

Running a gCOSY on the Varian

All written in **bold type** is direct input at the command prompt or a standard VNMR button
Note that the gcosy (gradient cosy) experiment is available on the Varian Inova 500 and 501 as well as the Varian Mercury 300. The standard cosy experiment is available on all of the facility NMR instruments.

- Insert your sample into the magnet in the usual fashion. Choose the nucleus and solvent and do not spin the sample.
- Type **pfgon?** This will query the instrument as to the status of the gradient amplifier.
 - If the response is **pfgon='nnn'**, then type **pfgon='nny' su** (this turns on the Z channel of the PFG amplifier)
- Set the temperature to 22°C: It's good practice to regulate the temperature during all NMR experiments and especially during 2D experiments.
 - Type **vttype=2**. This will allow the user to control the temperature.
 - Type **temp=22 su**. This will set and regulate the experimental temperature at 22°C.
 - Type **vttype=0**. This will turn off the ability to *change* the experimental temperature once it's regulated. This is an important step as it prevents turning off temperature regulation (i.e. run away or temperature 'drift') as we later move between experiments.
- Lock the sample:
 - After you have checked for lock saturation, increase the lock power by 8db and reduce the lock gain by 4db. The lock power varies during the pulses. By increasing the lock power this will help to prevent losing the lock during the experiment.
- Tune the probe. Skip this step if using the Mercury 300.
 - You might consider calibrating the 90° pulse but the COSY experiment is possible one of the least sensitive to pulse variations 2D experiments. If you want to calibrate the 90° pulse see the 90° calibration handout at: http://web.mit.edu/speclab/www/calibrate_a_90.pdf
- Shim the sample. Since the sample is not spinning you may wish to 'touch up' the x-y shims.
 - At this point you may wish to gradient shim. If you have not done this before, the gradient shimming handout is at: <http://web.mit.edu/speclab/www/varian%20gradient.pdf>
- Run a normal 1D-proton spectrum then choose the desired spectral width using the cursors and pressing the [**Expand**] button. Type **movesw au** and then wait for the experiment to complete.
 - **Note!** When changing the sweep width you can not exclude *any* peaks. It is best to use no less than 1.5 to 2.0ppm on each side of the full spectral region.
- Process and save the 1D file (using the **svf** command). Note: If you do not save the 1D now you will not be able to plot high-resolution projections later!
- Type **mp(x,y)**. This moves the experimental parameters from your current experiment number (x) to another experiment number (y). Under no circumstances should you use experiment number 5.
 - Example: **mp(1,2)** will move the current experiment #1 parameters to experiment #2
- Type **jexpy**. This will join experiment 'y' and display the new parameters.
- Type **gCOSY**. (small 'g' capital 'COSY')
- Type **nt=4** (the default is 1, so this should depend on your sample concentration)
- Type **time**. This will display the experiment time (w/ nt=4 the total duration should be about 15 to 20 minutes).
- Type **wexp='do2d'**. This will perform the auto-processing at the end of the experiment (wexp). The macro does some phasing, normalization, symmetrization, as well as generate a plot. This step is optional as you may wish to process the spectrum manually.

- Type **au**. This will submit the experiment to acquisition and process the data (if you have chosen `wexp='do2d'`).

Simple processing:

- If you have chosen to process the spectrum yourself, type **wft2da** (weight and Fourier transform phase-sensitive data).
- Upon completion, you will see the spectrum on the screen and a plot will automatically be generated.
 - If the plot is not generated or the spectrum is not displayed type **dconi**.
 - If you wish to symmetrize the spectrum along the diagonal type **foldt**.
 - The regions of interest can be “zoomed” by using first the left and then the right mouse buttons to define a region then clicking the **[expand]** button.
- To plot your cosy:
 - Select the desired window size then click **[expand]**.
 - Select the level you wish to plot by clicking the **[vs-20%]** or **[vs+20%]** buttons and then clicking the **[proj]** button for the projections.
 - Set the horizontal and vertical projections (press **[plot]** after each selection)
 - Type **ppc pap page** (plot peak contours, plot acquisition parameters, submit plot).
 - To change the contours type **dpcon(a,b)**, where a is the number of contours and b is the spacing between the lines. **dpcon(30,2)** works well.
- To plot your cosy (alternate):
 - Expand your window and select the level as above then type **plcosy(30,2,exp#)** where `exp#` is the experiment number where the 1D proton resides.
- When finished remember to turn off the temperature controller.
 - Type **vttype=2**
 - **temp='n' su**
 - **vttype=0**
- Log out in the usual fashion.