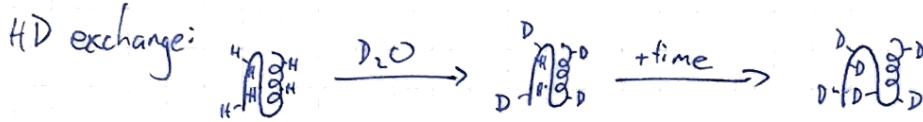


# H/D exchange

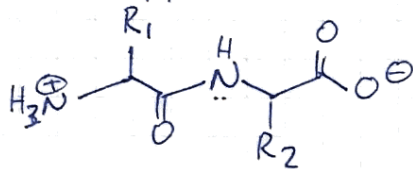


NMR + protein dynamics - have focussed on  $\tau_c$  timescale +  $R_{ex}$  + EXSY  
 - what about slower processes? ms - years



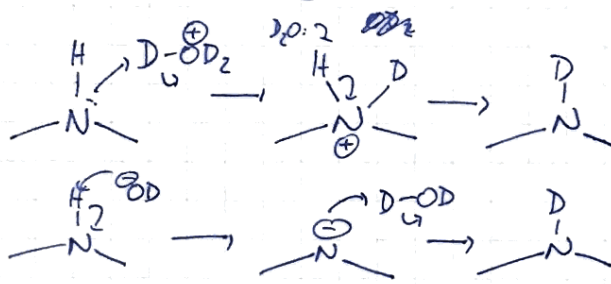
Monitor peak intensity over time:  $I \propto \exp(-k_{ex}t)$  Physical interpretation?

Consider a dipeptide:



What does rate depend on?

- pH
- temperature
- sequence
- isotope (H  $\rightarrow$  D, D  $\rightarrow$  H, H  $\rightarrow$  H...)

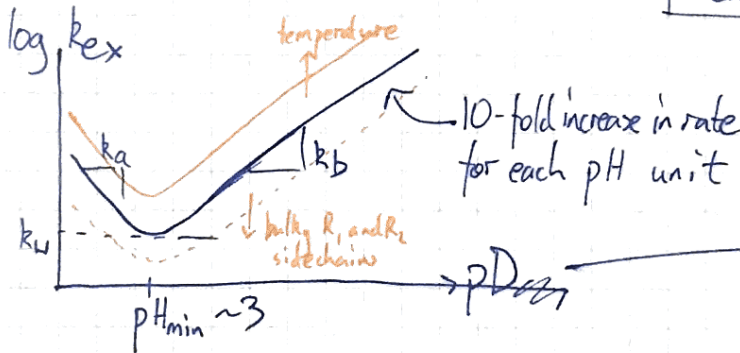


acid catalysis

+ water catalysis

base catalysis

$$k_{ex} = k_a [D^+] + k_b [OD^-] + k_w$$



pH vs pD (?)  
 $pD = -\log_{10} [D^+]$  (by definition)  
 but this is not measured directly by pH meter!  $pH^* = pD - 0.4$

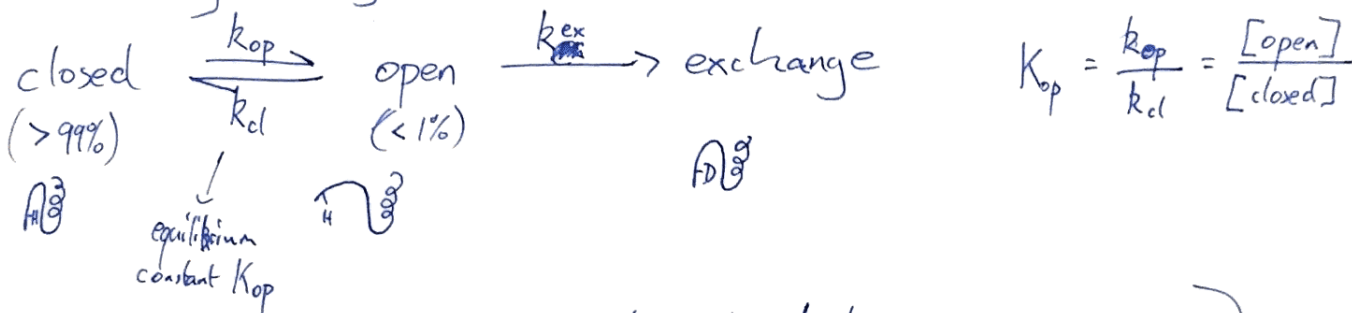
Temperature effect well characterised

Effect of sidechains also well studied (measured for all pairs)

$\therefore$  We can calculate 'random coil' exchange rates using database values  $\rightarrow$  SPHERE webserver.

