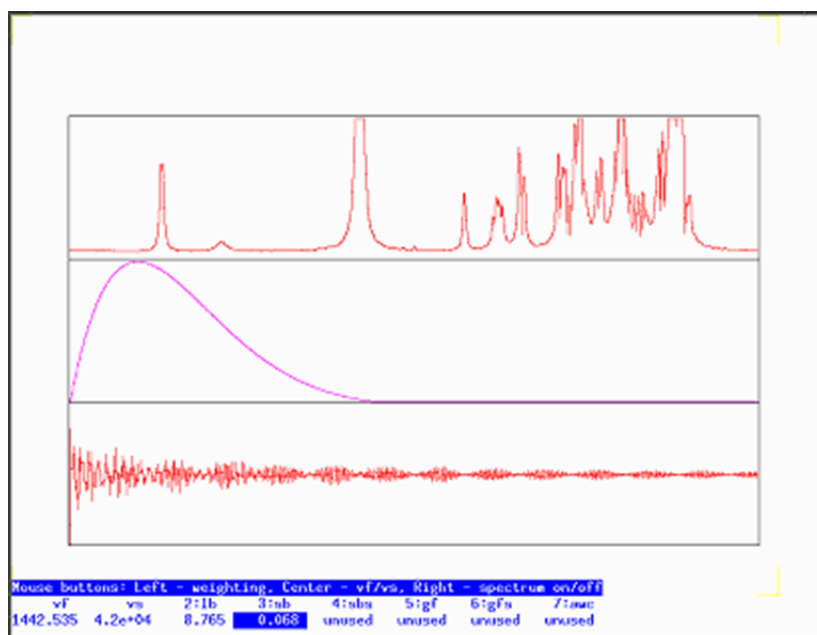
Step 2: Processing F2 dimension

From the menu: **Main** → **Process** → **Adj Weighting**

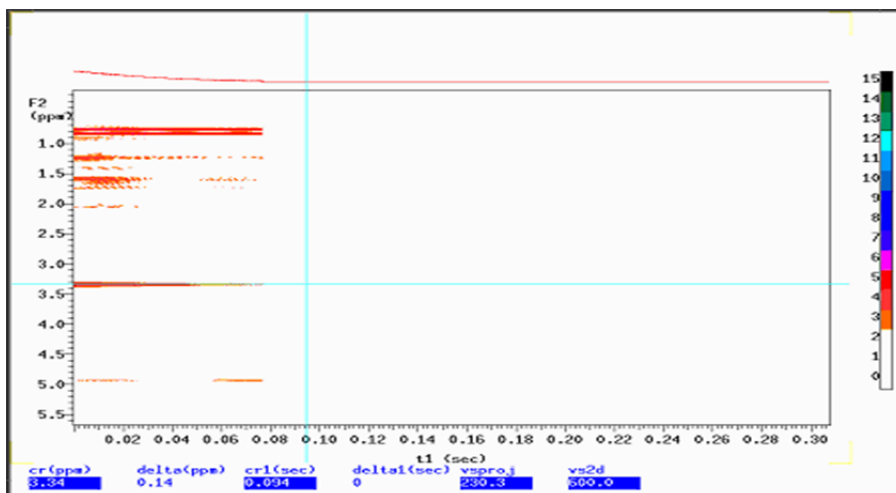
The following window will be displayed:



The top window is the spectrum that is the result after applying the weighting function and FT; the middle window is for the weighting function adjustment; the bottom window is the FID after applying the window function. From the menu, you could use **lb** (line broadening), **sb** (Sinebell weighting function), **sbs** (Sinebell squared weighting function), **gf** (Gaussian weighting function) and **gfs** (Gaussian squared weighting function) functions by clicking the icon. Then move the mouse to the middle window to adjust the weighting function. The purpose of this operation is to make the peak shape as following:



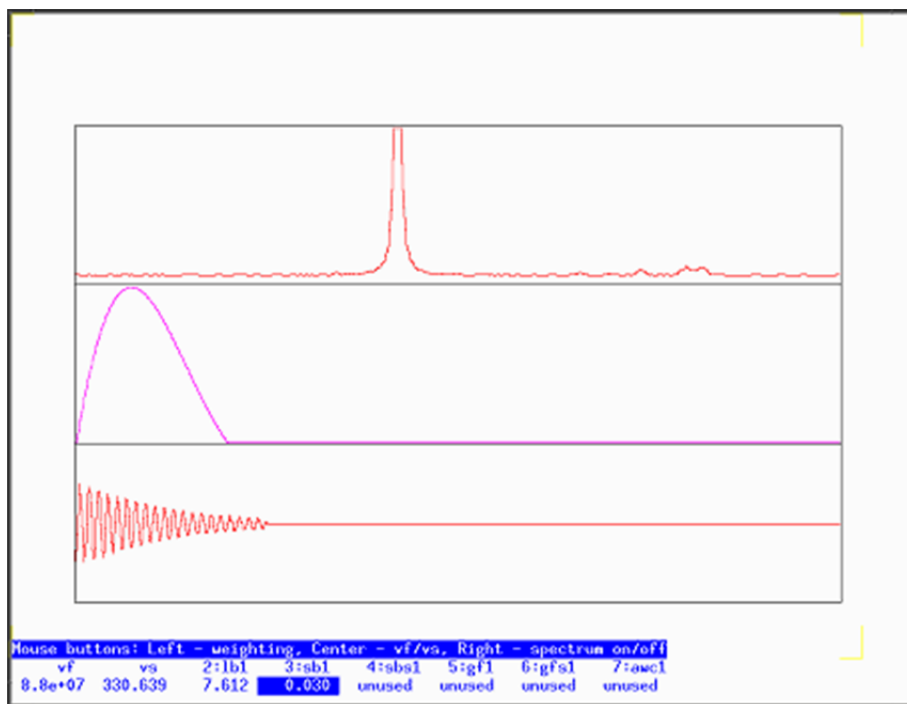
You could combine these weighting functions to change the shape of the peaks until you are satisfied with the spectrum. Then click **return**. If you acquired a phase sensitive 2D spectrum, there will be an icon “**phase F2**” on the menu, then you have to click **phase F2**. A 1D spectrum will be displayed. Phase it. If there is no “phase F2” icon, you acquired data is magnitude mode. You could click **Transform F2**. Computer will process the F2 dimension data. After it completes, a new window will be displayed.



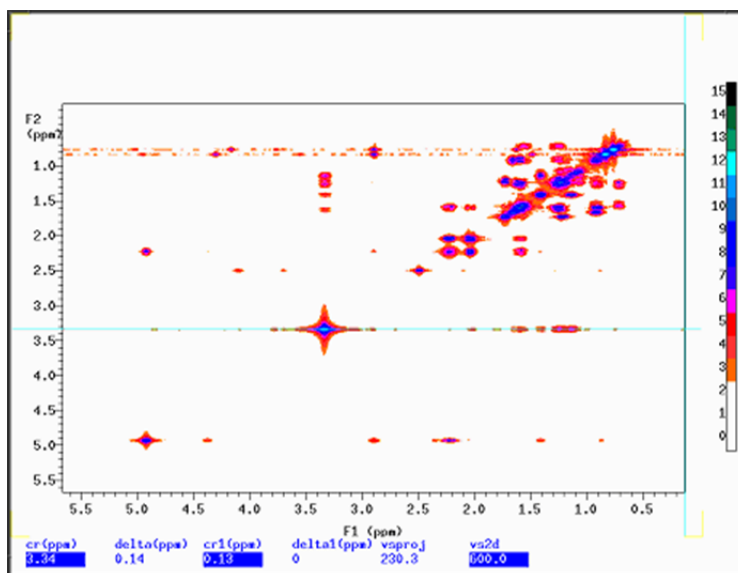
If there is nothing in the window, change **vs2d** parameter, by typing vs2d=5000 or bigger. This will increase the display intensity level. Then click **Redraw**. The red lines are your data, and white area is zero filling.

Step 3. Process the F1 dimension:

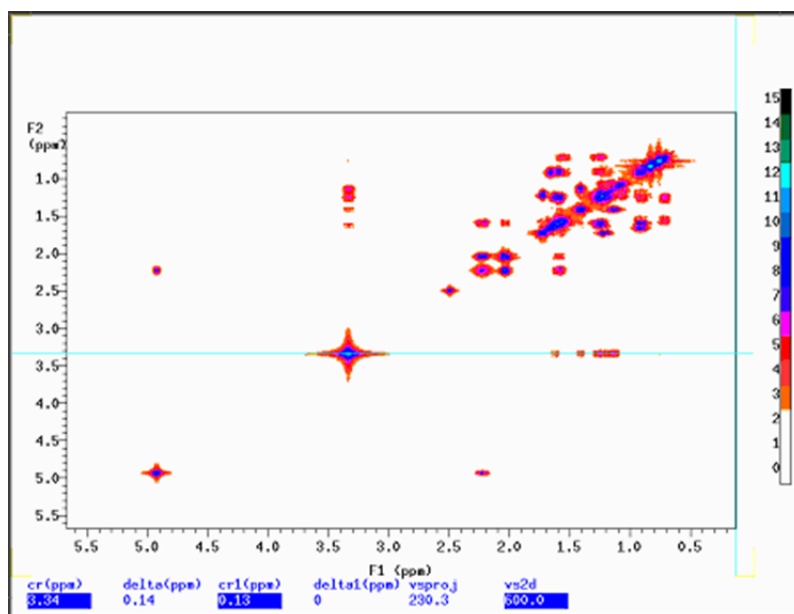
There will be red line in the middle of the spectrum, use mouse to move the line on a blue line, then click **Trace**. Then click **return** → **Adj Weighting**. A window will be displayed. Adjust the function as before.



Then click **return** → **F1 Transform**. The computer will process the F1 dimension. The 2D spectrum will be displayed on the screen after few seconds. If it is a COSY spectrum, you could type **foldt** to get rid of the unsymmetrical noise. Don't use **foldt** on NOESY!



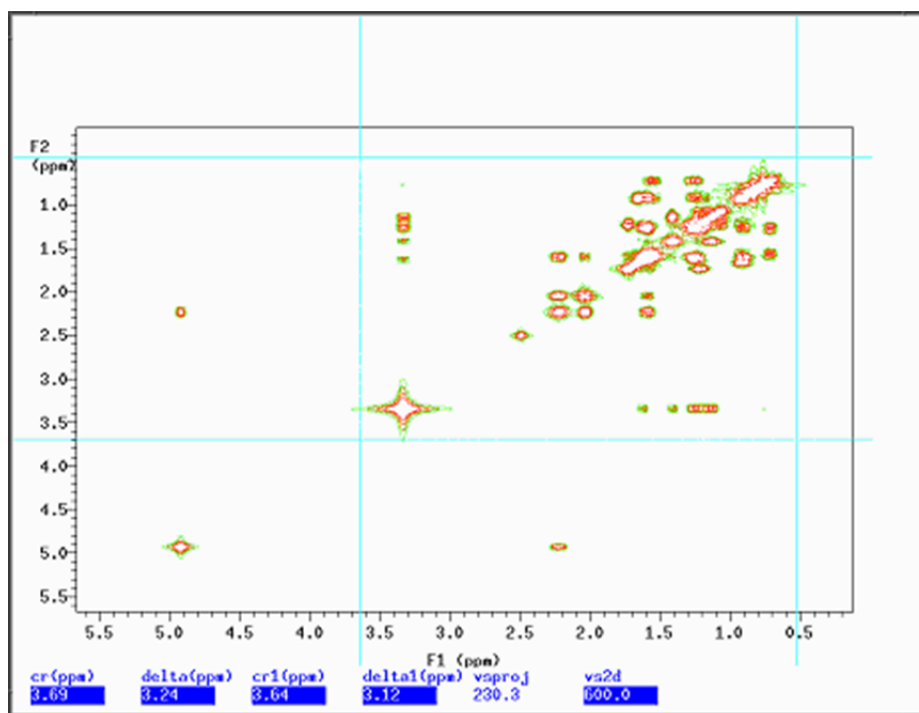
COSY spectrum before **foldt** operation



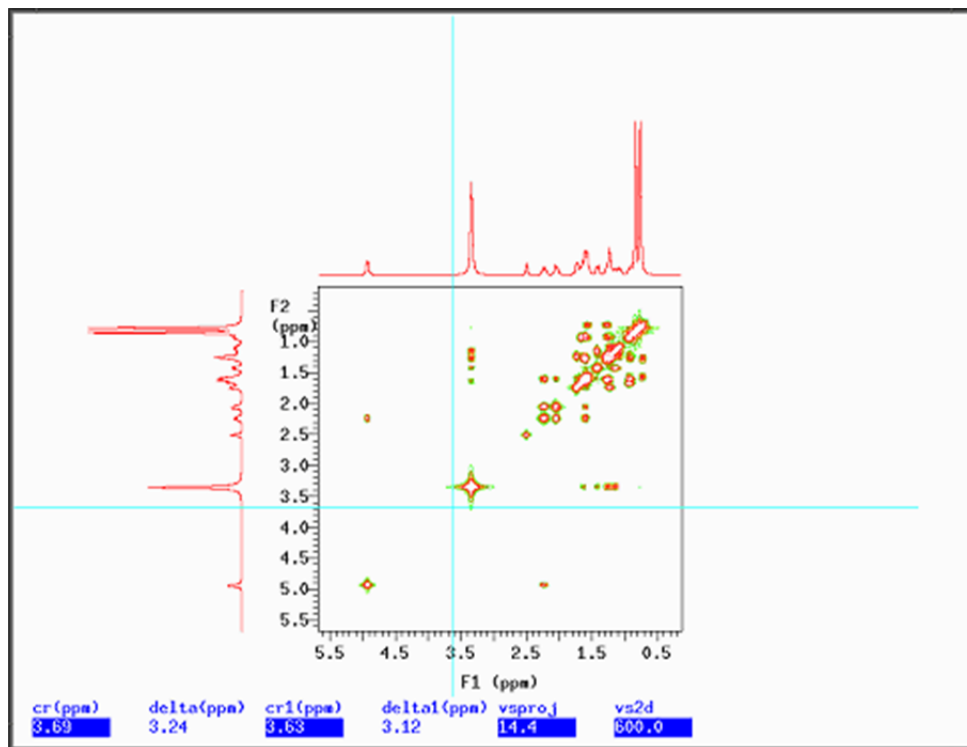
COSY spectrum after **foldt** operation

Step 4. Display and Printing:

On the menu, click **return**→**contour**, to display the spectrum as contour mode.
 Click **return** → **size**, to change the window size.



Click **project**→**Hproj(max)** to display 1D project spectrum. Click **Vproj(max)** to display 1D project spectrum on the side. You want to plot them with the 2D spectrum, you have to click plot after you click **Hproj(max)** or **Vproj(max)**.



To add text by typing text('your_text'). To print the text by typing pltex.

To print the spectrum, type **pcon(18,1.4)** page. The number 18 is the level, the 1.4 is spacing. If you have questions, please feel free to ask our service instructors.

Experiment 21: ^{19}F ^{31}P and Other Heteronuclear NMR: 1D Fluorine 19 Basic Operations

You must be an authorized user to run ^{19}F experiment. Probe tune is not required on INOVA400. However, on other NMR systems, you have to tune the probe or exchange probe for ^{19}F experiment.

Login and locking and shimming of your sample as usual.

Type **f19** to call up the standard fluorine experiment parameters with CDCl_3 solvent.

Enter **nt=64** or other nt number according to the nature of your sample.

Type **ga** to begin acquisition. After acquisition is done, a fluorine spectrum will be displayed. If not, enter **wft**. Type **aph** for automatic phasing. Other processing procedures are same as proton experiment.

Note: the standard fluorine 19 experiment parameters sets up a window width of 90 ppm and the chemical shifts shown on your spectrum have no meaning if you do not do referencing.

