Running COSY Spectra on the Gemini 200

Remember: When in doubt, ask John Layton or Rob Toreki about this procedure. The commands you need to type are listed in boldface type. Hit return after typing them.

NOTE: You can do H,H-COSY on either Gemini, but you will need to use the broadband instrument (the Gemini 200 in the rear of the NMR lab) if you want to run other nuclei.

COSY is a 2-D homonuclear decoupling experiment that determines which nuclei are coupled to each other in your spectrum. For more information, consult any introductory NMR textbook.

1. Set up your experiment and obtain a spectrum. To minimize the COSY run time, use only the minimum number of scans (nt) that you need to get a decent spectrum (nt=4 is usually fine for a normal proton sample).

2. To minimize the run time, narrow your spectral window to the area of interest. Simply place cursors on either side of your peaks of interest and then type **movesw**. To save times we'll reduce the number of iterations, so type **ni=32**.

3. Type **cosy** su to set up the experiment. If you'd like to get a time estimate on the experiment, type **time**. If the time is too long for your liking, you can reduce your number of scans (nt) or try reducing your spectral window. When you are satisfied, start the acquisition by typing **ga2d**.

4. When the run is completed type **wft2d foldt** then type **center**.

5. Your 2-D spectrum will be displayed in a square box as a colored intensity map. There is a colored bar numbered 0-15 on the right side of the screen that sets the threshold for peak display. To adjust the threshold, click on the colored bar using the middle mouse button.

   You may need to increase the vertical scaling to get your peaks to show up. Simply type **vs2d=xx** where xx is a number and then click on the **Redraw** button. A typical range for vs2d is 200-2,000 depending on the amount of sample you used and intensity of the peaks.

   Either way, adjust display so that all the peaks of your proton spectrum appear on the upper right to lower left diagonal (remember you'll be looking down on them from the top in a contour plot, not the side as you are used to doing). Don't increase the height too much or you will get excess noise and/or spurious cross peaks.

6. Once the contour map is to your liking we need to dump it to the plotter spool file. Do not try the **Plot** button at this point -- it won't work. Instead, hit the following buttons in order: **Return**, **Plot**, **All Contours**, **Params**, **Return**.

7. Now we can add the 1-D spectra along the axes. Click on either the **Contour** or **Color Map** button (whichever you like more...if you clicked on one and want to see the other, click on **Return** to back up one level of buttons).

8. Click on the **Proj** button and then the **Hproj(max)** button. Adjust the height of the plot, if desired, by clicking and dragging with the middle mouse button. Once you are happy, hit the **Plot** button to add it to the plot spool file.

9. Click on the **Vproj(max)** and scale it if desired. Then hit the **Plot** button.

10. When you are completely finished type **page**. This dumps the plot spool file to the plotter.

11. Restore the instrument to normal 1-D operation. The easiest way to do this is to simply set up a new proton experiment and type su. Example: **setup(h,cdcl3) su**.

12. Report any problems to John Layton or Rob immediately.