



KJM 9250

**CarbonT<sub>1</sub> Spectra on the DRX500 Spectrometer**

Version 5.0

Topspin 1.3 Windows XP DRX 500



© Professor Emeritus Alistair Lawrence Wilkins,  
University of Waikato, New Zealand.  
April 2018

# Carbon T<sub>1</sub> Spectra on the DRX-500 Spectrometer

## 1.0 Introduction

An **awcarbont1** parameter set and linked **VDLIST** file have been set up on DRX-500 spectrometer running under **TS1.3**.

The **awcarbont1** parameter set has **D1 = 10 sec** and a linked **VDLIST** file with 8 x delays in the range 0.03 to 10 sec with the longest delay (10 sec) the first used VDLIST value and the shortest delay (0.03 sec) the last used value.

**D1** and the longest (first) **VDLIST** value should be 3-5 times the longest T<sub>1</sub> in the sample compound.

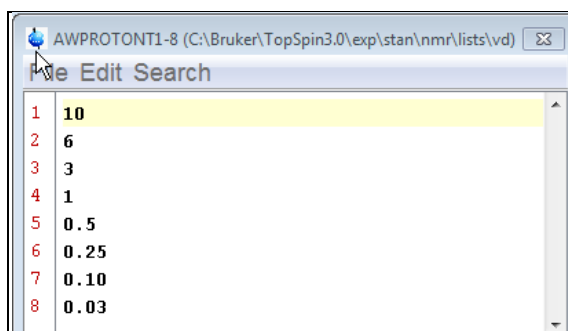
T<sub>1</sub> data sets can be processed on the spectrometer terminal or off line using any version of Topspin provided a copy of the linked **VDLIST** file is resident in the experiment's top level folder (= default set up: see below) or a copy of the originally named **VDLIST** file is recreated in the offline terminal's *C:\Bruker\Topspin...\exp\stan\nmr\lists\vd* folder.

 uxnmr.info	2/01/2017 10:50 p...	INFO File	4 KB
 uxnmr.par	2/01/2017 10:50 p...	PAR File	24 KB
 vdlst	10/01/2018 8:49 a...	File	1 KB

NB: The experimental copy of the variable delay file is named as **vdlst** irrespective of the name of the source vdlst file.

## 2.0 Experiment Set Up

- 1) Create an experiment and read in the **awcarbont1** parameter set (+ **getprosol**).  
Pulse programme = **t1irpg**
- 2) Review default settings. These settings can be adjusted if required.  
**TD(F2) = 32K, TD(F1) = 8.**  
**SW = 240 ppm, O1P = 110 ppm.**  
**D1 = 10 sec.**  
**NS = multiple of 4 or 8, DS = 4 or 8.**
- 3) Type **ased** (enter) and review other parameters used in the job including the linked **VDLIST** file = **AWCARBONT1-8**
- 4) The **VDLIST** file should have the entries shown below (next page). Values are in seconds. Do not alter the values in this file. An alternatively named **VDLIST** file should be created if different **VD** and **D1** values are required for a particular compound.

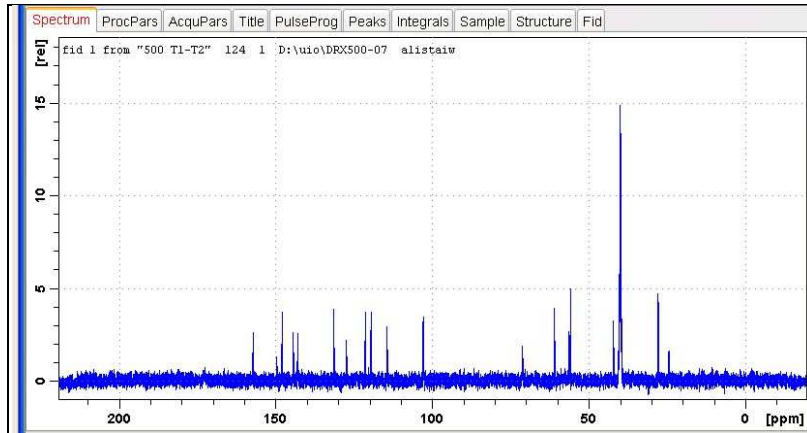


- 5) Set receiver gain using **RGA** (*important!*).
- 6) Type **edp** (enter) and check that **SI(F2) = 32K, SI(F1) = 8,**  
**WDW(F2) = EM, LB (F2) = 2 Hz** or other value of your choice.