The common reference compounds for ^{19}F experiment are C_6F_6 , CCl_3F and CF_3OOH . They can be used for both internal and external reference. The simple way to make an external reference is as follows:

Dissolve small amount of a reference compound in same deuteriated solvent as your sample in a NMR tube. Run a quick ^{19}F experiment with this solution after locking and shimming. Set reference compound peak to the correct chemical shift number. Then immediately run a ^{19}F experiment with your sample without change any parameter except **nt**. The chemical shift of resulting spectrum will not change much from the first experiment.

To run a more accurate experiment with an external reference, you need to buy a special capillary tube called 'Stem Coaxial Insert' from WilMad (product No. WGS-5BL for 5 mm NMR tube), which allows you to put the solution of reference compound into the capillary then insert it into your sample tube. In this way, you run sample with the reference but without contamination by the reference compound and your reference insert can be used again and again.

Experiment 20: VNMRJ ¹H Operating Instructions

Note: All the commands you have learn from the VNMR (INOVA600, INOVA400) works on the VNMRJ.

Login

Login to the system by entering your group's user name and password.

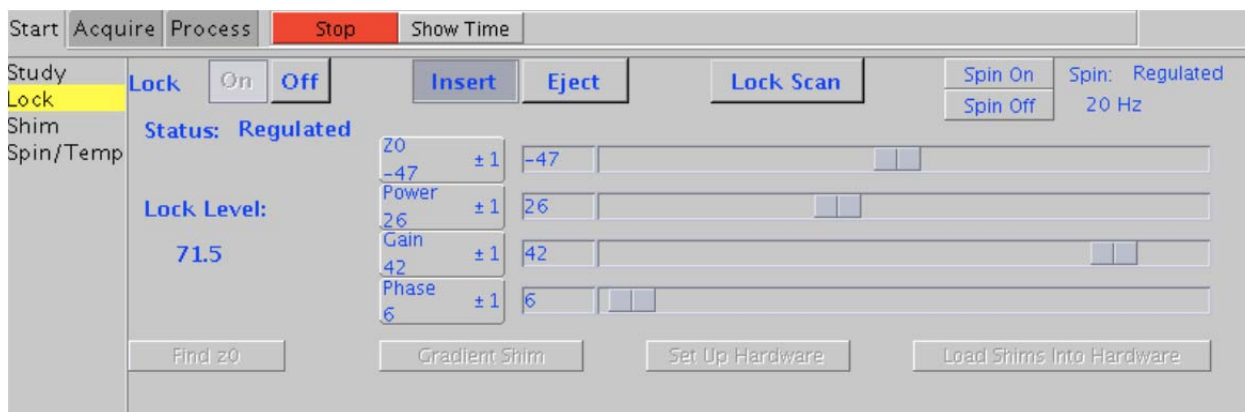
Starting vnmrj



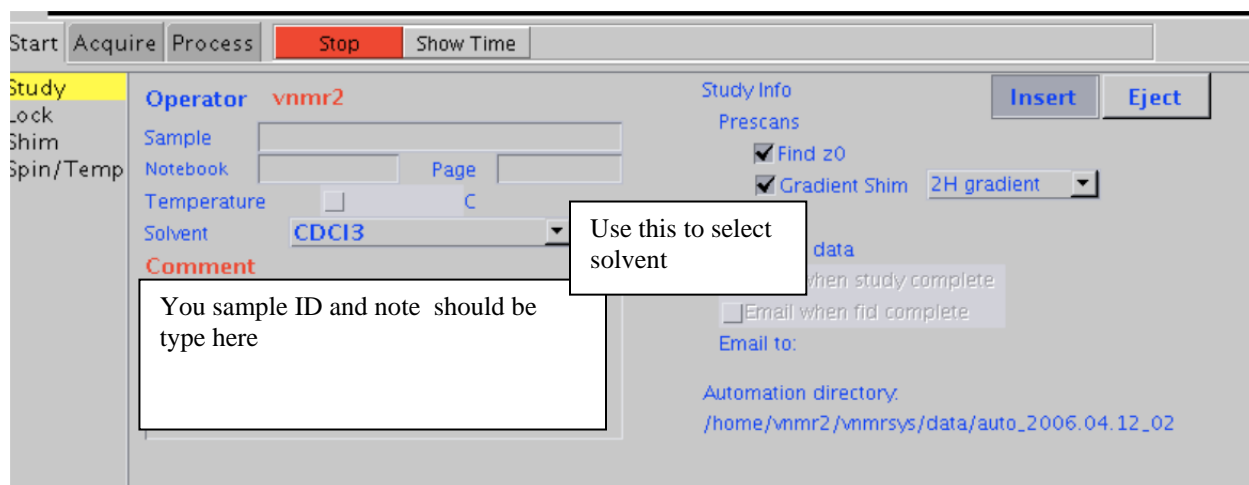
1. Start vnmrj by **single** clicking the vnmrj spectrum icon at the top of the screen.
2. Choose to run a ¹H experiment by dragging the proton icon on the left of the screen to the black area or type h1('solvent'). The default solvent is CDCl₃.

Inserting your sample

1. Click **spin off**, and Click **lock off** and then Click **eject** to remove the standard from the magnet.

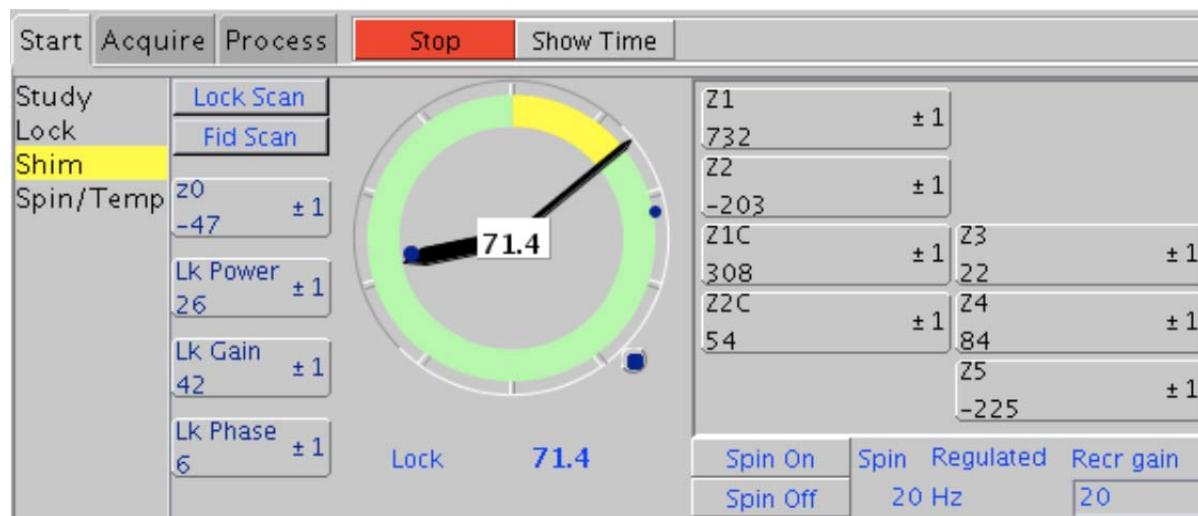


2. Replace the standard with your sample and click on **insert**. After the sample is proper inserted, then click **spin on**. The spin rate is displayed at the bottom.
3. If you wish to use a solvent other than CDCl₃, select which solvent you would like to use with the drag-down box on the following page. Click the **Study** tab.
4. If you would like to print a sample name/ID on your spectrum, insert this text into the comment box (The text will print later by the command **pap**).



Shimming and locking your sample

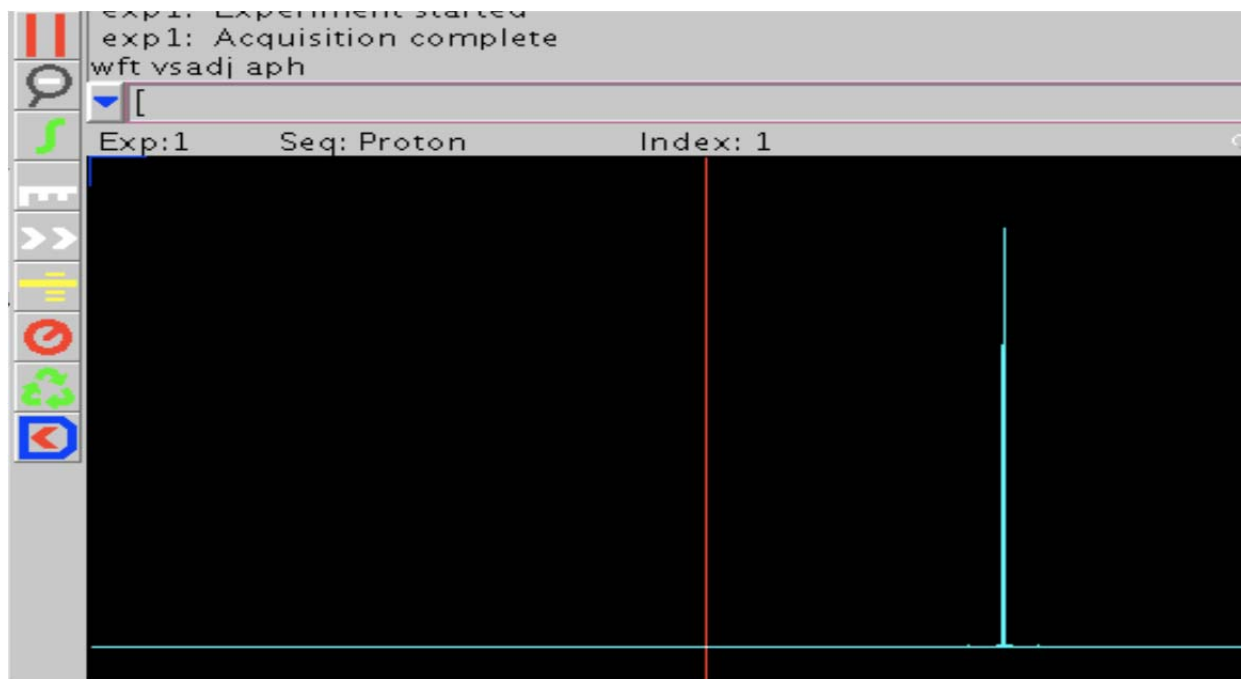
1. If you are using a solvent other than CDCl₃, click on the lock tab and change Z0, and then Power, Gain, and Phase as necessary to lock your sample. The values can be adjusted with the left and right mouse buttons as in the case with the other instruments, or by typing in the desired value and pressing enter.
2. Shim your sample by first clicking on the shim tab, then by adjusting the Z1 Z2 and Z3 values. Use command "loadshim" to reload standard shim file for the standard sample.



Acquiring your ¹H spectrum

1. Check the current acquisition parameters by clicking on the process tag, then by typing **dg** in the input box above the black box.
2. 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.

- 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).
- Start the experiment by typing **ga**.



Processing your spectrum

- After acquisition is complete, the spectrum should be displayed on the screen.
- Apply the same commands as used on the other instruments to process the spectrum (i.e., type **wft vsadj aph** in the input box for Fourier Transform, vertical scaling of peaks, and autophasing, respectively).
- Displaying the scale:*** Note the set of processing icons to the left of the spectrum. Display the scale by clicking on the white ruler icon.
- 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.
- Setting the solvent reference peak:*** As in the case with the other instruments, place the red cursor on your solvent peak, then type **rl(x.xxp)** in the input box to place the cursor directly on the peak and set the reference value (i.e., **rl(7.27p)** for CDCl₃).
- Integration:*** Click on the green integral icon, then take note of the two additional integration icons that appear just below it. Click the middle integration icon and use the mouse to cut the line, then return to the spectrum by typing **ds** in the input box. If necessary, you can also click on the top integral button or type **cz** to display the full integral.
- Setting a peak integral reference value:*** To set a specific peak integration value, click on the process tab, then the cursors/integration sub tab. Place the cursor on the desired

peak and type in the desired number of protons in the *normalization value* box. Save changes by clicking on the *set integral value* icon.

8. **Set a precise spectrum width:** To set a specific numerical range for your spectrum, use the same commands as used previously on other instruments (i.e., typing **cr = 9.5p delta = 10p** then clicking the expand icon will set the window from -0.5 to 9.5 ppm).
9. **Setting the peak threshold:** To choose the level of peaks for peak picking, press the icon labeled by the yellow threshold line and adjust the line accordingly.
10. **Plotting and printing the spectrum** To plot and print, type any combination of the following commands into the input box. Note that these are the same commands as the ones used for other instruments, but are listed here as a reminder.

??pl : print spectrum

??pir: print integrals

??pscale: print scale

??pltext: print text label (from the comment box)

??pap: print acquisition parameters

??pll: print peak locations (ppm and Hertz) and peak height

??ppf: print peak frequencies above each peak

??page: eject page from the printer

Saving the data

1. If you do not yet have a directory in your group's folder, make a new directory by typing the command **mkdir('directory_name')**. Alternately, you can open your group's folder (top left of the desktop) and create a new directory by selecting *File??Create folder*. Command "pwd" to check the current directory.
2. To save a file in an existing directory, first choose the directory by typing **cd('your_directory')**. Next, save the file by typing **svf('file_name')**.
3. To retrieve your data later, find your file in your group's folder on the desktop and drag it to the black processing window. Process as described previously.

Finishing the experiment

1. Eject your sample and replace with the standard sample.
2. If you used a solvent other than CDCl₃, adjust the lock parameters back to the required ones listed under the monitor.
3. Click on the *loadshim* icon at the top of the page, or type "loadshim" to reload the standard shim file.
4. Manually shim the sample to reach the required lock level.
5. Exit the system by choosing *File??Exit vnmrj* or by typing **exit** into the input box.
6. Logout by choosing *Actions??logout*, then click *OK*.

VNMRJ ¹³C Operating Instructions

Follow the VNMRJ ¹H instructions to login to vnmrj and insert, shim, and lock your sample. Remember all the commands on the inova400 could be used on the VNMRJ.

Acquiring your ¹³C spectrum

1. Choose to run a ¹³C experiment by dragging the carbon icon on the left of the screen to the black area or type **c13**
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 ¹H 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.xxxp)** in the input box to place the cursor directly on the peak and set the reference value (i.e., **rl(77.23p)** for CDCl₃).