What about HX within proteins? At a minimum, hydrogen bonding protects amide protons from exchange.

Lindstrom-Lang exchange model:



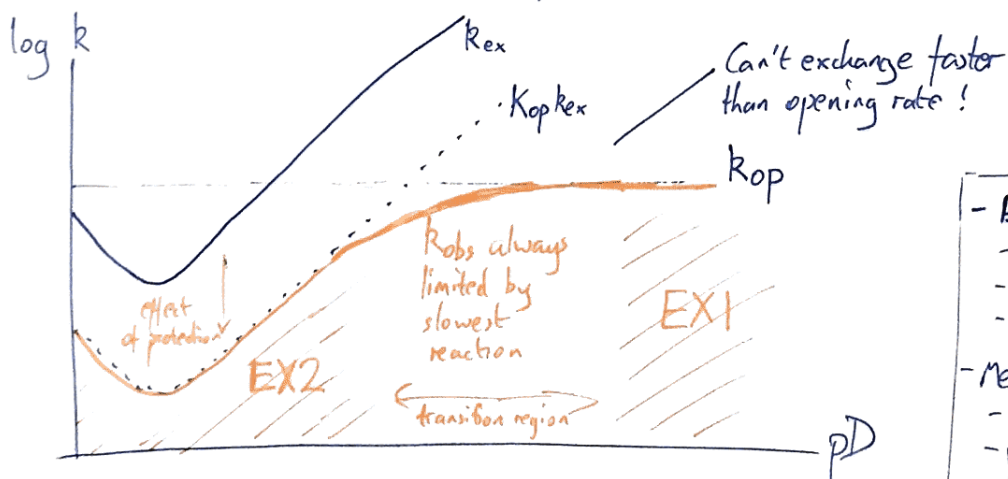
Two limits: Exchange of the open state is fast  
 - spend most of time waiting for rare opening events  
 - opening rate is RDS  $\Rightarrow k_{obs} \approx k_{op}$  } EX1

OR Equilibrium of open  $\rightleftharpoons$  closed is rapid - pre-equilibrium  
 Rate  $\propto$  % open  $\approx K_{op} \times$  exchange rate } EX2  
 $k_{obs} \approx K_{op} k_{ex} = \frac{k_{op} k_{ex}}{k_{cl}}$

From perspective of protein: so I've reached the open state... now what?

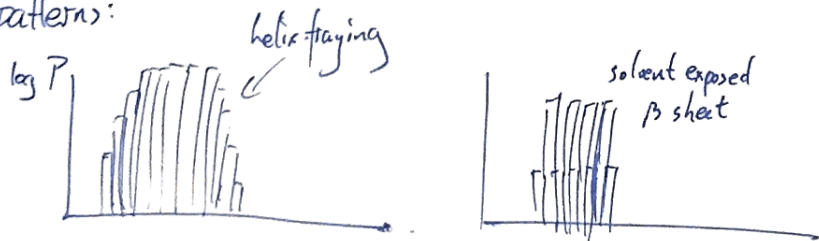
General solution:  $k_{obs} = \frac{k_{op} k_{ex}}{k_{cl} + k_{ex}}$

Information content? EX1 - kinetic! Tells you about  $k_{op}$   
 EX2 - thermodynamic! Tells you %open  
 or 'protection factor'  $P = 1/K_{op}$



- Examples:
  - IgG - N.B. PFs not pathway info
  - YFP
  - amyloid (quenched HX)
- Measurement strategies
  - sample prep (conc w/ lyophilisation)
  - why  $H_2O \rightarrow D_2O$ ?
  - dead time = SOFAST stopped flow
  - sample incubation/stability
- Isotope effects
- H-H exchange?

