Association reactions are limited by diffusion 2.1.2 Die bieter belegen reactions

The fastest association reaction is one where the two molecules react the instant they come together and so is determined only by diffusion reactions interest association reaction is one where the two molecules react the two reactants to diffusion. Instant they come together and so is actemning only by amasion f and so is determined only by diffusion

1 mole volume in litres

Association reactions have rates less than approximately 109 M-1 s-1 $\,$ \mathcal{N} we would like to convert these units to to able to \mathcal{N} to be able to compare with standard association of the standard association of the standard association of the standard association of the standard asso Association reactions have rates less than approximately TO? Ivi-FST rate than approximately 109 $M-1$ c -1 react in the product of the solution of the upper bound on \mathcal{L}_2 .

$$
f(\text{in M}) < f_{\text{max}} \times n_a \times 10^3 \qquad f_{\text{max}} = 4\pi Da
$$

Assuming D is 1000 μm² s⁻¹ (100 times faster than the typical diffusion of proteins) Remembering that *D* is measured in units of m² s¹, note that *f*max has units of volume per ter than the typical diffusion of proteins)

$$
f < 4\pi \times 10^3 \times 10^{-12} \times 10^{-9} \times 6 \times 10^{23} \times 10^3
$$

~ $\simeq 7.5 \times 10^9 \,\mathrm{M}^{-1}\mathrm{s}^{-1}.$

What is the lowest possible concentration in a bacterium?

The concentration of 1 molecule is

1 $n_A V$

and the volume of a bacterium is $1 \mu m^3$

The lowest possible concentration is 1 nM

Modelling signal transduction I.i
Modelling signal transduction I.i ig signal transduction i.i. waa generate is used by cells to diagram in the sec. 4, negative irreversible in t A bacterium such as *Escherichia coli* has a volume of approximately 1 *µ*m³ or 10¹⁸ m³ or Modelling signal transduction I .1²
Modelling signal transduction I .1 A bacterium such as *Escherichia coli* has a volume of approximately 1 *µ*m³ or 10¹⁸ m³ or

kinas
Di Signal (ligand) binding the receptor **Signalling** molecule, an activate *R* when by an activate *R* when by an activate *R* when by an extracellular signalling molecule, and a signalling molecule, and activate R and acti

$$
[\mathbf{R}] + [\mathbf{S}] \underset{b}{\overset{f}{\rightleftharpoons}} [\mathbf{R}^*]
$$

To allow the activated receptors to activate in turn a downstream signalling protein, *A* say, we and activated receptors a and activated receptors activate a downstream protein *A* say, we are also activated receptors activated protein include another binary reaction:

$$
[\mathrm{R}^*] + [\mathrm{A}] \xrightarrow{k} [\mathrm{R}^*] + [\mathrm{A}^*]
$$

Modelling signal transduction I.ii back can generate bis used by cells to divide by cells to divide by cells to divide \mathbb{R} . Negative in the sec. 4). Negative is used to divide the second section (Sec. 4). Negative is used to divide the second section o σ cause oscillations and drives biological rhythms (Sec. 5). membrane that enters an activated state *R*⇤ when bound by an extracellular signalling molecule, **S** (Fig. 1). We can define the can model the can model the can be a binary reaction: $\frac{1}{2}$ To begin our modelling signal transduction l.ii and plasma receptor, R , in the plasma receptor, R

$$
[\mathbf{R}] + [\mathbf{S}] \underset{b}{\overset{f}{\rightleftharpoons}} [\mathbf{R}^*]
$$

$$
[\mathbf{R}^*] + [\mathbf{A}] \overset{k}{\rightarrow} [\mathbf{R}^*] + [\mathbf{A}^*]
$$

.
a reaction, but catalyzes the conversion of A to its activities the conversion of A to \mathcal{A} and \mathcal{A} and \mathcal{A} are conversion of A to its activities of A to its activities of A to A to A to A to A The rate equations are reaction, but catalyzes the conversion of *A* to its activated form *A*⇤. The rate equations are

$$
\frac{d[S]}{dt} = -f[R][S] + b[R^*]
$$
\n
$$
\frac{d[R]}{dt} = -f[R][S] + b[R^*]
$$
\n
$$
\frac{d[R^*]}{dt} = f[R][S] - b[R^*]
$$
\n
$$
\frac{d[R]}{dt} = f[R][S] - b[R^*]
$$
\n
$$
\frac{d[R]}{dt} + \frac{d[R^*]}{dt} = 0
$$
\n
$$
\frac{d[A]}{dt} = -k[A][R^*]
$$
\n
$$
\frac{d[A^*]}{dt} = k[A][R^*]
$$