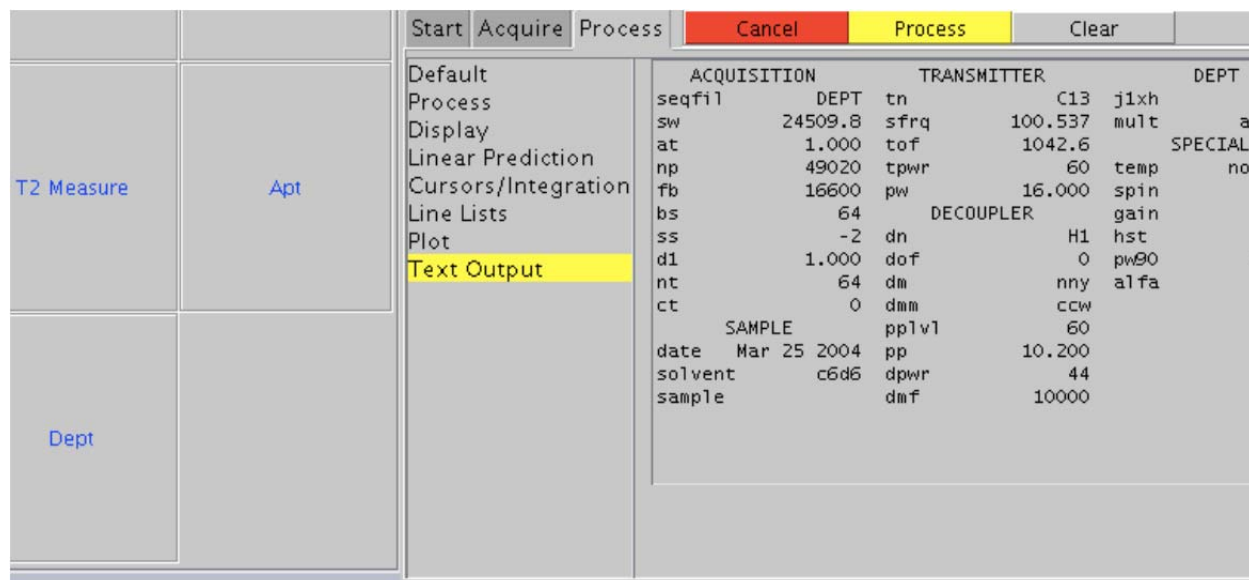
Follow the VNMRJ ¹H instructions to plot and print the spectrum, save the data, and replace your sample with the standard sample. **Before exiting the system, make sure to drag the proton icon to the black window then type su or type h1 to turn off the decoupler.**

VNMRJ APT Operating Instructions

Preparing for the APT experiment

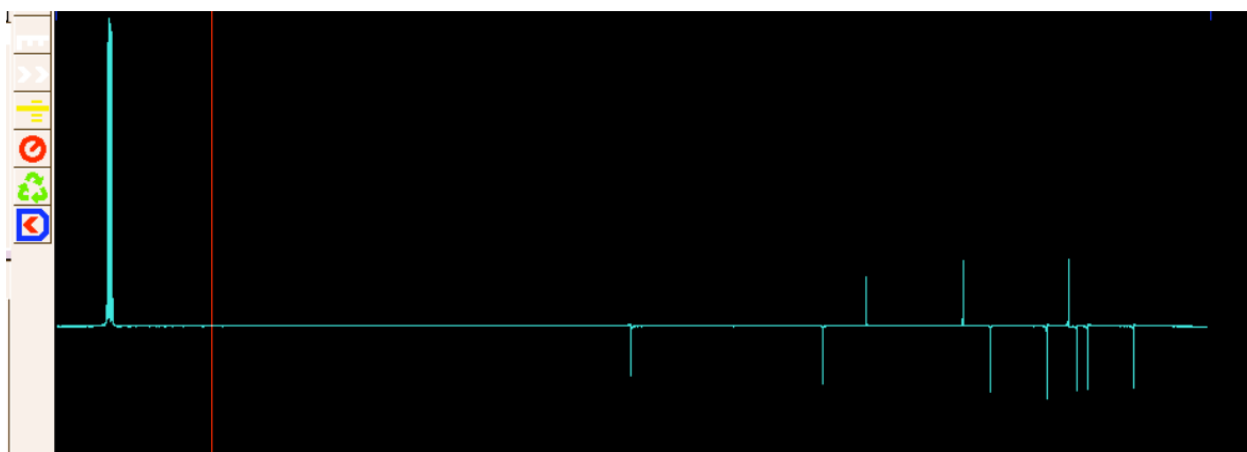
1. Use the VNMR 1H and 13C instructions to shim and lock your sample. Change solvent settings as necessary. Drag the carbon icon to the black window and acquire a carbon spectrum using standard parameters.
2. Type **wft aph** to process the spectrum.

- Use the toolbar to place the red cursors just to the left and right of the carbon peaks. Type **movesw** to select this as the new range for the experiment. Remember all carbons, include solvent carbons, will show up on the APT spectrum.
- Click on the Process and Text Output tabs. Type **dg** to load the updated parameters. Record the values for **sw** and **tof** for use later in the experiment.



Acquiring the APT spectrum

- Drag the *APT* icon from the left of the screen to the black window (this will return the experiment to default parameters).
- Using the values recorded previously in step 4, enter the new parameters for **sw** and **tof** by typing **sw = x** and **tof = x**. Type **dg** and verify that the parameters are correct.
- Enter the number of scans by typing **nt = x**, then type **ga** to start the experiment.
- After the experiment is finished, type **aptaph** to automatically phase the peaks. If the phasing is still off, you can adjust manually by choosing the red circle icon on the toolbar and then adjusting with the left and right mouse buttons.
- Set the solvent reference peak by typing **rl(x.xxp)**.



APT spectrum of Menthol in CDCl₃. UP: CH₂ and Cs and Down CH and CH₃s.

6. Print the spectrum using standard processing commands.

Finishing the Experiment

1. Remove your sample and replace with the standard sample, then turn on the spin and shim to the required lock level.
2. Drag the proton icon to the black window or type **h1** to load standard parameters.
3. Exit vnmrj and log out.

Additional information:

These instructions are very generalized. If you cannot obtain an acceptable APT spectrum, please see Dr. Wu for assistance, as additional parameters may need to be adjusted or the probe needs to be re-tuned for your sample.

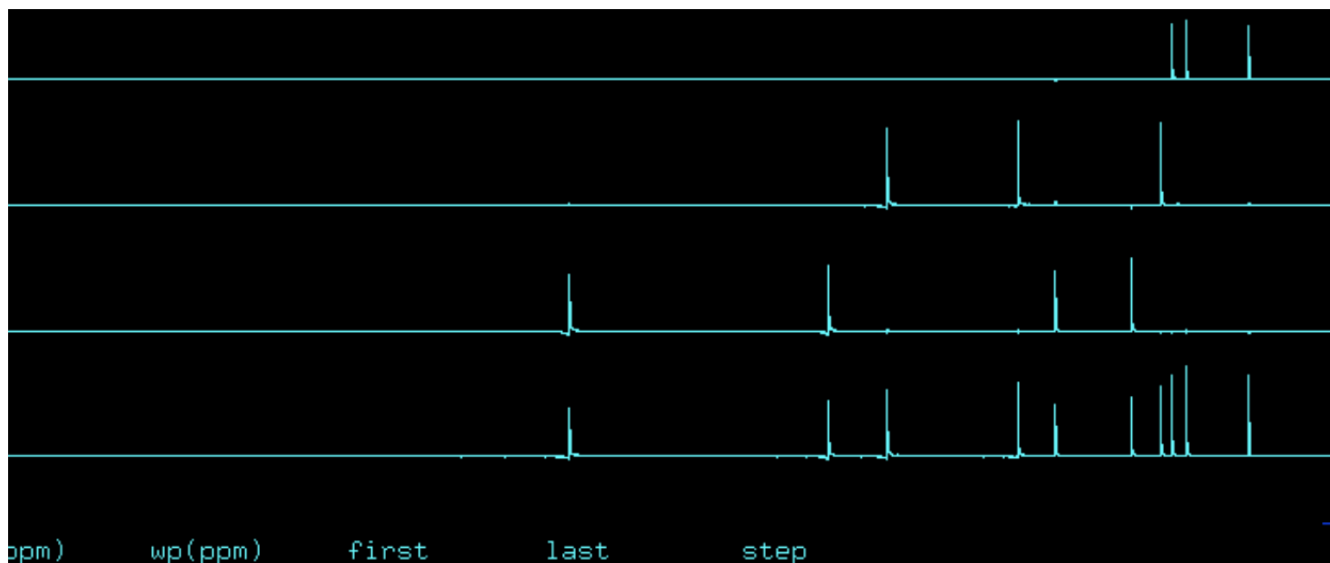
VNMRJ DEPT Operating Instructions

Preparing for the DEPT experiment

1. Use the VNMR 1H and 13C instructions to shim and lock your sample.
2. Change solvent settings as necessary. Drag the *carbon* icon to the black window and acquire a carbon spectrum using standard parameters.
3. Type **wft aph** to process the spectrum. Use the toolbar to place the red cursors just to the left and right of the carbon peaks. Type **movesw** to choose this as your range for the experiment.
4. Click on the Process and Text Output tabs. Type **dg** to load the updated parameters. Record the values for sw and tof for use later in the experiment.

Acquiring the DEPT spectrum

1. Drag the *DEPT* icon from the left of the screen to the black window (this will return the experiment to default parameters).
2. Using the values recorded previously in step 4, enter the new parameters for *sw* and *tof* by typing **sw = x** and **tof = x**. Type **dg** to update the parameters.
3. Enter the number of scans by typing **nt = x**, then type **ga** to start the experiment.
4. After the experiment is finished, type **autodept** to automatically plot and print the DEPT spectrum.



Finishing the Experiment

1. Remove your sample and replace with the standard sample, then turn on the spin and shim to the required lock level.
2. Drag the proton icon to the black window to load standard parameters.
3. Exit *vnmrj* and log out.

Additional information:

These instructions are very generalized. If you cannot obtain an acceptable DEPT spectrum, please see Dr. Wu for assistance, as additional parameters may need to be adjusted.

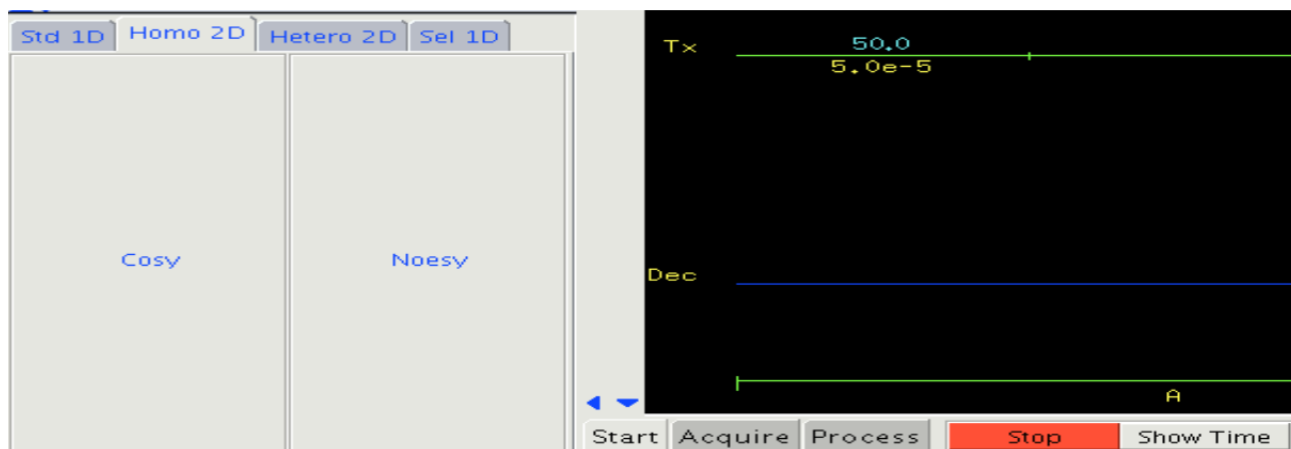
VNMRJ COSY Operating Instructions

Preparing for the COSY experiment

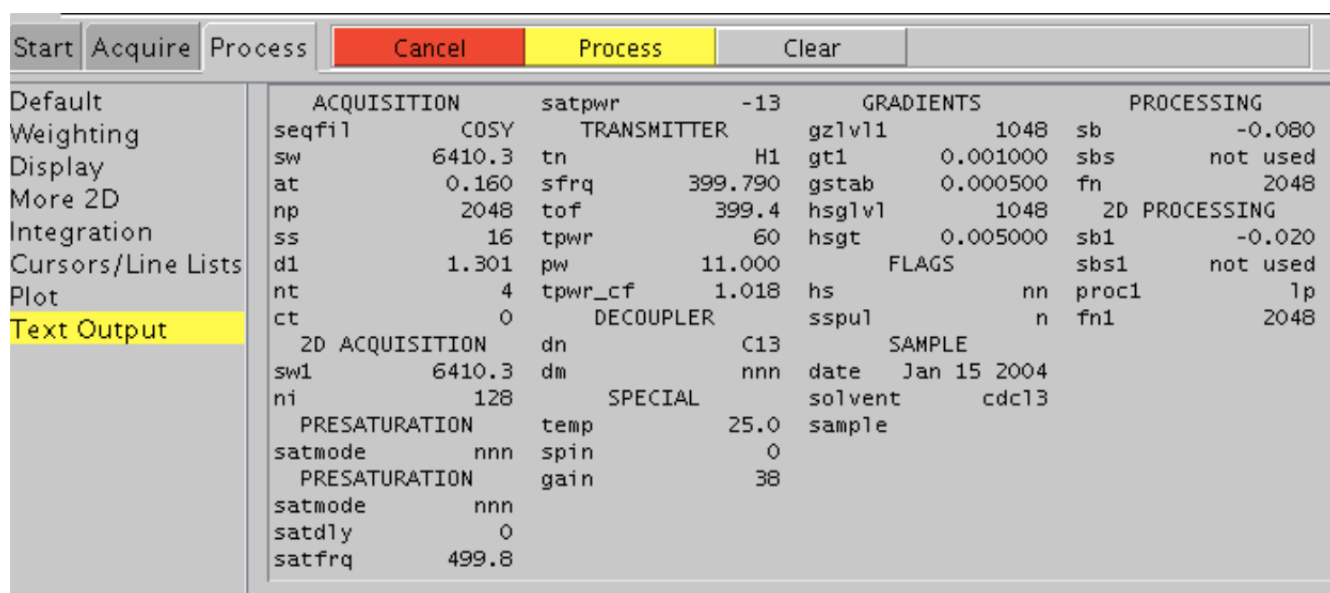
1. Use the VNMR ^1H instructions to shim and lock your sample. Change solvent settings as necessary. Drag the proton icon to the black window and acquire the proton spectrum using standard parameters.
2. Process the ^1H spectrum as listed in the instructions. Set the solvent reference peak, and save the file for later reference.
3. Type **gain?** in the command input box to determine the value to use for gain in the COSY experiment. For COSY or 2D experiments, you have set the gain, rather leave it as "autogain".
4. Use the ^1H spectrum to determine the spectral width for the COSY. Do this by placing the red cursor on both sides of the spectrum and typing **movesw**.

Acquiring the COSY spectrum

1. Click on the Homo 2D tab on the left of the screen.
2. Drag the COSY icon to the black window.



3. Type **dg** to view the current parameters. The parameters will be displayed after choosing the process tab (horizontal menu) and text output tab (vertical menu).
4. Change the gain value to the number used for the ^1H experiment in the previous section. This can be done by typing **gain = x** in the command input box.
5. Change the number of scans by typing **nt = x** (where $x = 16, 32$, etc.). Note that the minimum is 4 scans, and a larger number of scans will lead to a better spectrum.
6. Change the number of FID's by typing **ni = x**. Typically the desired values for x are 128, 256, 512, etc. It is best to start with at least $ni = 256$, and a larger value is better.
7. Check the parameters again as explained in step 3. $sw=sw1$, $np=1024$ or 2048 , $fn=2048$, $fn1=2048$, Type **time** to see the length of the experiment. Adjust nt and ni to fit your allotted time.



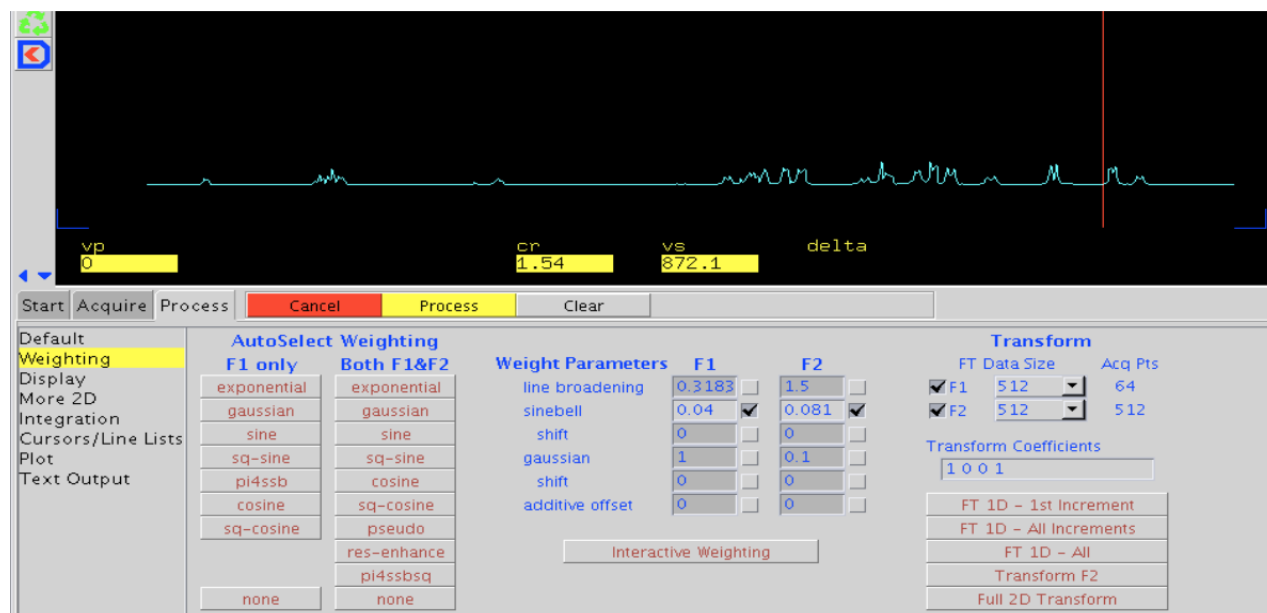
8. Turn off the spin (under the start and lock tabs), and type **ga** to begin the experiment.

