

2D NMR: TOCSY and HSQC

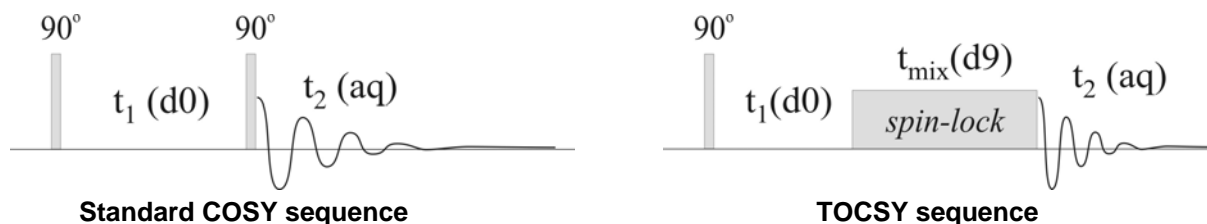
Use Artemis (Av-400) or Callisto (Av-500) for this week's HW.
Likely best to use the same sample as in HW#9 (but a change is OK).

Reading – TOCSY in Claridge sections 5.7;
– HSQC in Claridge sections 6-6.3 (much of this is overly technical)

Goals – Learn about the utility of these two experiments, more technical details about 2D experimental setup, and assignment aids in MNova.

I. TOCSY: Total Correlation Spectroscopy

COSY experiments provide information about ^1H - ^1H coupling, showing crosspeaks for proton pairs having direct J_{HH} couplings ranging 2.5 to 25 Hz for standard COSY and DQ-COSY, and smaller J_{HH} using (long-range) Ir-COSY. TOCSY¹ is the last variant of homonuclear 2D experiments that we'll investigate. The standard COSY is shown below next to TOCSY:



In TOCSY, the 2nd 90° pulse is replaced with a spin-lock pulse.² The spin-lock is *very* interesting (ya, ya, I know; maybe just to me): the spins are “fooled” into thinking that the large static magnetic field has disappeared, and interactions – like coupling and chemical shifts – now depend on the spin-lock strength, typically of about 12 kHz. That’s a lot smaller than 400 or 500 MHz. J -couplings do not scale with the field strength, but chemical shifts do. All couplings during a spin-lock are therefore *strong*: $J_{H_A H_B}^{\text{spinlock}} \gg \Delta\delta_{AB}^{\text{spinlock}}$. The strong coupling enables efficient mixing of all protons in a coupled spin system. The spin system will “stop” at heteronuclear bonds (e.g., an ether or amide bond), and other areas where J_{HH} is small (e.g., aliphatic to aromatic). Magnetization transfers occur faster with larger coupling, so 2- and 3-bond coupling occurs first. But as the mixing time is increased, the magnetization transfers further out.

Acquire a TOCSY spectrum with an 80ms mix time. **TD1**=2 should be fine, since TOCSY, like COSY, is fairly robust with respect to fast repetition times. If you are acquiring data on a research compound use a larger **TD1** (256 or 512). Acquiring another spectrum (or two) with shorter mix (e.g., **D9** = 0.03) is often best, and is fairly common.

¹ TOCSY is sometimes called homonuclear Hartmann-Hahn spectroscopy (HOHAHA).

² Two primary flavors of spinlock are used, MLEV and DIPSI. Bruker names their TOCSY parameter sets and pulses sequences by these names, and avoids the use of TOCSY. Facility generated parameters sets are named as TOCSY, located in /home/topspin3.1/uwchem/par.

Critical parameters for TOCSY, those that should always be checked, are:

- D1** ≥ 1×T₁(longest)
- NS** ≥ 2 (for the standard experiment; many other TOCSY variants require 8)
- TD1** = 128, 256, ... up to perhaps 800
- D9** = spinlock mixing time; it is common to acquire 2 or 3 spectra with different mix:
 - = 0.015 will observe 2-3 bond couplings only (1st shell)
 - = 0.03 start to see next shell (i.e., protons 2-3 bonds from 2nd)
 - = 0.05 2 shells, with some hints of 3
 - = 0.08 3 shells, with hints of 4
 - ≤ 0.12 120ms is the maximum spinlock that should be used; shows all shells

1. Work up the TOCSY spectrum, and compare to the COSY you acquired last week. The spectrum may need a slight amount of phase correction, but don't be surprised if some peaks simply won't phase very well. Crosspeaks as one moves to further shells will get less intense for D9=80ms. Some diagonal peaks may become weak, as magnetization transfers out.

