

Quick guide to performing a DEPT (Distortionless Enhancement by Polarization Transfer) experiment.

Please note that all **typed in bold** are entered at the command prompt

The basis for the DEPT experiment is simple. The transfer of polarization from protons to carbon enhances the carbon signal strength. By carefully calibrating the decoupler power it is possible to distinguish CH₃ (methyl), CH₂ (methylene), and CH (methine) groups using three pulse widths of 45, 90, and 135 degrees. Since quaternary carbons have no attached protons they are not detected.

The procedure:

- The dept experiment is best performed at a stable temperature. Therefore, if you wish to do your experiment at 20° type **temp=20 su**
- Acquire a ¹³C spectrum in the usual fashion. Note: You may wish to spin the sample but it is not necessary.
- Select and expand the region you are interested in observing and type **movesw ga** (move spectral window according to cursors and submit experiment to acquisition). Process and phase the data as usual. It is very important that the data be well phased. Also select a threshold level below the level of the smallest peak of interest.
- Type **mp(x,y) jexpy**, where x is the current experiment number and y is a second experiment number. This will move the current parameters to another experiment and 'join' that experiment. Note: Do not use experiment 5. This is reserved for special functions.
 - Example: to move from exp #1 to exp #2 type **mp(1,2) jexp2**.
- Type **dept** which will load the 'dept' parameters to the newly joined experiment. Note: from the ¹³C spectrum above how many transients were required for good signal to noise. Set nt to this value. If you wish to see how long this experiment will take type **time**.
- Type **au** (submit experiment to acquisition and process data). Once completed, the processed data will automatically be sent to the printer.
- If the automatic processing fails, type **ds(1)** to display the first spectrum. Rephase and expand region of interest. Place a threshold line just below the lowest peak.
- Type **adept dssa** to analyze the data
- Type **pldept** to plot the DEPT spectra.

Problems and Pitfalls:

The most common reason for failure of the *dept* experiment is failure to tune the probe. Both the proton and carbon channels need to be tuned (this is not necessary on the Mercury 300). Another common failure of the *dept* experiment is poor subtraction in the edited spectra. Poor subtraction is usually caused by improper calibration of the decoupler 90° pulse *pp*. If the *dept* experiment fails check the ¹³C 90° pulse width and the decoupler 90° pulse width calibrations. Other causes of poor cancellation are lock saturation (i.e., an unstable lock), poor vibration isolation of the NMR system, or temperature changes during the experiment.

Some Useful Related Commands:

- **adept**: automatically analyzes and edits a set of four DEPT spectra. Also writes a file named dept.out into the current experiment directory (if you are currently in experiment #2 the file would be found in /export/home/*your_home_directory*/vnmrsys/exp2). This file contains all of the results of the data analysis.
- **autodept**: processes the DEPT spectra, plots the unedited spectra, edits the spectra, plots the edited spectra, and prints out the editing information.
- **deptproc**: weights, Fourier transforms, phases each of the spectra in the data set and displays them on the screen.
- **padept**: performs the **adept** analysis and plots the resulting spectra with a scale and the assigned line listing.
- **pldept**: plots DEPT data, edited or not.