1. Introduction

The time constant T_1 is the longitudinal or spin-latittice relaxation time. It is a measure of the time that each nuclus needs to reach equilibrium with its surroundings in the direction of B_0 (z-axis). One popular method to measure T_1 is the inversion-recovery method. The magnetization (M_0) is inverted with a π pulse, then a time τ allowed to relax along the +z-axis. The magnetization, after time τ, is measured applying a $\pi/2$ pulse and then measuring the NMR signal. T_1 is, thus, determined by fitting the magnetization curve or direct calculation of $T_1 = \tau_n/\ln 2$, where τ_n is the τ at node ($M = 0$).

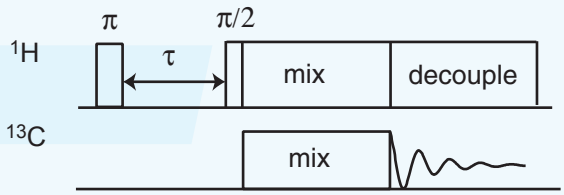
$$M = M_0(1 - 2e^{-\tau/T_1}), \qquad (1)$$

2. Pulse sequence

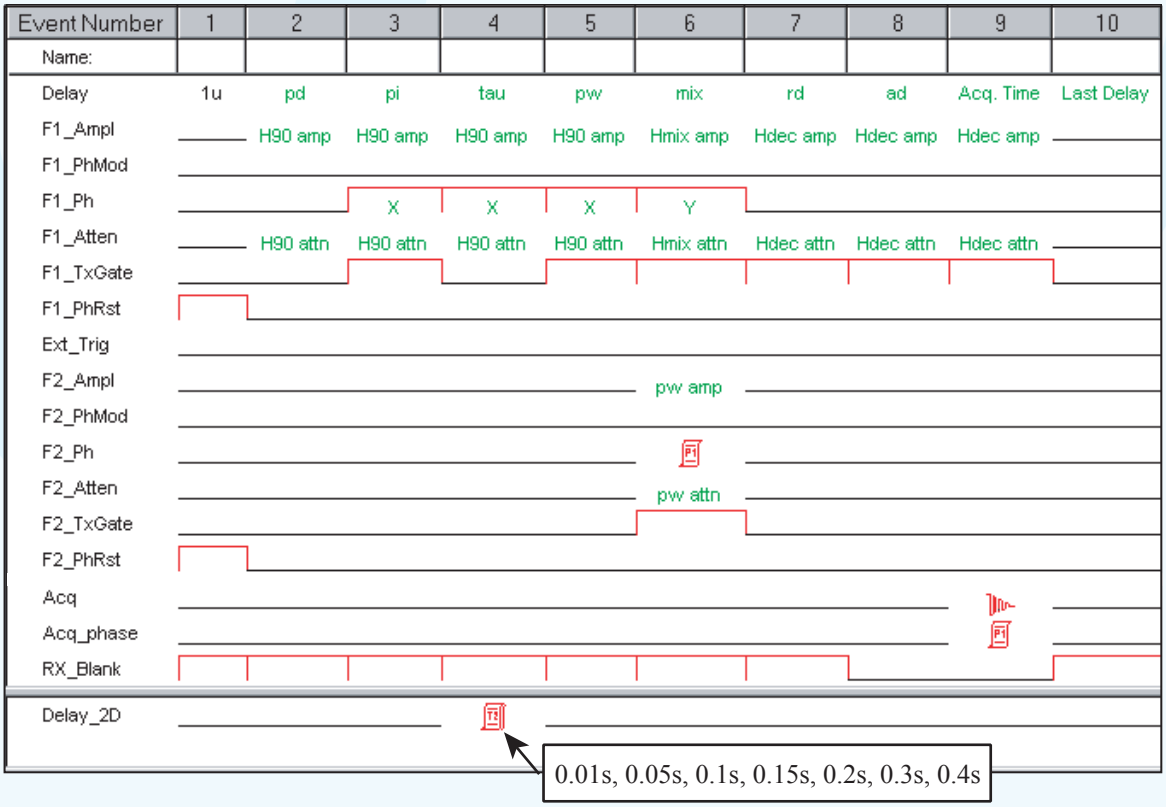
Figure 1 shows an example measuring proton T_1 through $^1H/^{13}C$ cross-polarization and ^{13}C observation.

Fig. 1a: the sequence for measuring ^1H T_1 of Gly-1-^{13}C, ^{15}N. Mixing time is 3ms and *rf* field is 50 kHz. The decoupling field is less than 50 kHz. b: the actual sequence in NTNMR sequence editor.

