

HSQC and HMBC for Topspin

These experiments are only possible on the 400 and 500. These experiments can be used to correlate both carbon-proton and nitrogen-proton. The procedure for ^{15}N and any differences from carbon are discussed at the bottom of this handout.

HSQC - Heteronuclear Multiple Quantum Correlation. This 2D experiment correlates the chemical shift of proton with the chemical shift of the directly bonded carbon. On the bottom axis is a proton spectrum and on the other is a carbon. Cross peaks give the shift of the corresponding proton and carbon. This experiment utilizes the one-bond coupling between carbon and proton ($J=120\text{-}215\text{ Hz}$).

HMBC - Heteronuclear Multiple Bond Correlation. This experiment utilizes multiple-bond couplings over two or three bonds ($J=2\text{-}15\text{ Hz}$). Cross peaks are between protons and carbons that are two or three bonds away (and sometimes up to four or five bonds away). Direct one-bond cross-peaks are suppressed. This experiment is analogous to the proton-proton COSY experiment in that it provides connectivity information over several bonds.

^{13}C HSQC and ^{13}C HMBC spectra of sucrose and ^{15}N HMBC of 1-methylpyrazole are shown at the bottom of this handout.

It is useful although not necessary to have already taken a carbon spectrum prior to taking HSQC or HMBC. This 1D can be used as a projection for the 2D. A 1D carbon spectrum, acquired from another NMR (like the 300wb), can be used as a projection. It is faster, however, to acquire an entire 2D HSQC spectrum than a single 1D carbon spectrum and thus, sometimes, it is impossible to obtain a 1D carbon while a 2D HSQC is possible. This is because these 2D experiments are proton-detected and have much higher intrinsic sensitivity than carbon (this is not an effect from the differing abundances of proton and carbon).

About sample size, tubes, and sensitivity: When sample quantity is very limited, it is advantageous to limit the amount of solvent in which it is dissolved. If a normal 5mm tube is used, however, this cannot be less than about 500 μL without causing serious lineshape (shimming) problems and the attendant loss of signal-to-noise. When one reduces the solvent quantity in a normal 5mm tube, it is important that the sample be centered within the coil. To do this, center the sample about the scored line on the plastic depth gauge.

There are special tubes (made by Shigemi) that can be used to restrict the active solvent volume without causing line shape problems. They are available from www.shigemi.com or Aldrich for a higher price. See John Decatur.

Choice of HSQC experiments

The following HSQC experiments are possible. The choice is made when you read in parameters with the rpar command. I recommend the edited version for normal work but if sensitivity is a concern, then use the standard HSQC.

| Parameter set | Experiment |
|---------------|--|
| hsqcedsp.top | edited HSQC with CH and CH ₃ carbons up, CH ₂ carbons down |
| hsqc.top | standard HSQC |
| hsqctocsy.top | HSQC-TOCSY – gives a TOCSY spectrum resolved into the carbon dimension |

HSQC Procedure

1. *Do not spin the sample.* Lock, shim and take a normal 1D proton spectrum. Be sure to tune the proton channel of the probe (**wobb**). Determine the proton spectral region to be used - values of **sw** and **o1p**. **sw** is the spectral width and **o1p** is the center of the spectrum. For example, if you have peaks over the range 1 to 6 ppm, the optimum region is from 0.5 to 6.5 ppm. Always leave at least 0.5 ppm on the edges of the spectrum. The value for **sw** is then 6 ppm and **o1p** is 3.5 ppm.
2. Note the file name of the 1D proton spectra taken above. You may wish to use it as the F2 projection for the 2D plot.
3. Type **new** to change the filename, or preferably, simply increment the experiment number.
4. Read in the parameters for the HSQC experiment by typing **rpar** or **hsqcdsp.top** or **hsqc.top**. Type **getprosol** to update the pulse parameters.
5. Type **wobb** and tune the *carbon* channel of the probe (The carbon channel comes up on the wobb screen when the HSQC parameters have been read in)
6. The parameters below may be changed. Click AcquPars. The F2 column refers to the proton (direct) dimension and F1 column refers to the carbon (indirect) dimension. The normal range for the carbon spectral width is from 0 -165 ppm since carbonyls do not usually have directly attached protons. If you suspect you have an aldehyde, then the carbon range should be increased to include up to 200 ppm or so.
 - **ns** - number of scans. By default =1 but this can be increased to give greater signal-to-noise.



