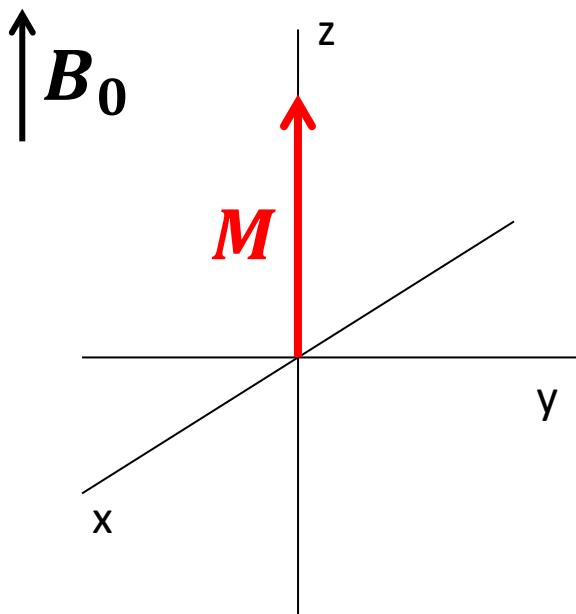
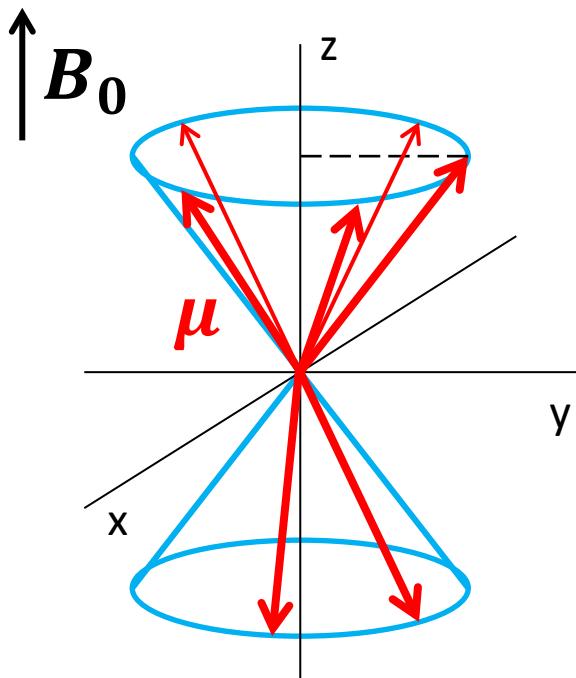


- Atomic nuclei have spin $\textcolor{blue}{I}$ and magnetic dipole moment $\mu = \gamma \textcolor{blue}{I}$
- ^1H , ^{13}C , ^{15}N have spin $\frac{1}{2}$ - good for NMR!
- Nuclei (with spin $\frac{1}{2}$) have two states (up and down) in a magnetic field
- The energy difference between the states is $\Delta E = \gamma \hbar B$, which corresponds to frequency of electromagnetic radiation $\omega = \gamma B$ ($\nu = \frac{\gamma B}{2\pi}$) (Larmor frequency)
- The populations of the two states differs slightly ∴ the bulk sample has a magnetic dipolar moment along z (aligned with $\textcolor{blue}{B}$)



- The magnetic field at the nucleus differs from the external magnetic field due to the movement of electrons around the nucleus ∴ different nuclei in a molecule have slightly different Larmor frequencies

Reference:

500.1306885 MHz



688.5 Hz

1.3766 ppm

500.1300000 MHz



0 Hz

0 ppm

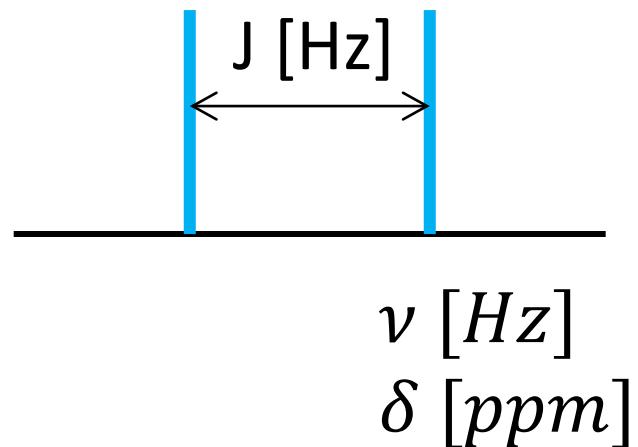
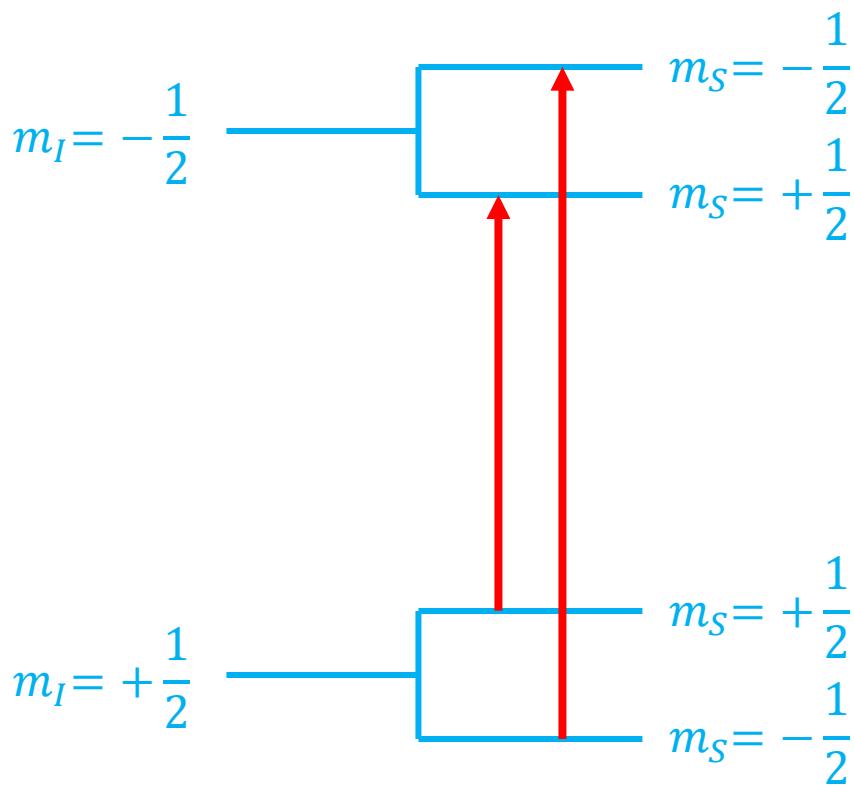
ν [Hz]

δ [ppm]

- Chemical shift (does not depend on external magnetic field!):

$$\delta = \frac{500.1306885 - 500.1300000}{500.130000} * 10^6 = 1.3766 \text{ ppm}$$

- J-coupling (scalar coupling) = interaction between nuclear spins mediated by electrons that form the bond(s) between the nuclei
- Energy of spin I in the presence of J-coupling to spin S:



- J-coupling constant [Hz] does not depend on external magnetic field (but the splitting in ppm units will!)

