Anasazi EFT60 Nuclear Magnetic Resonance Spectrometer

Solution height must be 4.0 cm (0.7 mL in tube).

Remove previous sample by opening top door (lift front edge), holding in the *launch* button and catching tube. (Be ready when the tube pops up!) Place tube in spinner, and adjust the height using front gauge. Place spinner and tube in sample shaft and use your thumb to seal the shaft. Use the flashlight to check if the lowered tube is spinning.

Sign the logbook. (Always note any difficulties to alert others to potential problems.)

The Anasazi NMR uses two programs, one to collect data (PNMR) and one to analyze data (NUTS). Usually PNMR is the left window and NUTS is the right window. You can use *alt tab* to switch between them or use the tabs at the bottom of the window. The advantage of the two programs is that you can examine collected data without interrupting ongoing data collection. Unfortunately, the PNMR program requires you to press *enter* (return) to accept a value and the NUTS program uses *enter* (return) to cancel the command.

zg enter in PNMR (left window) to **collect dat**a.

Enter file name or use default (pnmrfid) by pressing *enter*.

Wait for data collection to finish, then *alt tab* or click NUTS (right window).

a0 in NUTS to **import and Fourier transform** data (*ga bc ft qp fb l ^m ^f*).

Enter file name or use default (pnmrfid) by pressing *enter*.

Optional:

While holding mouse down over known peak, *sz* [value] *return* to set ppm.

Use mouse wheel to adjust peak heights so tallest sample peak reaches the top.

To phase use *qp* or *ap* (no enter) or *zo* (select left area) *0 enter zo* (select right area) *1 enter pe* (phase left with left drag, phase right with right drag) *enter*.

a8 (no enter) to **integrate** (*ai id z*)

Click within a region then *v* [integer] *enter* to set the region integral value.

Enter enter to leave integral mode.

Optional:

Drag far left slider to adjust integral scale.

Drag near left slider to adjust vertical zero.

c to clear all regions and start again.

Double click to left of peak and single left click to right of peak to add new region.

pp updates and labels peak positions, *pf* turns labels off, *mh* minimum height for labeling, *dp* manually labels peaks.

a9 (no enter) to **print** (*zo f ^m ^e pl*).

Normal response is *12 tab -.5 enter* for proton or *250 tab -10 enter* for carbon.

Inset plots: *zo* and drag to select region, CTRL-E (or right click) to expand, *enter*. *mo* to inset, click *A* to add view, drag, then CTRL-F (or right click) to resume full scale. Can *mo* again to position or remove box. *Delete inset* for every new sample.

The previous page assumes nucleus (*nu H1* or *nu C13*) *fo* and *shim* are set. See below.

Acquisition parameters (PNMR software)

Nucleus *nu enter H1* or *nu enter C13*

(Choose either proton or carbon-13 after which the choice will be displayed as the command prompt.)

Size *si enter 16384* (8 sec) or *si enter 8192* (4 sec) or *si enter 4096* (2 sec)

(To set the acquisition time, you change the data size *si*.)

Number of scans *ns enter* value

(Reasonable values for proton are 1, 4, or 8 and for carbon are 64, 128, 256. For more scans see *bapr* below.)

Relaxation delay *rd enter* value

(seconds. Shorter relaxation delays require smaller pulse widths.)

Pulse width *pw enter 17.8* or less

(μseconds. Use the 90° pulse, which can be measured with *h90cal*, or less.)

Receiver gain *gs enter*

(This displays the FID signal, which should not reach the red horizontal lines. Press CTRL-G to get a dialog box and enter a new value, 1-100. For protons in water the correct gain is about 5; for a typical organic molecule dissolved in chloroform the gain is about 60. In this mode you can also change the pulse width using CTRL-P and the relaxation delay in seconds using CTRL-R. When you are finished use CTRL-Q to quit the adjustment.)

Field Offset *fo enter*

(Run a spectrum, *alt tab* NUTS, find position of known peak, *alt tab* to PNMR, *fo enter* value for found and known position.)

Collect data *zg enter*

(Erases previous data file, starts acquisition, and saves new data. To collect more scans without erasing, for example a second set of 256 scans for carbon-13, use *go enter* instead. CTRL-S to stop.)

*B*lock *a*veraging with *p*eak *r*egistration (for longer runs than *ns* 256) instead of *zg* above

ns value *bapr enter enter 24 enter enter*

Uses default filename, my_bapr, and 24 blocks of data. *Alt tab* to NUTS, *a1, zo* to select a single strong isolated peak *0 enter*, CTRL-F12 to select my_bapr and process. Can examine while still collecting data. *lb 1*

Write/Read file *wr enter* or *re enter*

(Write/Read the FID data file, current parameters to a .ini file, or current shim settings to a .shm file.)

Other commands: COSY (F5), HET(F6), T1(F7), DEPT(F11)