L. Zhu (& DLO)
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Selective Decoupling: Homo-Decoupling of ^{1}H-^{19}F

This document describes how to set up a selective homo-decoupling experiment between ^{1}H and ^{19}F (it's called homo-decoupling because ^{1}H and ^{19}F use the same coil of the probe, homo='y').

Two parts:

- ^{1}H-decoupled ^{19}F spectrum
- ^{19}F-decoupled ^{1}H spectrum

A. ^{1}H-decoupled ^{19}F Spectrum

(1) In exp1, setup a normal **proton** experiment, and collect a ^{1}H spectrum
(2) Set **dn='H1'**
(3) Set the cursor in the center of a proton peak, and type **nl**
(4) Type **sd**, this gives you a dof value. **Write down the dof value: ______________________________**
(5) If you have more than one proton peak that are potentially coupled to F-19, repeat step 3 and 4 for all the peaks, and write down all the dof values. Or you can put the cursor in the middle of multiple peaks if they appear relatively close to each other, and use that placement to find the dof value.
(6) Type **jexp2** and setup a normal **F-19** experiment, and collect a ^{19}F spectrum; save the spectrum
(7) Move the FID in exp2 to exp3 by typing: **mf(2,3) jexp3 wft**

(8) In exp3, make sure:

dn='H1'
homo='y'
gain='y'
dm='nny'
dmm='ccc'
dof = the value found in exp1 (step 4 above), or arrayed dof values if you have a series of proton peaks to decouple from F19 (step 5 above); such as dof=dof1,dof2,dof3….., you can use **da** to look at the arrayed values and **dg** to go back to the normally parameter display

(9) (optional) You can array **dpwr** to find the best decoupler power (in this case, don't array dof, use one dof value found above to avoid complication), normally dpwr=20 should be good enough, don't use a dpwr value larger than 25.
(10) Once you have a desired **dpwr** value, collect the selectively ^{1}H-decoupled ^{19}F spectrum.
(11) You may find the arrayed ^{19}F spectra are very similar if the decoupled proton peaks you are very close to each other in the proton spectrum and the **dpwr** power setting is strong enough to decouple all proton peaks from the ^{19}F spectrum.
(12) Process and print the spectrum as usual. If you are not familiar with an arrayed experiment, following the detailed instructions in the HOMODECOUPLING document.

B. ^{19}F-decoupled ^{1}H spectrum

This experimental procedure is analogous to the ^{1}H decoupled ^{19}F experiment. Basically you can follow the above instructions but first interchange ^{1}H and ^{19}F. Here is the revised procedure:

1. In exp1, setup a normal **F-19** experiment, and collect a ^{19}F spectrum
2. Set **dn='F19'**
3. Set the cursor in the center of a proton peak, and type **nl**
4. Type **sd**, this gives you a dof value. **Write down the dof value: ______________________________**
5. If you have more than one proton peak that are potentially coupled to H-1, repeat step 3 and 4 for all the peaks, and write down all the dof values. Or you can put the cursor in the middle of multiple peaks if they appear relatively close to each other, and use that placement to find the dof value.
6. Type **jexp2** and setup a normal **H-1** experiment, and collect a ^{1}H spectrum; save the spectrum
7. Move the FID in exp2 to exp3 by typing: **mf(2,3) jexp3 wft**

8. In exp3, make sure:

   dn='F19'
   homo='y'
   gain='y'
   dm='nny'
   dmm='ccc'
   dof = the value found in exp1 (step 4 above), or arrayed dof values if you have a series of proton peaks to decouple from H-1 (step 5 above); such as dof=dof1,dof2,dof3….., you can use **da** to look at the arrayed values and **dg** to go back to the normally parameter display

9. (optional) You can array **dpwr** to find the best decoupler power (in this case, don't array dof, use one dof value found above to avoid complication), normally dpwr=20 should be good enough, don't use a dpwr value larger than 25.
10. Once you have a desired **dpwr** value, collect the selectively ^{19}F-decoupled ^{1}H spectrum.
11. You may find the arrayed ^{1}H spectra are very similar if the decoupled proton peaks you are very close to each other in the proton spectrum and the **dpwr** power setting is strong enough to decouple all proton peaks from the ^{1}H spectrum.
12. Process and print the spectrum as usual. If you are not familiar with an arrayed experiment, following the detailed instructions in the HOMODECOUPLING document.