

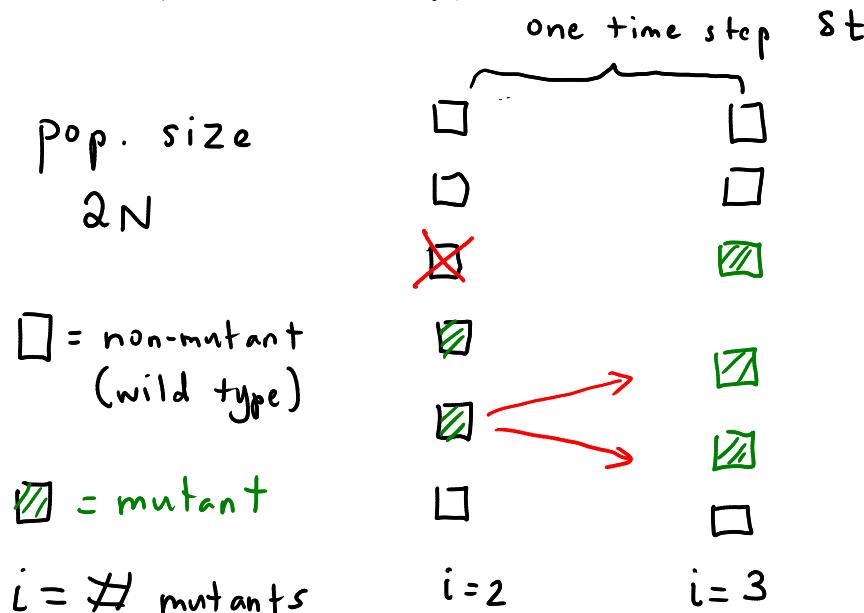
substitution rate

k = rate at which new mutants appear + fix

$$= \underbrace{2N_M}_{\substack{\text{new mutants} \\ \text{appears}}} \pi_{\text{fix}} \quad \downarrow \text{prob. of fixation}$$

Consider a "micro" version of WF model:

Moran model



\Rightarrow same p.p. size

reproduction step: either wild type or mutant

gets a chance to reproduce first, moving sys. to next time step

g = repr. rate of wild type

f = repr. rate of mutant

wild type first : $\frac{g(2N-i)}{f_i + g(2N-i)}$

define:

$$s = \frac{f}{g} - 1$$

selection coefficient

$|s| \ll 1$ typically

mutant first : $\frac{f_i}{f_i + g(2N-i)}$

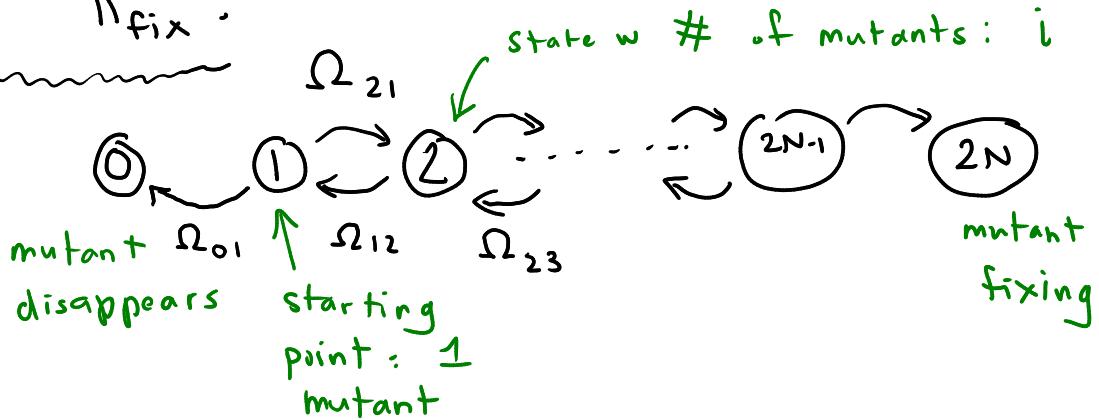
$s > 0 : f > g \Rightarrow$ beneficial mutant