SI	65536	8	Size of real spectrum
SF [MHz]	125.7577890	500.1300000	Spectrometer frequency
OFFSET [ppm]	219.39250	4.99974	Low field limit of spectrum
SR [Hz]	0	0	Spectrum reference frequency
HZpPT [Hz]	0.458222	125.000000	Spectral resolution
SPECTYP	UNDEFINED		Type of spectrum e.g. COSY, HI
Window function			
WDW	EM	SINE	Window functions for trf, xfb,...
LB [Hz]	2.00	0.30	Line broadening for em

- 7) Start the acquisition using the **ZG** command.
- 8) When the experiment has run type **rser 1** (enter) to read in the first serial file which will appear in a TEMP screen display window.

- 9) Type **EFP** (return) to transform it and phase it as per a normal carbon spectrum. The **multiabsn** command with **n = 30-40** can be used to straighten the baseline.



- 10) Type **edp** (enter) and note the phase constants for this spectrum.

Phase correction	
PHC0 [degree] =	252.218
PHC1 [degree] =	12.970
PH_mod =	pk

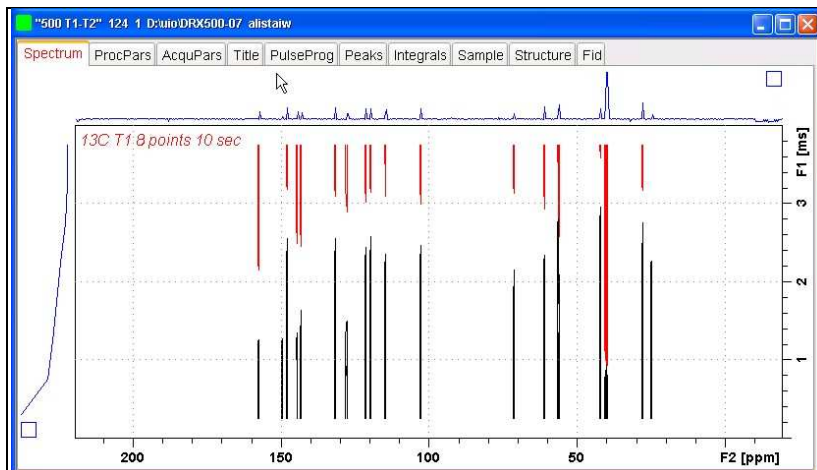
- 11) Close the **TEMP** window and reload the T<sub>1</sub> data set file.

- 12) Type **edp** (enter) and enter the phase constants noted in step 10 above into the **F2 PHC0** and **F2 PHC1** cells and check **PH\_MOD = pk**. **F1** cell info is not used.

Phase correction			
PHC0 [degree] =	252.218	0.000	0th order correction for pk
PHC1 [degree] =	12.970	0.000	1st order correction for pk
PH_mod =	pk	mc	Phasing modes for trf, xfb, ...

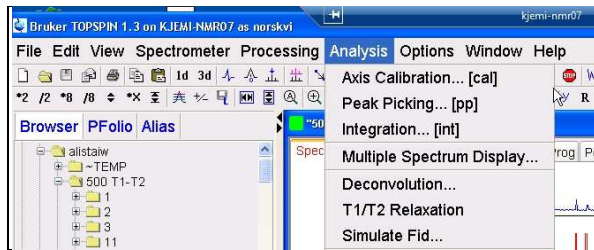
- 13) Type **xf2** (return) to transform the 2D data set followed by **abs2** (return) to baseline smooth it.

- 14) Provided phase constants have been correctly set up the transformed data set plot should resemble that shown below. Black = a positively phased signal, red = a negatively phased signal.