Processing the spectrum

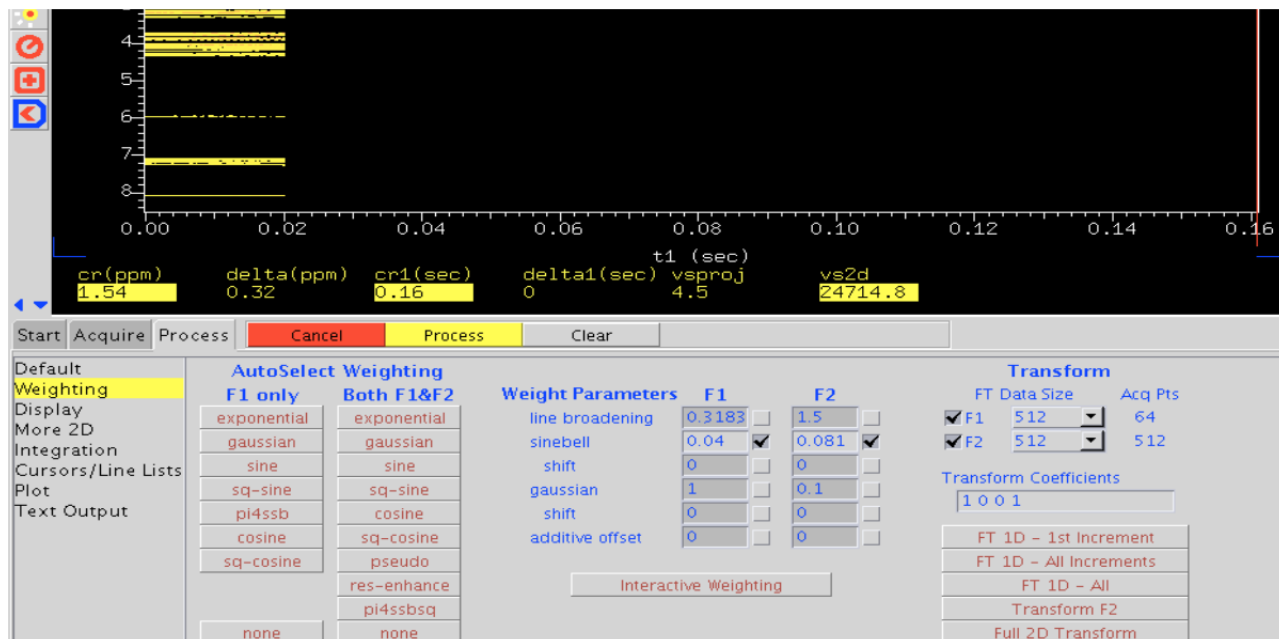
1. If you would like to use the default processing/plotting method, you can print now by typing **pcon page** in the command input box. If you would like to manually process the spectrum, continue below.

2. Peak shape adjustment (F1 and F2):

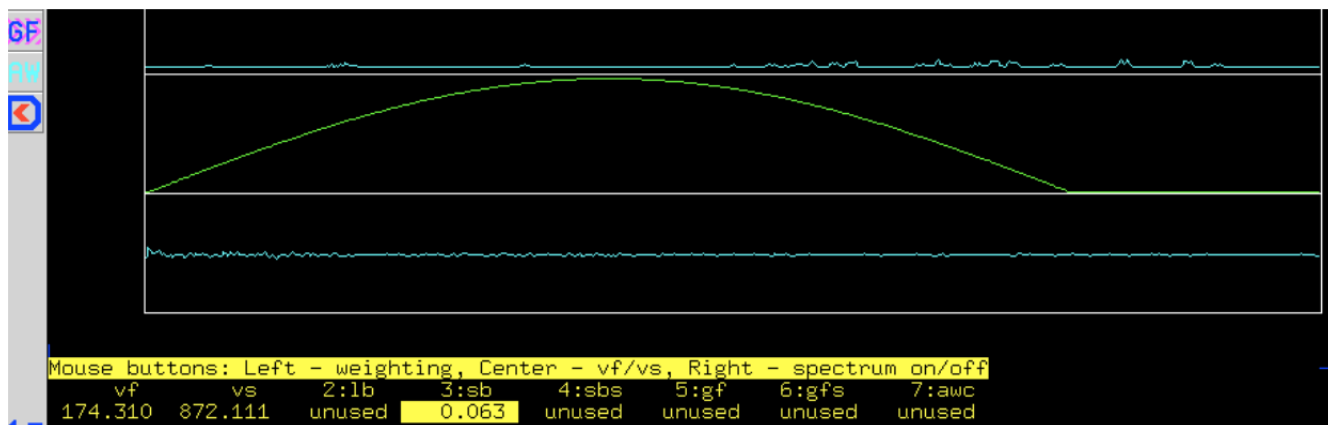
After selecting the process tab on the horizontal menu, choose the weighting tab on the vertical menu. To adjust F2, first click on *FT 1D - 1st increment*. If the full spectrum is not shown, type **full** followed by **f** to show the whole spectrum.



There are two options for adjusting the values for F2. You can simply input new values for F2 by entering numbers in the boxes under the weight parameters heading and F2 subheading, and then clicking the *Transform F2* icon.



Alternately, you can manually adjust F2 by clicking on *interactive weighting* and adjusting the Gaussian curve with the left mouse button until the desired peak shape is obtained. When adjustment is finished, click the *transform F2* icon.



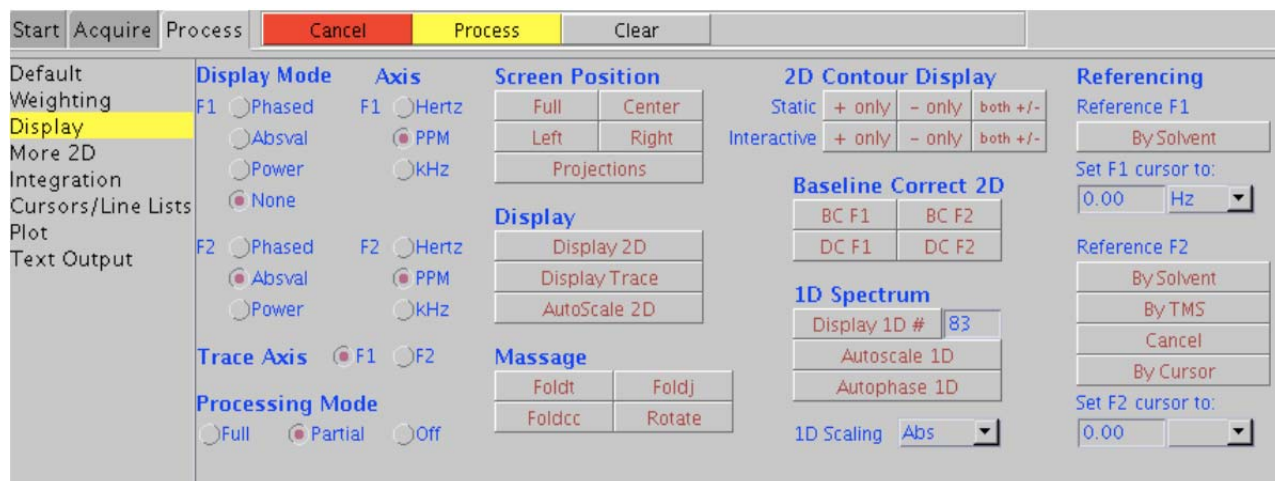
To adjust F1, choose any single line of the spectrum using the red cursor lines, then click on *interactive weighting* and manually adjust the curve as described in the last step. When adjustment is finished, click the *full 2D transform* icon.

3. **Eliminating peak noise:** To remove excess unsymmetrical noise, type **foldt** in the command input box.

4. **Setting the solvent reference peak:** Note that this step is unnecessary if you have already set the reference peak in your 1H NMR experiment at the beginning of these instructions. However, if necessary, you may set this value by using the cursor and zoom

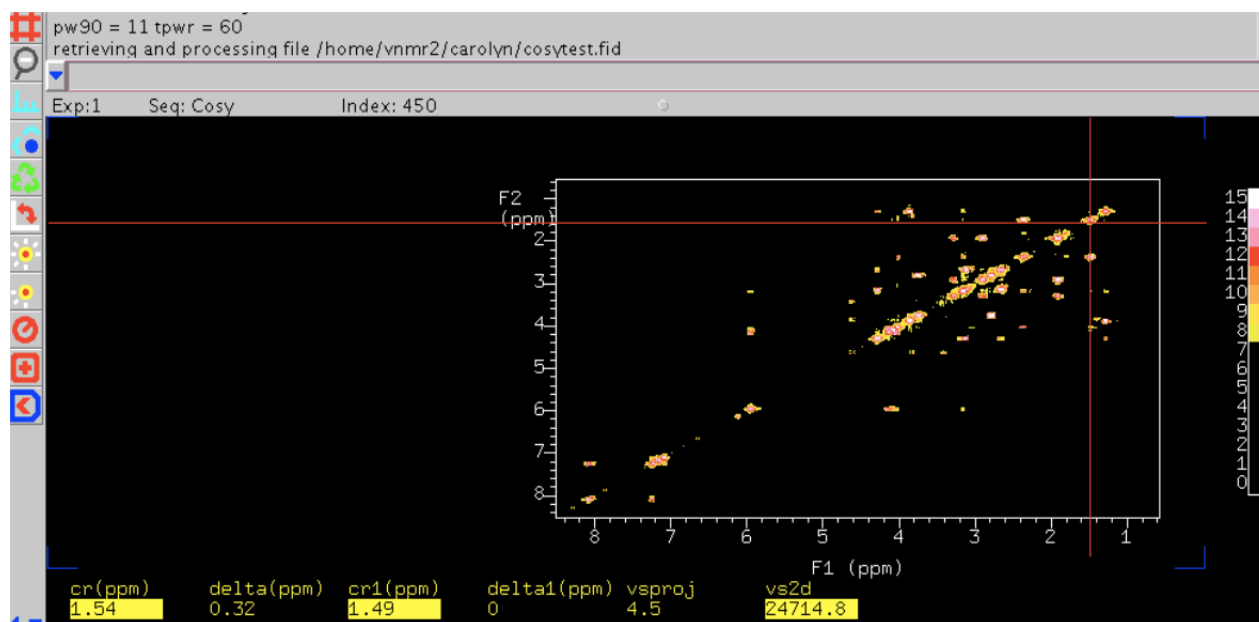
(magnifying glass) icons to expand the area containing the solvent peak. Place the cursor on the desired peak and type in the command **rl(x.xxp)** to set the reference value.

5. **Decreasing static noise:** Click on the display tab on the vertical menu. Check to make sure that “none” is selected under Display Mode, then look for the 2D Contour Display heading. Select the static *both +/-* icon to decrease static noise.



6. **Changing the screen position of the spectrum:** look for the Screen Position heading. You may choose from the *full*, *center*, *left*, and *right* icons, depending on how you would like to plot your spectrum. Typically it is best to choose the *center* option since it will allow for easier plotting of the peaks and spectrum later.

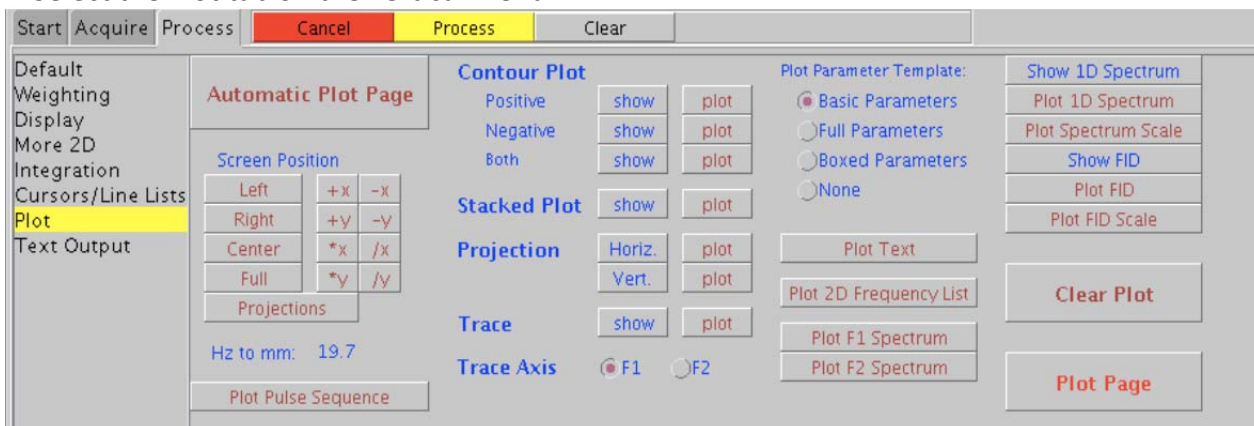
7. **Increasing/decreasing intensity of peaks:** Adjust intensity of peaks by using the yellow bulb icons on the toolbar.



8. Expanding regions of the spectrum: Choose the red cursor icon on the toolbar. Use the left and right mouse buttons to select the area to be expanded and click on the zoom icon to expand. Also use this icon to return to normal size.

Plotting and printing the COSY spectrum

1. Select the Plot tab on the vertical menu.



2. Look for the Contour Plot heading, then click on the *show* icon next to the *both* subheading. Click on the *plot* icon just to the right to mount the vertical and horizontal contour.


3. To add your proton peaks to the spectrum, look for the Projection heading, then click on *Horizontal* and *plot* (icon directly to the right) to add the horizontal peaks. Add the vertical peaks in the same manner, by clicking on *vertical* and then *plot*.

