Relaxation Process in NMR

Spin-Lattice Relaxation, T₁

The absorbed energy is lost through vibrational and rotational motion to the magnetic components of the "lattice" of the sample. Problem: The temperature of the sample can rise over time. Spin-Lattice relaxation processes cause an exponential decay of the excited state population. The more viscous a sample is, or the more restricted the motion of a molecule is, the <u>longer</u> the T_1 .

Spin-Lattice relaxation is the <u>slowest</u> of the relaxation processes.

Spin-Spin Relaxation, T₂

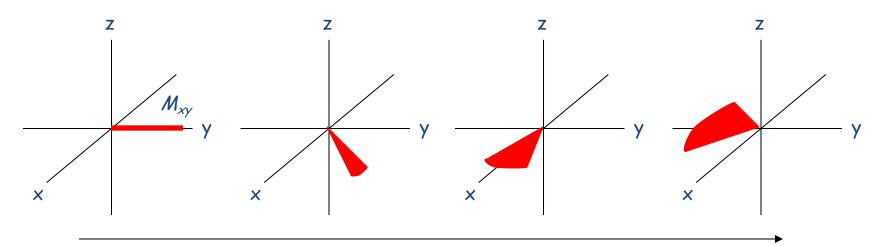
Several processes are "lumped" under this term, but one of the predominant techniques is spin diffusion, a process requiring neighboring nuclei to have the same precession rates, but different magnetic quantum numbers.

Another cause is a disruption in the homogeneity of the magnetic field through the sample caused by the sample itself. (*e.g.* – formation of dimers, trimers, *etc*. that change the relaxation rates of nuclei.)

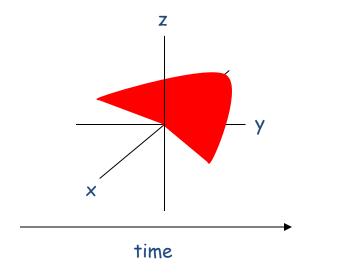
Spin-Lattice relaxation is the <u>slowest</u> of the relaxation processes $(T_1>T_2)$. Thus, T_2 is the primary influence on <u>line broadening</u> in the spectrum.

- **Spin-lattice relaxation** converts the excess energy into translational, rotational, and vibrational energy of the surrounding atoms and molecules (the lattice).
- **Spin-spin relaxation** transfers the excess energy to other magnetic nuclei in the sample.

Spin-Spin Relaxation, T₂

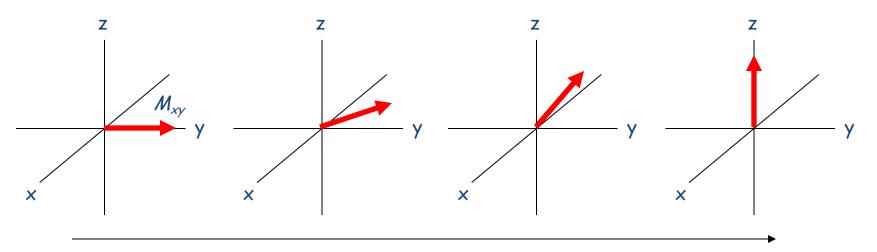




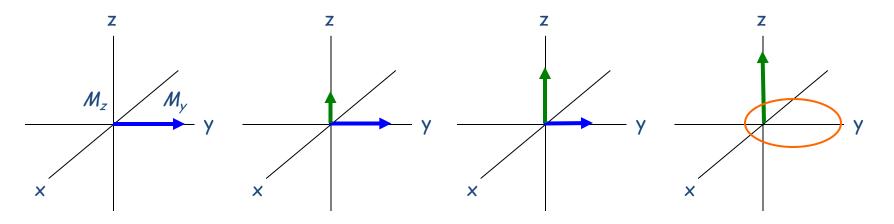


$$M_{xy} = M_{xy_0} \exp\left(\frac{-t}{T_2}\right)$$

Longitudinal Spin-Lattice Relaxation, T₁



time



Longitudinal Spin-Lattice Relaxation, T₁

The time constant, T_1 , describes how M_z returns to its equilibrium value. The equation governing this behavior as a function of the time *t* after its displacement is:

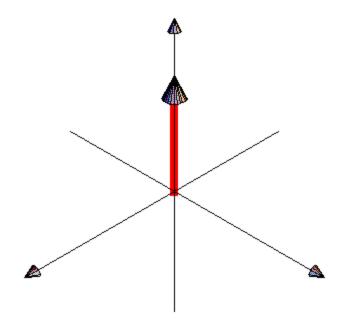
$$M_{Z} = M_{0} \left(1 - \exp\left(\frac{-t}{T_{1}}\right) \right)$$
 for pw $\leq 90^{\circ}$

T₁ is therefore defined as the time required to change the Z component of magnetization by a factor of e.