NMR spectrum of ubiquitin
(76 amino acid residues, MW=8,565 Da)

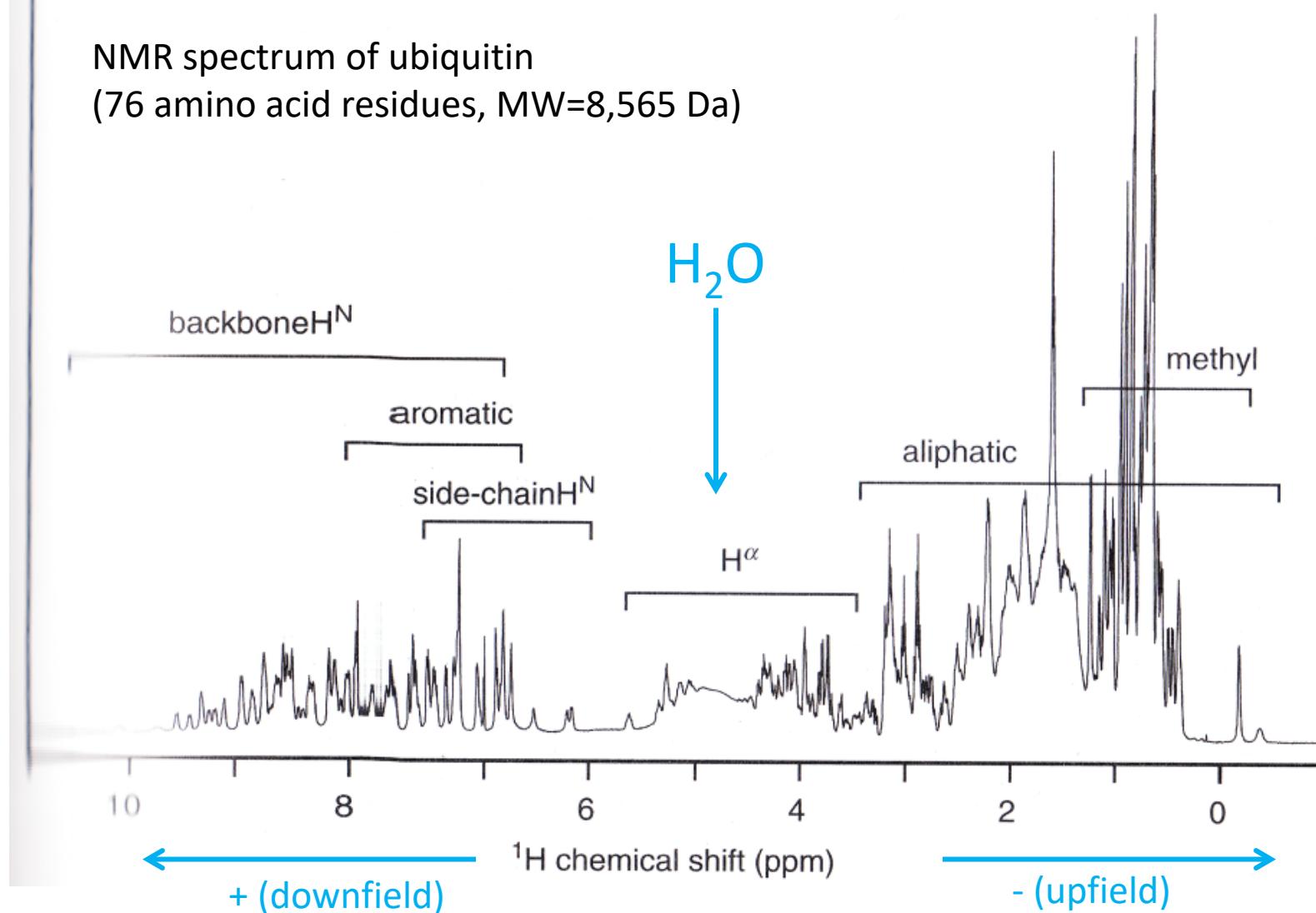


TABLE 1

RANDOM COIL ^1H CHEMICAL SHIFTS FOR THE 20 COMMON AMINO ACIDS WHEN FOLLOWED BY ALANINE

Residue	NH	H^α	H^β	Others
Ala	8.24	4.32	1.39	
Cys (reduced)	8.32	4.55	2.93, 2.93	
Cys (oxidized)	8.43	4.71	3.25, 2.99	
Asp	8.34	4.64	2.72, 2.65	
Glu	8.42	4.35	2.06, 1.96	γCH_2 2.31, 2.31
Phe	8.30	4.62	3.14, 3.04	2.6H 7.28; 3.5H 7.38; 4H 7.32
Gly	8.33	3.96		
His	8.42	4.73	3.29, 3.16	2H 8.58; 4H 7.29
Ile	8.00	4.17	1.87	γCH_2 1.45, 1.16; γCH_3 0.91; δCH_3 0.86
Lys	8.29	4.32	1.84, 1.75	γCH_2 1.44, 1.44; δCH_2 1.68, 1.68; ϵCH_2 2.99, 2.99; ϵNH_3^+ 7.81
Leu	8.16	4.34	1.62, 1.62	γCH 1.59; δCH_3 0.92, 0.87
Met	8.28	4.48	2.11, 2.01	γCH_2 2.60, 2.54; ϵCH_3 2.10
Asn	8.40	4.74	2.83, 2.75	γNH_2 7.59, 6.91
Pro	—	4.42	2.29, 1.94	γCH_2 2.02, 2.02; δCH_2 3.63, 3.63
Gln	8.32	4.34	2.12, 1.99	γCH_2 2.36, 2.36; δNH_2 7.52, 6.85
Arg	8.23	4.34	1.86, 1.76	γCH_2 1.63, 1.63; δCH_2 3.20, 3.20; ϵNH 8.07
Ser	8.31	4.47	3.89, 3.87	
Thr	8.15	4.35	4.24	γCH_2 1.21
Val	8.03	4.12	2.08	γCH_3 0.94, 0.93
Trp ^a	8.25	4.66	3.29, 3.27	2H 7.27; 4H 7.65; 5H 7.18; 6H 7.25; 7H 7.50
Tyr	8.12	4.55	3.03, 2.98	2.6H 7.14; 3.5H 6.84

Chemical shifts are referenced to internal DSS at 25 °C, pH ~5.0.

^a Measured using a peptide with free N- and C-termini.

Wishart DS, Bigam CG, Holm A, Hodges RS, Sykes BD. ^1H , ^{13}C and ^{15}N random coil NMR chemical shifts of the common amino acids. I. Investigations of nearest-neighbor effects. J Biomol NMR. 1995 Jan;5(1):67-81.

TABLE 2

RANDOM COIL ^{13}C CHEMICAL SHIFTS FOR THE 20 COMMON AMINO ACIDS WHEN FOLLOWED BY ALANINE

Residue	C=O	C ^a	C ^b	Others
Ala	177.8	52.5	19.1	
Cys (reduced)	174.6	58.2	28.0	
Cys (oxidized)	174.6	55.4	41.1	
Asp	176.3	54.2	41.1	γCO 180.0
Glu	176.6	56.6	29.9	γCH_2 35.6; δCO 183.4
Phe	175.8	57.7	39.6	1C 138.9; 2,6CH 131.9; 3,5CH 131.5; 4CH 129.9
Gly	174.9	45.1		
His	174.1	55.0	29.0	2CH 136.2; 4CH 120.1; 5C 131.1
Ile	176.4	61.1	38.8	γCH_2 27.2; γCH_3 17.4; δCH_3 12.9
Lys	176.6	56.2	33.1	γCH_2 24.7; δCH_2 29.0; ϵCH_2 41.9
Leu	177.6	55.1	42.4	γCH 26.9; δCH_3 24.9, 23.3
Met	176.3	55.4	32.9	γCH_2 32.0; ϵCH_3 16.9
Asn	175.2	53.1	38.9	γCO 177.2
Pro	177.3	63.3	32.1	γCH_2 27.2; δCH_2 49.8
Gln	176.0	55.7	29.4	γCH_2 33.7; δCO 180.5
Arg	176.3	56.0	30.9	γCH_2 27.1; δCH_2 43.3; ϵC 159.5
Ser	174.6	58.3	63.8	
Thr	174.7	61.8	69.8	γCH_3 21.5
Val	176.3	62.2	32.9	γCH_3 21.1, 20.3
Trp ^a	176.1	57.5	29.6	2CH 127.4; 3C 111.2; 4CH 122.2; 5CH 124.8; 6CH 121.0; 7CH 114.7; 8C 138.7; 9C 129.5
Tyr	175.9	57.9	38.8	1C 130.6; 2,6CH 133.3; 3,5CH 118.2; 4C 157.3

Chemical shifts are referenced to internal DSS at 25 °C, pH ~5.0.