4. To print, click on the *plot page* icon.

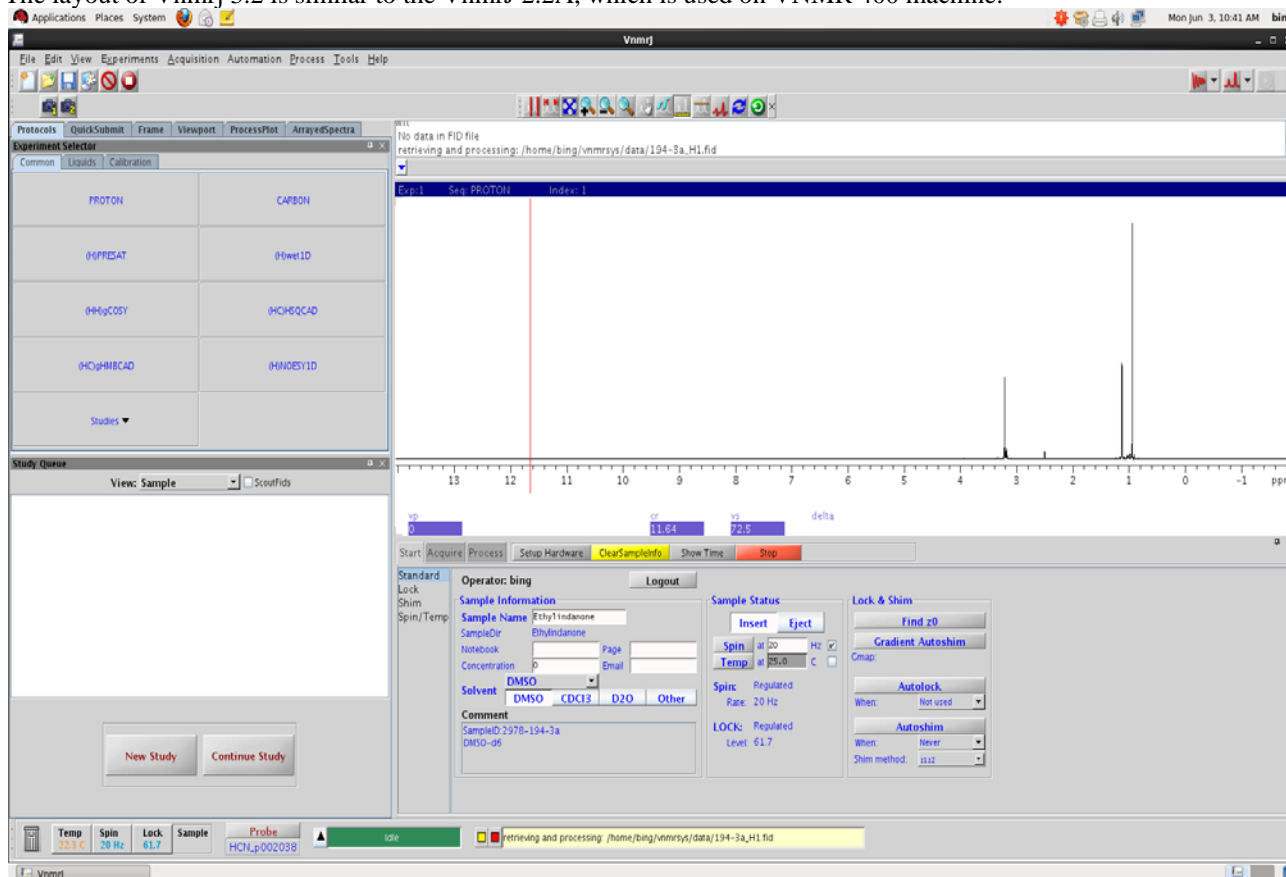
Finishing the Experiment

1. Remove your sample and replace with the standard sample, then turn on the spin and shim to the required lock level.
2. Under the Standard 1D tab, drag the proton icon to the black window to load standard parameters.
3. Exit vnmrj and log out.

Instruction to VnmrJ 3.2 (Installed on inova600 II)

Login to the computer using your group user name and password. Double click on the VnmrJ icon  to open the VnmrJ3.2 window.

The layout of VnmrJ 3.2 is similar to the VnmrJ 2.2A, which is used on VNMR 400 machine.



The big area of left panel is the Experiment Selector, under which there are several tabs and buttons. For routine use, you just click PROTON or CARBON button (note: there are no h1 and c13 commands for use).

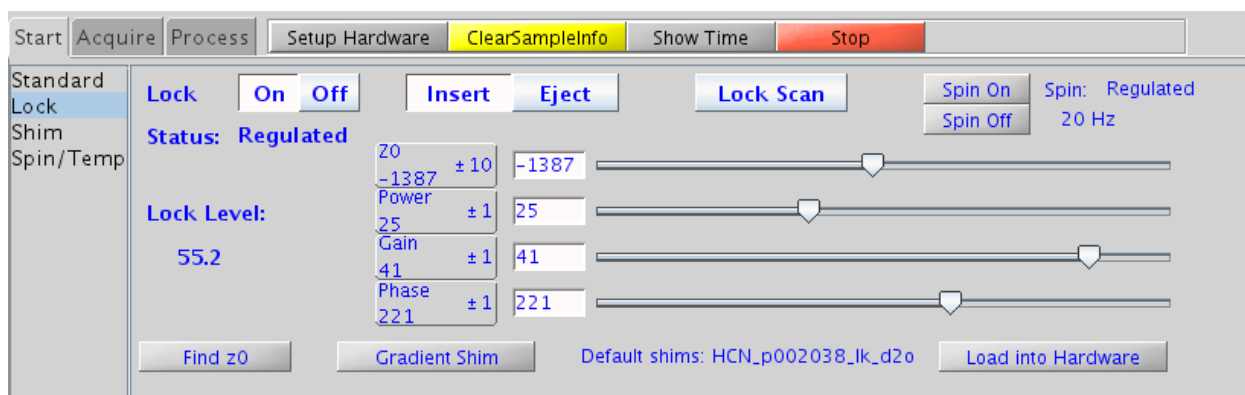
The middle right area is the screen showing the spectrum or lock signal. Immediately on top of it is the command line where you can input the old vnmr commands you have learnt for years. Most of them are still working. Above the command line is the message box showing the command you have just inputted, execution of the command, and error message if command cannot be executed.

On top of the message box there are a set of processing buttons we will discuss in the processing section. The underneath the spectrum screen is the panel used for loading the sample and setup the experiments.

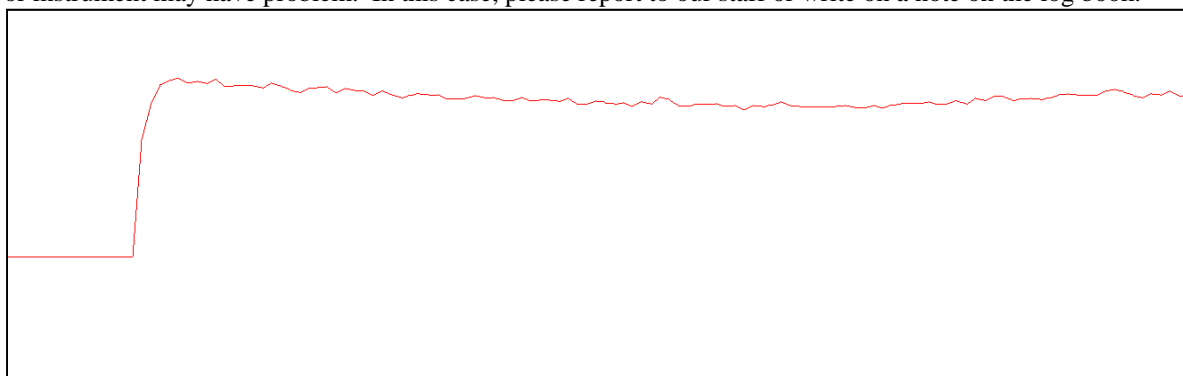
Checking the lock level with our standard sample

We require every user to put a standard CDCl₃ sample back into the magnet and do locking and shimming on it after he or she have done with their own samples to make sure the machine is in good condition for the following users. So we advise that after you login to the computer, the first thing you do is making a quick check to see if the previous user has done their requirement by following procedure. It only takes a second but will save you a lot of guessing afterwards.

Click on black Start > Lock tabs, the bottom right panel will look like as follow:



Click on Lock Scan and lock line will be shown in the middle screen. If the lock line looks like a flat plateau, as shown in the following picture, and lock level is above 70% with the values of parameter Z0, Power, gain and phase are same as the ones on a note we put beside the computer, that means the previous person has done the requirement and the machine is in good condition to use. Otherwise it means that the machine is not locked or shimmed properly or instrument may have problem. In this case, please report to our staff or write on a note on the log book.

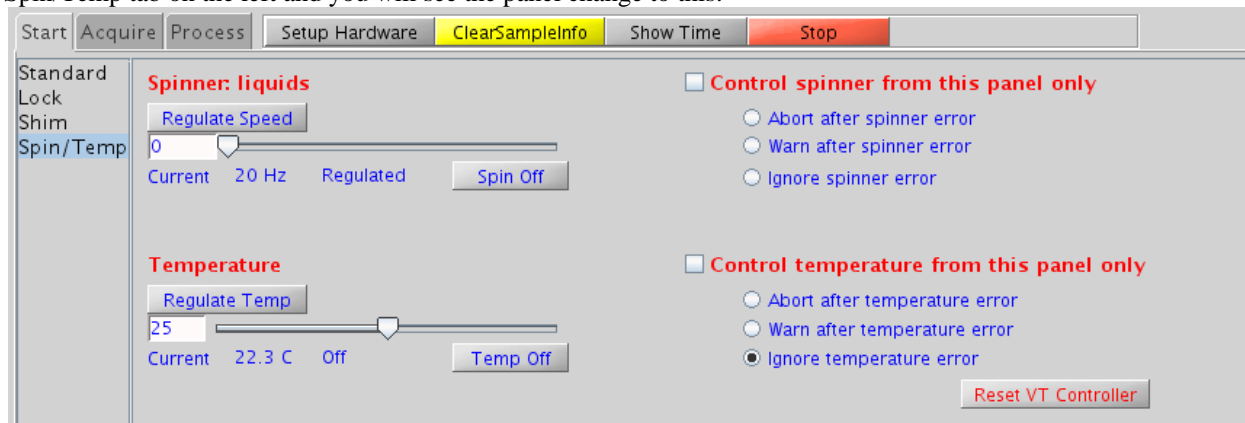


The shape of the lock signal

Loading Sample

Stay on the Lock panel, click on the blue Lock Off and Spin Off button and wait until the spin speed shown beside the button turn to 0, and then click on Eject button. You will hear the hissing of the compressed air which pushes the spinner up with our standard sample to the top of the magnet. Remove the spinner together with the standard sample from the magnet and take out the standard sample from the spinner, Insert your sample tube into the spinner using a depth gauge to make sure the sample tube is inserted all the way into the gauge and then place the spinner on top of the magnet with the compressed air still hissing. **(Warning: The glass sample tubes are fragile, be careful when you take them out or insert them into the spinner)**

Click on the Insert button to load the sample into the magnet and then click on Spin On button. Usually you will see the increase of the spin speed beside the button and reaches 20 Hz in seconds. If the spin speed stays on 0, click on Spin/Temp tab on the left and you will see the panel change to this:

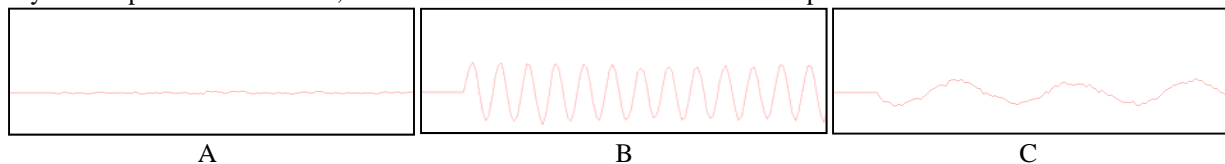


Move the Spinner slide to 20 Hz by pressing down the left mouse button and drag it and click on Regulate Speed.

Locking

If your sample is in CDCl₃, the lock line most likely will become a flat, plateau shape as shown before, you only need to click on Lock On button and click on Shim tab on the left to go to shimming step.

If your sample is not in CDCl₃, the lock line will look like one of three shapes as follows:



Then you need to find lock signal yourself.

The first is to make sure the Lock Off button is clicked. Increase the Power and Gain several unites each by click on the correspondent buttons using right mouse button. Then click left or right mouse button to change Z0 value (middle button is used to toggle the changing unit between 1, 10 and 100) to see if you are able to see the sine-wave signal like B and number of sine waves in the line is increase or decrease. If it is decrease, continue change Z0 using the same mouse button. You will see the line turns to C and eventually becomes a flat line shown before. Then click on Lock On button. Usually the lock level will increase a lot after you click on the Lock On button when it is on resonance. If the lock level higher than 100%, reduce the power and gain a couple of unites each to maintain lock level at about 70%. If it is too low, increase the power and gain. The last step is to increase or reduce the value of lock phase a little bit to make sure the lock level is the highest. After you have done all these, record the lock parameters on the form we provided by the computer. These parameters may help you and others to find lock quickly for the same solvent in the future.

If the lock line looks like A and does not change much after you adjust Z0 all the way from - to +, there are several possible causes: i) The sample is very concentrated and lock signal is weak. In this case, increase power and gain several units more and continue to try. ii) You have added too little solvent in the sample. In this case, increase a little more power and gain. We suggest using about 0.75 ml solvent. iii) The shimming is way off. If you have followed this instruction and checked the lock level with the standard sample the first thing after you login, this is not the case. If you are not sure, type “loadshim” to re-load the shimming file we saved for the standard sample. iiiii) The sample is not dissolved in a deuterated solvent.

Some notes about Locking:

Because of the slow drifting of the magnet field or changes due to external interference, all modern NMR spectrometers are equipped with a lock system which maintains the stability of the magnetic field.

The key step to lock is finding the lock signal or resonance frequency of the deuterium for a particular deuterated solvent you are using. There are four parameters, Z0, lock power, lock gain and lock phase, to adjust to find the lock signal. We always keep a set of these parameters for our standard CDCl₃ sample on a note by the computer, which are also good if your sample is in CDCl₃.

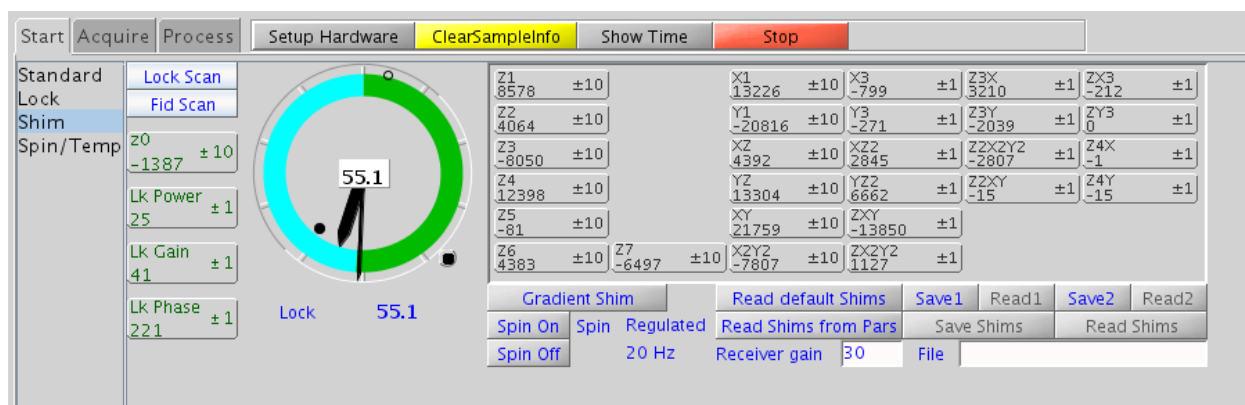
Usually, you only need to change Z0 to find the lock signal.

The Lock level is related to the nature of the deuterated solvent – the number of the deuterium atoms per molecule and the relaxation time of the deuterium. Usually, the more concentrated sample the lower the lock level because the deuterium concentration becomes lower and more viscosity reduces the T1.

Increase the power and gain only increase the lock level electronically, just like you turn on the volume of the radio, which does not increase the signal strength received. If the lock power is too high, the deuterium nuclei become “saturated,” the signal oscillates (goes down and then back up quickly), and it is difficult to establish lock. As long as the machine is locked, the lock level, high or low, does not affect the result of your experiment. But if you leave the lock level too low (lower than 20%), the machine may lost lock in the middle of the experiment, especially during a long experiment.

Shimming

After you have made lock, click on Shim tab on the left to show shimming panel:



There are 7 Z-direction coils from Z1 to Z7, called Z shims, which are parallel to the vertical direction of the probe. We mainly only adjust these shims in our routing experiments. Others such as X1, Y1 et al are called non-spin shims and usually there is no need to adjust these shims.

The lock level is used to monitor the shimming process. The higher the lock level the better the shimming. Here again, the value of the lock level we have got from the locking process above is not important. What we need to do in shimming is to maximize the lock level by adjusting the values of these Z shims using the right or left mouse buttons to click on those shim buttons. Again, the middle mouse button is used to change the unit for each click, which toggles between 1, 10 and 100. 10 is suggested.

