2D HMQC ($^{1}H\{^{13}C\}$) Directions For Bruker NMR

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Directions:

1. Obtain a proton spectra of the sample you wish to run an HMQC on.

   Parameters used for ^{1}H Acquisition
   - "rpar PROTON all" (for future reference things in " " are input commands)
   - "NS" = 16, "DS" = 2
   - "ZG" (1 min 30sec experimental time)

2. Process the $^{1}HNMR$.

   Process parameters used for $^{1}HNMR$

   - "EDC" (LB = 0.01)
   - "APK" (phase correction)

3. The "o1" and "1sw" values were recorded from the $^{1}HNMR$

4. From $^{1}HNMR$ create new file ("edc")

5. To load 2D HMQC acquisition process type "rpar HMQC all". (Don't forget to "getprosol"!)

6. Check the parameters of the experiment ("edsp"). Set NUC2 to C13. Change the value of OSF1 to the value of o1 (obtained earlier). **Make sure that the value of OFS2 is approximately 4 times the value of OSF1.** If it is, click save to exit parameter window.

7. Set "cnst2" to 145 hz

8. "rga" and obtain 2D HMQC spectra using "zg"

9. Process data using "xfb" (a sine bell shift of 5 on both axis and 5th order polynomial baseline correction were applied to improve resolution)

If you have followed these instructions you should now have a 2D HMQC spectra of your sample (see example below).