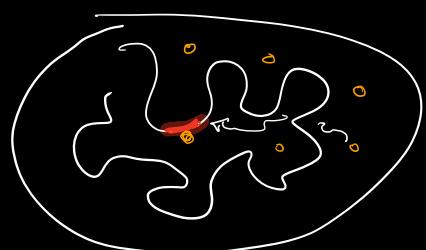


Protein-DNA kinetics

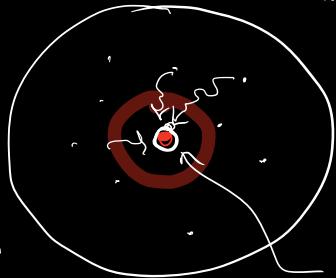


t_s time takes for a protein to find its site

$$t_s = \left(k_{on} \cdot [S] \right)^{-1}$$

- Diffusion: bind

$k_{on} - ?$



Marian

Smoluchowski

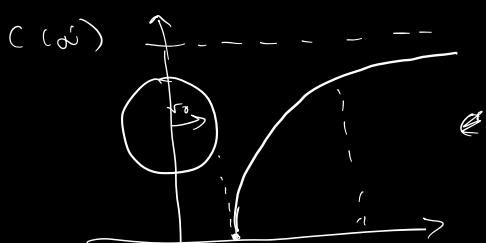
(1917) Lviv

target of radius r_0

$$C(\infty) = \text{const}$$

$$\Delta C(r) = 0$$

concentration of the protein



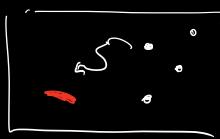
$$\frac{1}{r^2} \frac{\partial}{\partial r} \left(r^2 \frac{\partial C(r)}{\partial r} \right) = 0$$

$$\boxed{C(r) = \left(1 - \frac{r_0}{r} \right) C(\infty)}$$

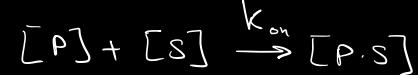
$$C(r) = A \frac{1}{r} + B$$

\Leftarrow no effect beyond $r \approx 2r_0$
no local crowding!

Bimolecular reaction



t_{search} for a protein to find its target



k_{on} -units? related to t_{search}

$$\frac{d[P \cdot S]}{dt} = k_{on} [P][S] \quad k_{on} = [M^{-1}s^{-1}]$$

$$t = \left(k_{on} [\text{concentration}] \right)^{-1}$$

$$[P] \quad [S]$$

$$\frac{d[P \cdot S]}{dt} = k_{on} [P] = k_{on} [S]$$

$$\frac{d[P \cdot S]}{dt} / [S] = k_{on} = \frac{d[P \cdot S] / [S]}{dt} = k_{on} [S]$$

$$k_{on} = \frac{C(\infty)}{r_0} = \left\{ \begin{array}{l} \text{total flux} \\ \text{through the} \\ \text{surface of} \\ \text{the target} \end{array} \right\} = 1$$

$$C(r_0) = 0$$

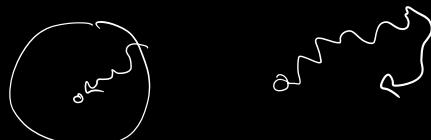
$$C(\infty) = \text{const}$$

$$\frac{1}{r^2} \frac{\partial}{\partial r} \left(r^2 \frac{\partial C(r)}{\partial r} \right) = 0$$

$$\frac{r^2 C''(r)}{r^2} = A$$

$$\boxed{C(r) = \left(1 - \frac{r_0}{r} \right) C(\infty)}$$

$$(\infty) k_{on} = \frac{\text{flux}_{\infty}}{I} = 4\pi r_0^2 \cdot J$$



$$J = -D \nabla C(r) \Big|_{r=r_0}$$

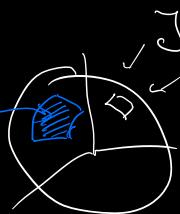
$$= D \frac{V_0}{r_0^2} C(\infty)$$

$$\bar{C}(\infty) k_{on} = 4\pi r_0^2 D \frac{1}{r_0} C(\infty) = 4\pi D r_0 S(\infty)$$

