

Optimizing 1D Array Acquisition Parameters

Preparations - Tune, lock, and shim as usual. If possible, determine T1 if it's unknown.

Step 1 – Optimizing acquisition time (at). Reducing **at** by half will cut your final data size by half. It will also cut the time required for each fid by up to half.

- a) **gain='n'** **nt=1** **ga**
- b) **ds** and check the range of linewidths in the spectrum, then set **lb** accordingly.
- c) **df dscale** to determine optimal **at**, and set **at** to the determined value
- d) **gain='y'** **ga**. Check the sharpest signal in the spectrum and see if it's well defined with sufficient data points. If not, try setting **fn=2*np wft**, and check again. If not, increase **at** accordingly.

Step 2 – Optimizing spectral width (sw). Reducing **sw** by half while maintaining **at** will also cut your final data size by half.

- a) **ds f full**. Place cursors to include just enough empty baseline on both ends of the spectrum to ensure a good baseline, and enter **movesw**.
- b) **ga**, phase spectrum, and make sure the spectral window has been set correctly.

Step 3 – Optimizing relaxation delay (d1).

- a) If you need to accurately compare integrals from different signals in the same spectrum, set **d1 = 5*T1(longest) – at**
- b) If not, set **d1 = 1.3* T1(longest) – at**. If $1.3 * T1(\text{longest})$ is less than **at**, set **d1=0**.

NOTE: The above procedures apply to the acquisition of 1D array data for ¹H as well as for other nuclei. However, since all other nuclei are less sensitive than ¹H, you may need to take more scans in Step 1 in order to have a good fid to look at. The other nuclei's lower sensitivity also places more importance in Step 1 and 3, since setting **at** and **d1** too long will be a waste of time.