

# Kinetic NMR Experiments

## Using Topspin

When doing a NMR kinetics experiment, one wants to take a series of spectra over a period of time. There are two possible ways to do this: with the `kineticzg` program or in pseudo 2D mode. The simplest is with the `kineticzg` program. If the kinetics are fast and the time delays between spectra are short (less than a minute), `kineticzg` is NOT a good option since the timing is not 100% accurate. You should use the 2D mode procedure, described at the bottom. The 2D procedure also allows non-linear sampling of the kinetic data.

For either method, one needs to consider the number scans taken for each spectrum since it will affect the time resolution of your experiment. That is, if your delay between spectra is only 5 minutes and each spectra requires 5 minutes then your time resolution would be poor. Limit the number of scans (ns) to be as small as necessary for adequate signal-to-noise to improve time resolution.

### Kineticzg Method

This results in a series of spectra that are linearly spaced over time, i.e., each spectrum is separated from the next by the same amount of time. `Kineticzg` is simple: it simply increments the experiment number a specified number of times, recording spectra according to the parameters in the beginning experiment number.

Set up as for a normal 1D experiment. Define data set. Read parameters. Lock, shim, tune the probe, as well as adjust SW, O1P, NS, etc. Be sure to take a simple 1D spectrum first and thus adjust RG (rga or start command). Do not spin.

- 1) Type "**edau kineticzg**", then *Return*.
- 2) The program is displayed. The time between spectra needs to be specified. This done by changing the number next to '*sleep*' (**sleep (number)**). ONLY CHANGE this number, which is in seconds. This is the time from the end of one experiment to the beginning of the next.
- 3) Click "**Save**", then "**Quit**" buttons on the top of the window
- 4) You will be asked '*compile*', '*ack*' and '*quit*'. Type "**c**", then *Return*. Since the `kineticzg` program is shared between users, this step must be done each time, since other users may have altered the sleep time.
- 5) Type "**kineticzg**", then *Return*. **This replaces the `zg` command.**
- 6) You will be asked '*number of experiments*'. This is the total number of spectra (max256). Enter and type *Return*. Experiment starts.

Good homogeneity (shim) is maintained during the experiment (even overnight) at 300K and 310K, borderline at 320K, but above 320K, the shim may drift. One can shim

manually after each experiment or use autoshim. To use autoshim, simply press the autoshim button at the bottom of the BSMS (lock) keypad.

### Processing: Multi efp

The program **multiefp** performs **efp** to a series of 1D NMR spectra that have sequential experiment numbers, which is the case here.

- 1) Go to the first experiment number of the series and phase it.
- 2) Type "**xau multiefp**", then *Return*
- 3) In the popup window, type the experiment number of the first spectrum you want to do efp.
- 4) In the next window, type the total number of spectra you want to do efp.

### Multi Integration

The programs **multi\_integ** or **multi\_integ3** automatically integrate a series of 1D NMR spectra. They each send the output to a text file, but differ in the output format.

**Multi\_integ3** is appropriate for Microsoft Excel.



- 1) Go to the first spectrum you want to integrate.
  - 2) Do integration as usual on the region you are interested in (including phasing, calibration, etc.), then click "**return**" and "**save**".
  - 3) Use must now "export" this integration region for subsequent use. Type "**wmisc**", then *Return*.
  - 4) click "**intrng**" button.
  - 5) Type '*a filename*' (any name, but not your experiment folder name) at the bottom or click one of file names (if owned by you!) listed on top, then *Return*.
  - 6) Now you are ready to integrate all the spectra. Type "**multi\_integ**" ( \_ is underline), then *Return*.
  - 7) On the next window
    - type "**0**" if your spectra are stored by a series of experiment number. **This is the usual case.**
    - type "**1**" if your spectra are stored by a series of process number.
    - then *Return*.
  - 8) In the next window, type '*the experiment (or process) number of the first spectrum*', then *Return*.
  - 9) In the next window, type '*total number of spectra*' you want to integrate, then *Return*.
  - 10) In the next window, type '*the filename*' you decided at step 5, then *Return*.
- When processing is completed, a pop-up window shows the directory and file name of your result. Note this or keep the window open for reference.
- 11) Open new unix shell.
  - 12) Change to the directory shown on the pop-up window above.
    - \*\*\* for example: type "**cd /300wb/data/(user name)/nmr/(folder name)/(first exp number)/pdata/1/**
  - 13) **Multi\_integ** stores the results in the file under the name of "**int.all**".
  - 14) To see the integration result on screen, type "**more int.all**", then *Return*.