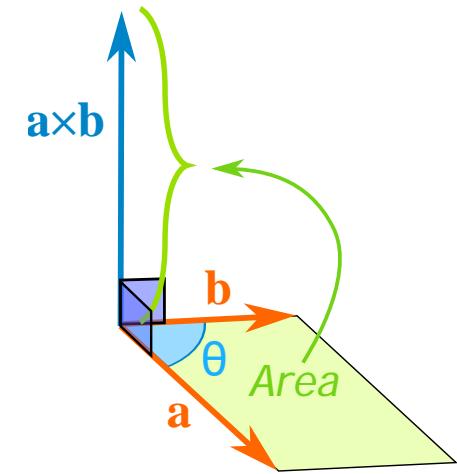
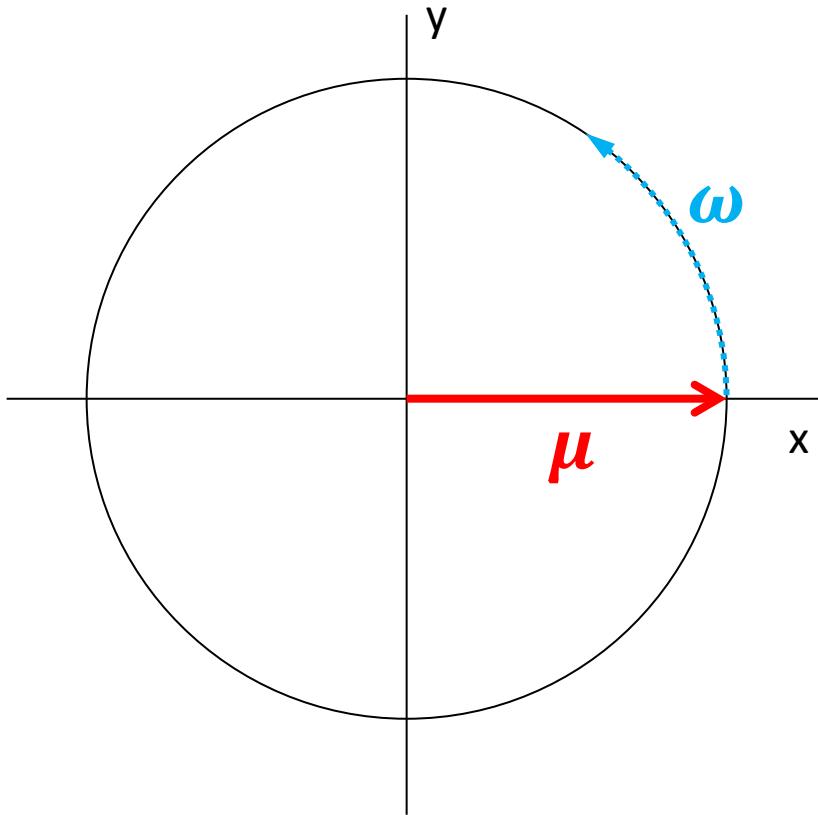
^a Measured using a peptide with free N- and C-termini.

Wishart DS, Bigam CG, Holm A, Hodges RS, Sykes BD. 1H, 13C and 15N random coil NMR chemical shifts of the common amino acids. I. Investigations of nearest-neighbor effects. J Biomol NMR. 1995 Jan;5(1):67-81.

Description and analysis of rotations (oscillations)

Rotation with angular velocity ω :

$$\frac{d\mu(t)}{dt} = \omega \times \mu(t) = -\mu(t) \times \omega$$



ν : frequency in $s^{-1} = Hz$

$$\omega = 2\pi\nu$$

angular velocity
(angular frequency) in
radians/s

Semi-classical model (Bloch equations)

Magnetic dipole μ experiences torque in magnetic field:

$$\mu(t) \times B = \frac{dI(t)}{dt} = \frac{1}{\gamma} \frac{d\mu(t)}{dt}$$

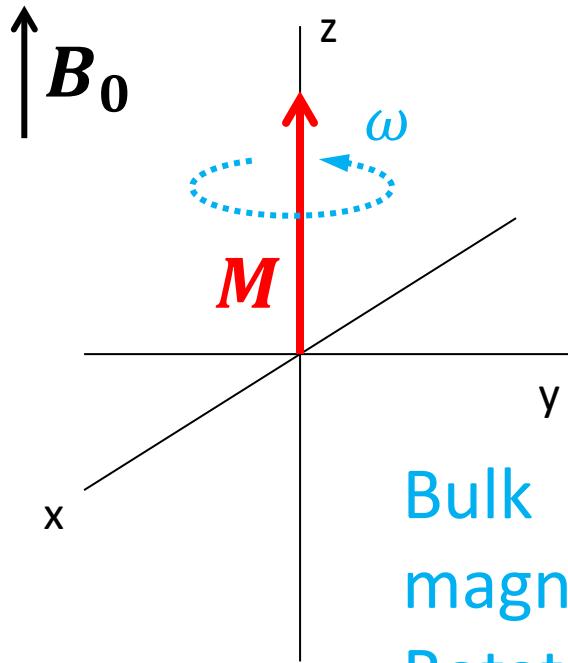
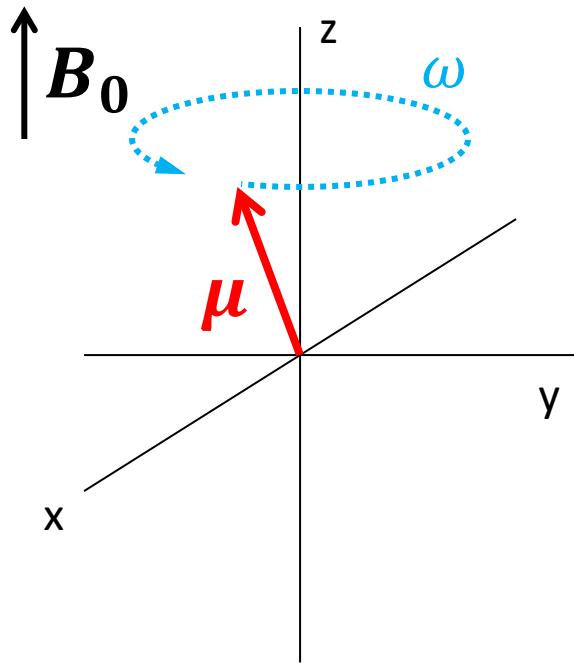
torque

$\mu = \gamma I$

$$\frac{d\mu(t)}{dt} = \mu(t) \times \gamma B = \boxed{-\gamma B} \times \mu(t)$$

$\mu(t)$ rotates (precesses) with angular velocity $\boxed{\omega = -\gamma B}$

Larmor frequency



Bulk
magnetization:
Rotation not
observable

Note: $\omega = -\gamma B \therefore \omega$ and B have opposite direction for positive γ and the same direction for negative γ .
In all the diagrams, I'll draw them in the same direction.

Application of perpendicular (horizontal) magnetic field $\mathbf{B}_1(t)$ that oscillates with angular velocity $\omega = -\gamma B$:

