# Stochastic Model and Optimization of SELEX

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## Outline

- Introduce SELEX: a process to select aptamers.
- Review the traditional deterministic model.
- Build a stochastic model for SELEX and analyze its properties.
- Search for the optimal protocol of SELEX.

- Aptamers are oligonucleotide or peptide molecules that bind to a specific target molecule.
- Some aptamers have high affinity to a pathogen. If we can isolate such aptamers, they can be used as an alternative of antibodies.
- In general, we start with a large library of randomly generated aptamers, and they have different affinities to the target.
- How to select the best aptamers in an easy way?

- Systematic Evolution of Ligands by EXponential enrichment (SELEX): a convenient method to select the best aptamers.
- Aptamers with higher affinities to the targets are more likely to bind to the targets. We can use the targets to pick out such aptamers.
- It is similar to a population evolution process.

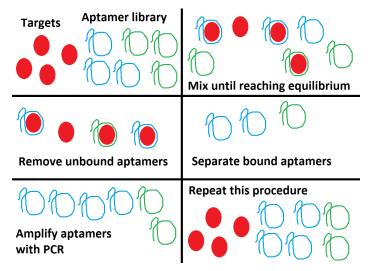


Figure: Protocol of SELEX

- We start with some target molecules and different types of aptamer molecules.
- Mix targets and aptamers until they reach equilibrium.
   Aptamers with higher affinities are more likely to bind to targets.
- Unbound aptamers are removed. Then we separate bound aptamers.
- Separated aptamers are amplified with PCR.
- One round of SELEX finishes. Aptamers with higher affinities are more concentrated.
- Start more rounds of SELEX to further concentrate aptamers with higher affinities.



- When starting one round of SELEX, we can control the quantity of targets and the quantity of aptamers, but the proportions of different aptamer types cannot be controlled.
- The goal is to maximize the proportion of the best aptamer (with the highest affinity) after this round of SELEX.
- A bad choice: add too many targets, so that almost all aptamers are bound. No selection is made, and the proportion of the best aptamer is invariant.
- We need a mathematical model to study the optimization of SELEX.

- A traditional approach uses the law of mass action, which is valid when the number of molecules is sufficiently large.
- Notations: [S]: total concentration of targets; [A<sub>i</sub>]: total concentration of aptamer type A<sub>i</sub>; [a<sub>i</sub>]: concentration of aptamers A<sub>i</sub> that are bound to targets at equilibrium. K<sub>i</sub><sup>+</sup>: reaction constant of S + A<sub>i</sub> → SA<sub>i</sub>; K<sub>i</sub><sup>-</sup>: reaction constant of SA<sub>i</sub> → S + A<sub>i</sub>.
- At stationary, for each reaction  $S + A_i \rightleftharpoons SA_i$ , we have:

$$\left( [S] - \sum_{j=1}^{N} [a_j] \right) ([A_i] - [a_i]) \, K_i^+ = [a_i] K_i^-.$$

unbound unbound bound target aptamer aptamer

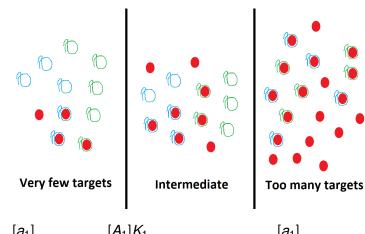
We can use M equations for M aptamer types to solve [a<sub>i</sub>].



- Define  $K_i = K_i^+/K_i^-$ , and assume  $K_1 \ge K_2 \ge \cdots \ge K_M$ , so that  $A_1$  is the best aptamer with the highest affinity.
- The goal is to maximize the proportion of bound  $\mathbb{A}_1$ :  $[a_1]/\sum_{i=1}^{M} [a_i]$ .
- We can set different values of target concentration [S] and aptamer concentration  $[A_i]$ , but the ratio  $[A_1]/[A_i]$  is fixed.
- $[a_1]/\sum_{i=1}^{M} [a_i]$  increases with  $[A_1]$  (and other  $[A_i]$ ), and decreases with [S].
- The optimal policy in the deterministic model: add as many aptamers as possible, and as few targets as possible.



Optimal policy:  $[A_i] \gg [S]$ .



$$rac{[a_1]}{[a_1] + [a_2]} = rac{[A_1]K_1}{[A_1]K_1 + [A_2]K_2}$$
upper bound

$$\frac{[a_1]}{[a_1] + [a_2]} = \frac{[A_1]}{[A_1] + [A_2]}$$

lower bound

- The optimal policy in the deterministic model requires very large aptamer concentration [A<sub>i</sub>] and very small target concentration [S].
- When [S] is too small, randomness is inevitable, and the law of mass action does not hold.
- We need a stochastic model.
- There is something different in this stochastic model.

