

Processing and analysis of ^{15}N R_1 , ^{15}N $R_{1\rho}$ relaxation experiments

Spectra has been recorded on a Bruker system

^{15}N R_1

1. Copy the files from the attached folder T1 to the working directory (experiment folder).
2. `$ chmod u+x *.com`
3. `$ bruker` to open the NMRPipe Conversion Utility and generate the `fid.com` file.
4. `$ fid.com`
5. `$ split.com` (For R_1 the Bruker `vclist` must be converted into a `vplist` with ms entries beforehand: `$ mv vclist vplist` and edit the `vplist`).
6. `$ nmrproc.com` (Edit the tauValues [`vplist` values] beforehand).
7. `$ nmrDraw` to draw the spectrum and pick the peaks. If the phase is not correct press v for vertical 1D-signal projection and h for horizontal 1D-signal projection. With P0 you can adjust the phase, remember the phase difference and correct the phase in the `nmrproc.com` file.
8. `$ ass.com` (copy a peak list in your working directory beforehand) to assign the spectra. Left mouse button to assign, right mouse button to deassign peaks.
9. `$ python3 NoneDeleter.py` to create `relax.tab`.
10. `$ relax.com`
11. `$ autoFit.com`
12. `$ model.com`
13. `$ modelExp.com`
14. `$ bash summary.tcl -in relax.tab > t1.tab`
15. Copy `t1.tab` into a newly created directory `data`.

^{15}N $R_{1\rho}$

1. Copy the files attached from the folder T1rho to the working directory (experiment folder).
2. `$ chmod u+x *.com`
3. `$ bruker` to open the NMRPipe Conversion Utility and generate the `fid.com` file.
4. `$ fid.com`
5. `$ split.com`
6. `$ nmrproc.com` (Edit the tauValues [`vplist` values] beforehand).
7. `$ nmrDraw` to draw the spectrum and pick the peaks. If the phase is not correct press v for vertical 1D-signal projection and h for horizontal 1D-signal projection. With P0 you can adjust the phase, remember the phase difference and correct the phase in the `nmrproc.com` file.
8. `$ ass.com` (copy a peak list in your working directory beforehand) to assign the spectra. Left mouse button to assign, right mouse button to deassign peaks.
9. `$ python3 NoneDeleter.py` to create `relax.tab`.
10. `$ relax.com`
11. `$ autoFit.com`
12. `$ model.com`
13. `$ modelExp.com`
14. `$ bash summary.tcl -in relax.tab > t1rho.tab`

15. \$ Copy the following header in the *t1rho.tab* file (you get the values from the *fid.com* file):

REMARK 600MHz for T1rho

REMARK -γOBS = 60.818

REMARK -γCAR = 119.06

16. \$ *extract_PPM.com* will generate a table called *fusionOffset.tab* that contains the offset of the peak ¹⁵N frequency relative to the carrier frequency (which will be needed to calculate the angle θ for the extraction of R_2 data from the R_1 and R_{1p} data).

17. Copy the *t1rho.tab* and the *fusionOffset.tab* into the directory *data*.

18. Adjust spectrometer frequency, and spin-lock power in the script *crtR1p.tcl* and execute:

\$ *crtR1p.tcl* | *sort -n* > *R1R2.tab*

19. *R1R2.tab* will contain the fitted R_{1p} rates, theta angle, R_2 rates, and R_1 rates.