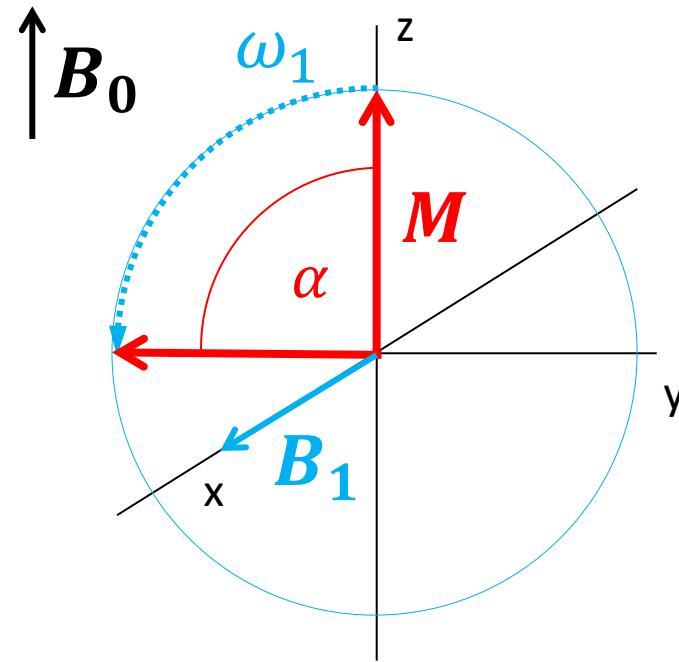
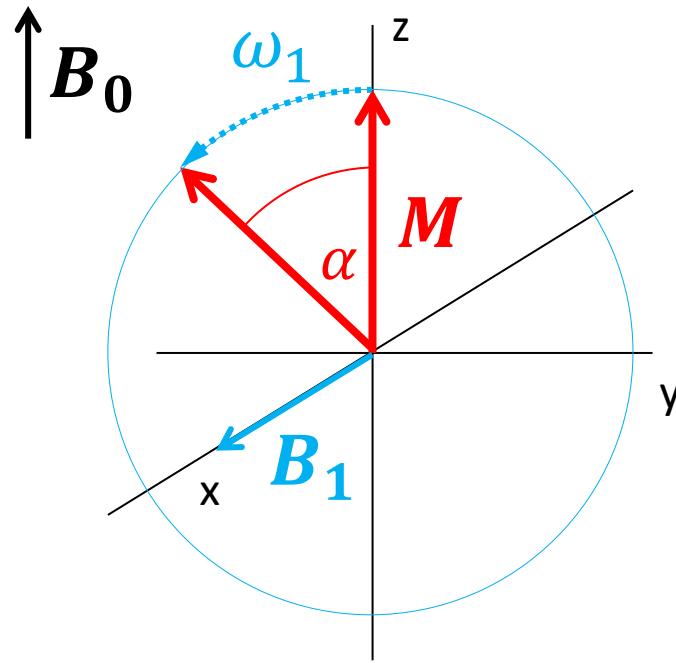
$$\frac{d\boldsymbol{\mu}(t)}{dt} = -\gamma(\mathbf{B} + \mathbf{B}_1(t)) \times \boldsymbol{\mu}(t)$$

Switch to a coordinate frame that rotates with angular velocity $\omega = -\gamma B$:

$$\frac{d\boldsymbol{\mu}(t)}{dt} = -\gamma \mathbf{B}_1 \times \boldsymbol{\mu}(t)$$

$\boldsymbol{\mu}(t)$ rotates with angular velocity $\boldsymbol{\omega}_1 = -\gamma \mathbf{B}_1$ around \mathbf{B}_1 in the rotating frame!

Rotating frame (angular velocity $\omega = -\gamma B$):



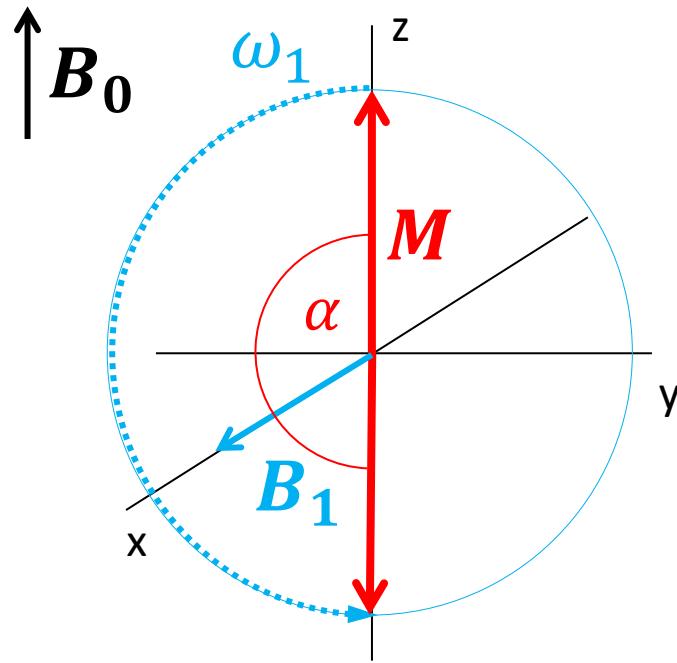
B_1 along x:

Rotation in the y-z plane
with angular velocity ω_1
 $\alpha = \omega_1 t$

90° pulse: $\alpha = \omega_1 t = \frac{\pi}{2}$

$$M_z = M_0 \rightarrow -M_y = M_0$$

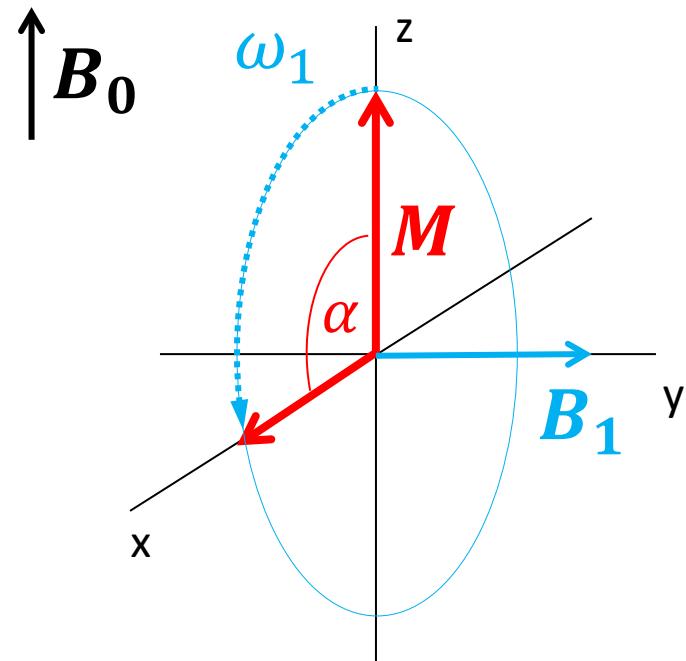
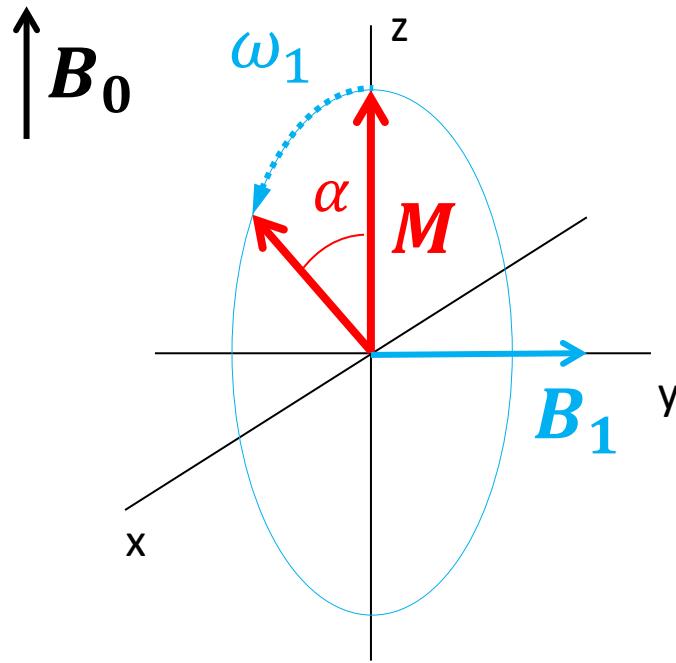
Rotating frame (angular velocity $\omega = -\gamma B$):



180° pulse: $\alpha = \omega_1 t = \pi$

$$M_z = M_0 \rightarrow -M_z = M_0$$

Rotating frame (angular velocity $\omega = -\gamma B$):



B_1 along y:

Rotation in the x-z plane
with angular velocity ω_1

$$\alpha = \omega_1 t$$

90° pulse: $\alpha = \omega_1 t = \frac{\pi}{2}$

$$M_z = M_0 \rightarrow M_x = M_0$$

When the angular velocity ω_{rf} of the perpendicular magnetic field $B_1(t)$ differs (somewhat) from Larmor frequency $\omega = -\gamma B$:

Pulses still work as long as $|\gamma B_1| \gg |\omega - \omega_{rf}|$

Rotating frame (angular velocity ω_{rf}):

$$\frac{d\mu(t)}{dt} = -\gamma(\textcolor{blue}{B} + \textcolor{red}{B}_1) \times \mu(t) - \omega_{rf} \times \mu(t)$$

$$= (\boxed{-\gamma \textcolor{blue}{B}} - \omega_{rf} \boxed{-\gamma \textcolor{red}{B}_1}) \times \mu(t)$$

ω

ω_1

Rotation around B_1 (stationary in the rotating frame)