dt rocherved = *f*[*R*][*S*] + *b*[*R*⇤ ce that <mark>1</mark> *dt* ⁼ *^f*[*R*][*S*] *^b*[*R*⇤ notice that the number of receptors is

$$
\frac{d[R]}{dt} + \frac{d[R^*]}{dt} = 0
$$

Modelling signal transduction I.iii σ cause oscillations and drives biological rhythms (Sec. 5). membrane that enters an activated state *R*⇤ when bound by an extracellular signalling molecule, **S** (Fig. 1). We can define the can model the can model the can be a binary reaction: $\frac{1}{2}$ α α β β β β $\overline{}$ $\overline{}$

$$
[\mathbf{R}] + [\mathbf{S}] \underset{b}{\overset{f}{\rightleftharpoons}} [\mathbf{R}^*]
$$

$$
[\mathbf{R}^*] + [\mathbf{A}] \overset{k}{\rightarrow} [\mathbf{R}^*] + [\mathbf{A}^*]
$$

kinase cascade We are interested in downstream effects – the rate of change of activated A.

reaction, and the conversion of *a the conversion* of *A* to its activities of *A* and *A* any of the receptor and signal is at equilibrium *i*libr *dt* ⁼ *f*[*R*][*S*] + *^b*[*R*⇤ Let's assume the binding of the receptor and signal is at equilibrium cell that molecules of *S* are present exterior to the cell. Let's assume the binding of the receptor and signal is at equilibrium

 $f[R][S] \simeq b[R^*]$]*.* (2.20) $f[R][S] \sim h[R^*]$ $\lim_{\epsilon \to 0} \frac{\log |z|}{z}$ neither created nor destroyed but only change state from inactivated to activated and vice versa.

G D_z $S = 100$ d CONStant R_0 *d*[*R*⇤] That the receptors are conserved means – for a constant $R_{\rm 0}$

> $R_0 = [R] + [R^*]$]*,* (2.21)

and so

and so
$$
[R^*] \simeq \frac{[S]R_0}{\frac{b}{f} + [S]}
$$

Modelling signal transduction I.iv back can generate bis used by cells to divid by cells to div σ cause oscillations and drives biological rhythms (Sec. 5). membrane that enters an activated state *R*⇤ when bound by an extracellular signalling molecule, **S** (Fig. 1). We can define the can model this activities are active to \mathbb{R} and \mathbb{R} and \mathbb{R} and \mathbb{R} and \mathbb{R} are active to \mathbb{R} and \mathbb{R} are active to \mathbb{R} and \mathbb{R} are active to \math Modelling signal transduction Liv reaction, but catalyzes the conversion of *A* to its activated form *A*⇤.

$$
[\mathbf{R}] + [\mathbf{S}] \underset{b}{\overset{f}{\rightleftharpoons}} [\mathbf{R}^*]
$$

$$
[\mathbf{R}^*] + [\mathbf{A}] \overset{k}{\rightarrow} [\mathbf{R}^*] + [\mathbf{A}^*]
$$

kinase cascade We are interested in downstream effects – activated *A* ownstream effects – activated A t real We are interested in downs: m effects – activated A

$$
\frac{d[A^*]}{dt} = k[A][R^*]
$$
 [R^{*}]

$$
\frac{d[A^*]}{dt} = k[A][R^*]
$$
\n
$$
[R^*] \simeq \frac{[S]R_0}{\frac{b}{f} + [S]}
$$
\nand so

and so but our main focus of A because A because A because A because A because A signals to the interior of the interior

and so
$$
\frac{d[A^*]}{dt} \simeq \frac{k[S]R_0}{\frac{b}{f} + [S]}[A]
$$

or
\n
$$
\frac{d[A^*]}{dt} \simeq \frac{k[S]R_0}{\frac{b}{f} + [S]}(A_0 - [A^*])
$$
\nbecause the number of A molecules is also conserved

because the number of *A* molecules is conserved (with a total concentration of *A*0) because *A*

cell that molecules of *S* are present exterior to the cell.

because the numbe
molecules is also cor because the number of *A* (*because the number of A*

molecules is also conserved molecules is also conserved

because the number of *A* molecules is conserved (with a total concentration of *A*0) because *A*

or