SS patterns:



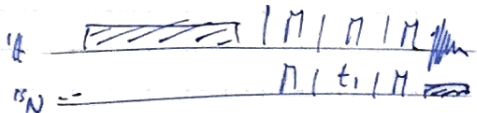
- EXSY (NOESY)
- Saturation transfer
- CLEANEX
- Diffusion
- Scalar coupling
- SOLESY

General:  
 $k_{ex} > 1/T_1(H_2O)$



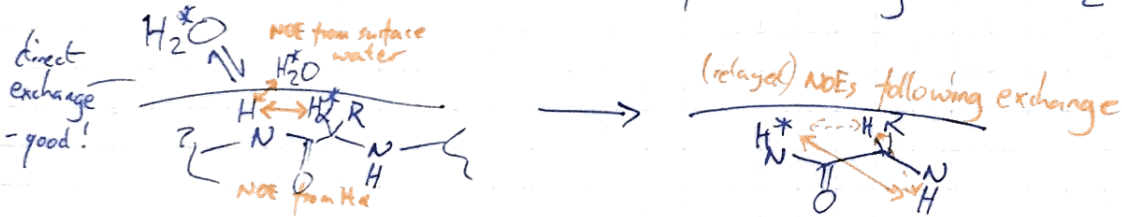
### H-H exchange:

#### SATURATION TRANSFER:



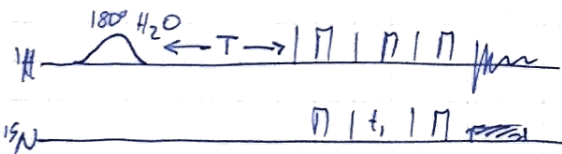
- Long presaturation period during which saturated  $H_2O$  protons exchange onto protein  $\alpha$  protons
- Loss of intensity for labile residues

- Temperature picture - heat diffuses from saturated spins
- saturation of Hx along with  $H_2O$



- Hard to quantify - depends on  $T_1$ , degree of saturation, length of sat. pulse

#### MAGNETISATION TRANSFER:



- Short selective inversion pulse followed by well defined mixing time
- Can observe buildup at small times
- Still potential for NOE effects

How to eliminate NOE effects? Recall NOE vs ROE:

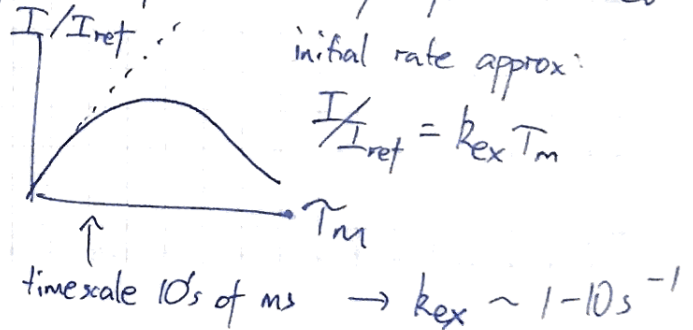
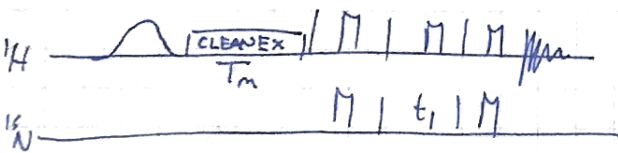
$|t_1| T_m$   
 longitudinal cross-relaxation  
 $< 0$  in macromolecular  
 limit ( $\omega_0 T_c \gg 1$ )

$|t_1| T_m$   
 transverse cross-relaxation always  $> 0$   
 $\sigma_{tr} = -2\sigma_{long}$

Solution - lock magnetisation at  $35^\circ$  angle to cancel NOE and ROE contribution