$s = 0 : \text{neutral mutant}$

$s < 0 : \text{deleterious mutant}$

Calculating π_{fix} :

mutants



find $\pi_i = \text{prob. that mutant reaches } 2N \text{ given start at } i$

we need $\pi_1 \equiv \pi_{fix}$ (start at $i=1$)

let's say current state is at $1 \leq i \leq 2N-1$:

$$i \rightarrow i+1 : \Omega_{i+1, i} = \underbrace{\frac{2N-i}{2N}}_{\text{prob. wild type dies}} \cdot \underbrace{\frac{f_i}{f_i + g(2N-i)}}_{\text{prob. mutant reproduces}}$$

$$i \rightarrow i-1 : \Omega_{i-1, i} = \underbrace{\frac{i}{2N}}_{\text{prob. mutant dies}} \cdot \underbrace{\frac{g(2N-i)}{f_i + g(2N-i)}}_{\text{prob. mutant reproduces}}$$

$$\Omega_{1,0} = 0 = \Omega_{2N-1, 2N} \quad i=0 + i=2N$$

cannot escape

let's say i is $1 \leq i \leq 2N-1$:

before reaching $2N$ we have to pass thru either $i-1$ or $i+1$:

$$\begin{aligned}\pi_i &= \left(\begin{array}{l} \text{prob. to} \\ \text{jump to } i-1 \end{array} \right) \pi_{i-1} + \left(\begin{array}{l} \text{prob. to} \\ \text{jump to } i+1 \end{array} \right) \pi_{i+1} \\ &= \frac{\Omega_{i-1,i}}{\Omega_{i-1,i} + \Omega_{i+1,i}} \pi_{i-1} + \frac{\Omega_{i+1,i}}{\Omega_{i-1,i} + \Omega_{i+1,i}} \pi_{i+1} \\ &= \frac{(1+s)}{(2+s)} \pi_{i+1} + \frac{1}{2+s} \pi_{i-1} \quad \text{recursion relation}\end{aligned}$$

$$\text{BC: } \pi_{2N} = 1 \quad \pi_0 = 0 \quad |s| \ll 1$$

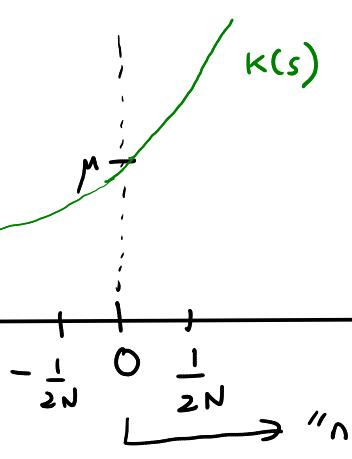
$$\text{Solution: } \pi_i = \frac{1 - (1+s)^{-i}}{1 - (1+s)^{-2N}} \approx \frac{1 - e^{-is}}{1 - e^{-2Ns}}$$

$$\pi_{\text{fix}} = \pi_i \approx \frac{1 - e^{-s}}{1 - e^{-2Ns}}$$

$$\text{substitution rate } k = 2N\mu \frac{1 - e^{-s}}{1 - e^{-2Ns}} \quad \text{Motoo Kimura 1962}$$

strongly deleterious

$$s \ll -\frac{1}{2N}$$



$s \gg \frac{1}{2N}$: strongly beneficial

$$s = \frac{f}{g} - 1$$

"nearly" neutral

$$|s| \ll \frac{1}{2N} \quad K \approx 2N\mu \frac{1-(1-s)}{1-(1-2Ns)} = \mu$$

\Rightarrow nearly constant rate of
subst. for neutral mutations
indep. of N (Kimura, Ohta 1971);
"molecular clock"