[the rest are optional]

- **O1p [ppm]** - center of proton spectrum
 - **sw [ppm]** for F2 - proton spectral width
 - **O2P [ppm]** - center of carbon spectrum
 - **sw [ppm]** for F1 - carbon spectral width
 - **td** for F1 - # of points in F1 dimension (# of FID's)
 - **fidres** - digital resolution. *Should be 3-5Hz/pt in F2 . Should be 20-80 Hz/pt in F1.* **Fidres** is given by the ratio **sw/td**. Set the values of **td** in F1 and F2 accordingly. The digital resolution should be set according to your needs, i.e., use better (lower **Fidres**) resolution if you are interested in carbons that have nearly identical shifts and nearly identical proton shifts. Better digital resolution in F1 dimension requires longer experimental time. Often 80Hz/pt is sufficient.
6. Type **expt** to determine the time required for the experiment. Values of **td in F1** and **ns** greatly affect the time.
 7. Type **zg** to acquire data. Do not type **rga** or **start**. You will see the lock signal fall and rise. This is normal.

PROCESSING

When data acquisition is complete, type **xfb** to transform the data. You may transform the data before the acquisition is finished but the resolution of the 2D spectrum will be reduced. (Don't forget to re transform after the experiment is finished).








Display control

To expand around a region, simply depress the left mouse button and drag the box around the desired region. To return to the full spectrum, click . To adjust the intensity, use .

Phasing

The HSQC spectrum that you have just run is phase sensitive. You must phase it. An out-of-phase spectrum will look strange and will show dramatic intensity differences on either side of all peaks. To phase a 2D spectrum, one extracts individual 1D rows or columns and phases the 1D spectra. The columns and the rows must both be phased and they must be phased separately.

If you have run the edited version, the color of the cross peak indicates the phase and thus the multiplicity. Blue and yellow/green represent opposite phase. CH and CH₃ will have one color (yellow/green) and CH₂ will have the other (blue). When printing with a black-and-white printer, the color information will have to be added by hand by the user (You!).

Click  to enter phasing. **Phase the rows first.** Position the cursor on a row that contains peaks. Click the right mouse button and select add. Then position the cursor on a row with a peak that has a different shift than the first, and right click and select add. The idea is to choose rows such that the peaks cover a large shift range. You may add more rows but usually two is sufficient. To phase rows, click . There will now be a red line on the largest peak. Adjust its phase using the zero-order button, . Then adjust the phase of other peaks in the other row(s) using the first-order button, . Click  to save and return. Click  to repeat the above process on columns. The columns will often not need much phase correction. When finished, click  to exit phasing.

Linear Prediction (optional)

Linear prediction is a powerful method of improving the resolution of 2D spectra. Normally the FID in the F1 dimension is not fully sampled –it is cut off. To sample it more completely requires more points (greater TD in F1) and a longer experiment time. Each doubling of TD (in F1) doubles the number of FIDs and thus requires a doubling of experimental time. Linear prediction is a processing method which predicts these cut-off points. It improves resolution in the F1 dimension without any increase in experimental time. It is done after the data is collected and can be optimized by varying the extent of prediction and the NCOEF parameter. It is by default turned off and must be turned on.

The price of linear prediction is somewhat lower signal-to-noise. If the signal-to-noise of your spectrum is marginal, then linear prediction is not recommended.

Crucial parameters are based on the value of TD (in F1) that was used for the experiment. Click the acqpar tab find this value. The following parameters must be set and are found within the propar tab:

ME_mod: set to LPfr

NCOEF: set to 3 times the number of cross peaks in your spectrum. For NOESY spectra, count symmetric peaks as two. Values that are incorrect by more than a factor of two can degrade the resolution.


LPBIN: set to 2*TD(in F1)

SI (in F1): set to 2*TD(in F1) or 4*TD(in F1) SI is the number of points actually transformed and determines the amount of zero-filling. Caution: Large values of will creat huge data sets. SI should never be smaller than TD (in F1).

To execute linear prediction, you must re-transform the spectrum with xfb. Larger values of LPBIN and SI MAY give even higher resolution. It is possible to use 4*TD for LPBIN and 4*TD for SI. If you make LPBIN larger, also increase the value of SI. Trial and error is necessary to get the optimum spectrum.

Linear prediction is normally done only in the F1 dimension. In the F2 dimension, it is better to adjust the digital resolution (Fidres) to the appropriate value before acquiring the spectrum.

