Solvent Pre-Saturation - Suppression of the Solvent Peak

SCS NMR Lab; DLO 10 Jan 2013

Introduction

Suppression of the solvent peak makes the digitization of the vertical range of the data match the *analyte height* instead of the *solvent height*. This improves the baseline and also improves integration of areas. Solvent suppression works by exciting the spins of the solvent, but they are not allowed to relax and give a signal.

Solvent suppression takes extra acquisition time. Type **time** to see how long the total experiment will take before you acquire.

Solvent suppression can affect the quality of signals near the saturation frequency. Sometimes the signals are improved, and sometimes they are worsened. It often depends on how big the solvent peak is initially.

Procedures

To begin this example, take a normal ^{1}H spectrum in the Exp1 window.

(If you are using a protonated solvent, see handout for No-D NMR.)

Type (this moves the standard data to another window for the suppression step; this is optional)

- **mf(1,2)**
- **jexp2**
- **wft**

Expand around the peak of interest, then Left Click on the peak you want to saturate (suppress). Use **nl** to put the red cursor exactly on the peak, then type **sd <rtn>**

- This sets the proper saturation frequency as dof

Type **presat <rtn>**

- The dof frequency will appear as the satfrq.

The saturation parameters (which are on the right side of the dg window) are optimized for small amounts of H_2O in D_2O. The default value for **satpwr = 2**.

- If you have a strong solvent peak a satpwr = 10 will probably work nicely.
- Adjust satpwr as needed to give a suppressed solvent peak that looks like a "glitch", which should be shaped like a horizontal "Z".
- The presat experiment can ruin the integrity of NMR data near the solvent peak, so use it carefully.

Type **gain='n'** so it will autoscale the gain with the suppressed signal.

Type **nt=4** (or more as needed; generally, don't take just 1 scan; instead, acquire 4, 8, 16, 32, etc. scans).
Type **ga**

Process as usual, and adjust **satpwr** as needed.

- Many times the saturated peak will not phase properly. Ignore the saturated peak and make sure the baseline on either side of it is phased properly.