(a)



(b)



3. Experiment and results

A set of spectra at different τ's is obtained in a 2D experiment. A 2D delay table is used in event 4 (see Fig. 1b). Fig. 2 shows the fully labeled Gly-1-^{13}C CPMAS spectra aquired with the sequence shown in Fig. 2a and ploted as a function of τ.

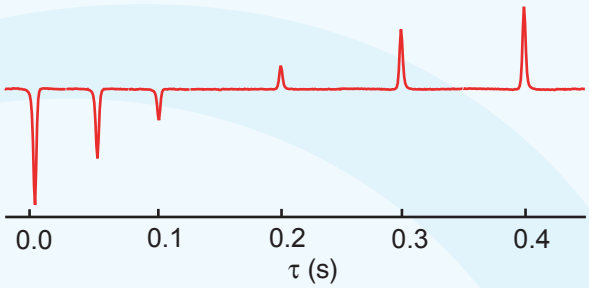


Fig. 2 The centerband array of Gly-1-^{13}C CPMAS ^{1}H spectra. Spin speed is 2.5 kHz.

4. T_1 calculation

NTNMR has a built-in data analysis toolwhich can be used to calcullate T_1. First, the spectra are phased such that the first spectrum is inverted. Then the desired peak is highlighted for T_1 calculation. The NMR Data Analysis" window is open from "Tools" menu, the τ table as "x-axis" and "Intensity" as "source" are selected, the "Draw" button is clicked, and the result will appear in the window as shown in Fig. 3.

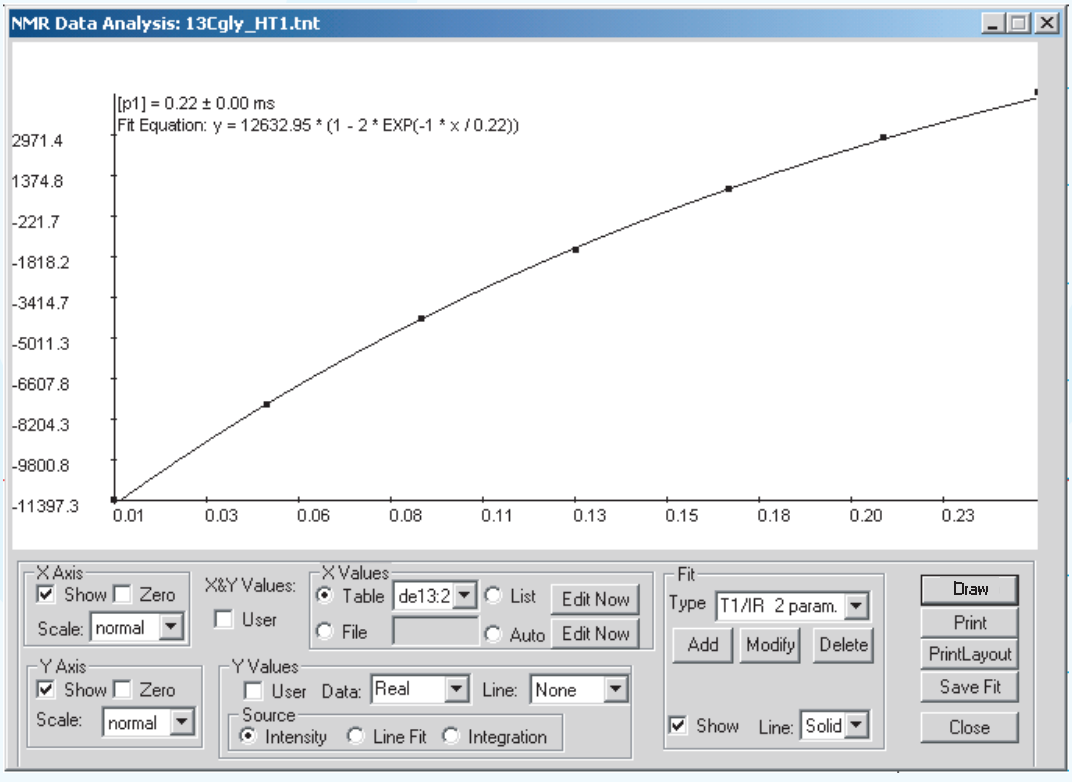


Fig. 3. T_1 fitting for glycine-1-^{13}C in the "NTNMR Data Analysis" window. Fitting results: T_1 = 0.22 ms.