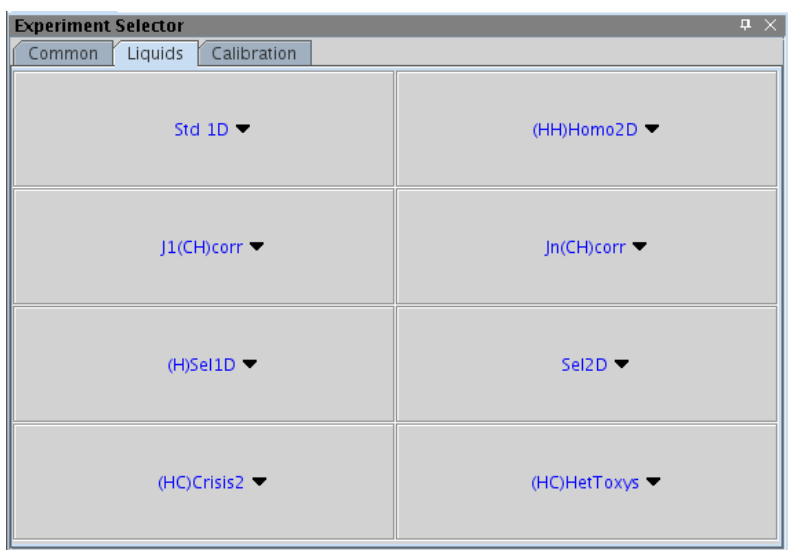
Starting with Z1, click on Z1 button using left or right mouse button to find which way to make the lock level increases. If the lock level increase, continue the same way until the lock level does not go any higher (which starts to go back down) and then shim on Z2 the same way and then go back to Z1 again. If the lock level goes above 100%, reduce the power and gain a couple of units to keep the level at 70% and continue to shim on Z1 or Z2, as such go back and forth until lock level is not able to be increased any higher.

In most cases, this concludes the shimming. However, if you find that the shape of the signal is not good after you have done shimming on Z1 and Z2, a second level of shimming may be needed:

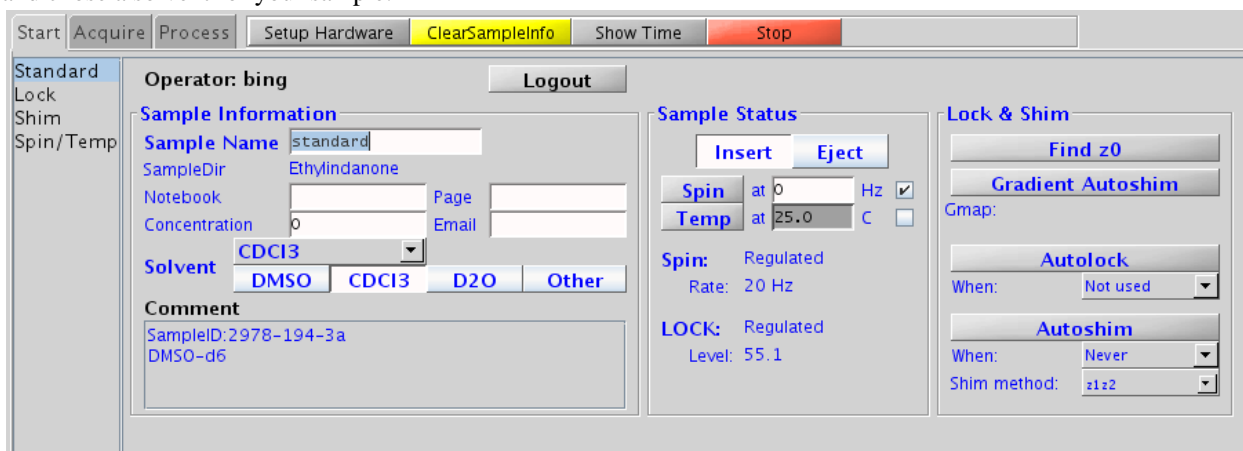
1. After shimming on Z1 and Z2, write down the lock level, adjust the Z3 in one direction, say by 8 units (no matter the lock level is going up or down), and then re-optimize Z1 and Z2 interactively until the lock level is at a maximum. If this lock level is higher than the one that you wrote down, continue to change Z3 in the same direction and adjust Z1 and Z2 again. Every time Z3 is changed, Z1 and Z2 are needed to be re-optimized again until the lock level is a maximum.
2. Repeat step 1 with Z4.
3. Repeat step 1 and step 2 interactively until the highest possible lock level is obtained.

Set Up Experiment

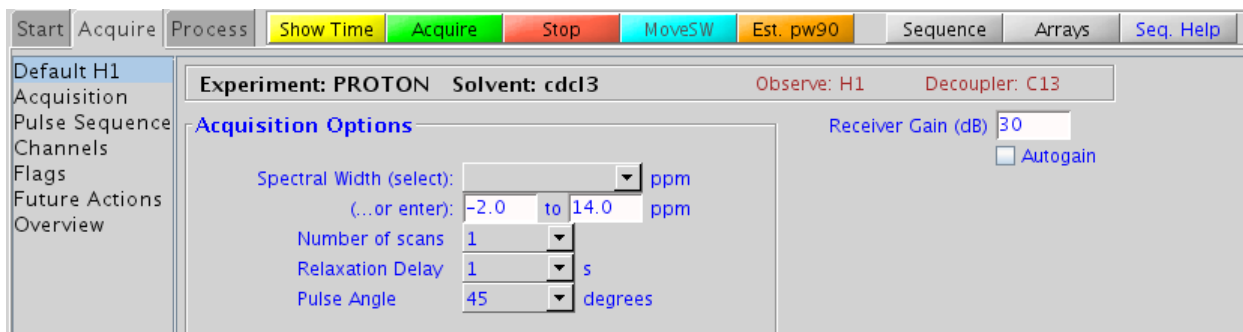
1. On the left panel under the Experiment Selector, click a button of your experiment such as PROTON, or CARBON. If your experiment is not in the list, click on Liquids tab and it will show a list of types of experiments. Under each name, there is a pull-down list of experiments. You can click on a type, to show the list and chose an experiment you want.



- Go back to bottom right panel and click on Start tab. Filling your sample name in the Sample Name box and chose a solvent for your sample.



- Click on Acquire tab. Under Acquire there are 7 tabs on the left you can chose. The first one is the Default H1 (or Default C13 if you click on CARBON in step 1). In this area, you can change spectral width, number of scans (nt) and relaxation delay (d1). Remember, you can always change these parameters on the command line.



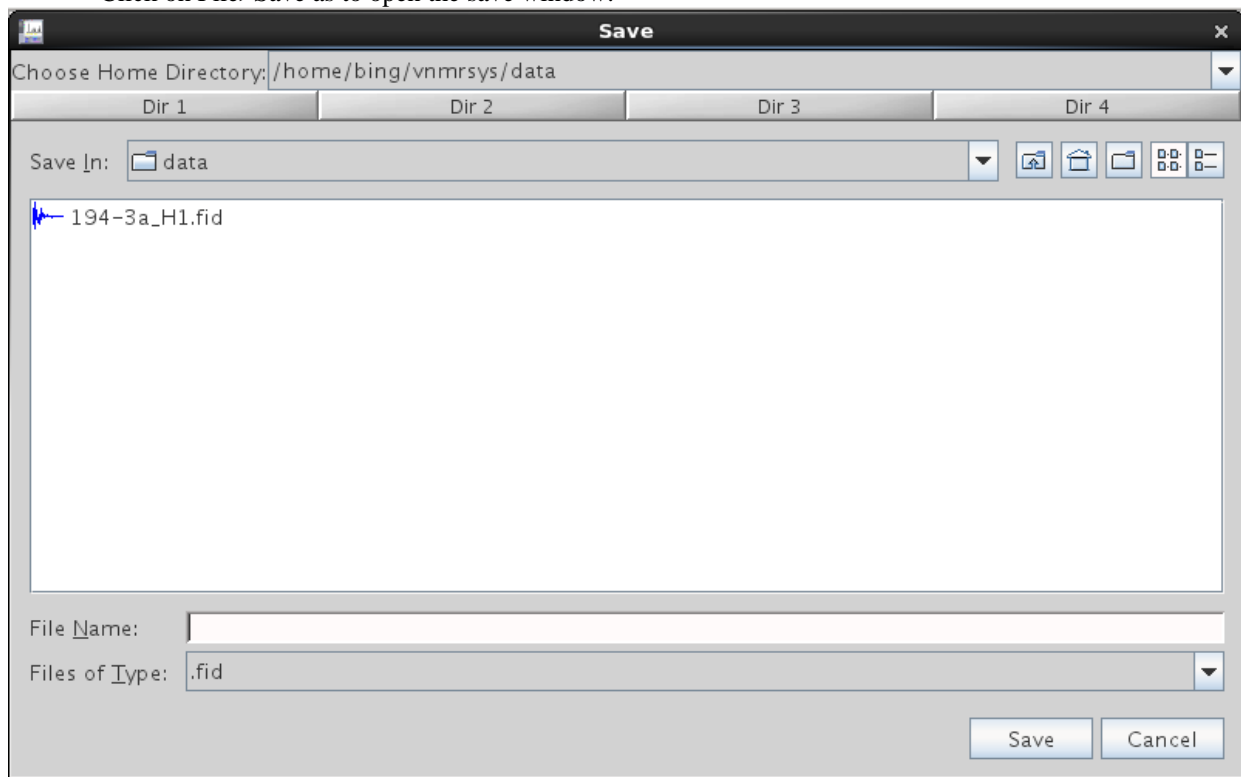
- Click on Overview, it will show all the experiment parameters. Type dg to update the parameters you have just changed above.
- On the command line (immediately above the spectrum screen), type ga to start the experiment.** You can monitor the experiment progress at the bottom of the window. There will show how much time left, how many scans have been completed et, al.



SAVE YOUR DATA

We advise you that the first thing after data acquiring is to save the data.

The following procedure is to save your data on a server lined to the internet so it is convenient for you to download the data later on from your computer. The path of server directory is /media/data_server/your_group_name.

Click on File>Save as to open the save window:



Notice that your home director (folder) on the top of the window. You need to click button  several time to go up to the root (/), and click Media>data_server>your_group_name in the box. Click  button to create your own directory, and click on your directory after you done. Then type your file name in the File Name box and click Save. To retrieve your file, do the sample thing above to find your file and double click your file name.

You are also able to save your data on the command line:

Type goserver and your_group_name as prompted

Type mkdir('your_directory_name')

cd('your_directory_name')

svf('your_file_name')

To retrieve your file, type rt('your_file_name')

To see your working director, type pwd.


PROCESSING

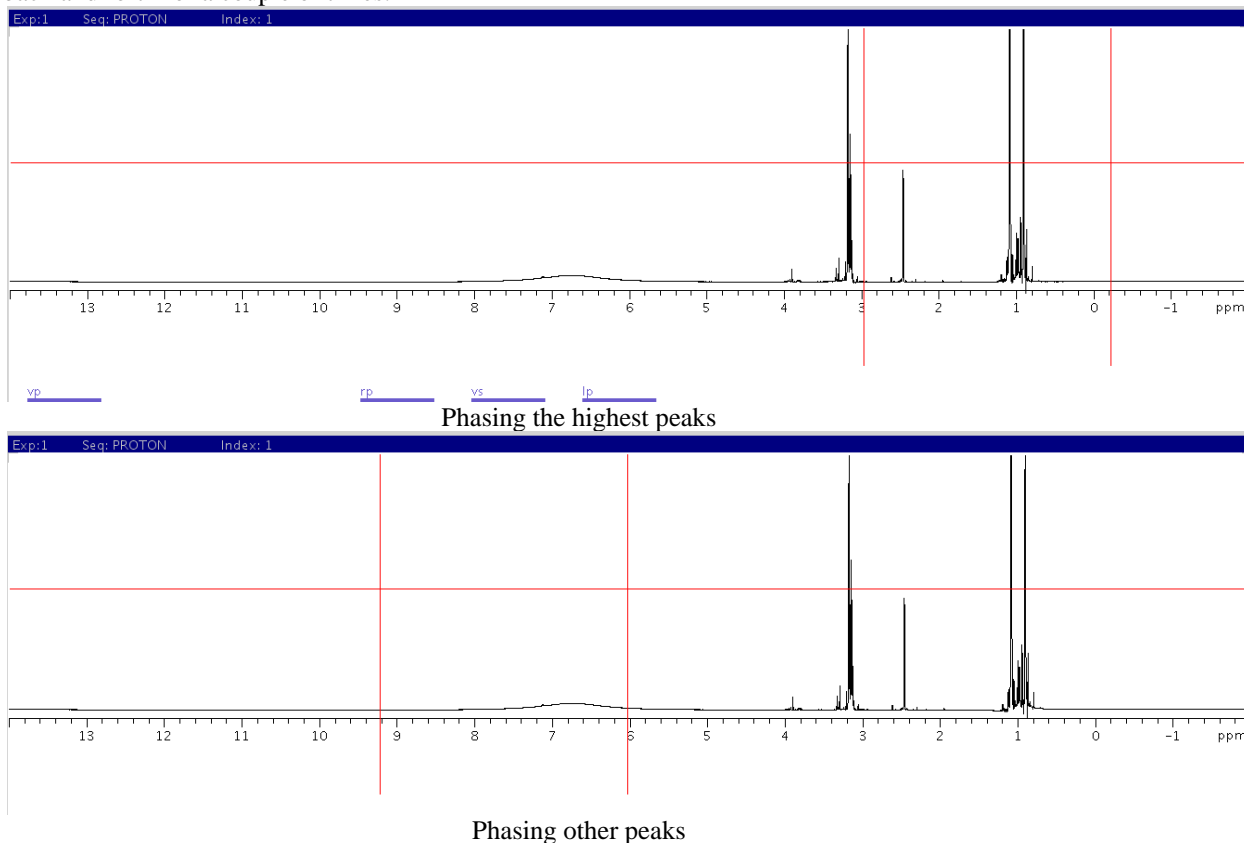
1. After the experiment is completed, usually the spectrum will be shown automatically on the screen. If it is not, type wft aph and enter.
2. Adjust the intensity of the peaks:
 - i. Type vsadj (vertical scale adjustment). or
 - ii. Use the middle wheel on the mouse to adjust the intensity. Roll to front, increase the intensity. Roll to back decrease the intensity

Now you need to use a set of processing buttons on top of the screen: (Please read the note at the end this instruction for a full explanation of the functions for each button)






3. Phasing:

If the phase is still not good after you typed `aph`, you can do manual phasing. Click on phase mode button  and then press and hold the mouse button on the strongest peak and move the mouse up and down to get a good phase for the peak (left mouse button is for coarse adjustment and right mouse button is for fine adjustment). The peak is boxed by two red cursors. When you move the mouse up and down, only the peaks inside of the cursors change their phase. Then do the same thing for other peaks. You may need to do this back and forth for a couple of times.




4. Zoom in and out

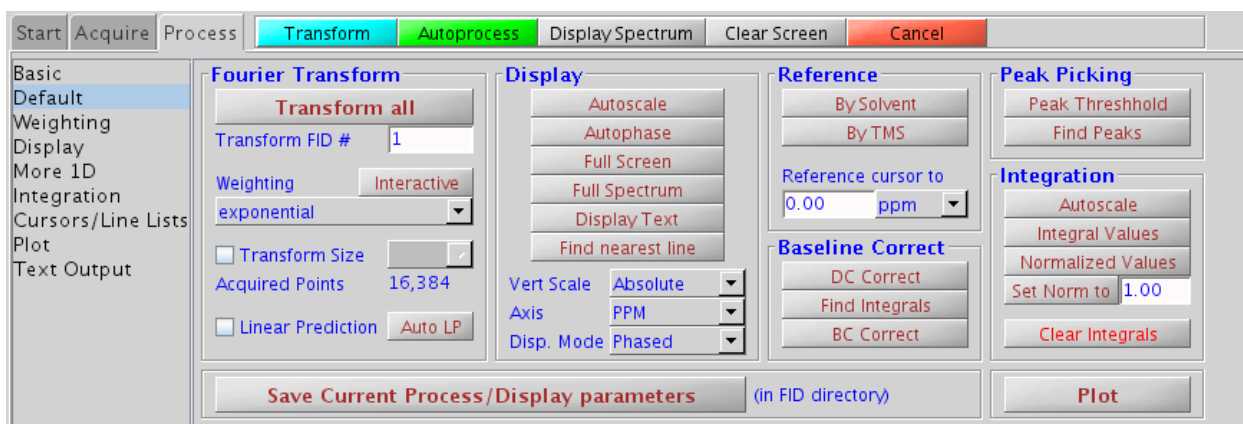
Click on two red cursor button , and use these two red cursors to define the region you want it to be expand by click left and right mouse buttons. Then click on Zoom in button .