II. HSQC: ¹H-¹³C 1-bond heterocorrelation

You have acquired HSQC spectra in an earlier HW. Here we'll examine a few additional setup issues.

a) Choice of experiment: *Multiplicity-edited* HSQC — analogous to DEPT-135 with -CH₂- inverted from -CH₃ and -CH< moieties — is the most common experiment run for small molecules. As samples get more complex, being comprised of mixtures of compounds or simply by increased molecular weight, partial overlap of two oppositely phased peaks may become a serious concern. In such cases, the DEPT-45 analog — all peaks positive — of the experiment may be better. There are two primary experiments covering these choices:

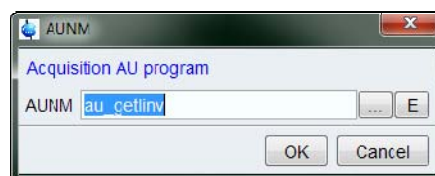
HSQCEDETGPSISP:	edited HSQC, DEPT-135 analog
HSQCETGP:	non-edited HSQC, DEPT-45 analog

b) Manual setting of ¹H spectral region: If your sample has large dynamic range in peak intensities — usually arising from protonated solvents, but also from tert-butyl or when trying to identify impurities or other minor constituents in a mixture — the automatic spectra region determination used for any 2D experiment may fail: e.g., the spectral region cuts out the aromatic region, rendering the acquired spectrum useless.

The following procedure for manually setting the spectral region is correct for any composite experiment (experiments having a C, rather than N, prefix) in IconNMR:

i) Go into **Parameters** → **Edit all Acquisition Parameters** .

ii) When viewing **All parameters**, click on **Automation** in lefthand links; or simpler might be to type **AUNM** in TopSpin, which will open a panel like that on the right. Open the **Au Programs** listing using the button and then select the following, or type the au name in directly:



Experiment Type	AUNM for Automatic SW,O1p	AUNM for Manual SW,O1p
HSQC, HMQC, HMBC	au_getlinv	au_zg
all COSYs, TOCSY, NOESY, ROESY	au_getlcosy	au_zgcosy

The screenshot shows the Bruker TopSpin software interface. The main window displays the 'Automation' panel with the following settings:

- AUNM: au_getlinv
- PYNM: (empty)
- EXP: PROTON
- GRDPROG: (empty)
- CHEMSTR: none
- USERA1: (empty)
- USERA2: (empty)
- USERA3: (empty)

The 'AU Programs' window is open, showing a list of programs. The 'au_zg' program is highlighted in blue. The list includes:

au_dosy	au_get1d	au_getlcosy	au_getlinv
au_getlxhco	au_lc1d	au_lc2d	au_lgrdonflow
au_mult	au_noediff	au_noemult	au_prof
au_profrga	au_sel180zg	au_selhmbc	au_uvnmr
au_watersc	au_zg	au_zg135	au_zgcosy
au_zgnr	au_zgonly	au_zgsino	au_zgte
autoflist	autoplot_6_of_6	batman	bsms_exam
butselau	buttonau	c13cryo	ca1d_report
calcphinv	calcplen	calcpowlev	calctemp
calibo1p1	clev	clspec	cmcq_acquQuar
cmcq_procQuant	cmcq_water	cmcqviewer	coltemp
convfid2asc	convgradshim	convto1d	convvc
cor_MULT_lin	cor_MULT_log	covariance	dccorr

iii) Change F2 values for **SW** and **O1p** based on the ^1H spectrum (see the COSY lab, HW 9, for notes on how best to do this: i.e., expand the spectrum in TopSpin and click).

iv) Check **AQ**, **TD**, and **SI**.

2. Choose the experiment that best matches your compound, and acquire a relatively high-resolution (e.g., **TD1** = 400) and good quality (**NS**=2) HSQC. Manually set the ^1H spectra region. Make some assignments of your compound based on COSY, TOCSY and HSQC data. Look in particular for entry points in the spectra, some proton and/or carbon that can be assigned with definiteness that show correlations in the COSY/TOCSY spectra. Next week we'll do HMBC. The more assignments made in the HSQC, the better for that.

Plot the TOCSY and HSQC spectra. Provide as many assignments as you can via annotations (or just write on paper if you prefer). Put a ? after tentative assignments. Upload 2 plots as .mnova and .pdf files, and turn in a paper copy if you've hand written the assignments.