Kinetics / reaction monitoring

Introduction

As an intrinsically quantitative analytical technique, NMR spectroscopy can be used to measure concentrations of different components during chemical reactions for period of a few minutes to multiple days. One can either take a series of 1D spectra or acquire the data in pseudo 2D mode over the period of reaction. The best way to analyze the resulting data is to use MNOVA.

Before starting, you should have good estimates of the timeframe for your reaction and T1 relaxation time for your sample. Setup the **d1** and **aq** accordingly to make sure the relaxation time (**d1+aq**) is at least $5*T_1$. In general, the aliphatic protons on small molecules have T1 around 2 s and aromatic proton at about 4 s. You should run T1 experiment to get the numbers since it is very sample/solvent dependent.

1D method is a very versatile. Setup the 1D you will repeat and run **multi_zgvd**. It can be either a single pulse or single pulse with decoupling, i.e. F19 or F19CPD. The drawback of this method is that the timing between spectra can be off by a few seconds especially when your kinetics are fast and take less than an hour. The pseudo 2D, on the other hand, gives perfect timing for each fid, but it can be used only for single pulse experiment.

Once you decide how often you take a spectrum, you need strike a balance between the time resolution of the kinetic measurement and the amount of time needed to obtain sufficiently good signal-to-noise for each experiment. Limit the number of scans (ns) to be as small as necessary for adequate signal-to-noise to improve time resolution.

Before starting your reaction, please setup the experiment you want to repeat with a test sample with conditions similar to your real one. Do the locking, tuning, and shimming. Find the appropriate number of scans (ns) for adequate signal-to-noise. If resolving peaks is not a concern, you do not have to do lock/tune/shimming after putting the real sample in. Simply start acquiring the data, especially for F19.

Separate 1D Spectra w/ multi_zgvd

This works for any nucleus, including proton.

1) Assume you already determined how often you want to run your recurring 1D experiment, let's call it **D20**, delay between start of different 1D spectra
2) Start with a normal 1D spectrum to adjust the spectral sweep width **SWH**, acquisition time **aq,** offset **O1p,** number of scans **NS**, and other parameter obtain sufficiently good signal-to-noise if necessary. Type **expt** to calculate how much time it takes. Let's call it "$\mathbf{T_{expt}}$". The delay between the end of one fid and start of next one equals $\mathbf{D20\text{-}T_{expt}}$. Let's call it $\mathbf{D_{fix}}$.
3) Create a new dataset with exactly same parameters from step 1. Start your reaction and load your sample to NMR instrument as fast as you can. Since you have already done locking/tuning/shimming on a test sample with similar conditions, you have following options:
   a) Do a topshim session first if your kinetics takes hours to finish.

b) Skip the topshim if your reaction is really fast

4) Run **multi_zgvd**, when asked for a fixed or variable delay, answer with the default (fixed delay), then give the $\mathbf{D_{fix}}$ as the input for next question. For the question of "Enter number of experiments", give the numbers of experiment you want to run.

5) During the run, you can use **multiple display** to check peak intensity changes to evaluate if you reaction finishes or not.

Pseudo 2D Mode Procedure

The following procedure can be used for any nucleus.

1) Following step 1 and 2 of previous section to optimize the 1D experiment you want to repeat.

2) Create a new dataset and load the parameter set "**kx_zg2d_nu**".

3) Input the **D20** (delay between start of different 1D spectra) as shown in **Fig 1** and **TD** on F1 dimension (how many 1D spectra you want to acquire) as shown in **Fig 2.**

4) Start your reaction and load your sample to NMR instrument as fast as you can. Since you have already done locking/tuning/shimming on a test sample with similar conditions, you have following options:
   a) Do a topshim session first if your kinetics takes hours to finish.
   b) Skip the topshim if your reaction is really fast

5) Start your experiment by typing **zg** or click on "**run**".

6) During the run, you can use **rser** to check each individual fid as long as it is finished. For example, "**rser 1 10**" will write the 1st fid to experiment number 10; "**rser 20 11**" will write the 20th fid to experiment number 11. Then you can use **multiple display** to stack or superimpose them.

Fig 1. ACQUPARS display in “pulse program parameters” view

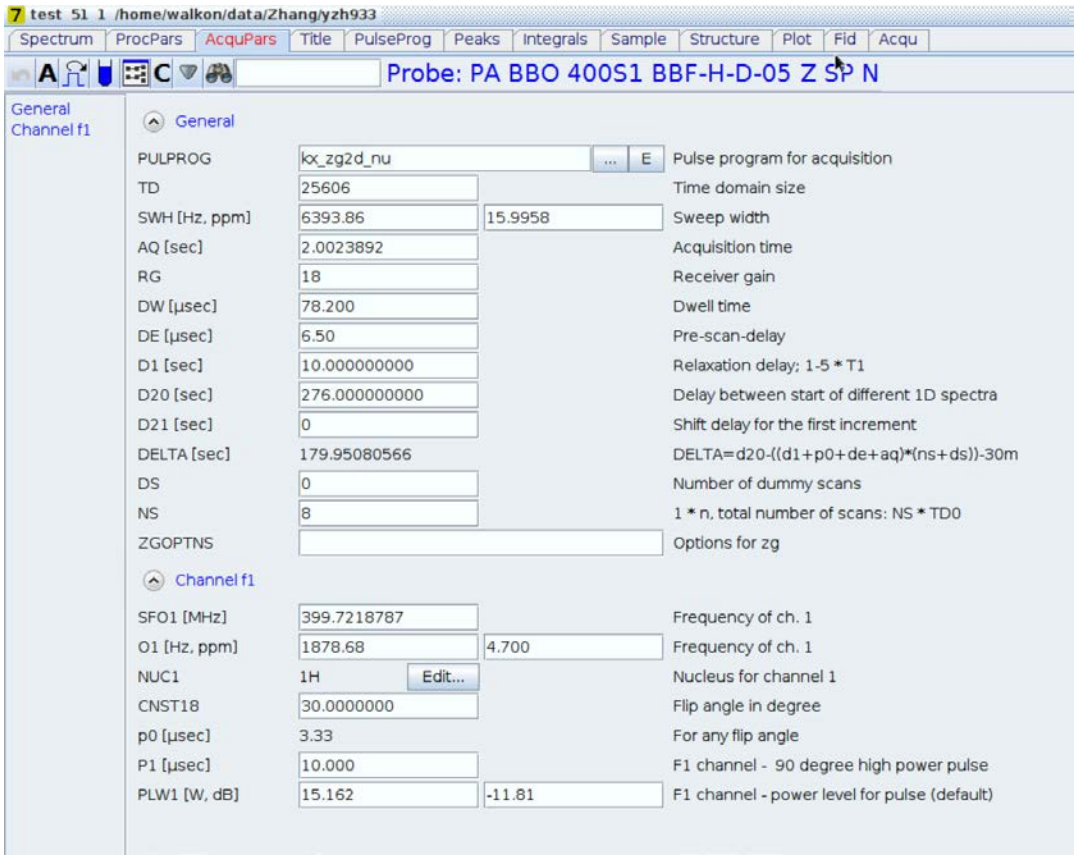

Fig 2. ACQUPARS display in “all acquisition parameters” view