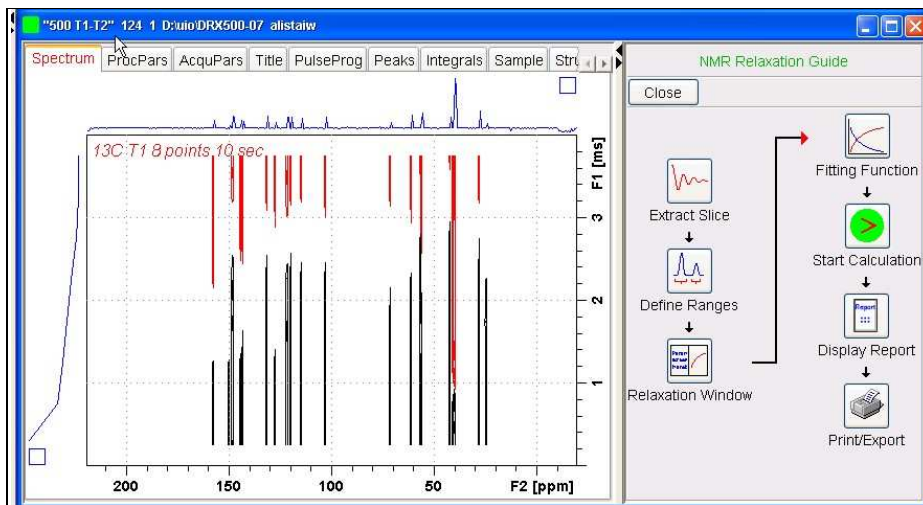


### 3.0 T<sub>1</sub> Data Set Processing

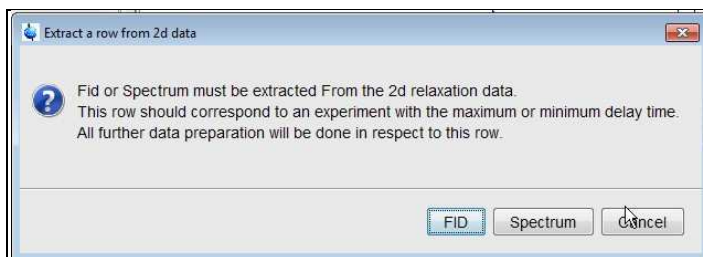
15) Open Topspin's **Analysis** menu and click its **T1/T2 Relaxation** tab.



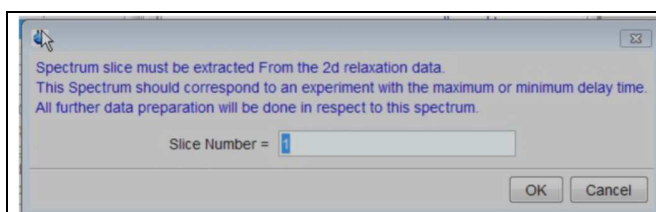
This will open up the screen display shown below.



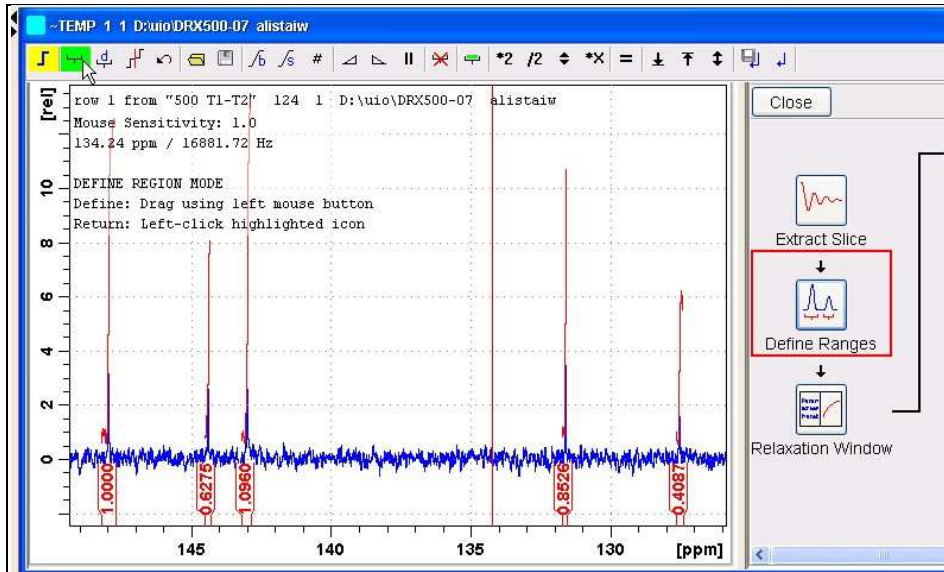
16) Click the **Extract Slice** button and then click the **Spectrum** button in the panel that appears.



