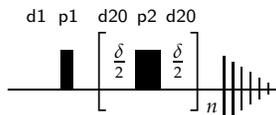


## Measurement of T<sub>2</sub> Values

The T<sub>2</sub> relaxation time of NMR peaks may be measured through the Carr-Purcell-Meiboom-Gill (CPMG) pulse sequence,



which prevents the z-magnetization from relaxing while the transverse magnetization undergoes coherence loss. This sequence is repeated for a series of loop counts ( $n$ ), and the resulting signal intensity is regressed *vs.* the total delay time.

### Setup/Acquisition

1. Inject a sample, lock, shim, and acquire a proton spectrum as normal, without spinning (ro off).
2. Change pulprog to cpmg. Select the AcqPars tab (or type eda) and use the  button to convert the parameters to 2D.
3. Create the vc-list, which contains the  $n$ -values to be used, and set the vclist parameter:
 

```
edlist vc t2delay
vclist t2delay
```
4. Adjust other parameters for the CPMG sequence:
 

d1	=	$5 \times T_1$ for <sup>1</sup> H	typically 20 s; long is critical
td(F1)	=	number of items in vc-list	
d20	=	10m	relaxation delay ( $\frac{\delta}{2}$ )
ns	=	8	a multiple of 8
ds	=	2 or 4	
5. Start the acquisition (rga; zg). Type expt to see how long the experiment will run — usually about 40 min.

### Processing

6. Set si (F1) to a power of 2 greater than td (F1). Set the F2 line broadening, lb (F2), to 1.
7. Type xf2 to Fourier transform data-set.
8. Enter “rser 1” to select the first slice of the spectrum in a new window. Type efp to Fourier transform the slice.
  - a. Expand on the region of interest.
  - b. Phase the spectrum. Ensure that the baseline looks good and multiplets are symmetric, even if the multiplets do not properly phase.
  - c. Integrate the peaks of interest:
    - Type .int and integrate each peak for which T<sub>2</sub> should be calculated.
    - Save as “intrng” and return, using the  and  buttons.
    - Type wmisc intrng t2rng to write the integration-region list as “t2rng”.
  - d. Set the frequencies for which T<sub>2</sub> will be calculated. As you do this, it is important to only choose *one* line within each integral region, and to choose the line with the maximum intensity.
    - Type .bas1 to enter baseline-correction mode.
    - Use the  button to pick baseline points.

- Save and return. The software will complain about insufficient points. You can verify that the points are indeed picked by clicking  again: red boxes with arrows should appear on the peaks. Click .
  - Return out of the peak-pick subroutine.
  - Type `wmisc baslpnts t2bas` to write the baseline-points file as "t2bas".
- e. Create a delay list from your `vc-list` (loop-count list).
- Open the terminal emulator (right-click on desktop, choose "Konsole") and, at the command prompt, enter `vc2vd`.
  - Enter the acquisition parameters it asks for (`d20`, `p2`, and `vc1list`) from the acquisition parameters (`ased`) or pulse sequence (`spdisp`).
  - Write the new `vdlist` to `t2delay`.
9. Return back to the 2D spectrum and enter `proc_t1` into the TopSpin command line. The macro will ask for a series of parameters. Reply with the following:
- ```

FID number      = 1
limits          = 1000 to -1000
drift           = 20
baselinepoints file = t2bas
integrals file   = t2rng
vd file         = t2delay      (or other filename chosen through vc2vd)
calculation type = 2

```
10. Once the calculations have been performed, obtain the results by clicking the  :  :  :  buttons from the top tabs. If any bad data-points need to be omitted,
- a. Click the check-list icon to verify that the Function Type is UxNMRT2.
  - b. Click the +/- buttons to select the peak you wish to modify.
  - c. Click the  button, move the cursor to select a data-point, then right-click on it.
  - d. Once the point is deleted, the  and  buttons will recalculate the fit.