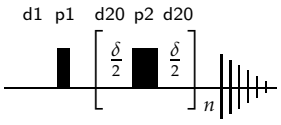
Measurement of T2 Values

The T2 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 AcquPars tab (or type `eda`) and use the $\boxed{\downarrow_{1,2,..}}$ 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 × T1 for ^{1}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 T2 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 T2 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 `.basl` 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 cancel.
- 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 `vclist`) 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 Analysis : Dynamics : T1/T2 : Relaxation 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.