15) To print the integration result, type "**lp int.all**", then *Return*. You can also move to a PC formatted zip disk for further analysis.

## 2D Mode Procedure




The 2 mode is better and more versatile. It allows non-linear spacing between spectra and the timing between spectra is exact. It uses the  $T_1$  subroutines for processing so getting intensity data for the whole series is simple. Like a  $T_1$  experiment, a list of delays must be specified, which in this case is the time between spectra. For a constant time between spectra, the list need have only one value. The program “loops” if the number of spectra exceeds the number of values in the list. The following procedure is very general and thus can be used for any nucleus.










### Acquisition setup

1. Read standard 1D parameters for your nucleus of choice (rpar protonstd). Lock, shim, tune the probe, take a normal 1D spectrum.
2. Create the file with a list of delays times between spectra. Type edlist vd filename, where filename may already exist or be new. Delay values are in seconds and define the time between spectra. The first value should be nearly zero, say, 0.00001 sec., since the variable delay comes before each spectrum. Delay times can be spaced non-linearly for optimal sampling. You may need tens to even a hundred values. A single delay entry is sufficient if you want a constant delay and thus linear spacing. Save.
3. Change to 2D mode: click AcqParms, and then click  and select 2D and then OK.
4. Change the pulse program: in AcqParms find the parameter pulprog and change to zg\_kinetics.
5. Set several parameters. In AcqParms, set td in F1 to the number of 1D spectra you intend to take. Click  to access pulse-program parameters Adjust ns and d1 as appropriate. For the parameter vdlst, enter the name of the file just created or modified above. Click the Spectrum tab to save.
6. Type start to begin.

NOTE: If you have completed the above setup in the past and have kinetic data, the above parameters may be reused by simply creating a new data set (new) from an existing data set. All parameters are copied into the new data set.





### Processing

Processing is similar to  $T_1$  experiments. You must first phase all the spectra. Click ProcParms. For the parameter si in F1, make equal to or slightly greater to td in F1. Set PH\_mod to pk in the F2 dimension. Click the Spectrum tab to save. Type rser # to read in one 1D spectrum (if there are 15 delay values, then # may rang from 1 to 15). Type ef and phase this spectrum. After adjusting the phase, save the phasing to both 2D and 1D by clicking on , , and then to exit .

You should now see a 1D spectrum. Next, you will choose which peaks are to be analyzed, based on intensity or area. Click peak pick  and then add one or more peaks manually by clicking  and select peak with cursor and left click. Click  to export to the relaxation analysis routine. Then, click save+return . You also need to define integral regions. Click integrate . Click  to define beginning and end of integral; press left button and drag to define. After adjusting integral, export to relaxation module by clicking  and then choosing Export Regions to Relaxation Module. Then, click save+return . Click  to close the 1D spectrum and return to 2D.


Type xf2 to transform all the spectra.

(If at any time you wish to return to the above 1D spectrum, type rsr #.)

Type t1/t2 to enter the relaxation sub-routine. Your points should be automatically picked. To pick them manually, click . To adjust the settings, click . If your points are not all being picked, you may also need to increase the number of drift points are then re-pick. Click  to calculate T1. To delete a particular, possibly outlying point, right-click over the point and select delete. If you have picked more than one peak in your spectrum, click + or – to change to the next peak. Click  to generate a report. This report is saved as a text file in your process number directory of the NMR data and can be easily downloaded from the NMR server and then cut-and-pasted into Excel for further processing.

The time axis of your data will not be correct because the program is only aware of the time between points. You will need to construct the cumulative time in order to have the proper time axis. This can easily be done in Excel.

## Plotting

You may wish to generate a stack plot of all or only certain spectra. To do so, you must “export” each 1D spectrum you wish to a separate 1D process number. Then, the selected 1D spectra can be imported into Topspin editor for plotting. Under Processing, select rows and columns, and then choose interactive row/column display. Then click  to scan rows of data. Choose the desired row and right-click the mouse and choose extract row/column. Give a Procno not yet taken (usually 1 is taken by the 2D data so start with 2) and click OK. You are transferred to 1D spectrum. To close this spectrum, simply click its X box in the upper right corner. Repeat if desired.

To export all rows to 1D spectra, use the command splitter, which puts every 1D into a different experiment number.