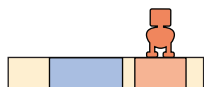


statistical mechanics of gene regulation

thermodynamic states

states



weights

1

$$\frac{P}{N_{NS}} e^{\beta \epsilon_P}$$

$$\frac{R}{N_{NS}} e^{\beta \epsilon_R}$$

allostery

inducer-TF binding

K_A

ϵ_{AI}

TF-DNA binding

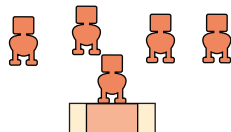
ϵ_{RA}

K_I

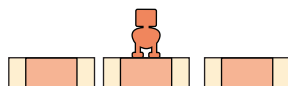
ϵ_{RI}

abundances

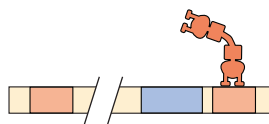
TF excess



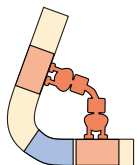
titration



DNA looping

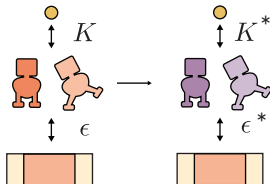


distance of binding sites

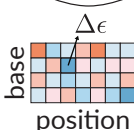


mutations

TF mutation



binding site mutation



unifying data collapse

$$\text{fold change} = \frac{1}{1 + e^{-\beta F(\epsilon, K, c, \dots)}}$$

