

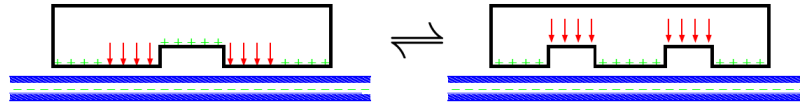
C. Kinetics of target search

- consider simple additive model of binding energy:

$$G_n = G^* + m(n) \cdot \varepsilon \quad \text{where} \quad m(n) = \|S_n - S^*\|$$

if valid for all $0 \leq m \leq L$, then the kinetics of target search would be **slow** since $G_n - G_{n\pm 1}$ is typically of the order $\text{std}(G) \approx \sqrt{L} \cdot \varepsilon \gg kT$

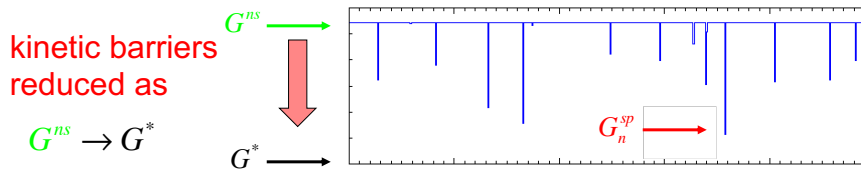
- two-state model** of TF-DNA binding [Winter, Berg, von Hippel, 81]



specific binding: $G_n^{sp} = G^* + m(n) \cdot \varepsilon$

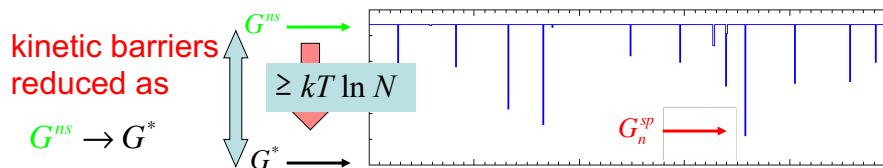
non-specific binding: G^{ns}

Boltzmann weight: $e^{-G_n/kT} \rightarrow e^{-G_n^{sp}/kT} + e^{-G^{ns}/kT}$



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- if G^{ns} is too low, thermodynamic specificity will be lost



statistical mechanics of the two-state model:

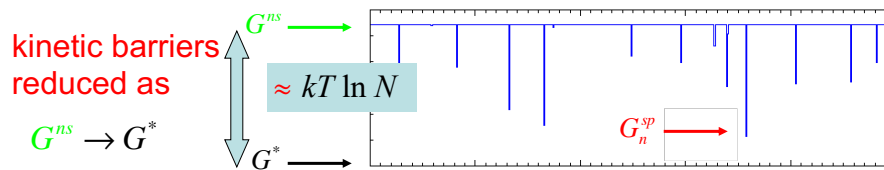
$$Z \equiv \sum_{n=1}^N e^{-(G_n - G^*)/kT} \rightarrow \underbrace{\sum_{n=1}^N e^{-(G_n^{sp} - G^*)/kT}}_{Z^{sp}} + \underbrace{\sum_{n=1}^N e^{-(G^{ns} - G^*)/kT}}_{Z^{ns} = N \cdot e^{-\frac{G^{ns} - G^*}{kT}}}$$

→ for $Z = Z^{sp} + Z^{ns} \approx 1$, need to have $Z^{sp} \approx 1$ and $Z^{ns} \leq 1$

→ $G^{ns} - G^* \geq kT \ln N \approx 16 kT$

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- effect of kinetic slow down ?



-- for each trap with binding energy $G_n^{sp} < G^{ns}$

escape time (Kramer): $\tau_n = \tau_0 \cdot e^{(G^{ns} - G_n^{sp})/kT}$ τ_0 : sliding time

density of state

-- average escape time: $\bar{\tau} \geq \frac{\tau_0}{N} \sum_G [1 + e^{(G^{ns} - G)/kT}] \cdot \Omega(G)$
 $= \tau_0 \cdot [1 + e^{(G^{ns} - G^*)/kT} \cdot Z^{sp}/N]$

→ for $Z^{sp} \approx 1$, kinetic slowdown insignificant if $G^{ns} - G^* \leq kT \ln N$

→ both thermodynamics and kinetics okay if $G^{ns} - G^* \approx kT \ln N$

[Note: for the Lac and Arc repressors, $G^{ns} - G^* \approx 15 kT$]

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D. Global search dynamics (smooth landscape)

- 1D diffusion along the chromosome: [Elf & Xie, 2007]

$$\left. \begin{array}{l} N = 5 \times 10^6 \text{ bp} \approx 1 \text{ mm} \\ D_1 \approx 0.1 \mu\text{m}^2 / \text{sec} \end{array} \right\} T_{1D} \sim \frac{N^2}{D_1} \sim 10^7 \text{ sec}$$

-- may be overcome by increasing # of TF; for parallel search, $T_{1D} \sim 1/(\#\text{TF})^2$

-- cost: covers the chromosome with lots of "useless" TFs

- 3D diffusion directly from the cytoplasm:

$$T_{3d} \approx \frac{1}{4\pi} \frac{V_{cell}}{\ell_{TF} \cdot D_{cyto}} = \frac{1}{4\pi} \underbrace{(V_{cell}/\ell_{TF}^3)}_{\text{search volume}} \cdot \underbrace{(\ell_{TF}^2/D)}_{\text{search time per volume}} \sim 10 \text{ sec}$$

$V_{cell} \approx 3 \mu\text{m}^3$
 $\ell_{TF} \approx 15 \text{ bp} = 5 \text{ nm}$
 $D_{cyto} \approx 10 \mu\text{m}^2 / \text{sec}$

– faster mainly due to the reduced redundancy of 3D random walk

– but TFs typically associate strongly to DNA (sub-compartmentalization)

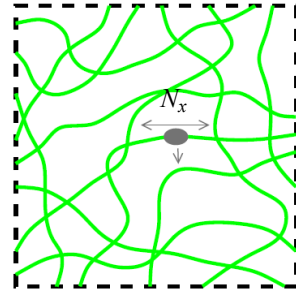
[e.g., for the Lac repressors, $G^{cyto} - G^{ns} \approx 15 kT$]

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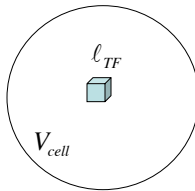
- **combined 1D/3D search:**

- dense DNA packing in cell
- short-time: slide on DNA (over scale N_x)
- long-time: random walk on 3D network
- slide dist: $N_x \sim 300$ bp
- slide time: $T_x \sim N_x^2 / D_1 \sim 0.1$ sec

$$T_{1D/3D} \sim \frac{1}{4\pi} \frac{V_{cell}}{N_x \cdot (N_x^2 / T_x)} \sim 100 \text{ sec}$$



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Summary:

- specificity of target recognition: $Z^{sp} \approx 1$
 $\rightarrow \varepsilon \approx 2 \text{ kT}, L \approx 15 \text{ bp}$, gives $\tilde{K}_j \equiv \sum_{n \neq j}^N e^{(G_j - G_n)/kT} \approx e^{m_j \varepsilon / kT}$
 \rightarrow **affinity of target sites become “programmable”**
- kinetic accessibility of target predicts $G^{ns} - G^* \approx 15 \text{ kT}$
- combined 1D/3D search

- \rightarrow to what extent is “programmable” interactions used ?
- \rightarrow search process for multimer?
- \rightarrow eukaryotes?

many differences, e.g., $N_p = 10^2 \sim 10^4$ in budding yeast
 (need another von Hippel!)

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