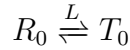


Monod-Wyman-Changeux Model

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First, assume that protein X has n binding sites for ligand F and protein X has two states, R and T . The binding of different numbers of ligands to protein X leads to transitions between R and T states. We denote the protein X bound with k ($0 \leq k \leq n$) ligands in the two states as R_k and T_k , respectively. The dissociation constants K_R and K_T are independent of how many ligands are bound to protein X. When no ligands are bound, we have the following equilibrium:



where

$$L = \frac{[T_0]}{[R_0]}.$$

Moreover,

$$R_{k+1} \xrightleftharpoons{K_R} R_k + F, \quad T_{k+1} \xrightleftharpoons{K_T} T_k + F, \quad 0 \leq k \leq n-1.$$

To find the expression of K_R and K_T , we only need to know the concentration of F , R_k , R_{k+1} and T_k , T_{k+1} . However, R_k is a mixture of different configurations and the actual participants in the dissociation reaction are the individual configurations. Therefore, we need to determine the concentration of each single configuration. Since R_k has C_n^k configurations, the concentration for each configuration in R_k is

$$\frac{[R_k]}{C_n^k}.$$

therefore, we have

$$K_R = \frac{(C_n^k)^{-1}[R_k][F]}{(C_n^{k+1})^{-1}[R_{k+1}]} = \frac{n-k}{k+1} \cdot \frac{[R_k][F]}{[R_{k+1}]}, \quad K_T = \frac{(C_n^k)^{-1}[T_k][F]}{(C_n^{k+1})^{-1}[T_{k+1}]} = \frac{n-k}{k+1} \cdot \frac{[T_k][F]}{[T_{k+1}]}.$$

Define

$$c = \frac{K_R}{K_T}, \quad \alpha = \frac{[F]}{K_R},$$

Thus, we can calculate the proportion of binding sites occupied by F relative to all binding sites as:

$$\bar{Y}_F = \frac{\sum_{k=1}^n k([R_k] + [T_k])}{n(\sum_{k=0}^n [R_k] + [T_k])} = \frac{Lc\alpha(1+c\alpha)^{n-1} + \alpha(1+\alpha)^{n-1}}{(1+\alpha)^n + L(1+c\alpha)^n},$$

and the proportion of protein X in the R state relative to the total amount of protein X is:

$$\bar{R} = \frac{\sum_{k=0}^n [R_k]}{\sum_{k=0}^n ([R_k] + [T_k])} = \frac{(1+\alpha)^n}{(1+\alpha)^n + L(1+c\alpha)^n}$$

References

- [1] Monod J, Wyman J and Changeux J-P. On the nature of allosteric transitions: A plausible model. Journal of Molecular Biology, 1965(12) : 88-118.