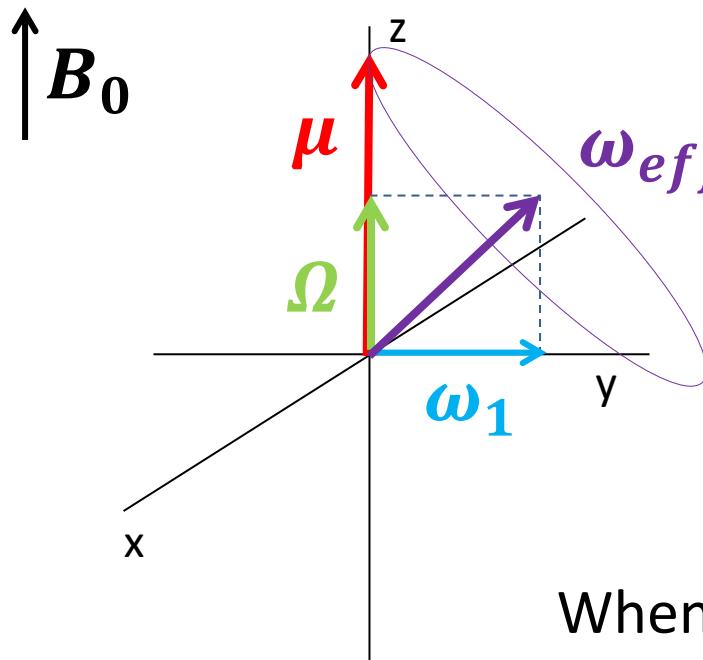
Correction for rotation of the rotating frame

Rotation around B with Larmor frequency

Rotating frame (angular velocity ω_{rf}):

$$\frac{d\mu(t)}{dt} = (\boxed{\omega - \omega_{rf}} + \omega_1) \times \mu(t)$$

Ω (offset)



When $|\omega_1| \gg |\Omega|$

$\omega_{eff} \approx \omega_1$

Rotation around axis in a horizontal plane

Rotation around a tilted axis

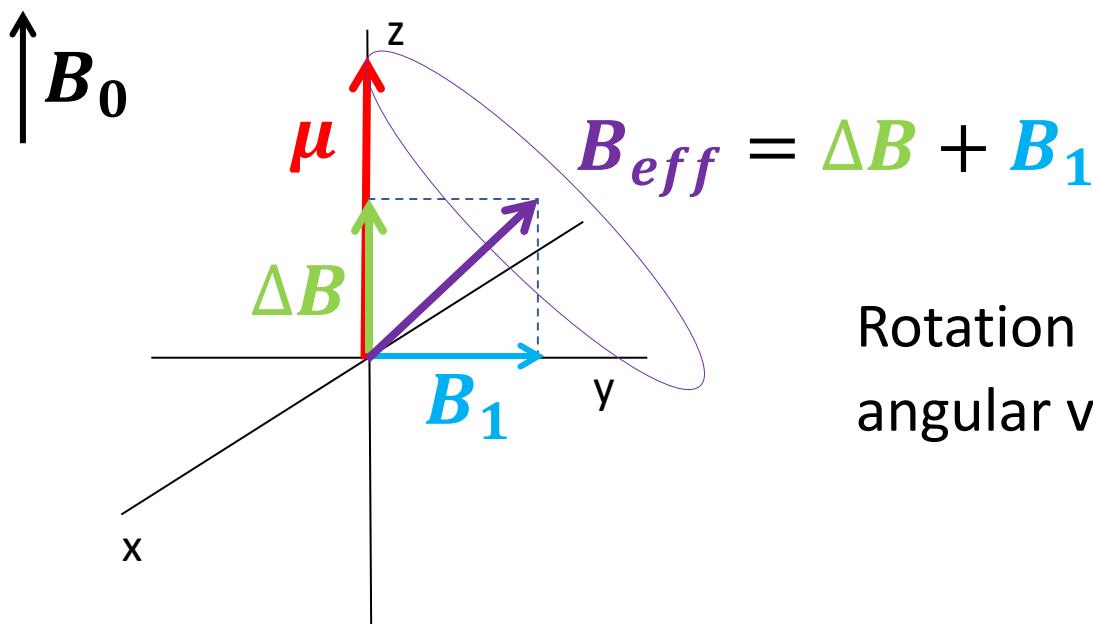
$\omega_{eff} = \Omega + \omega_1$

Another way to look at it:

Rotating frame (angular velocity ω_{rf}):

$$\begin{aligned}\frac{d\mu(t)}{dt} &= -\gamma(\mathbf{B} + \mathbf{B}_1) \times \mu(t) - \omega_{rf} \times \mu(t) \\ &= -\gamma \left(\boxed{\mathbf{B} + \frac{\omega_{rf}}{\gamma}} + \mathbf{B}_1 \right) \times \mu(t)\end{aligned}$$

$\Delta\mathbf{B}$ (residual vertical magnetic field
in the rotating frame)



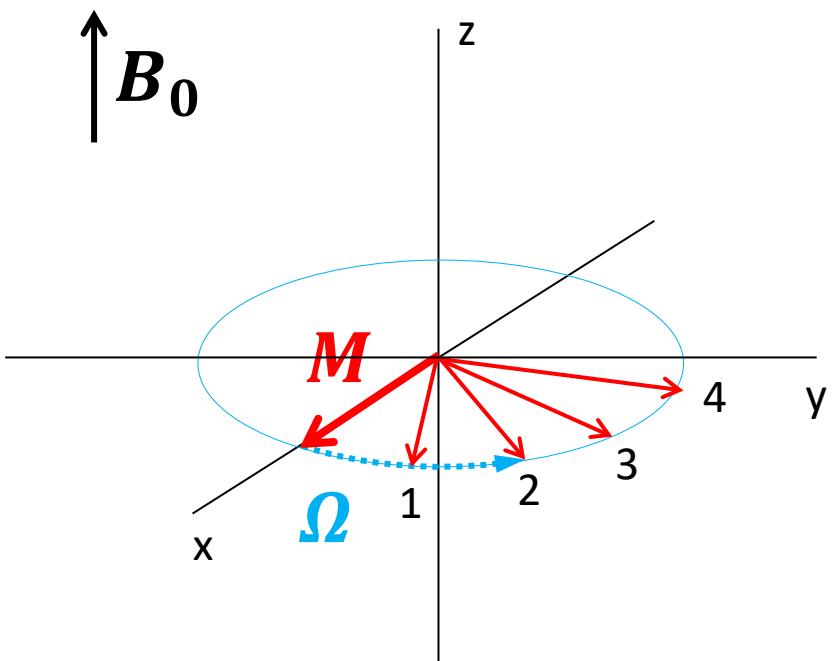
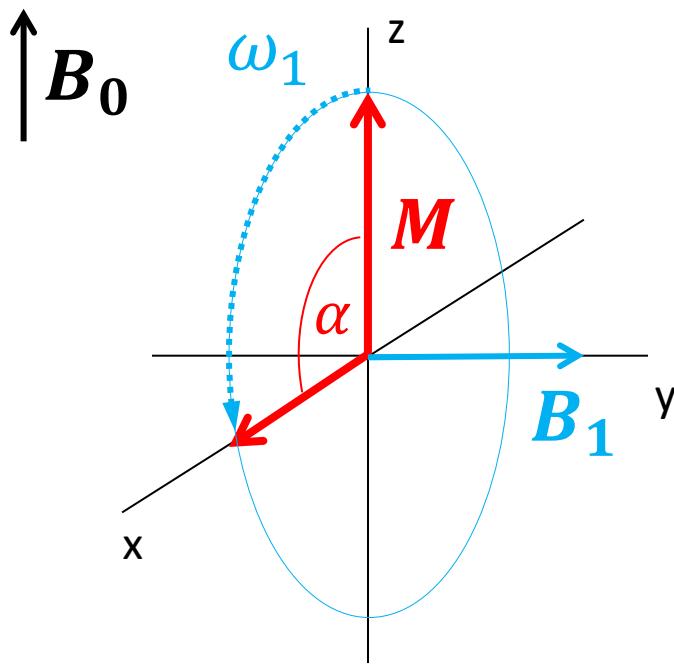
Rotation around B_{eff} with
angular velocity $\omega_{eff} = -\gamma B_{eff}$