You can click on Zoom mode button , and then press, hold the mouse button and then drag the mouse to define the region you want to expand.

To Zoom out, click on Zoom out button  or click on reset to full display button .

5. Referencing


Click on single cursor button , and place the red cursor on the peak you want it to be the reference peak. Type `nl`, and then click on Process tab and Default tab under the spectrum screen. Fill the ppm number you want the reference peak to be in the "Reference cursor to" box and hit enter key.



Process > Default Panel

If you know the rl command, you can always type rl(x.xxp) on the command line after type nl.

6. Peak picking

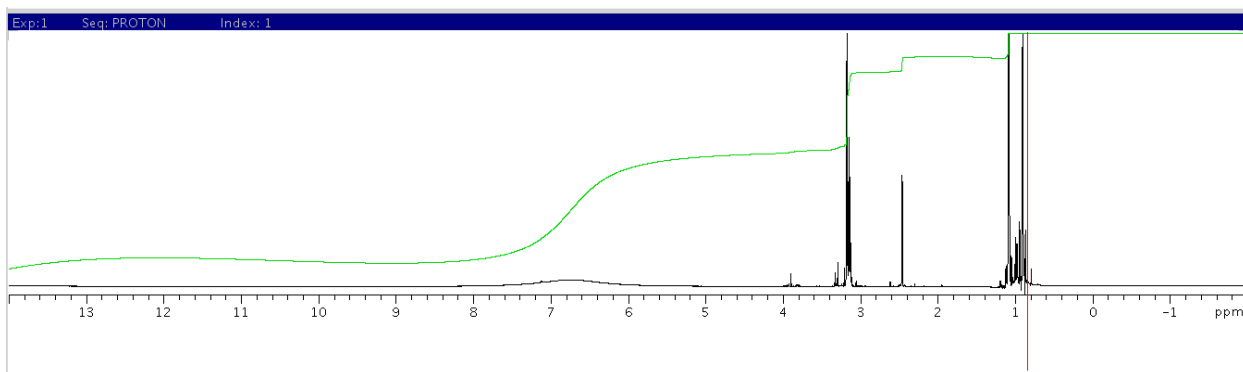
Click on Show threshold button  to show threshold line and use mouse button to drag the line to below all the peaks you want to pick up.

Type dpf to show the peak picking (for print peak picking type ppf)

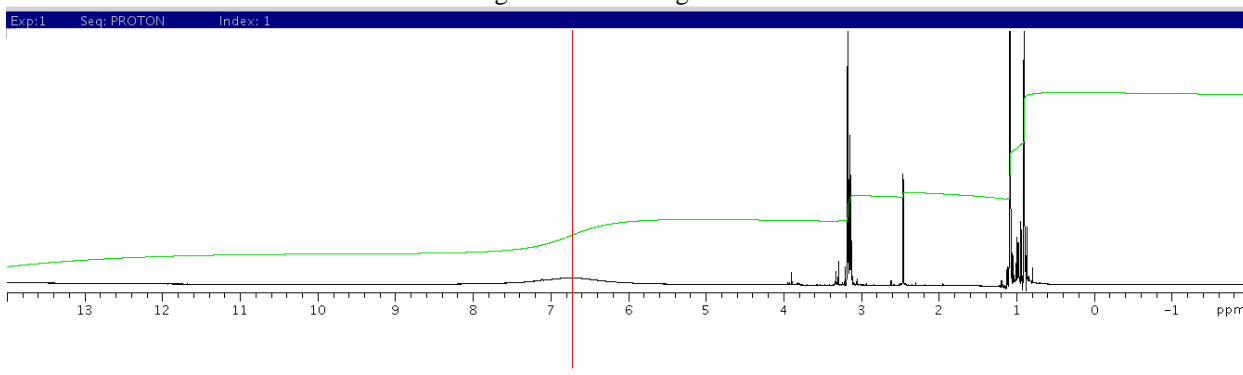
7. Integration

Click on Show integral regions button  to show a full integral line.


If the integral line is too high (goes up to the top of the screen), use the middle wheel of the mouse to adjust it (now the wheel is not able to be used for adjusting the intensity of peaks. If you want to adjust the intensity of the peaks, you need to delete the integral line, which will be explained later).



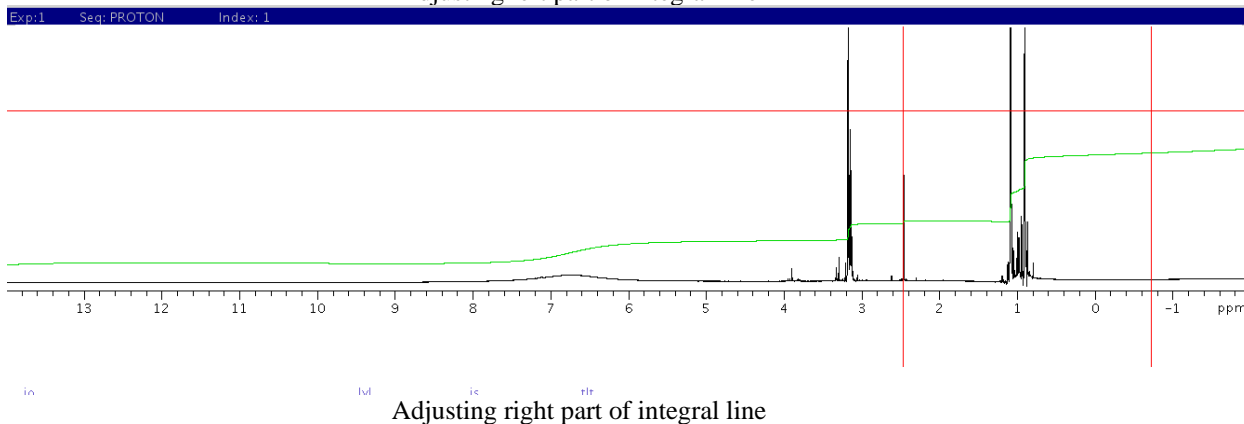
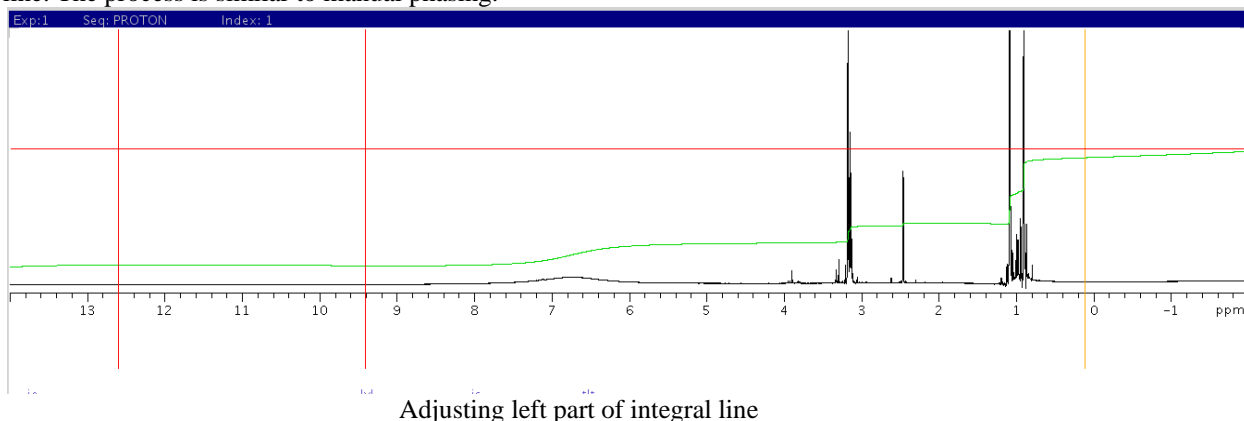
Integral line is too high






After adjusting the height of integral line

The full integral line should look like a nice stair and go up from left to right. The horizontal portion of the line should be perfect flat. If it is not, that means that the baseline of the spectrum is not flat. In this case you are able to adjust it by clicking on Integral Lvl/Tilt button , then move the cursor on the left part of integral line and press and hold left or right mouse button, move the mouse up and down to try to make the

horizontal line between two red cursors flat, and then move the mouse cursor to the right part of the integral line and do the same thing. So do as such back and forth a couple of times until you satisfy with the integral line. The process is similar to manual phasing.



Click on define integral region button  and use left mouse button to cut the integral line by click on both sides of a peak. After you finish with all the peaks, type ds.

If you made some mistakes during the cutting, you can always re-do it by click on show full integral button  and click on delete integral regions button  (same as cz command) and then re-do the cutting.

Define the integral areas:

Put a red cursor on a peak with a integral line, then click on the process tab and then integral tab under the spectrum screen. Type the number of protons related to that peak in the "Integral Area" box and click Set Integral Value underneath the box.

Integral	start(ppm)	end	value
1	3.34188	3.07901	6.447
2	2.56523	2.386	1.000
3	1.227	0.99998	12.450
4	0.99998	0.725166	14.087

Process>Integration

Show integral value under each peak:

Type vp=12 and dpir

8. Plotting

Using plotting commands are simpler and quicker. The plotting command always start with pl and finish with page. Any other commands are put between these two commands, such as:

pscale – print scale underneath the spectrum

dpir – print integral value under each peak

ppf – print the result of peak picking on top of each peak

ppa – print parameters

ptext – print text message


eg: pl pscale dpir page




You are always welcome to explore the Process>Plot panel for more sophisticated plotting purpose.


Finishing up experiment


After you have done all the things listed above, take out your sample and replace our standard CDC13 into the magnet. **Do not forget to lock and shim on the standard sample.** Check the locking parameters on the note we placed by the computer. If you think the shims have been changed a lot during your experiment, type “loadshim” to re-load the shimming parameters we saved for the standard sample.

The functions of the processing buttons:

Note: If you do not see these buttons on your VnmrJ window, click on View on top of the window and chose toolbar> graphic. You can also move this set of buttons around by pointing the mouse cursor to the three-dot  button and drag the buttons to wherever you like.


 The first one is Cursor button. It changes between one cursor  and two cursors .


 Show full Spectrum



 Reset to full display


 Zoom in

 Zoom out

 Zoom Mode. After click on this button, you can press and drag your mouse to define the region you want to expand.

 Pan & Stretch mode. Move spectrum up and down by press and move your mouse.

 Show integral regions. After you click on this button, three other buttons appear: 


 Show full Integral


 Define Integral Region


 Integral Lvl/Tilt, which used for flattening the base line.


If you click on Show full Integral button , another set of two buttons appear: 

 Hide Integral (no integral)

 Delete all Integral regions (cz)


 Show/Hide axis (dscale)

 Show/Hide Threshold for peak picking (Th)

 Phase mode for manual phasing

 Redraw

Return

 Close (for closing this set of toolbar)

Experiment 230: Solid-State NMR CP-MAS Operations

Sample to be used: Uniformly ^{13}C ^{15}N labeled Glycine

Step 1. Sample Preparations

- 1.1 For Natural Abundance samples 100 mg of solid sample will be needed. For ^{13}C or ^{15}N enriched samples >30 mg of sample will be required.
- 1.2 Pack sample into a Bruker solid-state NMR Rotor. Rotors can be obtained through Dr. Wu. Training on sample packing see solid-state NMR service instructor.
- 1.3 After packing sample spin-test rotor using Bruker MAS Manual Controller-C. Set Bearing Pressure to 20 psi and slowly increase Drive pressure until a spin rate of ~10 kHz. Spinning should be stable at ~10 kHz for 30-45 seconds. Then slowly reduce drive and bearing pressure and eject sample. Consult Dr. Wu for detailed training on using spinning module.

Step 2. Change Sample

- 2.3 Verify FTS System for temperature requirement.
- 2.4 Insert sample. Open the AVANCE 600 panel door and press **INSERT** on MAS Controller. Climb ladder and insert sample at top of magnet. At MAS Controller, press **SPIN RATE** and adjust with **up arrows** to 3500 kHz and press **GO**.
- 2.5 Once the temperature has reached 258K, press **SPIN RATE** and adjust with **up arrows** to 10000 kHz and press **GO**.
- 2.4 Have Dr. Wu or solid-state NMR Instructor assist you with the following steps in preparing the equipment: (1) tune the probe, (2) measure ^1H and ^{13}C pulse widths.

Step 3. Measure ^1H T1

- 3.4 Type **ased** and set **PULPROG** to cpecho_1H_T1_adcaq.av.akm.
- 3.5 Set dipolar dephasing delay (**d8**) to $1\mu\text{s}$ and **ns** to 1. Type **za** then phase a negative carbon signal.
- 3.6 Try different values of **d8** to find the value of **d8** that eliminates all signal (i.e. This value is T_{null}).
- 3.7 Approximate T1 as $T1 = T_{\text{null}}/\ln 2$. The recycle delay (**d1**) should be set to a value greater than $5 * T1$ (Typical T1 samples for peptides are between 0.2-1.5s).

Step 4. Measure Cross-Polarization (CP) Build-up

- 4.1 Type **ased** and verify **SPNAMO=ramp70** and **CPDRG2=spinal64.13**.
- 4.2 Type **ns=128** (or scans with sufficient signal to noise). Type **gs** and Zoom in on peak of interest and set **dp1** and **dp2** to define ppm range for peak.
- 4.3 Use **popt** program to array the contact time (**p15**) starting at $500\mu\text{s}$ to $3000\mu\text{s}$ in steps of $250\mu\text{s}$. Choose the contact time that yields the maximum signal.

Step 5. Record ^{13}C CP-MAS for Sample

- 5.1 Type **ased** and setup the following parameters

p3	^1H 90 pulse width	$1.9\mu\text{s}$
p12	^1H 90 power level	Obtain from Solid-State NMR Instructor
p15	CP Contact Time	Measure in Step 4
p11	^1H CP Power Level	Obtain from Solid-State NMR Instructor
p13	^1H Decoupling Power Level	Obtain from Solid-State NMR Instructor
p1	^{13}C Power Level	Obtain from Solid-State NMR Instructor
p2	^{13}C Hahn echo pulse	Obtain from Solid-State NMR Instructor
d1	Recycle Delay	Measure in Step 3
p11	^{13}C CP pulse width	$10\mu\text{s}$

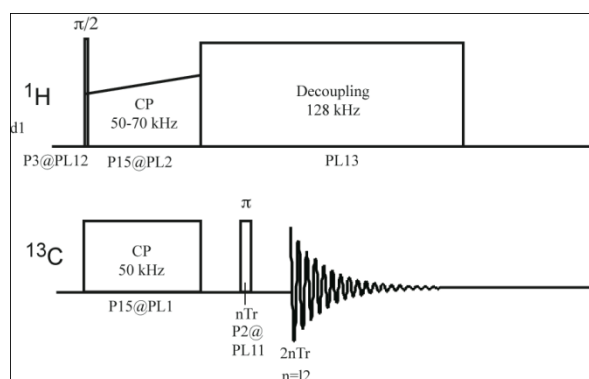


Figure 1: CP-MAS Pulse Sequence

- 5.2 Set **ns=1** and type **gs**. Verify FID takes between 1/2-2/3 of the screen. If not adjust receiver gain (**rg**). Type **gs** and have solid-state NMR instructor verify probe is properly tuned.
- 5.3 Set **ns=16-32k** of scans for natural abundance samples, and **ns=1-8k** for ^{13}C enriched samples.