If the net magnetization is placed along the "-Z" axis (*i.e.* – $\mathbf{pw} = 180^{\circ}$), it will gradually return to its equilibrium position along the "+Z" axis at a rate governed by T₁. The equation governing this behavior as a function of the time *t* after its displacement is:

$$M_{Z} = M_{0} \left(1 - 2 \exp\left(\frac{-t}{T_{1}}\right) \right) \text{ for } pw = 180^{\circ}$$

Relaxation of *M_{xy}* **During Fourier Transform NMR**

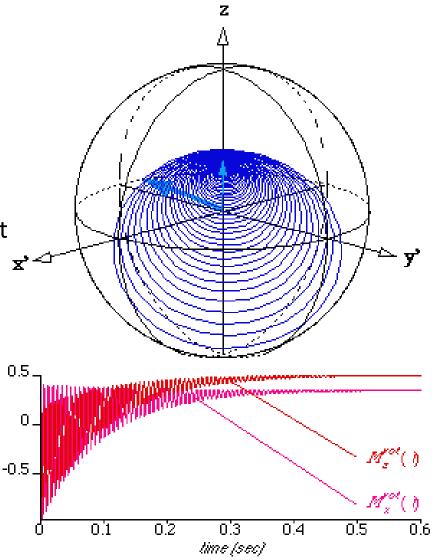


Responses Due to T_1 AND T_2

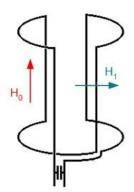
The Bloch Equations

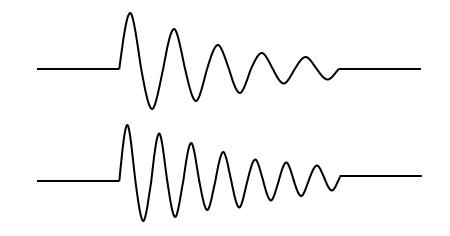
magnetization vector's trajectory

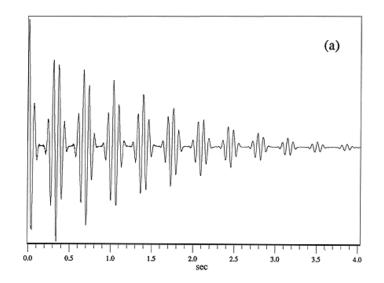
The initial vector, M_o , evolves under the effects of $T_1 \& T_2$ relaxation and from the influence of an applied rf-field. Here, the magnetization vector M(t) precesses about an effective field axis at a frequency determined by its offset. It's ends up at a "steady state" position as depicted in the lower plot of x- and y- magnetizations.

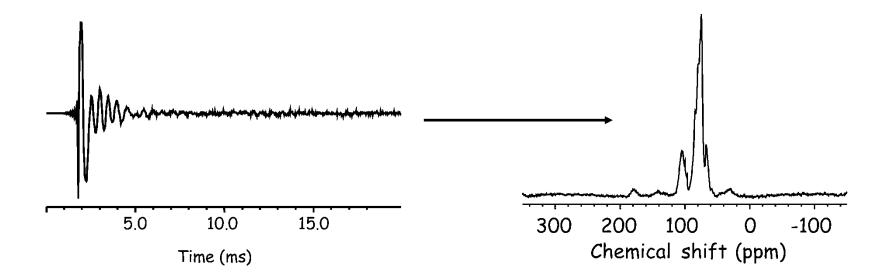


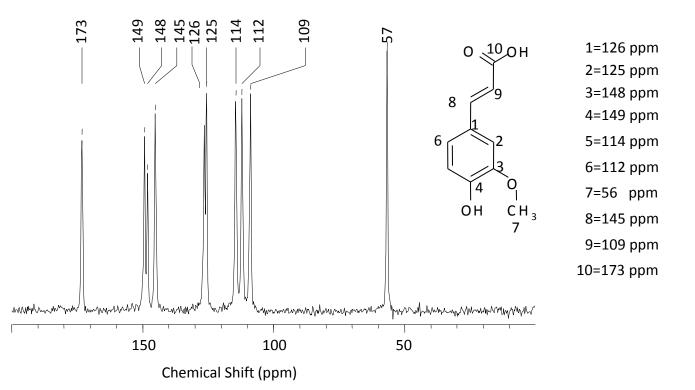
Basics of Fourier Transform NMR: The Free Induction Decay







