BARE BONES GUIDE TO DEPT
on the Varian NMR Instruments with VNMRJ 3.2

This guide is written assuming proficiency in basic operation of the Varian NMR instrument. You should be experienced in performing basic 1-dimensional NMR experiments before attempting to perform more advanced experiments on your own. Please ask for help the first time you perform this, to minimize your frustration

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Considerations: The new DEPT sequence in VNMRJ 3.2 incorporates adiabatic pulses, and the ability to either exclude, or include quaternary/unprotonated carbon signals (with Q-carbons in-phase/up, or anti-phase/down). The experiment can be done as a single 1D spectrum, with multiplicity selection, or as a full, edited DEPT experiment; however, this requires that four (4) complete spectra be acquired and processed for subsequent editing (which requires significantly more NMR time).

1) Setup for normal ^{13}C Observation, and then type DEPT <Enter>
   a) or, select DEPT from the Experiments/[Setup NEW Parameters to Do…]/13C-1H Multiplicity Determiniation/DEPT pull-down menu.
      i) DO NOT setup DEPT from a normal 1H spectrum or 1H parameters… bad things can happen.

2) Go to the [Acquire]/[Defaults] panel to setup the experiment as you wish:
   a) Enter your desired spectral window in the boxes provided, or choose available pre-sets.
   b) Select the number of scans and the relaxation delay desired
   c) Select the Editing desired {i.e. a FULLY Edited, or CH/CH3 "up", CH2 "down" spectrum (aka DEPT-135)}
      i) Fully edited will take 4x to 8x the amount of time, depending upon the options chosen for Q-carbons in the editing process.
   d) Decided how to handle Quaternary carbons (traditional experiment would suppress them, but you can choose how to handle the unprotonated carbons)… select the appropriate menu item.
3) Type **time** (or *click* on [Show Time]) to see how long the experiment will take (*optional*).

4) If you did a single DEPT-135 (or other single-trace DEPT), you should save the data and process/analyze in MestReNova.

Fully, Edited DEPT: Depending on which options you selected, processing/analysis (which includes scaled addition & subtraction of spectra) might best be done in the VNMRJ software directly.

1. Go to the [Process] Panel and select the [Default] sub-panel, where you will find a number of processing options under the "DEPT process" heading, which should be self-Explanatory.
   a. "Full Editing" will show Quaternary, CH, CH_2, and CH_3 carbons in separate spectral traces.
   b. "CH Only Edit" will show All Protonated, CH, CH_2, and CH_3 carbons in separate traces.

2. After choosing the processing that you desire, you can go to the [Process]/[Plot] sub-panel, and select [Automatic Plot Page] to plot to the currently defined printer (you can first change this by selecting a different printer under the "Send Plot To…" widget.
   a. You can choose [Automatic Plot Preview] and preview as a .PDF and save the .PDF file in your directory if you so choose.