→ CLEANEX experiment

- Doesn't cancel NOE, from rapidly rotating molecules eg. hydration water



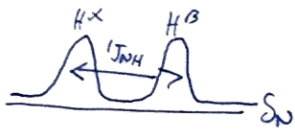
DIFFUSION:  $D_{obs}$  = population weighted average of protein + solvent

$D_{protein} \sim 10^{-10}$  to  $10^{-11} \text{ m}^2 \text{ s}^{-1}$   
 $D_{water} \sim 10^{-9} \text{ m}^2 \text{ s}^{-1}$

$\left. \begin{array}{l} \text{residue resolved} \\ \text{diffusion measurements} \end{array} \right\} k_{ex} \sim 1 - 10^4 \text{ s}^{-1}$

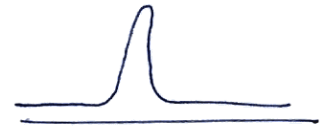
SCALAR COUPLING:  $^1J_{NH} \approx 92 \text{ Hz}$

$^1\text{H}$  coupled  
 $^{15}\text{N}$  spectra:



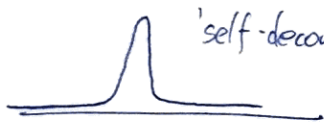
in absence of exchange

decoupling



$\alpha/\beta$  states rapidly interconverting

effect of rapid exchange:  
 $k_{ex} \gg J$



'self-decoupling' as exchanging spins have random states

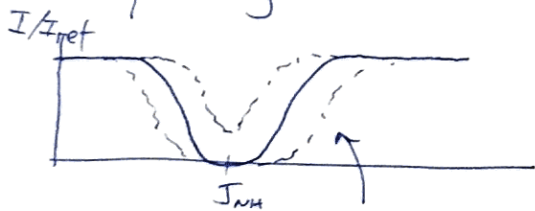
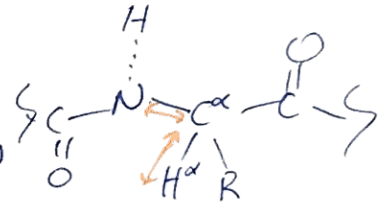
Intermediate exchange:



$k_{ex} \sim J_{NH}$

Problem - broad signal, no INEPT transfers!

- use a different detection scheme eg. HACAN
- compare signal  $\pm$   $^1\text{H}$  decoupling, which gives reference signal

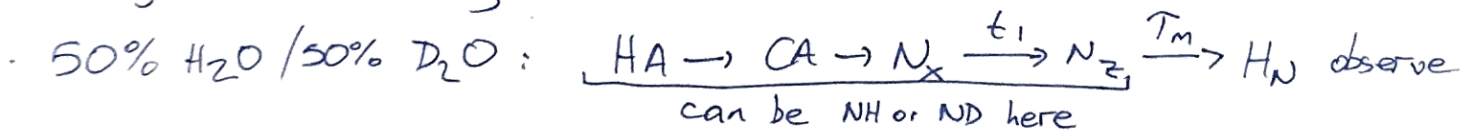


- magnitude of signal dip depends on time spent as  $N_x$  magnetisation

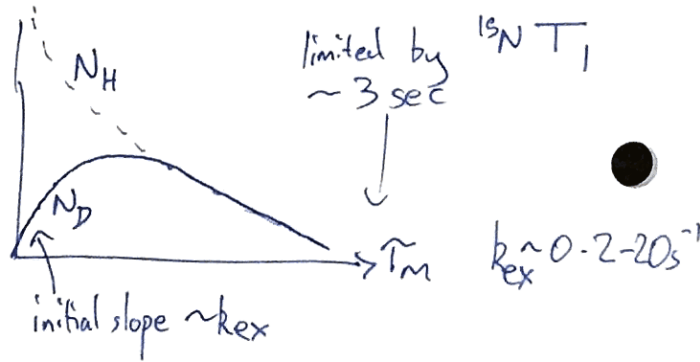
$k_{ex}$  up to  $10^5 \text{ s}^{-1}$  (sidechains)

SOLEXSY

- Observe that  $^{15}\text{N}$  chemical shifts have an isotope effect
  - shift upfield of  $\sim 0.7 \text{ ppm}$  in ND vs NH
  - just not commonly observed!



