DCIF Training Guide
Kinetics
Bruker 400/401/600

(20080919)

As with all of the other DCIF tutorials, the conventions used in this guide are as follows:

- **Boldface** type indicates commands that are typed into the Topspin command line or in a terminal window
- Italic ***[Boldface]*** type with square brackets indicates a button in the Topspin menu that is to be pushed.
- **<Boldface>** type surrounded by a bracket indicate keyboard strokes.
- **LMB** indicates the Left Mouse Button
- **MMB** indicates the Middle Mouse Button
- **RMB** indicates the Right Mouse Button
- Unless otherwise noted, all commands typed into the input window are followed by an <↵ Enter> keystroke.

1. Insert, lock and shim your sample.

2. Setup the parameter set; tune the probe if necessary.
    a. In order to measure accurate integrals you should determine the T1 relaxation time for your molecule. Your delay should be 5x longer than T1 for quantitative measurements.

3. Acquire a trial run and note how long the acquisition takes.

4. Type **dcif-kinetics**
    a. "This program will automatically increment the experiment number for a given number of acquisitions." Continue (y/n) **y**
    b. "How many data sets will you acquire (total)?" **#**
    c. "How long of a delay (in seconds) between experiments?" **#** (seconds)
        i. This is the delay between when each experiment starts. Make sure this delay is longer than the total acquisition time needed.
    d. The acquisition should start automatically.

5. When the entire array is complete Topspin should display " Kinetics Experiment Complete"

6. The resulting experiment numbers will be contiguous. If you setup and start the array of 10 spectra in expno 1, expno 2 through 11 will have your data.
    a. The command **dpa** will display the time the acquisition started.
    b. To review each experiment type **re <#>** or type **search.**

7. Use the TopSpin Plot Editor to print stacked spectra.