Rotating frame (angular velocity ω_{rf}):

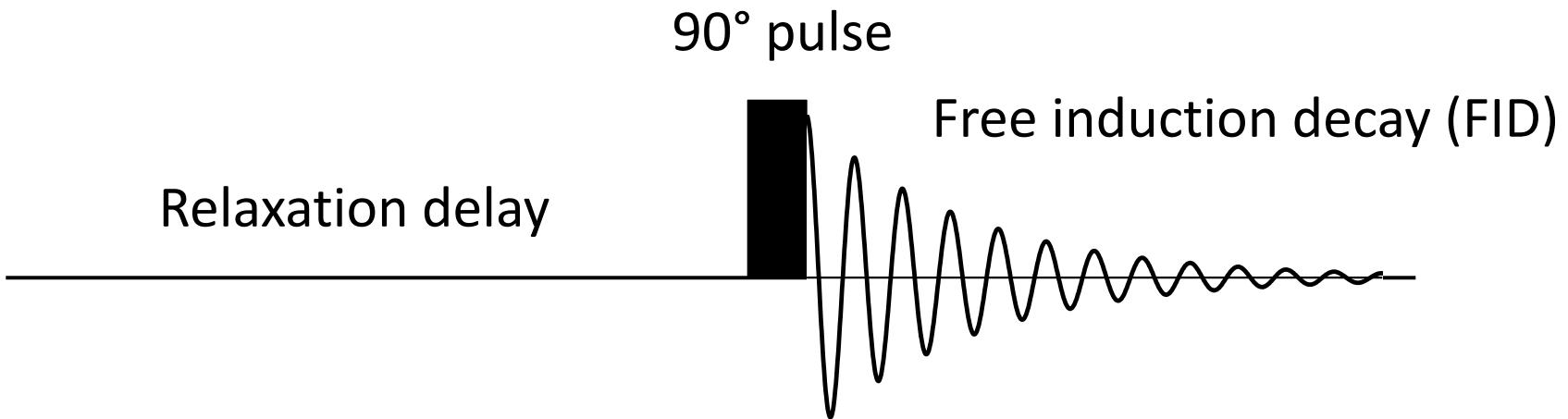
$$\frac{d\mu(t)}{dt} = (\boxed{\omega - \omega_{rf}} + \omega_1) \times \mu(t) = -\gamma \left(\boxed{B + \frac{\omega_{rf}}{\gamma}} + \mathbf{B}_1 \right) \times \mu(t)$$

Ω (offset)

ΔB (residual vertical magnetic field
in the rotating frame)



Basic NMR experiment



Relaxation delay - Allows magnetization to return to equilibrium along z

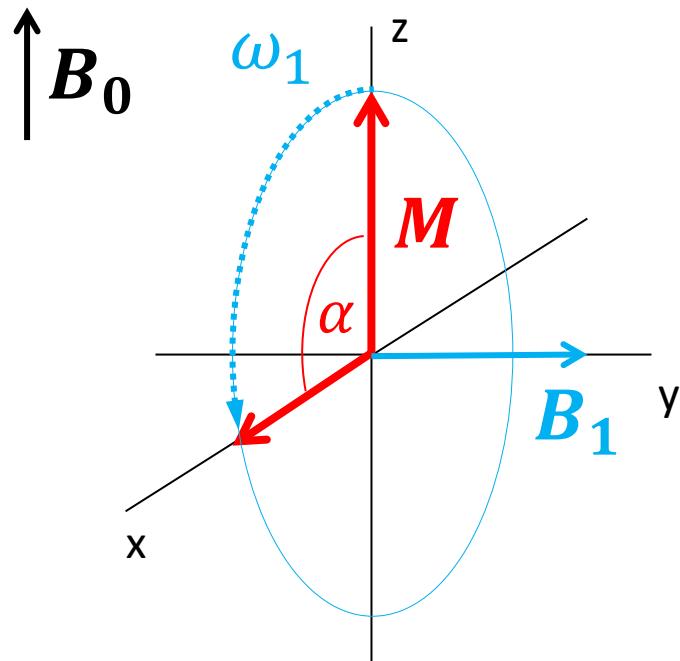
90° pulse - Tips magnetization into the x-y plane

Free induction decay (FID) - Magnetization precesses in the x-y plane, this induces electrical current in a coil and is detected

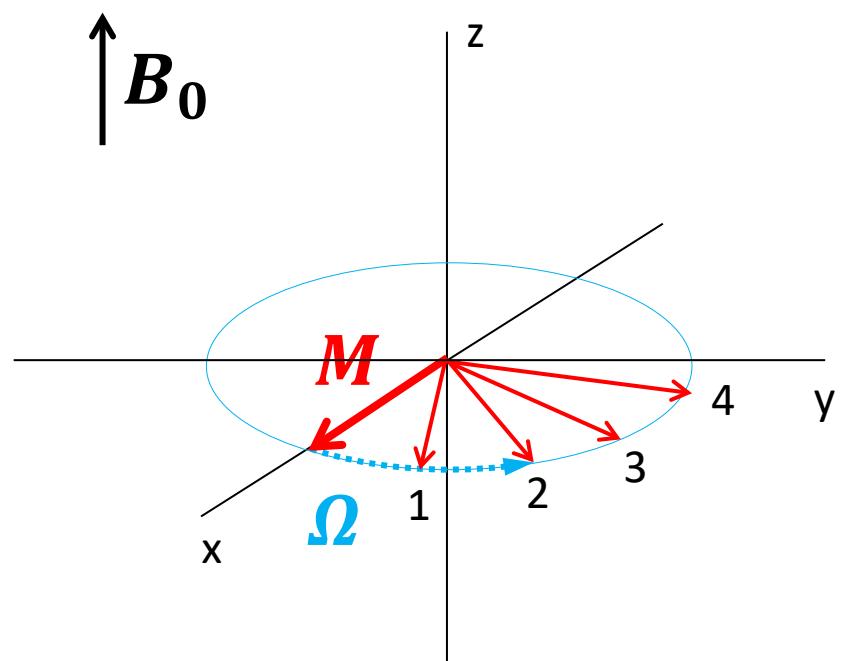
Repeat n times (to improve signal to noise ratio)

Rotating frame (angular velocity ω_{rf})

90° pulse



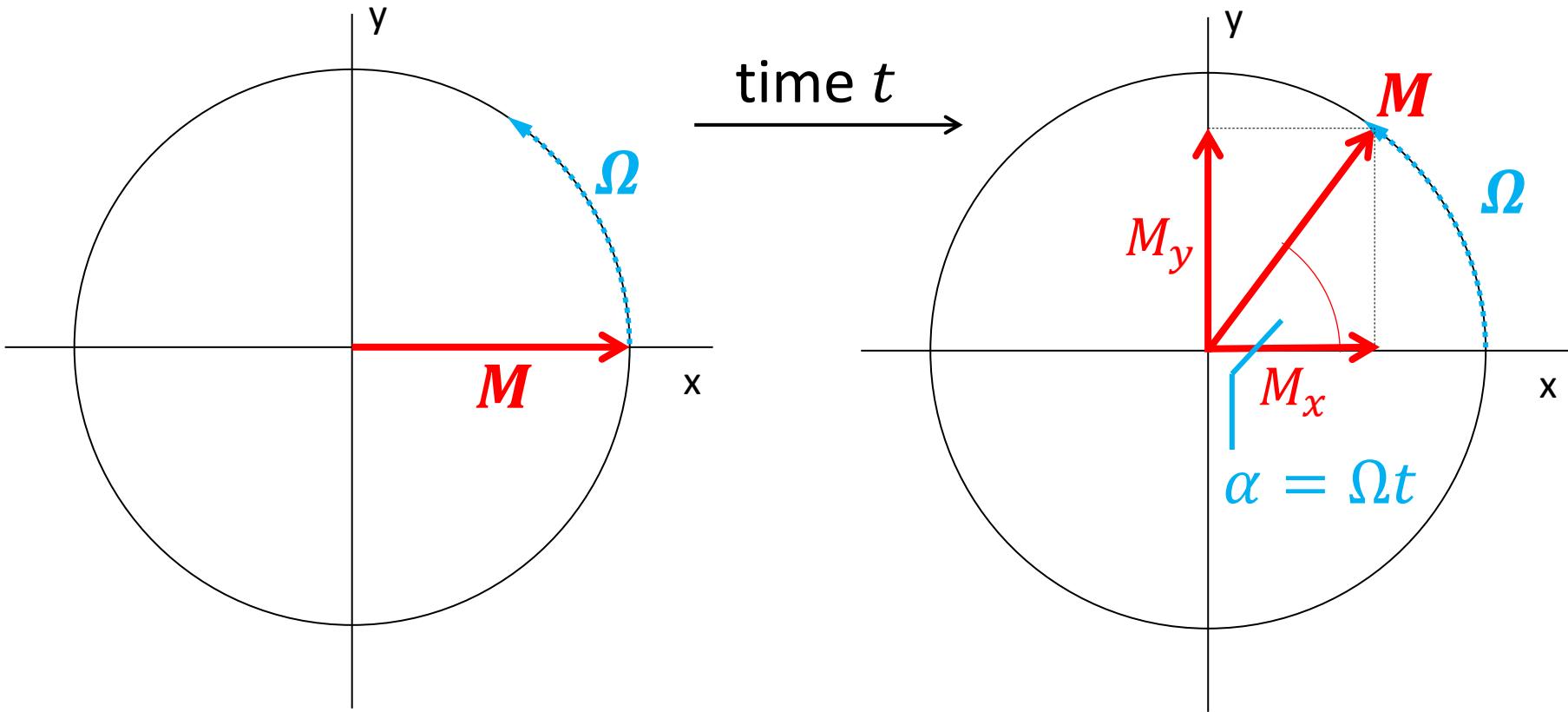
Free induction decay (FID)