Observe 2 peaks as function of mixing time:





### Bimolecular rxns



$$k_{-1} = k_{off}$$

$$k_1 = L_{free} \cdot k_{on}$$

$$K_d = \frac{k_{off}}{k_{on}} \Rightarrow k_1 = k_{off} \cdot \frac{L_{free}}{K_d}$$

$$(L_{free} = K_d, k_1 = k_{-1}, \text{OK})$$

Calculating  $L_{free}$ :  $K_d = \frac{P_{free} \cdot L_{free}}{PL} = \frac{(P_0 - PL)(L_0 - PL)}{PL}$

$$\Rightarrow K_d \cdot PL^2 = PL^2 - P_0 PL - L_0 PL + P_0 L_0 - K_d PL$$

$$\Rightarrow PL = \frac{1}{2} \left[ K_d + P_0 + L_0 + \sqrt{(K_d + P_0 + L_0)^2 - 4 P_0 L_0} \right] \text{ and } L_{free} = L_0 - PL$$

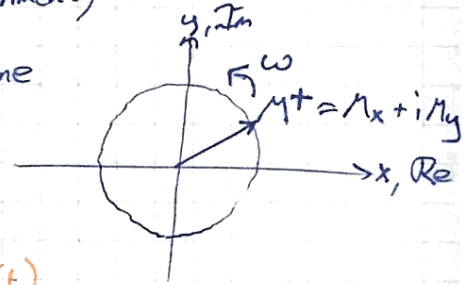
### Bloch-McConnell equations (single pulse experiment)

Free precession of single spin in complex plane

$$M^+(t) = M^+(0) e^{i\omega t} e^{-R_2 t}$$

$$\frac{dM^+}{dt} = i\omega M^+(0) e^{i\omega t} = i\omega M^+(t)$$

$$(i\omega - R_2) M^+(0) e^{i\omega t} e^{-R_2 t} = (i\omega - R_2) M^+(t)$$



Two isolated spins  $M_a^+$  and  $M_b^+$   $\Rightarrow$  2 ODEs - write in matrix form

$$\frac{d}{dt} \begin{pmatrix} M_a^+ \\ M_b^+ \end{pmatrix} = \begin{pmatrix} i\omega_a - R_{2a} & 0 \\ 0 & i\omega_b - R_{2b} \end{pmatrix} \cdot \begin{pmatrix} M_a^+ \\ M_b^+ \end{pmatrix} \equiv \begin{pmatrix} [i\omega_a - R_{2a}] M_a^+ \\ [i\omega_b - R_{2b}] M_b^+ \end{pmatrix}$$

↑ No off-diagonal terms - spins are uncoupled (not in coupling sense!)  
Exchange ~~is~~ couples the spins evolution together

$\frac{d}{dt} \vec{M} = \Lambda \cdot \vec{M}$  is solved by combinations of  $e^{\lambda_i t} \vec{u}_i$   
where  $\{\lambda_i\}$  are eigenvalues of  $\Lambda$ .

Eigenvalues  $A \vec{x} = \lambda \vec{x} \Rightarrow (A - \lambda I) \vec{x} = 0 \Rightarrow |A - \lambda I| = 0$  (characteristic equation)

$$\vec{M} = e^{\Lambda t} \cdot \vec{M}_0$$

Simpler case: Symmetric 2-site exchange without relaxation ( $k_{ab} = k_{ba} = k$ )  
 $\omega_a = 0$  (choice of reference)

$$\Lambda = \begin{pmatrix} -k & +k \\ +k & i\omega - k \end{pmatrix}$$

$$|\Lambda - \pm \lambda| = \begin{vmatrix} -k-\lambda & k \\ k & i\omega - k - \lambda \end{vmatrix} = -(k+\lambda)(i\omega - k - \lambda) - k^2$$

$$= \lambda^2 + (2k - i\omega)\lambda + k^2 - ik\omega = 0$$

$$\Rightarrow \lambda = \frac{i\omega - 2k \pm \sqrt{(i\omega - 2k)^2 + 4ik\omega}}{2} = \frac{1}{2}i\omega - k \pm \frac{1}{2}\sqrt{-\omega^2 + 4k^2}$$

$$= \frac{1}{2}i\omega - k \pm \frac{1}{2}i\omega\sqrt{1 - \frac{4k^2}{\omega^2}}$$