*Sunderchowgshi
rate*

$$\boxed{k_{on} = 4\pi D r_0 a}$$

*fraction of the
surface of the target
that is reactive*

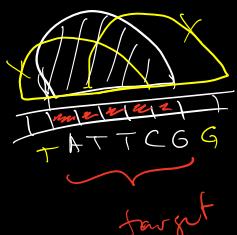


$$I = 4\pi r_0^2 J a$$

Estimate k_{on}

for protein-DNA interactions

$$D \sim 3 \cdot 10^{-7} \frac{\text{cm}^2}{\text{s}}$$

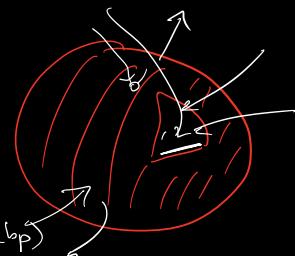


$$r_0 - ?$$

$$r_0 = \underline{\text{site size}} ?$$

$$= 0.34 \text{ nm} \cdot L(\text{bp})$$

$$a = 1/L$$



$$r_0 a = 0.34 \cdot \cancel{L} / \cancel{L} = 1 \text{ bp}$$



$$\boxed{k_{on} = 10 \cdot 3 \cdot 10^{-7} \frac{\text{cm}^2}{\text{s}} \cdot 1 \text{ bp} = 10 \cdot 3 \cdot 10^{-7} \frac{\text{cm}^3}{\text{s}}} \cancel{\frac{1}{3}} \cdot \cancel{10^{-7}}$$

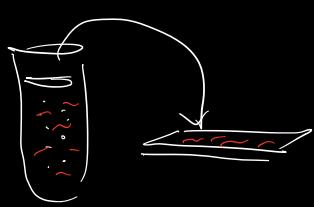
$$1 \text{ bp} = \cancel{1/3} \text{ nm} = \cancel{1/3} \cdot 10^{-7} \text{ cm}$$

$$= 10^{-13} \frac{\text{cm}^3}{\text{s}} = 10^{-13} \frac{\text{cm}^3}{\text{s}} \cancel{10^{-3} \text{ l}} \cancel{\text{cm}^3} = 10^{-16} \frac{1}{\text{s}} \times 6 \cdot 10^{23} \frac{\text{M}}{\text{l}} \frac{1}{\text{M}}$$

$$= 10^{-7} \text{ M}^{-1} \cdot \text{s}^{-1}$$

speed limit:

100 - 1000 fold



Art Riggs (1970)

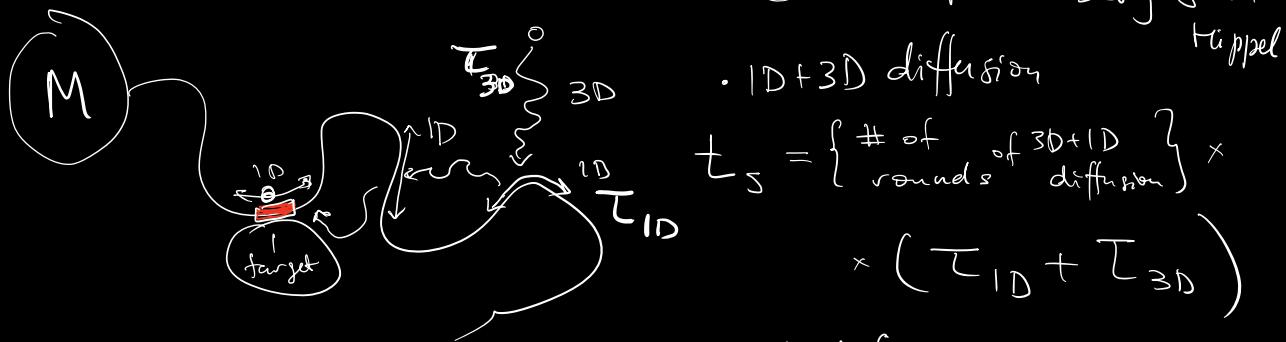
$$k_{on}^{\text{exp}} = 10 - 10^{10} \mu^{-1} s^{-1}$$

proteins
Bind
DNA

(100 - 1000 times
faster!)

Facilitated diffusion!

Max Delbrück : changing dimensionality often could help ... Peter Berg & von Hippel



. 1D + 3D diffusion

$$t_s = \left\{ \begin{array}{l} \# \text{ of} \\ \text{rounds} \end{array} \right. \left. \begin{array}{l} \text{of } 3D+1D \\ \text{diffusion} \end{array} \right\} \times \left(\tau_{1D} + \tau_{3D} \right)$$

$$\underbrace{\tau_{1D}}_{n \text{ bp scanned}} \leftarrow \frac{\text{prob to find}}{\text{the size } \cancel{\text{is}} \text{ on one round}} = \frac{n}{M}$$

$$\left\langle \begin{array}{l} \# \text{ of rounds} \\ \text{till success} \end{array} \right\rangle = \frac{M}{n}$$

$$t_s = \frac{M}{n} (\tau_{1D} + \tau_{3D})$$

$$n^2 = \underbrace{2D_{1D} \tau_{1D}}_{\substack{\uparrow \\ \text{size protein}}}$$

