Duke UNIVERSITY NMR Center

VnmrJ LIST OF USEFUL 1D COMMANDS FOR VARIAN/AGILENT NMR SPECTROMETERS

1D Setup/Acquisition

aa – abort acquisition, harsher than **sa**
array – array a parameter
at – acquisition time in seconds
bs – block size of data periodically stored to disk
cexp(#) – create experiment, example: **cexp(3)**
ct – current transient number
d1 – relaxation delay
dn/tn – 1st decoupler / observer transmitter nucleus
ds – number of dummy scans
e – eject sample
explib – list experiment library in "text output"
gain – receiver gain, if **gain='n'** == autogain
go/ga/au – start acquisition, **ga** adds **wft**, **au** does **wft** and **autoprocess**
i – inject sample
jexp# –join experiment, example: **jexp3**
man('command or macro name') – displays help for commands
mf – copy fid to another experiment, example: **mf(1,2)**
movesw – change the **sw** to cover the region between the 2 cursors
movetof – move **tof** (center of spectrum) to the cursor location
mp – copy parameters to another experiment, example: **mp(1,2)**
nt – number of scans
rts – retrieve the standard shim set
sa – stop acquisition, less harsh than **aa**
solvent – name of the solvent
ss – steady-state scans, scans with no data collection
sw – spectral width, example **sw=15p** to specify 15ppm width
sw1 – spectral width in 1st indirect dimension
su – send current parameters to the spectrometer: **load='y' su**
time – tells you how long the experiment will take
time(hours,minutes) – displays number of scans need for desired time of experiment
tof – transmitter offset, center of spectrum
unlock(#) – remove interactive lock and join an experiment

1D Processing

abc – auto baseline correction
aph0 – autophase zero order only
aph – autophase both zero and first order
bc – baseline correction with a spline or 2nd – 20th order poly
cdc – cancels the baseline drift correction offset (**dc** to turn it on)
dc – turn on baseline drift correction offset (**cdc** to turn it off)
ft – Fourier transform without window function
lb – line broadening, example: **lb=1**
lp/rp – 1st order / 0 order phase correction
lpbc(n+1) – back predict first n data points of FID, default n=63
peak – find tallest peak
process – runs the autoprocess macro to autophase, reference, baseline correct, etc.
rt('filename') – load saved data into current experiment
svf('filename') – save your data
wft – Fourier transform with window function Gaussian – automatically set up Gaussian window function
wtia – bring up interactive window to display and set window function

1D Display

ai – change to absolute intensity display, alternate is **nm**
av – display in absolute value mode, toggle with **ph**
adept – add/subtract set of DEPT expts
centersw – moves cursor to the center of the spectrum (**tof**)
cz – clears all integral reset points
cr – cursor position, example: **cr=8.0p**
da – display arrayed parameters
date – date of experiment
df – display 1D raw data (FID)
delta – print Hz difference between two cursors
dg – display standard parameters
dg1 – display plotting and display parameters
dli – list integral regions in the parameter window
dll – list lines in the parameter window above threshold set by
dpf – display peak frequencies over spectrum above threshold
dps – display pulse sequence
ds – display and refresh 1D spectrum
dscale – display scale if not shown
dssa – display 1D arrays stacked plot
dssh – display 1D arrays side by side
dssl – display array index, **dssl('value')** displays array values
dtext – display text string in graphics window
dres – calculates peak resolution/linewidth
dpir – display integral values below spectrum
dsn – measure/display signal-to-noise in region between cursors
f – expand data (spectrum and raw) to maximum size
full – expand display to full display and plotting sizes
ho – horizontal offset (mm) between staked spectra
isadj – automatic adjust of integral vertical display to fit page
nl – put the cursor on nearest line
nm – change to normalized intensity display, alternate is **ai**
ph – display in phase sensitive mode, toggle with **av**
r1 – recall display parameter set saved with s1, r1-r9 can be used
rl(shift) – set reference line on the cursor location, example: **rl(7.26p)**
s1 – save display parameters, s1-s9 can be used, recall with **r1**
text('string') – text saved with data, example: **text('sample aa2345-6')**
th – parameter to set threshold for line list
thadj(maxpeaks,noise_mult) – adjust threshold so that no more than max number of peaks are found
vsadj – adjust the vertical scale so that largest peak shown fits on screen
vp – vertical position (mm) of spectrum
vo – vertical offset (mm) between staked spectra
vs – vertical scale of spectrum
z – manual method to set integral reset points

1D Plotting

page – send to plotter, example: **pl pscale ppa pir ppf page**
pap – plot long list of parameters (**ppa** is short list)
pir – plot integral region amplitudes under the regions
pl – plot spectrum, will need to be followed by **page** or **iupage** command
pll – plot peak list in a column for peaks higher than the value
plotter –set common plotter use: **plotter='sun2lj'** full
pltext – plot text string, use **text('string')** to create
ppa – plot short list of parameters (**pap** is long list)
ppf – plot peak frequencies over peaks for peaks higher than the value
pps – plot pulse sequence