T1 relaxation time measurement

(T2 measurement is the same, just load the T2 measure protocol)

Click **T1 Measure** protocol, double click the protocol in the study queue panel. Type in sample name, select a solvent. Click **Acquire**, click **Default**, select the **T1 mode** (Inversion recovery or progress saturation), input the **Min T1, Max T1** and the **Total Exp time**. You may adjust other parameter, such as number of scans, spectral width, etc. Then click **Submit**. After it finishes, the spectra and T1 data will be printed.

You may reprocess the data by following procedures:

1. Open the file and Enter **wft** .
2. Display the last spectrum (for a *T*2 experiment to display the first spectrum).
3. Phase this spectrum properly.
4. Select a threshold and adjust the threshold line position.
5. Enter **dpf**, **dll**, or click on the appropriate button to display a line list and locate lines for the system.
6. Enter **fp** to measure the peak height of each peak in an array of spectra. If optional line indexes are supplied to fp as arguments (e.g., fp(1,3)), only the peak heights of the corresponding lines are measured.

The npoint parameter (if defined and set “on”) determines the range of data points over which the fp command searches for a maximum for each peak.

Analyzing the Data

*T*1 and *T*2 analysis is performed by the t1 and t2 macros, respectively. t1 and t2 measure relaxation times for all lines in the line listing and display an extended listing of observed and predicted peak intensities. t1s and t2s perform the same calculation as t1 and t2 but produce a shorter output, showing only a summary of the measured relaxation times.
The command expl displays exponential/polynomial curves resulting from *T*1, *T*2, or kinetic analysis. Optional input of line numbers as arguments allows displaying only selected lines. Similarly, the command pexpl plots the same curves.
The macro autoscale returns the command expl to autoscaling in which scale limits

(set by scalelimits) are determined that will display all the data in the expl input file. The macro scalelimits causes the command expl to use typed-in scale limits. If no arguments are given, scalelimits asks for the desired limits. The limits are retained as long as an expl display is retained.

To delete spectra from the t1 or t2 analysis (or from t1s or t2s), enter dels(index1<, index2>...). This command deletes the spectra selected by the indexes from the output file fp.out of the fp command used by the t1 or t2 analysis. Spectra can be restored by rerunning fp.

Exponential Analysis Menu

Most of the commands for working with *T*1 and *T*2 analysis are available by clicking on Main Menu button, followed by the Analyze button, and then the Exponential button. The following menu, called the Exponential Analysis menu, is displayed

***T*1 Data Workup: Step-by-Step**

The following procedures accomplish the same result.

1. Enter **rt('/data-directory/t1data.fid')**, or File → Open → … to load the data.
2. Enter **wft dssh full ds(arraydim) aph**.
3. Click on **Next** > **Th**. Use the left mouse button to set the threshold.
4. Enter **dll fp t1 center expl**.

If you want to print the detailed T1 analysis result, type **printon t1 printoff.**