

Laboration 10

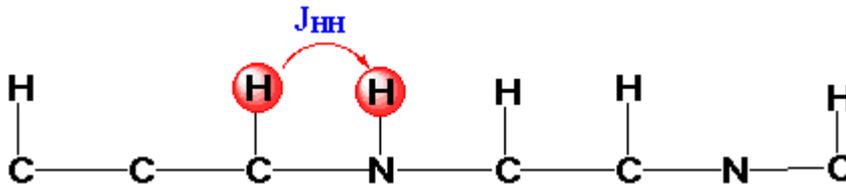
COSY
Magnitude mode

KR

Theory

COSY

The **2D COSY (COrrelation SpectroscopY) experiment** is the most simple and widely used 2D experiment. It is a homonuclear chemical shift correlation experiment based on the transfer polarization by a mixing pulse between directly J-coupled spins. Thus, homonuclear through-bond interactions can be traced out by simple analysis of the 2D map providing a more general and more useful alternative to classical 1D homodecoupling experiments.



Practical

1. Run a *PROTON* according to "Bruker run manual for 500 MHz NMR".
The 2-D exp should be recorded non spinning, so for a better result shim also the non spinning shims x, xz, y, yz manually (the auto-program topshim only shim the z shims)
2. Optimize the values of **o1p** and **sw**
3. Check the ^1H 90° -pulse (lab 3).

Experiment setup

1. **edc** or **new** and read the parameter set **A_COSY**
2. **getprosol** (get probe and solvent specific parameters from prosol)

or if the ^1H 90° -pulse value need to be changed

Set the measured **p1** (^1H 90° -pulse)

getprosol 1H 'p1-value' 'p11-value' (get probe and solvent specific parameters and use your adjusted p1 value to calculate related pulses)

3. If required, any acquisition parameter can be modified manually or in the *AcquPars* section, you can see what is valid for the parameters in *PulseProg*.



- a. **o1p** is the center of the ^1H spectrum
 - b. **sw** (F1) same exact value as **sw** (F2), you get it from ^1H spectrum
 - c. **td** (F2) is the time domain in the F2 dimension (usually set to 1K-2K)
Set it to **1024** (1K)
 - d. **td** (F1) is the number of experiments/increments to be recorded in the F1 dimension (usually set to 64w-512w)
Set it to **64**
 - e. Set appropriate **ns**, depending on the time you want the experiment to take.
4. turn off the spinner
 5. **rga**
 6. **zg**

Process recorded data

7. **xfb** add a window function and Fourier transform the data.
8. **abs1**, **abs2** perform a baseline correction
9. In the *Procpar*s section set **sr**(F1) and **sr**(F2) to the same value as in the ^1H spectrum (already calibrated)
10. If the spectrum is very noisy (t1-noise) you can try to symmetrizes the 2-D data with **sym**.
Be careful! Why?