Turn on B_1 for time t such that
 $\alpha = \omega_1 t = | - \gamma B_1 | t = \frac{\pi}{2}$

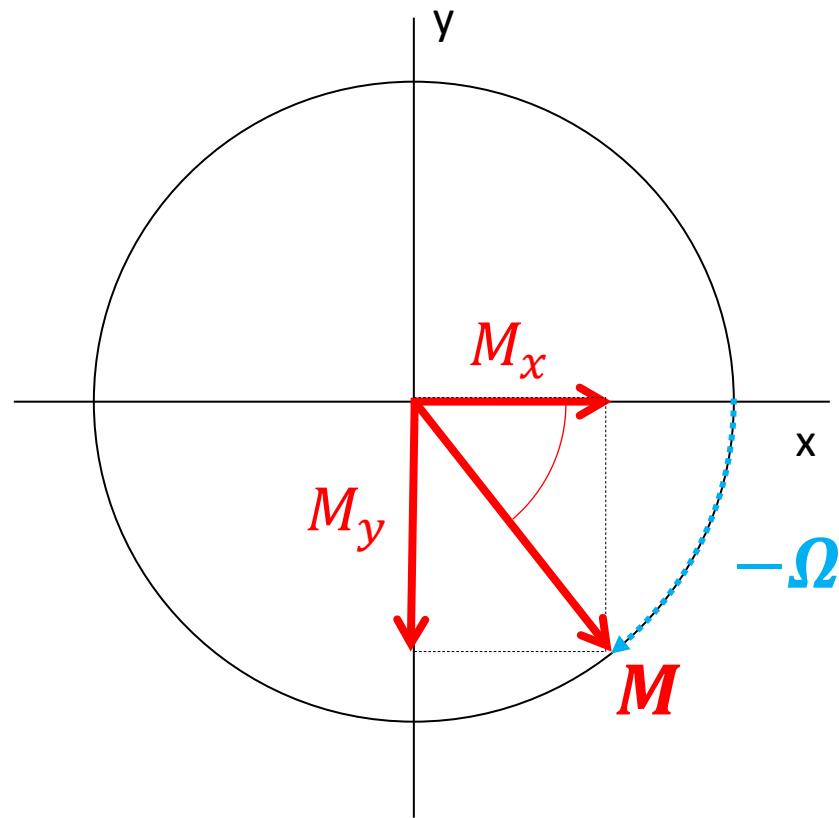
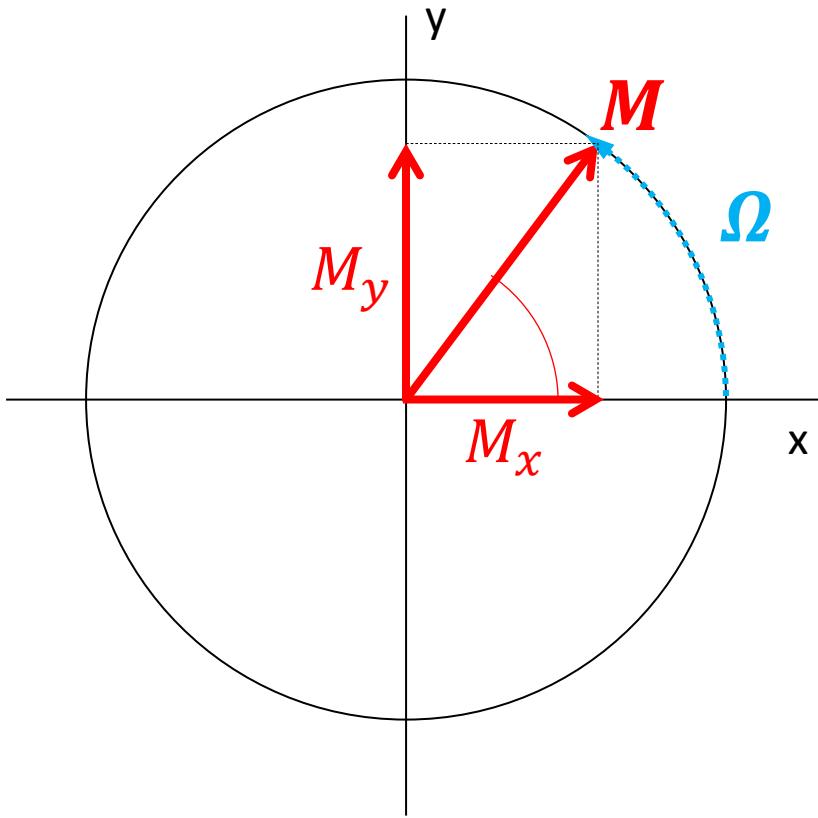
Magnetization precesses in the x-y plane with frequency Ω
(and relaxes back to equilibrium)

Description and analysis of rotations (oscillations): Rotation with angular velocity Ω



$$M_x = M_0$$
$$M_y = 0$$

$$M_x = M_0 \cos \Omega t$$
$$M_y = M_0 \sin \Omega t$$



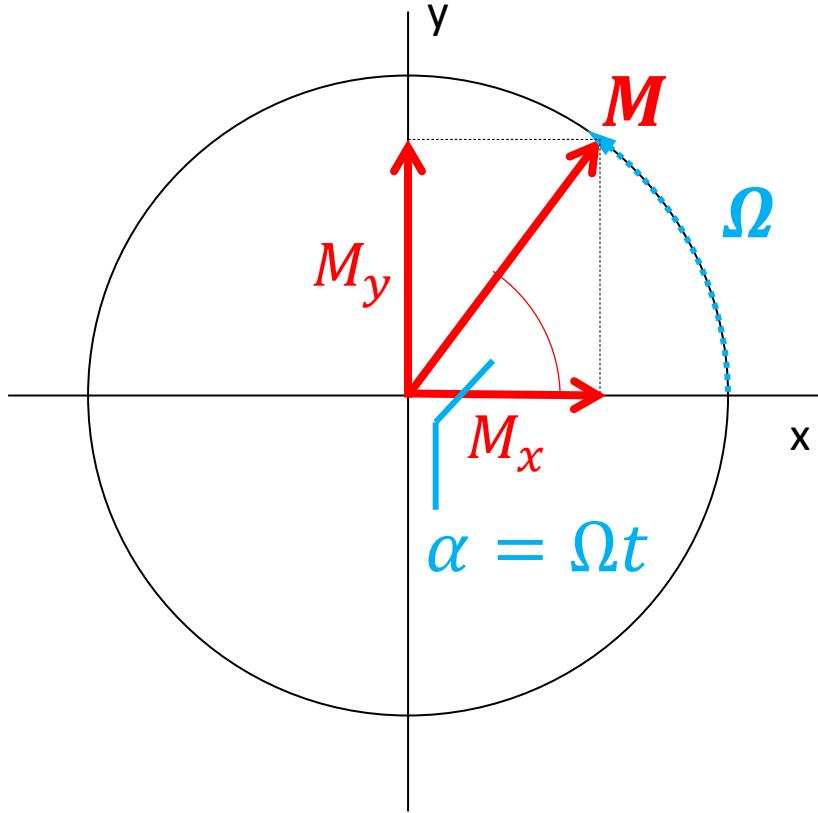
$$M_x = M_0 \cos \Omega t$$

$$M_y = M_0 \sin \Omega t$$

$$M_x = M_0 \cos(-\Omega t) = M_0 \cos \Omega t$$

$$M_y = M_0 \sin(-\Omega t) = -M_0 \sin \Omega t$$

Need both M_x and M_y components to distinguish the direction (sign) of rotation



M_x and M_y components formally treated like real and imaginary components of a complex number:

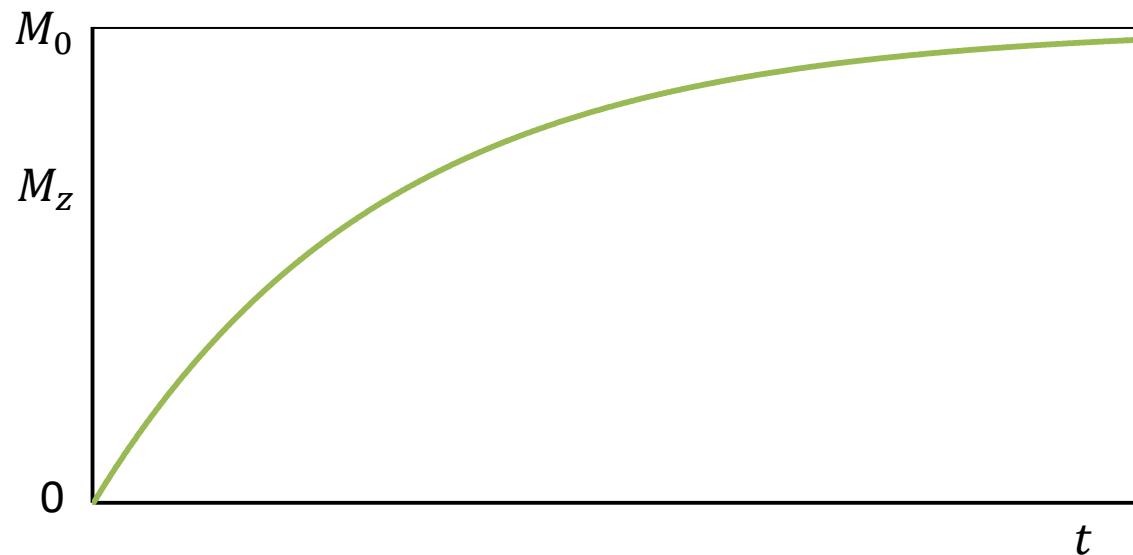
$$M = M_x + iM_y = M_0 \cos \Omega t + iM_0 \sin \Omega t$$

$$M = M_0 (\cos \Omega t + i \sin \Omega t) = M_0 e^{i\Omega t}$$

Return to equilibrium: relaxation

- Longitudinal (spin-lattice) relaxation

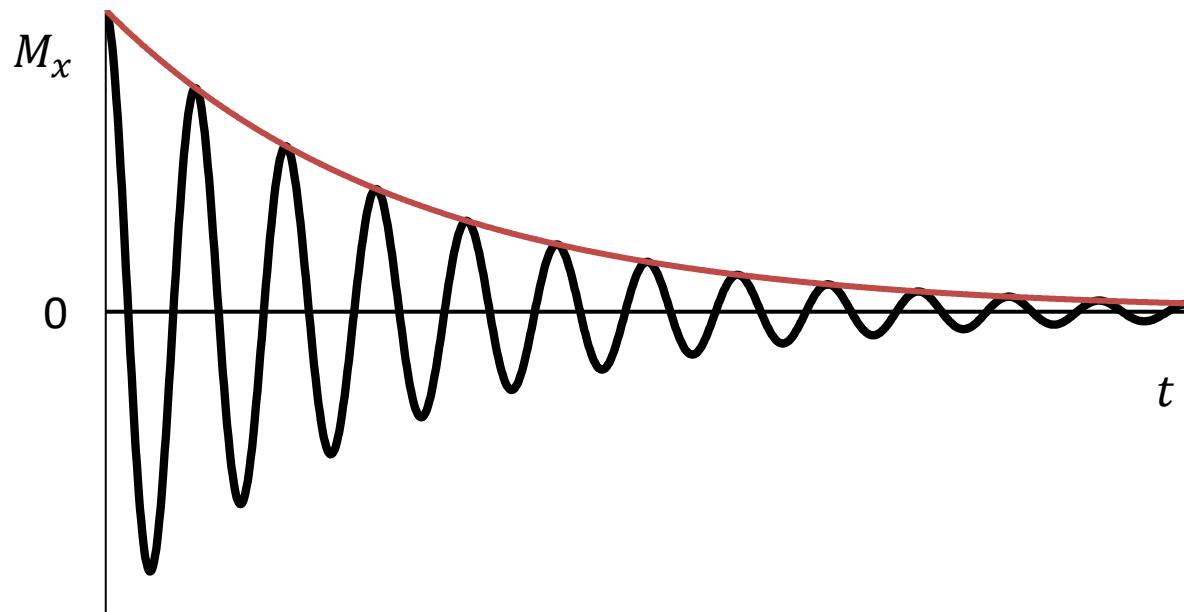
$$M_z = M_0(1 - e^{-R_1 t}) = M_0(1 - e^{-\frac{t}{T_1}})$$



Return to equilibrium: relaxation

- Transverse (spin-spin) relaxation:

$$M_{xy} = M_0 e^{-R_2 t} e^{i\Omega t} = M_0 e^{-\frac{t}{T_2}} e^{i\Omega t}$$



Converting oscillating signal to a frequency spectrum

Fourier transform $S(\omega) = \int_{-\infty}^{\infty} s(t)e^{-i\omega t} dt$

Oscillation $s(t) = M_0 e^{-R_2 t} e^{i\Omega_0 t}$

$$S(\omega) = \int_0^{\infty} M_0 e^{-R_2 t} e^{i\Omega_0 t} e^{-i\omega t} dt$$

$$\begin{aligned}[i(\Omega_0 - \omega) - R_2]t &= y \\ [i(\Omega_0 - \omega) - R_2]dt &= dy\end{aligned}$$

$$= \int_0^{\infty} M_0 e^{[i(\Omega_0 - \omega) - R_2]t} dt = \int M_0 e^y \frac{dy}{i(\Omega_0 - \omega) - R_2}$$

$$\int e^y dy = e^y + C$$

$$= \frac{M_0}{i(\Omega_0 - \omega) - R_2} \int e^y dy = \frac{M_0}{i(\Omega_0 - \omega) - R_2} [e^{i(\Omega_0 - \omega)t} e^{-R_2 t}]_{t=0}^{\infty}$$

(0-1)

$$(B + A)(-B + A) = -B^2 + A^2$$

$$S(\omega) = \frac{-M_0}{i(\Omega_0 - \omega) - R_2} = \frac{-M_0}{i(\Omega_0 - \omega) - R_2} \frac{-i(\Omega_0 - \omega) - R_2}{-i(\Omega_0 - \omega) - R_2}$$

$$= M_0 \frac{i(\Omega_0 - \omega) + R_2}{(\Omega_0 - \omega)^2 + R_2^2} = M_0 \left[\frac{R_2}{(\Omega_0 - \omega)^2 + R_2^2} + i \frac{\Omega_0 - \omega}{(\Omega_0 - \omega)^2 + R_2^2} \right]$$

Lorentzian line shape

$A(\omega)$
Absorption

$D(\omega)$
Dispersion