Shift scale calibration

To calibrate, click  and set the cross-hairs on a peak for which you know the shift in both dimensions, click the left mouse button, and enter the shifts. Generally, the shift scale will be approximately correct without performing this step.


Projections

By default, low resolution 1D projections are displayed at the top and left of your spectrum. One can replace the top projection with the high-resolution 1D proton spectrum you took earlier and the left projection with a carbon spectrum. Place the pointer over the projection, right click the mouse, and select external projection. Enter the exact filename as noted in step 2 above (including exact experiment number, etc...)

Sometimes, the chemical shifts of the 1D projection do not align with the 2D spectrum. See the above calibration procedure if this is true. Or, you may need to calibrate the 1D spectrum.

Peak Picking

You may create and annotate a list of peaks in 2D mode. It is easiest using manual mode. Under Analysis, select peak picking. At the bottom of the menu, select start manual picker. Place the cross-hairs directly over a peak and right-click the mouse to add or annotate a peak. One may delete an already selected peak.

When finished, select save, 

Setting the contour level

The Topspin plot editor uses the saved display contour level when it begins. To save the current contour levels, right-click over the spectrum, select edit contour levels, and then simply click OK to close.

Plotting

See the intro handout for printing. To print using the plot editor, select File, Print. Select "Print with layout – start Plot Editor (plot)". Select a LAYOUT such as 2Dinv208_11x17 and click OK. This automatically places the proton projection defined in the above step into the spectrum.

The carbon projection, however, isn't brought in automatically. To bring in the carbon projection, one must right-click over the spectrum (within Topspin editor) and select edit. Check the click-box for left projection and then select Left Data Set and then choose a spectrum.

To adjust intensities of the projections, right click the mouse over the spectrum and select 1D/2D edit.



These buttons control the projection, To print, select file, print.

HMBC

HMBC experiment is experimentally very similar to the HSQC. To run a HMBC, follow the above procedure for HSQC with the differences pointed out below.

Type **rpar hmbcea.top** or **hmbc.top** to read in the correct parameters for HMBC. The hmbcea.top gives better signal to noise and is preferred. To transform the data from hmbcea.top you must first type **xfb** and then **xf2m**.

Parameters for HMBC only

- ◆ **ns** - minimum number = $2 * n$ (must be a multiple of 2) the number of scans depends upon sample concentration..
- ◆ **SW in F1** (carbon) Since the HMBC experiment correlates carbons and protons that are 2 or 3 bonds apart, there are usually cross peaks involving carbonyls (if present). Use a carbon SW large enough to include both. The default is 220 ppm.
- ◆ **cnst13** - two or three bond J coupling constant. Default value is a compromise value for $J=8\text{Hz}$ but this can be set to 5 or 10 Hz when running two versions (see below).

The three bond couplings vary with dihedral angle (Karplus relationship) over the range 0-15 Hz. One problem with the HMBC is that one must pick a delay based on the value of the long-range carbon-proton coupling. A delay value that maximizes the intensity of cross peaks from 5 Hz couplings will minimize the intensity cross peaks from 10 Hz couplings. By default a compromise value of 8 Hz is set. If desired, however, one can run two HMBC experiments, with two different delay values of 5 and 10 Hz, in order to be sure that all cross peaks were observed.

The HMBC experiment is not phase sensitive. Simply type **xfb** (and then **xf2m** if you are doing hmbcea) to process. Skip the phasing section.

Nitrogen-proton HMBC

There are several differences between carbon and nitrogen HMBC. First, there is a difference in sensitivity. Since ^{15}N is about 1/3 as abundant as ^{13}C , the sensitivity of the ^{15}N experiment is 1/3 that of the ^{13}C experiment. Scan times are 9 times as long for equivalent sensitivity. Another main difference is the presence of long-range couplings in the ^{15}N HMBC. ^4J couplings are often larger than ^3J and 2 couplings so there will be cross peaks connecting atoms that are more bonds apart. The coupling values range from 3 to 15 Hz so it is important to cover this whole range by doing two versions with different values of cnst13. See the following paper for a series of examples of ^{15}N HMBC connectivities: Kline, M., Cheatham, S., Magn Reson. Chem., 2003, 41, 307-314.

To do ^{15}N HMBC, the differences in procedure are as follows. Type **rpar hmbc_n15.top** to read in parameters. To do two versions with different values of cnst13, use 5 and 10 Hz.