Slow EX:  $k \ll \omega$ ,  $1 - \frac{4k^2}{\omega^2} \approx 1$

$$\Rightarrow \lambda = \left(\frac{1}{2} \pm \frac{1}{2}\right)i\omega - k$$

*lifetime broadening*

*precession at 0 and  $\omega$  frequencies*

Fast EX:  $k \gg \omega$ ,  $4k^2 - \omega^2 \approx 4k^2$

$$\Rightarrow \lambda = \frac{1}{2}i\omega - k \pm k = \frac{1}{2}i\omega, \quad \frac{1}{2}i\omega - 2k$$

*peak average shift*      *zero amplitude, not observed.*

$$\lambda = \frac{1}{2}i\omega - k \pm k\sqrt{1 - \frac{\omega^2}{4k^2}}$$

Expand  $\sqrt{1-x} \approx 1 - \frac{1}{2}x + O(x^2)$

$$\approx \frac{1}{2}i\omega - k \pm k\left(1 - \frac{\omega^2}{8k^2}\right)$$

±ve root:  $\lambda \rightarrow \frac{1}{2}i\omega - \underbrace{\frac{\omega^2}{8k}}_{R_{ex}}$

*Fast intermediate.*

cf.  $R_{ex} = \frac{P_A P_B \Delta\omega^2}{k_{ex}}$

$$P_A = P_B = \frac{1}{2}$$

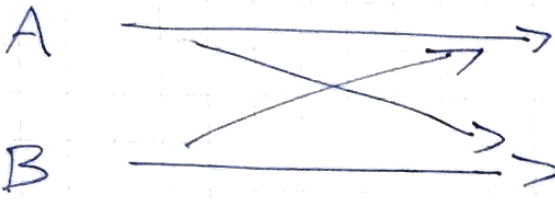
$$k_{ex} = k_{-1} + k_1 = 2k$$

OK

# EXSY

$t = 0$

$t = T$



$$\vec{M}_0 = \begin{pmatrix} p_A \\ p_B \end{pmatrix}$$

$$\vec{M}_T = \begin{pmatrix} p_A \\ p_B \end{pmatrix}$$

$$\vec{M}_T = \begin{pmatrix} A \rightarrow A & B \rightarrow A \\ A \rightarrow B & B \rightarrow B \end{pmatrix} \vec{M}_0$$

How to find matrix entries?

$$A(0) = \begin{pmatrix} 1 & 0 \\ 0 & 1 \end{pmatrix}$$

$$\frac{d\vec{M}}{dt} = (K+R)\vec{M}$$

$$K = \begin{pmatrix} -k_{ab} & k_{ba} \\ k_{ab} & -k_{ba} \end{pmatrix}$$

$$R = \begin{pmatrix} -R_{1a} & 0 \\ 0 & -R_{1b} \end{pmatrix}$$

$$\vec{M}(t) = e^{(K+R)t} \vec{M}(0)$$

$$\Rightarrow A = e^{(K+R)T}$$

Matrix exponential:  $e^X = 1 + X + \frac{1}{2}X^2 + \dots$

$$\therefore \text{For small } T, A \approx \begin{pmatrix} 1 - k_{ab}T - R_{1a}T & k_{ba}T \\ k_{ab}T & 1 - k_{ba}T - R_{1b}T \end{pmatrix}$$

General solution (simplified, for  $k_{ab} = k_{ba}$ ,  $R_{1a} = R_{1b}$ ):

$$A(t) = \begin{pmatrix} \frac{1}{2}e^{-Rt}[1+e^{-2kt}] & \frac{1}{2}e^{-Rt}[1-e^{-2kt}] \\ \frac{1}{2}e^{-Rt}[1-e^{-2kt}] & \frac{1}{2}e^{-Rt}[1+e^{-2kt}] \end{pmatrix}$$