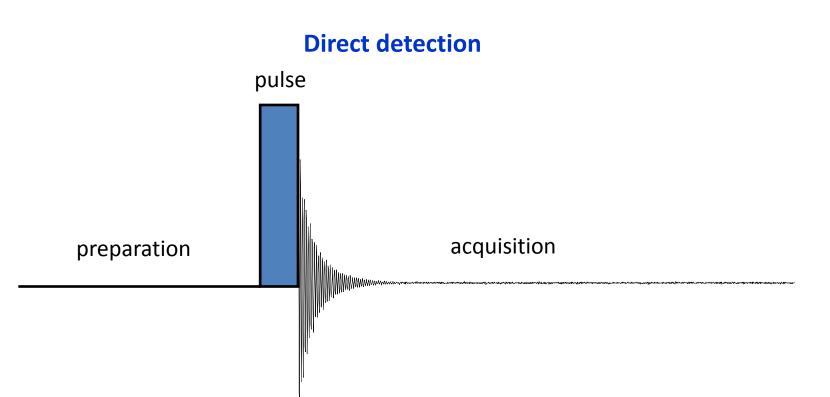




$$v = \frac{\gamma}{2\pi} B_0 (1 - \sigma) \longrightarrow \delta = \frac{v_s - v_R}{v_R} \times 10^6$$

Basic NMR experiment





How to measure T₂

$$M_{xy}(t) = M_{xy}(0)e^{-t/T_2}$$

At its most fundamental level, spin-spin relaxation corresponds to a decoherence of the transverse nuclear spin magnetization.

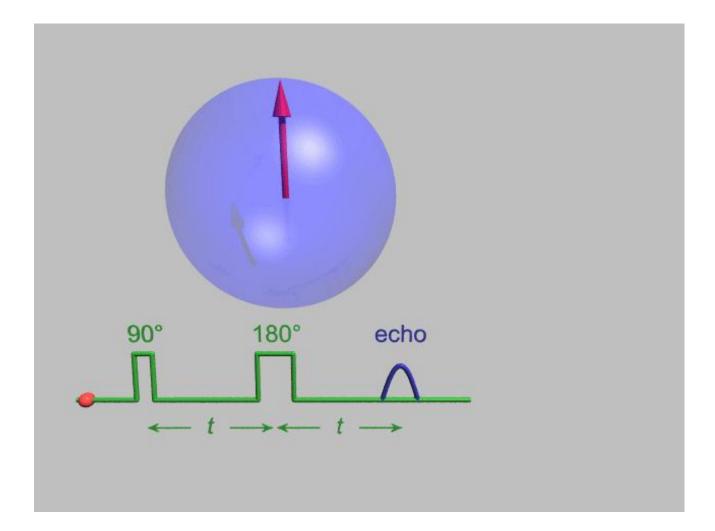
Random fluctuations of the local magnetic field lead to random variations in the instantaneous NMR precession frequency of different spins.

As a result, the initial phase coherence of the nuclear spins is lost, until eventually the phases are disordered and there is no net xy magnetization.

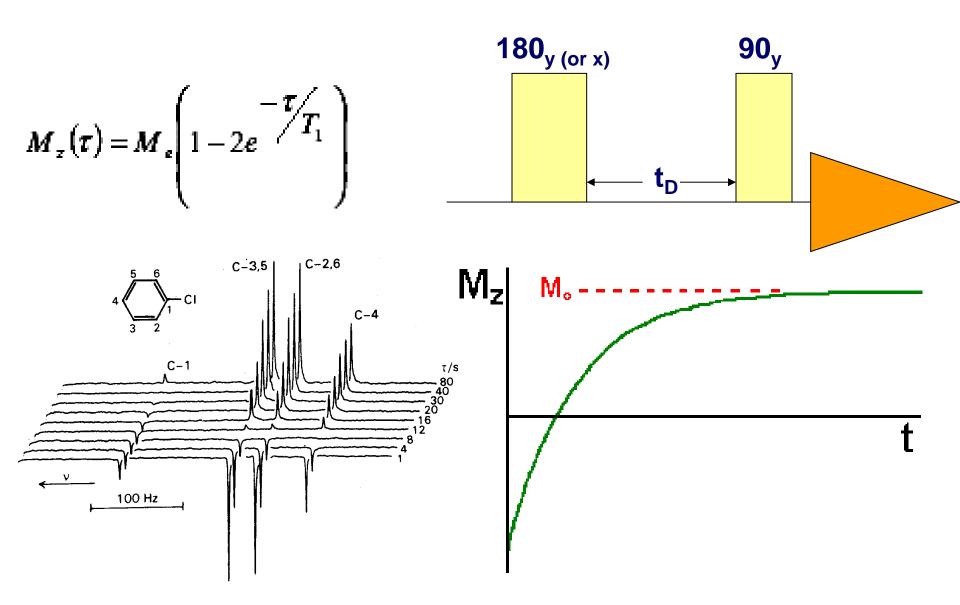
Because T₂ relaxation involves only the phases of other nuclear spins it is often called "spin-spin" relaxation.