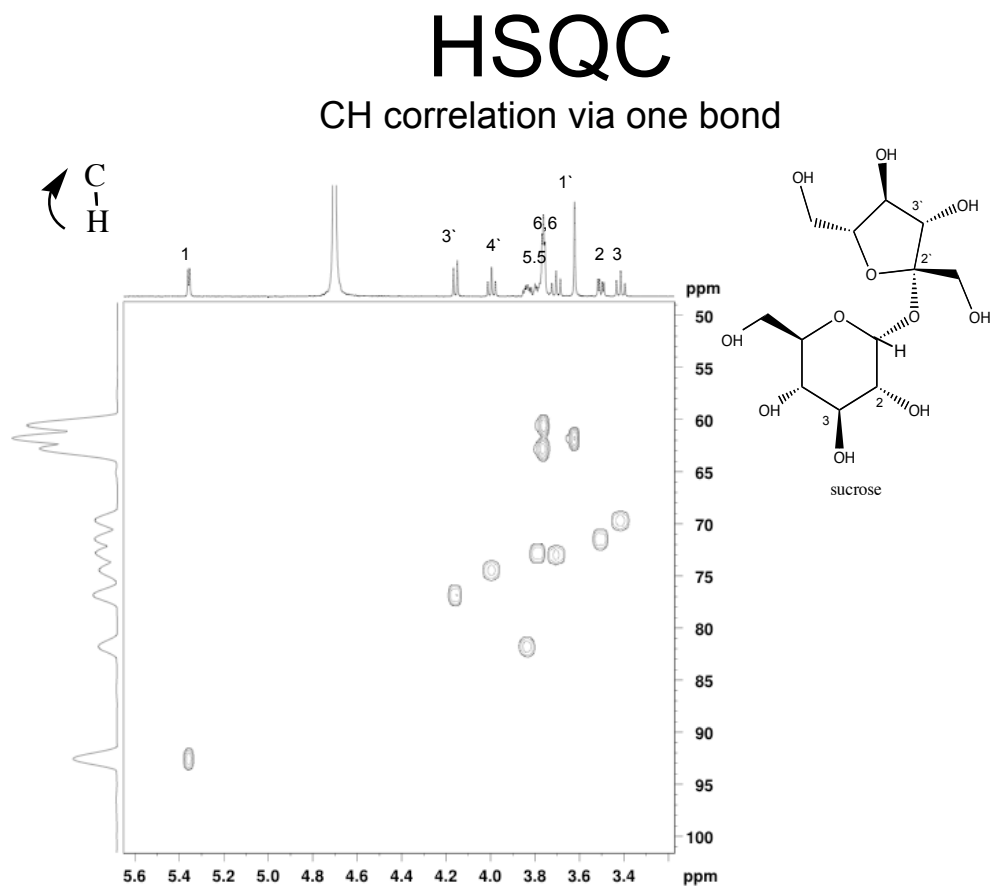
EXPERIMENTAL TIME REQUIRED

The following table indicates the approximate experimental time for each carbon-proton technique based upon a sample of strychnine (MW=334, natural abundance) using the standard 5mm probe. HMBC often benefits from longer scan times since some peaks may not be very intense. The minimum scan time is 10 minutes for HSQC and 20 minutes for HMBC.

Since ^{15}N is about 1/3 as abundant as ^{13}C , the sensitivity of the ^{15}N experiment is 1/3 that of the ^{13}C experiment. Scan times are about 9 times as long for equivalent sensitivity.

| <u>Technique</u> | <u>Quantity(per ml)</u> | <u>Molarity (mM)</u> | <u>Carbon Time</u> | <u>Nitrogen Time</u> |
|------------------|-------------------------|----------------------|--------------------|----------------------|
| HSQC | >5mg | 15 | 10 min | |
| | 2.5mg | 7.5 | 40 min | |
| | 500ug | 1.5 | 12 hours | |
| | | | | |
| HMBC | 25 mg | 75 | 20 min | 30 min |
| | 5 mg | 15 | 40 min | 6 hrs |
| | 2.5 mg | 7.5 | 3 hrs | 18 hrs |
| | 1 mg | 3 | 19 hours | |

Below is a ^{13}C HSQC spectrum with a low resolution $\text{C}13$ projection.



Example of ^{15}N HMBC of 1-methylpyrazole