- Notations: S: total number of targets;  $A_i$ : total number of  $A_i$  type aptamers;  $a_i$ : number of  $A_i$  aptamers that are bound to targets.  $\bar{K}_i = K_i/V$ : reaction coefficient, where V is the system volume.
- Consider a continuous-time Markov process on M-dimensional lattice  $\mathbb{Z}^M$ , where the states are the bound aptamer counts  $(a_1, \ldots, a_i, \ldots, a_M)$ .
- The transition rates satisfy

$$\frac{r[(a_1, \ldots, a_i, \ldots, a_M) \to (a_1, \ldots, a_i + 1, \ldots, a_M)]}{r[(a_1, \ldots, a_i + 1, \ldots, a_M) \to (a_1, \ldots, a_i, \ldots, a_M)]}$$

$$= \frac{(S - \sum_{j=1}^{M} a_j)(A_i - a_i)}{a_i + 1} \bar{K}_i.$$



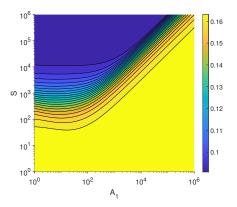
The stationary probability distribution satisfies

$$\mathbb{P}(a_1,\ldots,a_M) = \mathbb{P}(0,\ldots,0) \times \begin{pmatrix} S \\ S - \sum_{j=1}^M a_j, a_1,\ldots,a_M \end{pmatrix} \times \left[ \prod_{i=1}^M \binom{A_i}{a_i} \right] \times \left[ \prod_{i=1}^M \bar{K}_i^{a_i} \right]$$

- For simplicity, we only consider two aptamers  $A_1$ ,  $A_2$ .
- Due to stochasticity, we need to consider the expected proportion of  $\mathbb{A}_1$  and exclude the case that no aptamer is bound:  $\mathbb{E}[a_1/(a_1+a_2) \mid a_1+a_2>0]$ .



Contour plot of the A₁ proportion
 E[a₁/(a₁ + a₂) | a₁ + a₂ > 0] as a function of aptamer number A₁ (and A₂) and target number S:



•  $A_1$  proportion decreases with S, but does not always increase with  $A_1$ .



In the stochastic model, we still have similar bounds for  $\mathbb{A}_1$  proportion.

#### Theorem

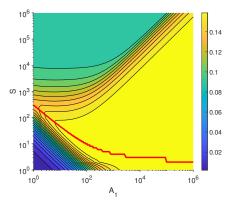
$$\mathbb{E}[a_1/(a_1+a_2)\mid a_1+a_2>0] \leq A_1\bar{K}_1/(A_1\bar{K}_1+A_2\bar{K}_2).$$

#### Theorem

$$\mathbb{E}[a_1/(a_1+a_2)\mid a_1+a_2>0]\geq A_1/(A_1+A_2).$$



- When  $a_1 = a_2 = 0$ , stipulate that  $a_1/(a_1 + a_2) = 0$ .
- $\mathbb{E}[a_1/(a_1+a_2)] = \mathbb{E}[a_1/(a_1+a_2) \mid a_1+a_2 > 0] \times [1-\mathbb{P}(0,0)].$

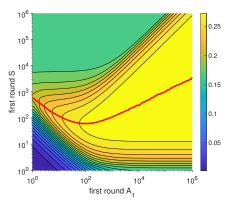


• In the contour plot of  $\mathbb{E}[a_1/(a_1+a_2)]$ , when the aptamer number  $A_1$  increases, the optimal target number S (red curve) decreases.

- Optimal policy in the stochastic model:
- When the aptamer number  $A_1$  (and  $A_2$ ) is not large, the target number S should not too small. Otherwise,  $\mathbb{P}(a_1 = 0, a_2 = 0)$  might be large.
- What if we make  $A_1$  (and  $A_2$ ) sufficiently large, so that  $\mathbb{P}(a_1 = 0, a_2 = 0) \approx 0$ ? Can we set S = 1 now?

- For one round of SELEX, S=1 and very large  $A_1$ ,  $A_2$  can reach the upper bound:  $\mathbb{E}[a_1/(a_1+a_2)] \approx A_1\bar{K}_1/(A_1\bar{K}_1+A_2\bar{K}_2).$
- However, since there is only one target molecule, after one round of SELEX, only one aptamer type is left.
- After further rounds of SELEX, the expected A<sub>1</sub> proportion does not increase.

• Contour plot of the  $\mathbb{A}_1$  proportion  $\mathbb{E}[a_1/(a_1+a_2)]$  after two rounds of SELEX:



• For the first round, a policy with large  $A_1$  and very small S does not perform well. The optimal target number S (red curve) first decreases and then increases with  $A_1$ .

- Optimal policy for multiple rounds of SELEX in the stochastic model:
- $A_1, A_2 \gg S$  and  $S \gg 1$ .
- After N rounds of SELEX, this policy has  $\mathbb{E}[a_1/(a_1+a_2)] \approx A_1 \bar{K}_1^N/(A_1 \bar{K}_1^N+A_2 \bar{K}_2^N)$ .
- Thus  $1 \mathbb{E}[a_1/(a_1 + a_2)]$  converges to 0 exponentially fast with the rate  $\approx \bar{K}_2/\bar{K}_1$ . This is the most important factor for the efficiency of multi-round SELEX.

## Section IV: Summary

- We discuss SELEX, a process to select the best aptamer for binding a target.
- In the traditional deterministic model, the optimal policy (for any rounds of SELEX) is to have a very large aptamer number and a very small target number.
- We develop a stochastic model, in which the optimal policy for multiple rounds of SELEX is to have a very large aptamer number but a moderate target number.
- This theoretical analysis can be applied to other scenarios, such as selecting drug-resistant cells.

# Thank you!