Step 6. CP-MAS Data processing

- 6.1 Set **tdeff** then type **fp** to lowest value so that it does not attenuate signals of interest, while minimizing noise level.
- 6.2 Determine type of processing needed (**fp**, **efp**, or **gfp**). If using **gfp** set **gb=0.0005**. Set **lb** (- value for **gfp**) and array until signal drops by 1/2. Compare **gfp** processing to **fp** to determine if any desired resolution has been lost (e.g. a shoulder in a carbonyl peak you wish to analyze). Array **lb** by decreasing the magnitude of the number until resolution has reached desired level.

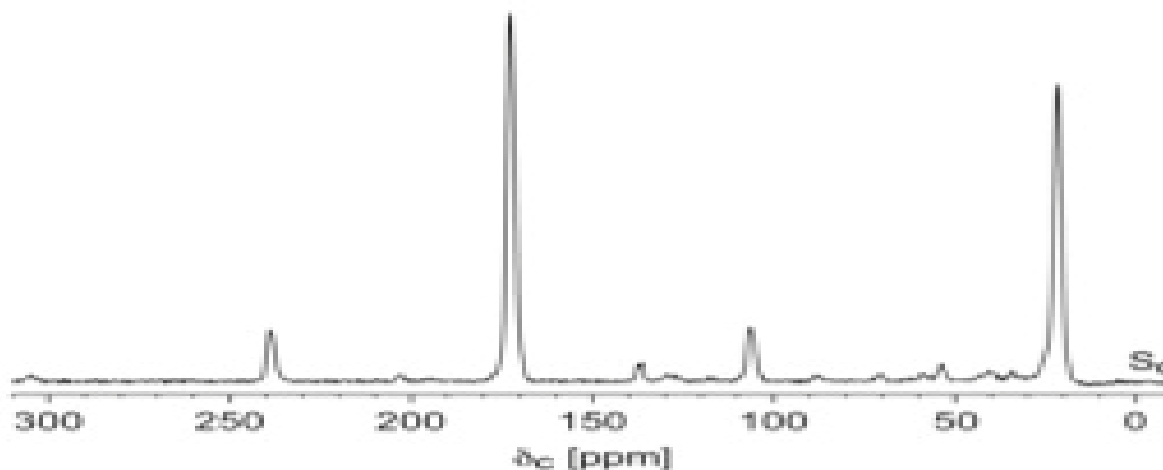


Figure 2: CP-MAS Spectra of peptide containing ^{13}C carbonyl label (172 ppm) on leucine and ^{13}C methyl label (23 ppm) on alanine collected at spinning speed=10 kHz. Note spinning side-bands from carbonyl peak at 238 ppm and 108 ppm – spaced 10 kHz from the center band. Remaining peaks represent natural abundance carbons from the peptide.

Appendix A: How to transfer data from NMR host computers to a PC or Mac

Step 1:

Download “CrossFTP” from Emory software distribute center.

<https://software.emory.edu/express/> You may use your Emory login ID and passwd. After installed, click file → connect → Use the following parameters to connect to NMR center server: SFTP/SSH Label: T310_server Host: 170.140.188.78 Part 22 uncheck anonymous User Name: ?????? Password: ?????? Proxy/firewall: Use global Setting Remote: /media/nmr_data Local Path: NMR_data in your own computer

Step 2:

Request a MNOVA license from NMR Center (License fee is required). Download the software from: <http://mestrelab.com/software/mnova-suite/download/> Software is available for both Mac and PC. Install the software and activate the license. Email your computer ID to Dr. Wu.

Step 3.

Save your NMR data to the server: After you complete the acquisition, type goserver ---- a micro that allows you to save NMR data to the right directory. Type your login ID. Click file, you will see the current directory of your group. You can make one your own under this directory. Type svf(‘file_name’).

Warning: Do Not Keep important data on the server, you have to back up your own data in case the system crashes, or hacked.

NMR Center has an internal network that is not connected to outside network. To access the NMR data on all NMR host computers, you have to use a PC to connect the internal network and download the data. There is a PC available in the NMR lab. Bring your own USB, or portable hard disk.

Login if screen is locked: username: nmr user
 password: nmr4me

Double Click on “Shortcut to Smart FTP” to open the Smart FTP window.

Type the IP address of the host computer you want to download data from in ‘Address’ box.

IP addresses for each host computers:

inova400: 170.140.188.70
inova600: 170.140.188.67
mercury300: 170.140.188.72

Type your group username in ‘Login’ box.

Type the password of your group in ‘password’ box and press Enter.

You maybe need to wait a couple of minutes to establish the connection.

When you see the folders and files appear in the panels, the connection is established.

Find your folders and files and drag them to the desktop (or you may want to create a temporary folder) on this computer.

Copy the data to the media you like: USB flash drive (flash key), zip disk, floppy disk or burn your data on a CD.

Delete your data and folders you created from this computer.

Appendix B: When and how to use command *su acqproc*

su acqproc is a command to connect or disconnect the communication between Sun host computer and CPU board in the NMR console. There are several occasions users need to use it.

When: The communication is lost. The computer seems not to respond to any command you typed in and you are not able to open the ‘acqi’ window. A word ‘inactive’ is usually shown after STATUS in the ACQUISITION STATUS window.

How: Open the Console window by double click on the Console icon on the up-right corner of the screen (Sometimes it is hiding behind ACQUISITION STATUS window). Type *su acqproc* and press **Return**. A message “Starting ‘Expproc’ will show up. At same time “Word ‘inactive’ will change to ‘idle’ in the ACQUISITION STATUS window. You should be able to operate the instrument again.

When: The Lock button is missing in the ACQUISITION window. It happens very often when you type h1, then immediately you clicked acqi. After you type h1, you should wait until “idle”, then click “acqi”.

How: Open the Console window, type *su acqproc* and press **Return** to disconnect the communication. Type *su acqproc* and press **Return** again to establish the communication.

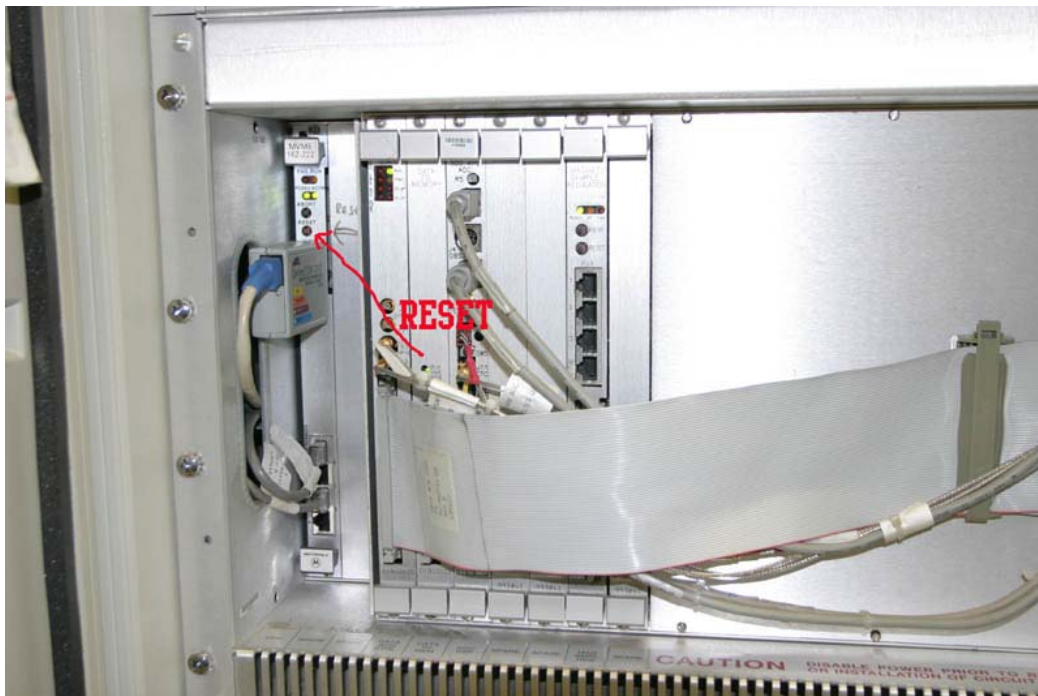
If above operation doesn’t work, you should call Dr. Wu for help. Sometime you have to reset the console when he asks you to do so. The following pictures show the reset button on different console.



UNITY600 Plus Console RESET button position.



Mercury 300 RESET Button position.



INOVA400 and INOVA600 RESET Button position

Appendix C: Most Useful Commands for VNMR and VNMRJ

aa—abort acquisition
ai—absolute intensity mode
alock='n' auto lock setting
alfa---Delay time before acquisition
aph—automatic phase correction
at—acquisition time (sec)
axis—scale units: axis='h' or axis='p'
bc—baseline correction
bs—block size
cd—change directory: cd('/data/nmryao')
cexp—create experiment: cexp(7)
cr—cursor value
ct—completed transients (scans)
cz—clear zeros (integral)
d1—first delay (relaxation delay in seconds)
d2—second delay in seconds
da—display array (parameters)
dc—drift correction
dconi—display contours interactively
delta—cursor difference
df—display fid
dfrq—decoupler frequency
dg—display group of parameters
dli—display integral list
dll—display line list
dlni—display normalized integral list
dm—decoupler mode: dm='nny'
dn—decoupler nucleus

dof—decoupler offset
dpcon—display plotted contours:
dpcon(10,1.2)
dpf—display peak frequencies
dpir—display integral regions
dpirn—display normalized integral regions
dps—display pulse sequence
dpwr—decoupler power
dres—digital resolution
ds—display spectrum
dscale—display scale descale(-10)
dssa—display stacked spectra
dssh—display stacked spectra horizontally
dtext---display text on the screen
f—display full spectrum
foldt—symmetrize 2D data (cosy)

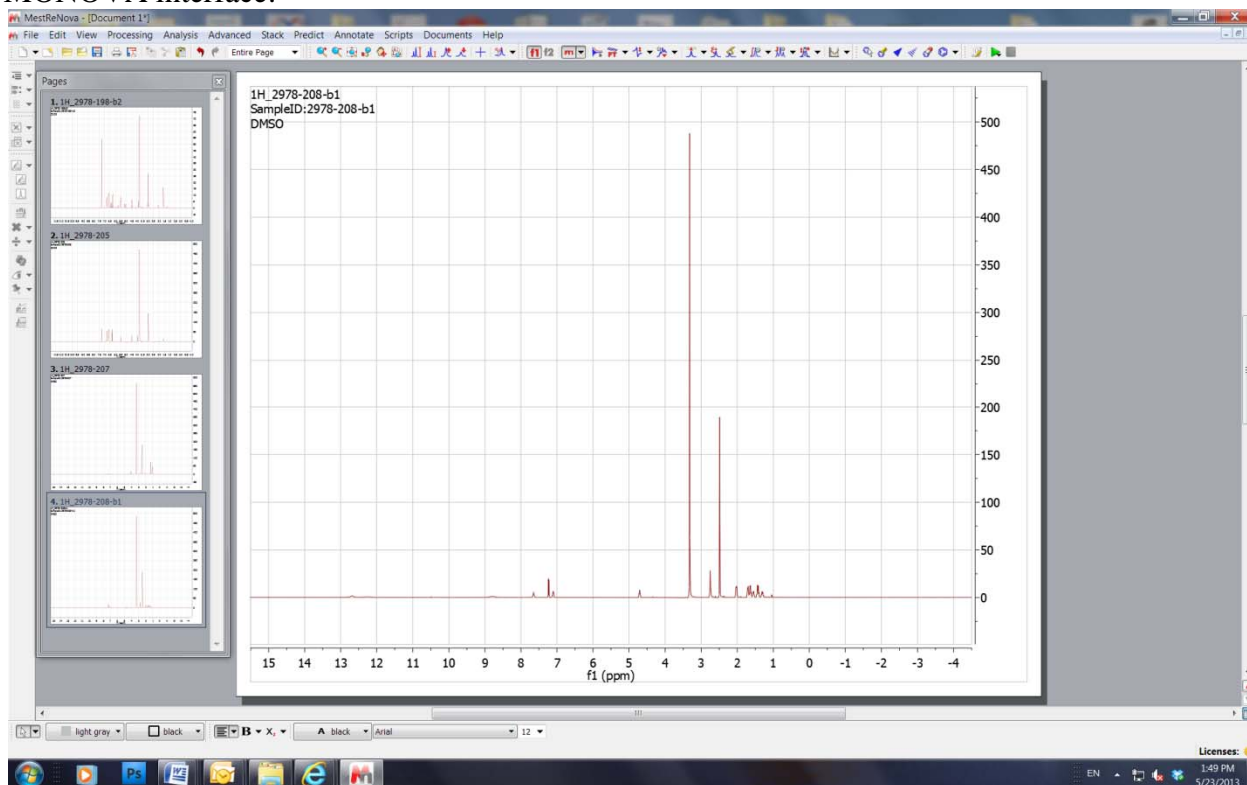
fn—Fourier number (zerofill)
fn1—Fourier number in 2nd dimension
full—display spectrum in full window
ga—acquire and process
gain—receiver gain: gain='n' for autogain
go—acquire spectrum
ho—horizontal offset
ins—integral normalization scale
io—integral offset
isadj—adjust integral scaling
jexp—join experiment: jexp2
lb—line broadening
lp—left phase
movesw—move sweepwidth
movetof—move tof
mp—move parameters: mp(1,2)
nl—nearest line
nm—normalized mode
np—number of points
nt—number of transients (scans)
pad—preacquisition delay
page—send to plotter
pap—plot all parameters
pcon—plot contours: pcon(10,1.2)
phase(180)—phase spectrum 180°
pir—plot integral regions
pirn—plot normalized integral regions
pl—plot spectrum
pll—print line list
plot—plot everything
plww—print spectra whitewashed
ppa—plot partial parameters
ppf—plot peak frequencies
process—transform, phase, integrate
spectrum
spsub---Subtract current spectra from exp5.
pscale—plot scale
pw—pulse width
pwd—present working directory
ra—resume acquisition (stopped by sa)
rl—reference line: rl(7.27p)
rof2---Receiver gating time
rp—right phase
rt—retrieve FID
rtp—retrieve parameters

rts—retrieve shims
sa—stop acquisition
sc—start of chart (in mm)
sc2—start of chart in 2nd dimension (in mm)
sd—set decoupler frequency
sda—add another decoupler value
sfrq—spectrometer frequency
sp—start of chart (in ppm)
sp1—start of chart in 2nd dimension (in ppm)
ss—steady state scans or dummy scans
su—setup hardware parameters
svf—save FID
svs—save shims only
svp—save parameters only
sw—spectral width or sweep width
temp—set temperature: temp='n'
tn—transmitter nucleus
tof—transmitter offset (middle of sweepwidth)
tpwr—transmitter power
text('your_ID\\date')
unlock—unlock a locked experiment:
unlock(2)
vo—vertical offset
vp—vertical position
vs—vertical scale
vsadj—vertical scale adjust
wc—width of chart (in mm)
wc2—width of chart in 2nd dimension (in mm)
wshim='n' start with auto shim
wp—width of chart (in ppm)
wp1—width of chart in 2nd dimension (in ppm)
wft—weighted Fourier transform
wft2d—transform 2D absolute value data
wft2da—transform 2D phase-sensitive data
wti—interactive weighting
z—cut integral reset

Appendix D: Processing NMR data with MNOVA

You can download the software from: <http://mestrelab.com>. If you don't have a license, you can use it free for 45 days. If you need a license, please talk to you advisor, if he agrees to pay for the license fee, then you can request a license from NMR center. MNOVA is friendly with window and Mac.

MONOVA interface:



After you transferred NMR data from NMR_data server to your PC or Mac. Then you can open the MONOVA software to process the data by dragging the data folder into the MONOVA window. The spectrum will be automatically processed.

Here is the complete operation manual: <http://mestrelab.com/resources/manuals/>