17) Enter **1** in the **Slice number** cell and click the OK button. This will display the transformed spectrum ex the first (longest) **VDLIST** value = the one that was phased via the **rser 1** routine in steps 7 and 8.



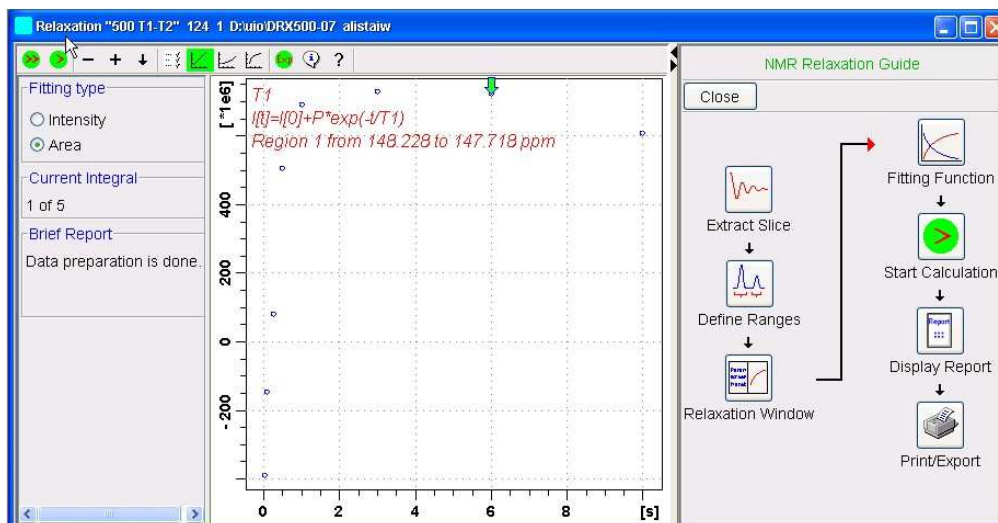
- 18) Expand the spectrum that appears in the usual way and integrate selected peaks in it. Integrals should start and terminate as close as possible to the edge of a peak.



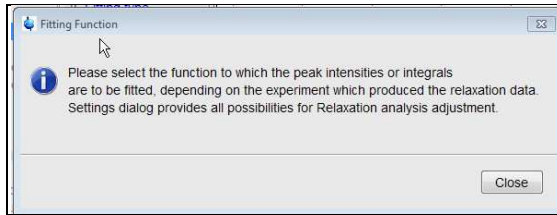
- 19) Click the "Save Region As" icon button (= 7th from the left in TS1.3's upper menu bar = *the one with the floppy disk icon*) and then its **Export Regions to Relaxation Module and .ret.** tab.



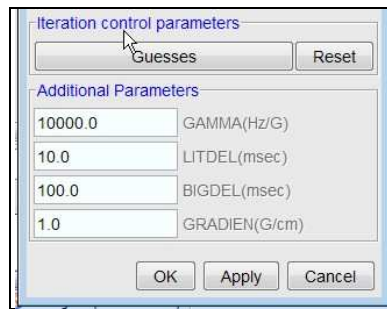
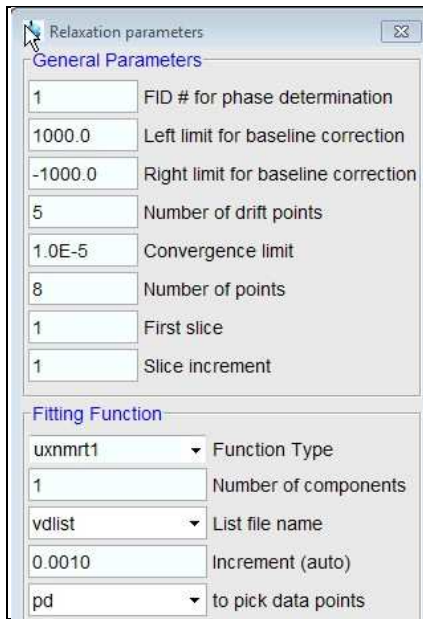
- 20) Click the **Relaxation Window** button, note any screen messages that may appear and close them. Select **Intensity** or **Area** in the plot window that appears. **Area** is often the better choice.