$$= \frac{M}{\sqrt{2 D_{1D} \tau_{1D}}} (\tau_{1D} + \tau_{3D})$$

Size
protein

depends on $[DNA]$

$\left. \begin{array}{l} \text{3D} \\ \tau_{3D} \end{array} \right\} \text{determined by protein-DNA non-specific Binding energy!} \quad \left. \begin{array}{l} E_{hs} \approx L \cdot kT \end{array} \right\}$

$$t_s = \frac{M}{\sqrt{2D_{1D}}} (\tau_{1D} + \tau_{3D}) \rightarrow \text{optimal?}$$

over τ_{1D}

$$\text{O: } \frac{dt_s}{d\tau_{1D}} = \frac{M}{\sqrt{2D}} \cdot \frac{d}{d\tau_{1D}} \left[\sqrt{\tau_{1D}} + \frac{\tau_{3D}}{\sqrt{\tau_{1D}}} \right] =$$

$$\cancel{\text{d}} \sim \frac{1}{\sqrt{\tau_{1D}}} + \frac{\tau_{3D}}{\tau_{1D}^{3/2}} = 0$$

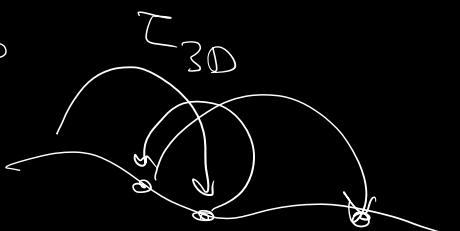
$$\boxed{\tau_{1D}^{\text{opt}} = \tau_{3D}} \approx \text{very general ...}$$

$$\boxed{t_s^{\text{optimal}} = \frac{M}{n} 2 \tau_{3D}} \quad \begin{matrix} \text{optimal} \\ \text{3D + 1D} \\ \text{Search} \end{matrix}$$

o How much faster is this 1D+3D?

3D only: $n=1, \tau_{1D}=0$

$$\boxed{t_s^{\text{3D}} = M \tau_{3D}}$$



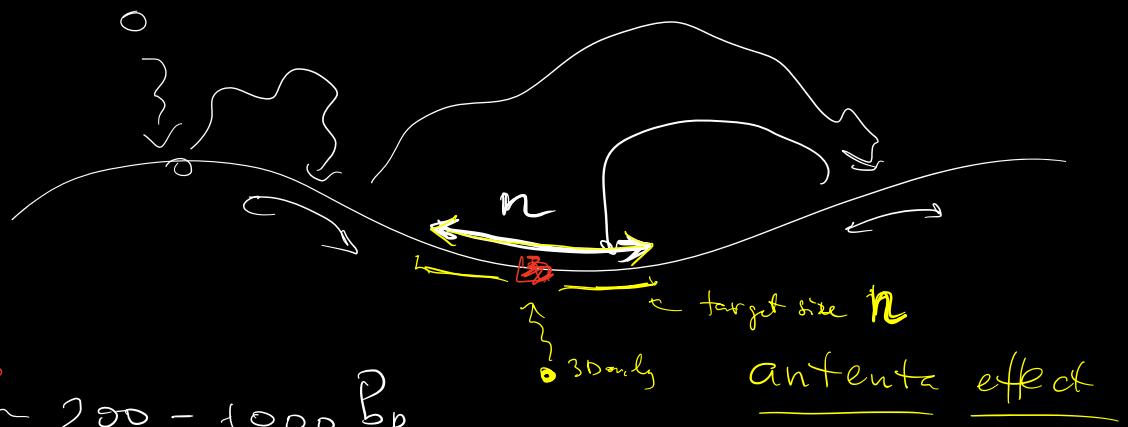
$$\frac{1D \text{ only}}{M^2} = 2 D_{1D} \tau_{1D} \quad \tau_{3D} = 0 \quad n = M \quad \tau_{1D} = \frac{M^2}{2 D_{1D}} \quad \boxed{t_s^{\text{1D}} = \frac{M}{M} \cdot \frac{M^2}{2 D_{1D}} \sim M^2}$$

$$\boxed{\frac{t_s^{\text{3D}}}{t_s^{\text{opt}}} = \frac{M \tau_{3D}}{2 M/n \cdot \tau_{3D}} = \frac{n}{2}}$$

$\tau_{\text{why?}}$

acceleration
due to
1D + 3D

Recall Smoluchowski $k_{b2} = 4\pi D_{3D} r_0 \cdot a$



$$n^{\text{exp}} \approx 200 - 1000 \text{ bp}$$

$$D_{1D}^{\text{exp}} \approx 10^6 \frac{\text{bp}^2}{\text{s}}$$

if $\tau_{\text{sp}} \approx 1 \text{ sec}$ $n \approx 10^3 \text{ bp}$

$\times 2$ reflects that
the protein spends
1/2 of its time
on reverse
places on DNA