 T_2 values are generally much less dependent on field strength, B, than T_1 values.

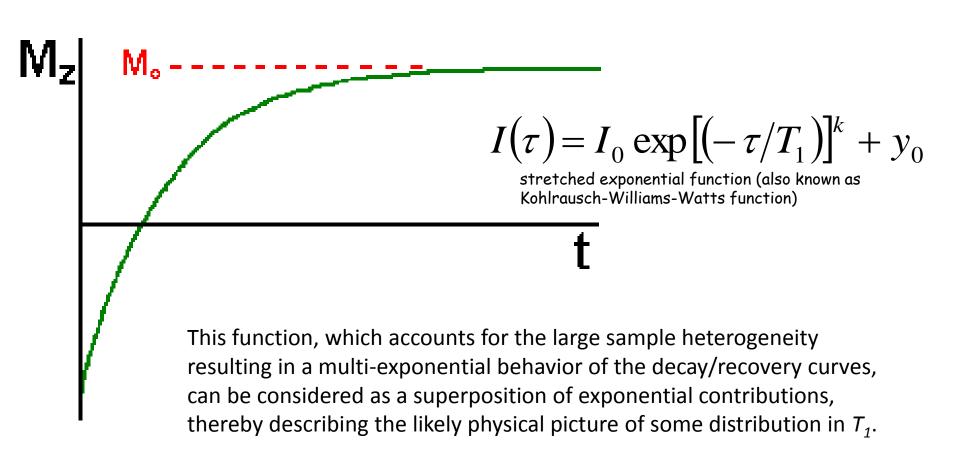
Spin echo sequence



How to measure T₁



How to measure T₁



The equation has the advantage that it is able to handle a wide range of behaviors within a single model. For this reason, assumptions about the number of exponentials to be used in modeling NMRD data are not necessary.

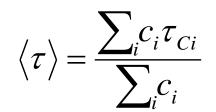
For peptides in aqueous solutions the dipole-dipole spin-lattice and spin-spin relaxation process are mainly mediated by other nearby protons

$$T_1^{-1} = \frac{2}{5} \frac{\gamma^4 \hbar^2}{r^6} I(I+1) \tau_c \left[\frac{1}{1+\omega^2 \tau_c^2} + \frac{4}{1+4\omega^2 \tau_c^2} \right]$$

$$T_2^{-1} = \frac{1}{5} \frac{\gamma^4 \hbar^2}{r^6} I(I+1) \tau_c \left[3 + \frac{5}{1+\omega^2 \tau_c^2} + \frac{2}{1+4\omega^2 \tau_c^2} \right]$$

Model free analysis

$$J(\omega_L) = \frac{\sum c_i \frac{\tau_{Ci}}{1 + (\omega_L \tau_{Ci})^2}}{\sum c_i}$$



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Bloembergen-Purcell-Pound (BPP) model

$$\left\langle \tau \right\rangle \!=\! \frac{\sum_{i}\! c_{i} \tau_{Ci}}{\sum_{i}\! c_{i}}$$

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 α represents the high-field relaxation rate and β is a constant related to the dipolar interactions. The latter contains the proton quantum-spin number, the proton gyromagnetic ratio, the Planck constant and the electron-nuclear hyperfine coupling constant which describes the interactions between resonant protons and unpaired electrons.

The correlation time is roughly defined as the time taken for a molecule to rotate one radian or move a distance of the order of its own dimension. Usually it is assumed that the correlation time depend on temperature according to an Arrhenius type of function;

$$\frac{1}{r_c} = v_0 \exp\left(-\frac{E}{RT}\right)$$