- 21) Click the **Fitting Function** button and note the comments about **intensity** or **area** options in the screen display that appears and close it.

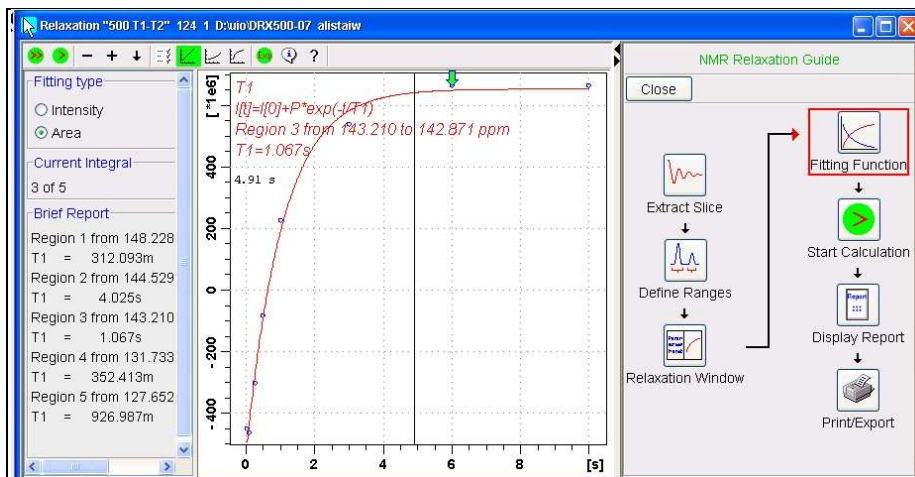


- 22) When the Fitting Function message screen is closed a panel with relaxation parameters (split into two screen captures below) will appear.



- 23) Check **Function Type = uxnmrt1** and **List file name = vdlist**. Other cells/values can be left as they are (= default settings)

- 24) Click the **double red arrow** in the menu bar at the top left of the plot window and **NOT** the single red arrow button in the NMR Relaxation Guide menu below the Fitting Function button.



- 25) The + and - buttons in the upper menu bar can be used to advance (or reverse) the individual T<sub>1</sub> plots.
- 26) Fitting type (**Intensity** or **Area**) can be changed in the plot display. If this is done clicking the **double red arrow** will recalculate the T<sub>1</sub> results and update their plots.
- 27) The NMR Relaxation Guide has buttons which can be used to display and/or print T<sub>1</sub> results. A sample report for one signal is shown below.

```

Dataset :
D:/uio/DRX500-07/data/alistaiw/nmr/500 T1-T2/124/pdata/1
AREA fit :
I[t]=I[0]+P*exp(-t/T1)

8 points for Integral 1, Integral Region from 148.228 to 147.718 ppm
Results      Comp. 1

I[0] = 9.608e-001
P     = -1.662e+000
T1    = 312.093m
SD    = 7.059e-002

      tau   ppm   integral   intensity
-----
10.000s  147.965  6.0951e+008  5.2728e+007
 6.000s  147.964  7.2678e+008  5.3574e+007
 3.000s  147.964  7.3254e+008  5.4515e+007
 1.000s  147.964  6.938e+008  4.7863e+007
500.000m 147.964  5.0898e+008  2.4473e+007
250.000m 147.965  7.868e+007   eliminated
100.000m 147.964 -1.508e+008 -1.7628e+007
 30.000m 147.965 -3.9873e+008 -3.3996e+007

```