Bio-NMR facility training protocol

1. Put the NMR tube in the sample holder; and use the gauge to find the proper depth.

2. <u>eject and insert</u> the sample tube into the magnet.

3. Adjust the temperature.

4. Lock Deuterium signal. Lock scan; lock level; lock power; lock gain; lock phase; Z0;

5. <u>mtune</u>, matching and tuning for the 1^{st} channel (H¹), check tuning for the 2^{nd} (C¹³) and the 3^{rd} (N¹⁵) channels,

6. Z gradient shimming, use the proper shimming map file and number of shim iteration,

7. H^1 90° pulse calibration using "water" pulse sequence: make sure to check "presaturation" off, nt = 1, ss = 0, gain = 0, array pw, increment = 0.4, do 360° pulse calibration; and then find tof, (also can find H₀ in this step if you use DSS as the internal reference, zoom DSS peak, put curser on it, <u>nl</u>, <u>movetof</u>, <u>spcfrq</u>, go to the text area and writer down the H₀ value.)

8. N^{15} 90° pulse calibration using "gNhsqc" pulse sequence: update the parameters: H^1 pw, tof, tpwr, gain, ni = 1, ss = 4, calN = 2; array pwN,

9. C^{13} 90° pulse calibration using "gChsqc" pulse sequence: update the parameters: H^1 pw, tof, tpwr, gain, ni = 1, ss = 4, calC = 2; <u>array</u> pwC,

The basic operation commands:

su	setup exp.; setup parameters, and communicates with console
go	acquire data
ga	acquire data and then wft
SSS	input the filename first and save it automatically after acquisition is finished
<u>ssq</u>	input the filename first and save it, and then quit VNMRJ and log your account out automatically after acquisition is finished
aa	abort acquisition
e	eject sample
i	insert sample

<u>underscore</u> – customized commands

Common basic spectra parameters:

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nt	number of transients	
SS	number of dummy scans	
bs	block size	
d1	relaxation delay, also called recycle delay	
sw	spectral width; sw1, sw2,	
tof	transmitter offset; be the center of spectrum	
solvent	for adjusting referencing; D ₂ O in most case here	
pw	pulse width in us	
tpwr	transmitter power level; dpwr decoupler power level	
pw90	changing pw90 has no effect; some macros use pw90 to determine other	
	pulse widths to be used in the experiment	
gain	receive gain	
at	acquisition time	
np	number of total points in direct detect dimension; not complex points	
tn	transmitter nucleus; dn decoupler nucleus	
sfrq	spectrometer frequency of the nucleus being detected in MHz; dfrq	
	decoupler frequency in MHz	
dm	decoupler mode; e.g. dm = nny	
dmm	decoupler modulation mode; e.g. $dmm = ccg$	
dmf	decoupler modulation frequency; the frequency range that needs to be	
	decoupled in Hz; $1/dmf = 90^{\circ}$ pulse at decoupling power level (e.g. 41dB)	
ni,ni2	number of complex points in indirect detect 2 nd or 3 rd dimension	
dof,dof2	decoupler offset; equivalent to tof for decoupler nucleus	
1 (2) 1		

dmf2, dpwr2, dmm2, dm2 are equivalent for 3rd channel decoupler nucleus

Common spectra display and manipulate commands:		
movetof	move tof to where the current cursor is; follow by tof?	
movesw	set spectral width as the range between both current cursors on the spectrum	
centersw	put cursor in center of spectrum	
aph	autophase spectrum	
ft, wft	Fourier transform, or weighted Fourier transform	
f, full	display full spectrum in current range or in full graphic area	
vs	vertical scale; press middle mouse button to adjust or type vs? vs = 34567	
vsadj	auto-adjust vertical scale	
df	display fid	
ds	display spectrum	
nl	nearest line; puts cursor on the nearest peak top	
th	threshold; in millimeters	
dpf	display frequency values for all peaks above certain threshold	
dscale	display scale	
rl	reference line, put cursor on the resonance peak, rl(4.772p)	
dps	display pulse sequence	
res	resolution; displays the line-width at 50%, 55%, and 10% of peak intensity;	
	for checking shims and the base of the resonance	
dres	display resolution; displays the line-width at 50% of intensity for analyzing	
	quality of shims and the digital resolution	
array	setup a series of values for a parameter	
dssh	display stacked spectra horizontally	
dssl	display stacked spectra with number	
svf	save fid as a directory (filename.fid) including (binary) fid, (parameters file)	
	procpar, (note) text, and log file in /home/username/vnmrsys/data	
SVS	save current shim settings to a file stored in /home/username/vnmrsys/shims	
jexp1	jump to exp1	
explib	List all created exp.	
mp	move parameters, mp(10,12) move parameters of exp10 to exp12	
wft		
wft2da	weighted Fourier transform 2D for phase sensitive spectra ($phase = 1,2$)	
rp	right phase correct	
lp	left phase correct	
time	show total exp. time	

Common spectra display and manipulate commands: