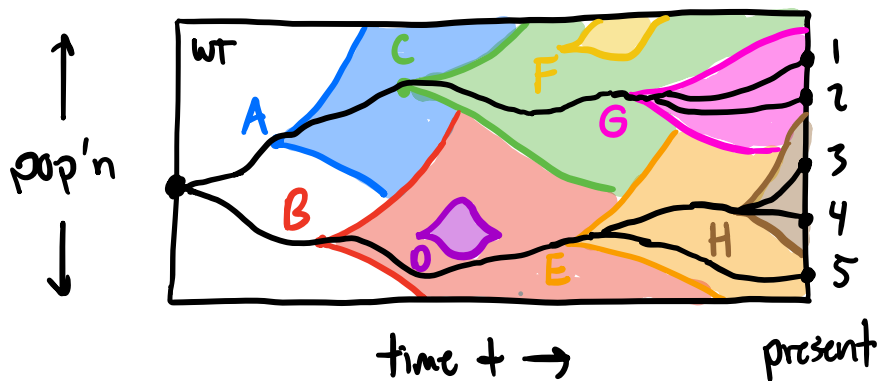


Chapter 15

Linked selection and clonal interference

Linked selection + clonal interference

(a.k.a. "Hill-Robertson Interference")



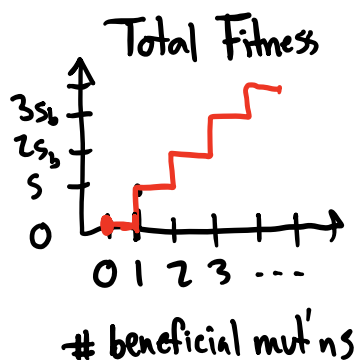
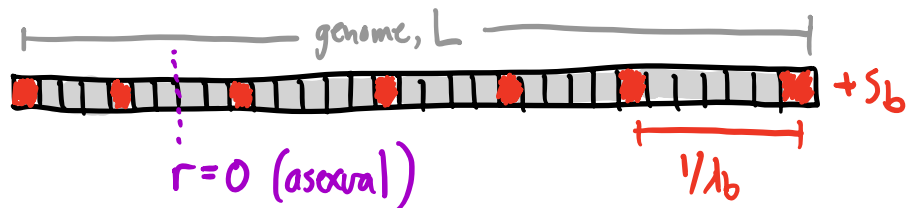
⇒ can't be reduced to $L=1$ or $L=2$ model (collective phase)

⇒ Most progress only recently, w/ big contribution from physicists

[e.g. Tsimring et al PRL '96, Rouzine et al '03, Desai + Fisher '07, ...]

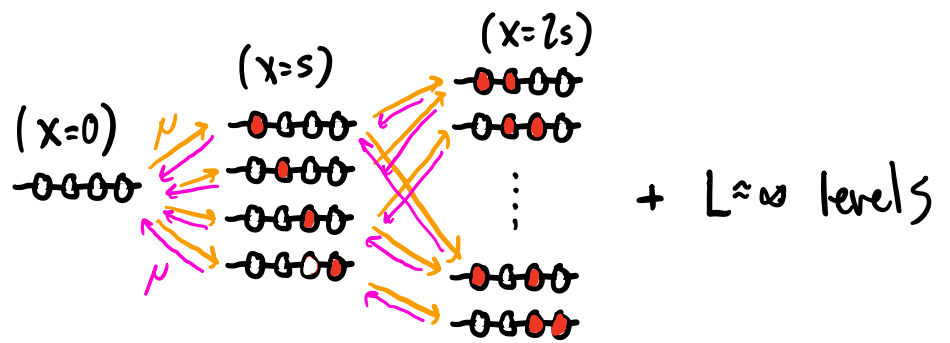
⇒ Analytical progress enabled by starting w/ very simple model:

"Staircase" Model



- ① All mutations provide same benefit (S_b)
- ② Occur @ total rate $U_b \equiv L\lambda_b\mu$
- ③ Never run out (e.g. $L\lambda_b \rightarrow \infty, \mu \rightarrow 0$)

Genotype network:



Key simplification:

"fitness class" $f(k,t) \equiv \sum_{|g|=k} f(g,t)$

Diagram illustrating the simplification of the genotype network into a sequence of fitness classes $(x=0)$, $(x=s)$, $(x=2s)$, ..., $(x=ks)$. The nodes are labeled 0 , 1 , 2 , ..., k . Transitions are labeled with U_b and ≈ 0 .

\Rightarrow coarse-grained SDE ($1+1$ dimensional vs 2^L+1 dim.)

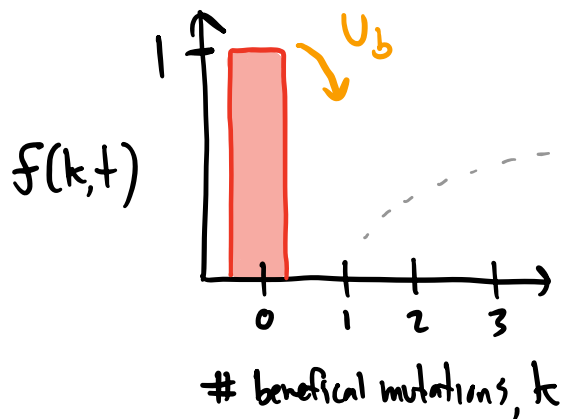
$$\frac{df(k)}{dt} = \underbrace{s_b(k - \bar{k}(t))f(k)}_{\text{selection (nonlinear)}} + \underbrace{U_b[f(k-1) - f(k)]}_{\text{mutation}}$$

$$+ \underbrace{\sqrt{\frac{f(k)}{N}} \eta(k) - f(k) \sum_{k'} \sqrt{\frac{f(k')}{N}} \eta(k')}_{\text{genetic drift (stochastic)}}$$

\Rightarrow let's consider behavior when $NS_b \gg NU_b \gg 1$

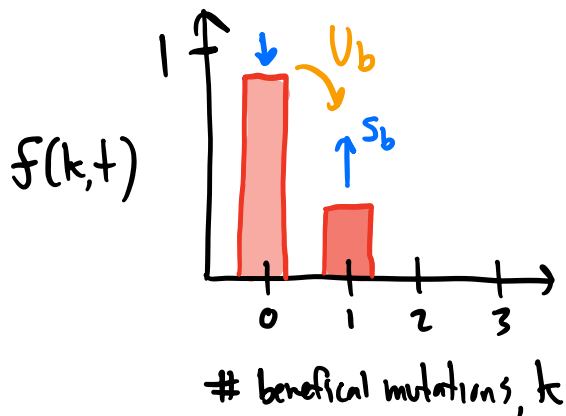
(e.g. yeast barcode experiment in HW 4 Problem #1)

① Start w/ wildtype population @ $t=0$



$$\frac{df(1)}{dt} \approx s f(1) + U_b + \sqrt{\frac{f(1)}{N}} \eta_1(t)$$

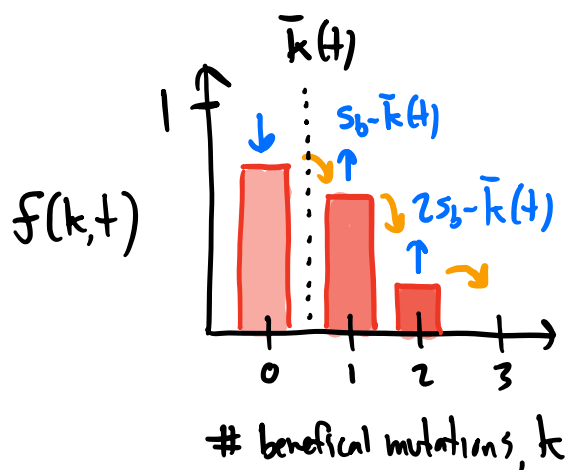
② First-step mutations ($k=1$) establish & grow exponentially



$$\Rightarrow f(1, t) \approx \frac{U_b}{s_b} (e^{s_b t} - 1)$$

(deterministic approx good @ first, since $NU_b \gg 1$)

③ Double mutants establish before single mutants take over,



\Rightarrow clonal interference!

$$\left(\text{since } \int_0^{z_{1/2}} N f(1, t) \cdot U_b \cdot s_b dt \sim NU_b \gg 1 \right)$$

\Rightarrow Is deterministic approx still useful?

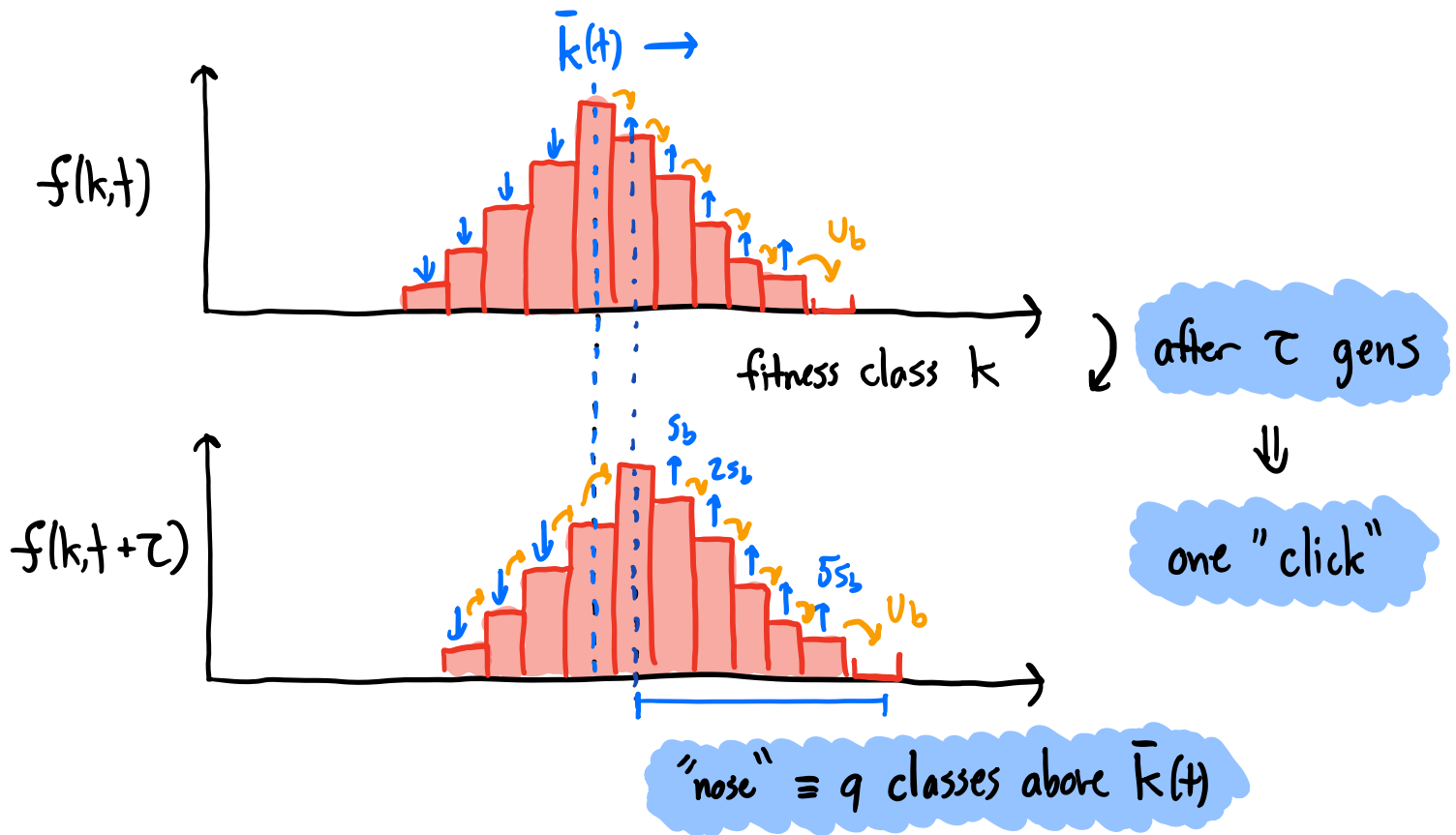
$$\frac{df(k)}{dt} = \underbrace{s_b(k - \bar{k}(t))f(k)}_{\text{selection (nonlinear)}} + \underbrace{U_b[f(k-1) - f(k)]}_{\text{mutation}} + \underbrace{\sqrt{\frac{f(k)}{N}}\eta(k) - f(k)\sum_k \sqrt{\frac{f(k)}{N}}\eta(k')}_{\text{genetic drift}}$$

~~$\rightarrow 0$~~

\Rightarrow can show: $f_{\text{det}}(k,t) = \frac{1}{k!} \left[\frac{U_b}{s_b} (e^{s_b t} - 1) \right]^k \cdot e^{-\frac{U_b}{s_b} (e^{s_b t} - 1)}$

\Rightarrow **Not self-consistent!** \Rightarrow Predicts $s_b \bar{k}(t) \approx U_b e^{s_b t}$
(eventually all $f(k,t) \ll 1/N!$)

\Rightarrow Instead, if we simulate model, observe "travelling wave":



\Rightarrow What determines $\tau(N, s_b, U_b) + q(N, U_b, s_b)$?

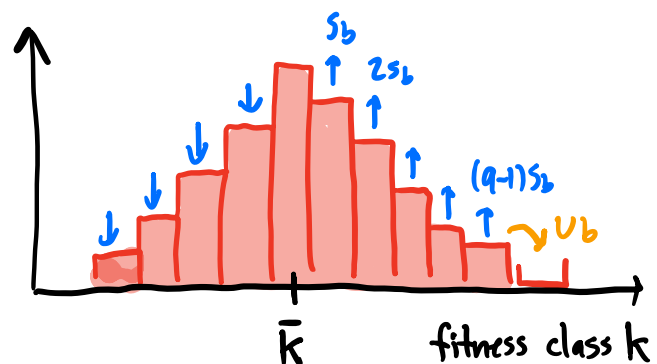
\Rightarrow Today: heuristic analysis [\sim Desai + Fisher 2007]

applies when: $Ns_b \gg Nu_b \gg 1$ + $s_b \tau \gg 1$ & $q \gg 1$

Leads to simplifications:

① mutations only important for establishing new "nose"

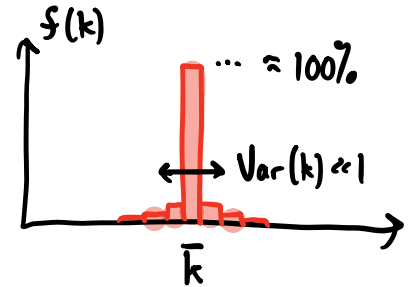
(since $s_b \gg U_b$)



② Genetic drift only important for establishing new nose

(since $\tau \gg 1/s_b$, individual mutations establish before next click.)

③ most of pop'n is near $k \approx \bar{k}(t)$

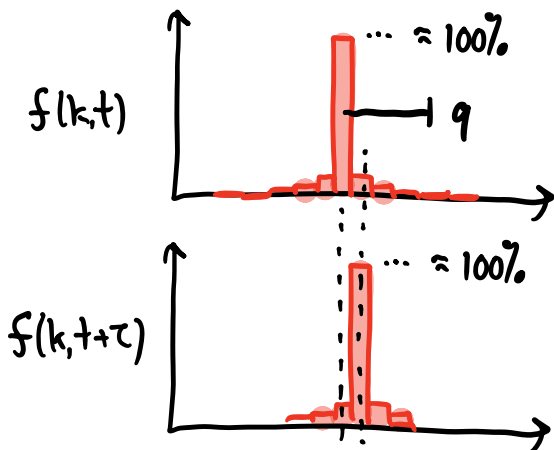


Problem 3 of HW 4:

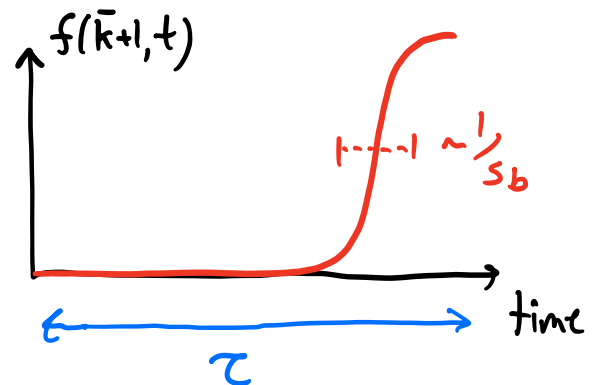
$$\underbrace{\frac{d\langle \bar{k} \rangle}{dt}}_{\equiv 1/\tau} = \left\langle \sum_k k \frac{df(k)}{dt} \right\rangle = \left\langle \underbrace{\sum_k s_b (k - \bar{k})^2 f(k, t)}_{s_b \text{Var}(k)} \right\rangle$$

$$\Rightarrow \text{Var}(k) = \frac{1}{s_b \tau} \ll 1 \quad (\text{by assumption})$$

④ Also implies that $\bar{k}(t)$ clicks suddenly:



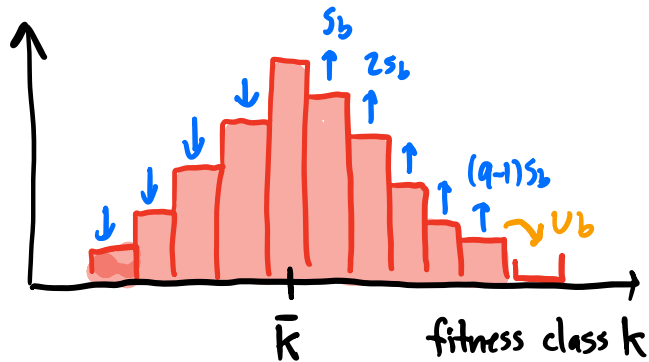
\Rightarrow



\Rightarrow i.e. for most $t \in [0, \tau] \Rightarrow \bar{k}(t) = \bar{k}(0)$

\Rightarrow everyone grows as $f(k, t) \sim f(k, 0) e^{(k - \bar{k}(0))st}$

\Rightarrow Now we have all ingredients to understand wave:

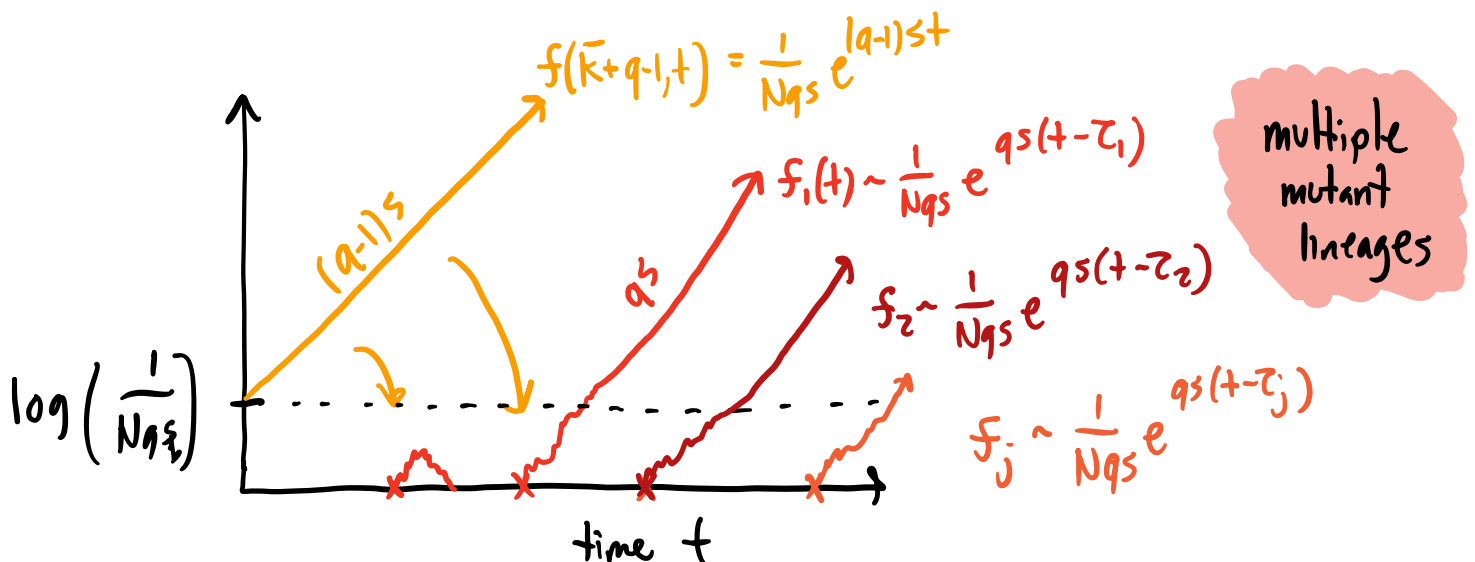


\Rightarrow in one click (τ), must establish new nose

\Downarrow

$$f(\bar{k}+q, t) = \frac{1}{Nq_s} e^{qs(t-\tau)}$$

$\Rightarrow \tau \approx$ establishment time of nose class!



$$\Rightarrow f(\bar{k}+q, t) = \sum_{j=0}^{j_{\max}} f_j(t) \equiv \frac{1}{Nq_s} e^{q_s(t-\tau)}$$

\downarrow
 establishment time
 for whole class.

$\Rightarrow j^{\text{th}}$ successful mutant establishes when:

$$\underbrace{\int_0^{\tau_j} N U_b \cdot f_{q-1}(t) \cdot q s_b dt}_{\sim O(j)}$$

Note: extra
little bit
will be
important
below!

$$\int_0^{\tau_j} N U_b \cdot \frac{1}{N q_s} e^{(q-1)s_b t} \cdot q s_b dt = \frac{U_b}{q s_b} e^{(q-1)s_b \tau_j} \sim O(k)$$

$$\Rightarrow \tau_j = \frac{1}{(q-1)s_b} \log\left(\frac{s_b}{U_b} \cdot q \cdot j\right)$$

$$\Rightarrow \text{Note: } \tau_j = \underbrace{\frac{1}{(q-1)s_b} \log\left(\frac{s_b}{U_b} \cdot q\right)}_{\tau_1} + \underbrace{\frac{1}{(q-1)s_b} \log(j)}_{\tau_j - \tau_1}$$

\gg
 (most time spent waiting for first mut'n)

\Rightarrow many mutations establish in quick succession ($\delta t \sim \frac{1}{qs_b} \ll \tau$)

\Rightarrow Typical size of j^{th} lineage:

$$\Rightarrow f_j(t) = \frac{1}{Nqs} e^{qs(t-\tau_j)} = \frac{e^{qs t}}{Nqs} \left(\frac{s_b q j}{u_b} \right)^{-1 - \frac{1}{q-1}}$$

↑
extra bit
will be
important!

\Rightarrow Size of entire nose class:

$$f(\bar{k}+q, t) = \sum_{j=1}^{J_{\max}} f_j(t) = \frac{1}{Nqs} e^{qs t} \left(\frac{s_b}{u_b} \right)^{-\frac{q}{q-1}} \sum_{j=1}^{J_{\max}} \frac{1}{(q \cdot j)^{1 + \frac{1}{q-1}}} \rightarrow 1$$

$$\equiv \frac{1}{Nqs} e^{qs(t-\tau)}$$

↙ set equal! ↘

\Rightarrow Time to establish new nose: $\tau = \frac{1}{(q-1)s} \log \left(\frac{s_b}{u_b} \right)$

vs $\tau_j \equiv \frac{1}{(q-1)s_b} \log \left(\frac{s_b \cdot q \cdot j}{u_b} \right)$

[Note: $\tau < \tau_j$ b.c.
multiple mutations
contribute @ once]

One task remaining... how to determine $q(N, s_b, U_b)$?

\Rightarrow follow new nose over time:

$$f(\bar{k}+q, \tau) \approx \frac{1}{Nq s} \xrightarrow{\tau} \frac{1}{Nq s} e^{(q-1)s\tau} \xrightarrow{\tau} \frac{1}{Nq s} e^{(q-1)s\tau + (q-2)s\tau} \rightarrow \dots$$

(right after est.)

\Rightarrow After q clicks, old nose is new mean! (majority of pop'n)

$$f(q\tau) \sim \frac{1}{Nq s_b} e^{(q-1)s_b\tau + (q-2)s_b\tau + \dots + s_b\tau} \sim \frac{1}{Nq s_b} e^{\frac{q^2 s_b \tau}{2}} \sim \mathcal{O}(1)$$

\Rightarrow system of 2 eqs for τ & q :

$$\frac{q^2 s_b \tau}{2} \approx \log(N s_b) + \tau = \frac{1}{q s_b} \log\left(\frac{s_b}{U_b}\right)$$

$$\Rightarrow \text{solution: } q = \frac{2 \log(Ns_b)}{\log(\frac{s_b}{u_b})} ; \tau = \frac{1}{2s_b} \frac{\log^2(\frac{s_b}{u_b})}{\log(Ns_b)}$$

$$\Rightarrow \left\langle \frac{d\bar{x}}{dt} \right\rangle = \frac{s_b}{\tau} = \frac{2s_b^2 \log(Ns_b)}{\log^2(s_b/u_b)}$$

(compare to $\sim N u_b s_b^2$ in *successive mutations* regime)

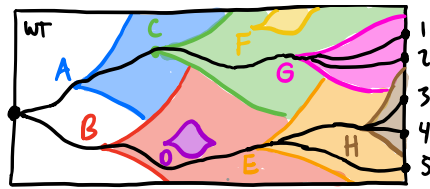
$$\Rightarrow \text{Self consistency: } s\tau \gg 1 \text{ + } q \gg 1$$

$$\Rightarrow \log\left(\frac{s_b}{u_b}\right) \ll \log(Ns_b) \ll \log^2\left(\frac{s_b}{u_b}\right)$$

Note: used heuristic derivation here...

for formal analysis (using branching processes)
see Appendix A and B below

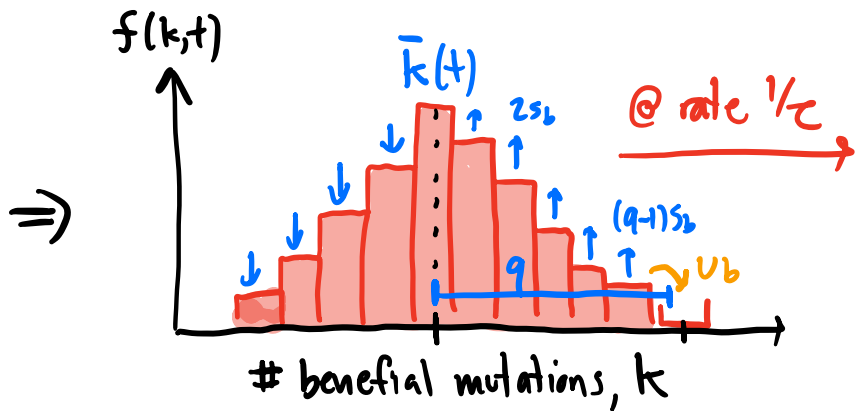
Recap : clonal interference



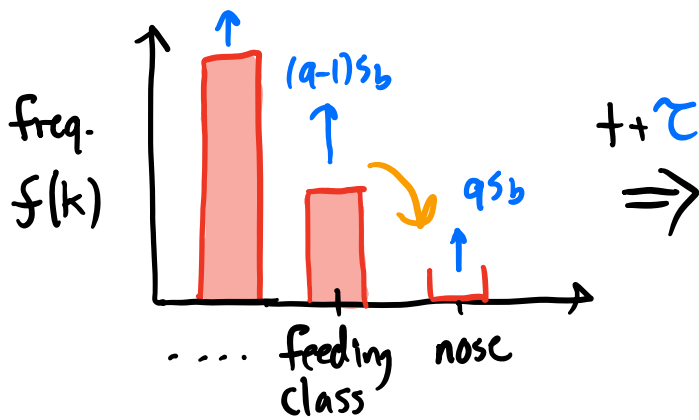
"Staircase" model

← Genome, $L \gg 1$ →

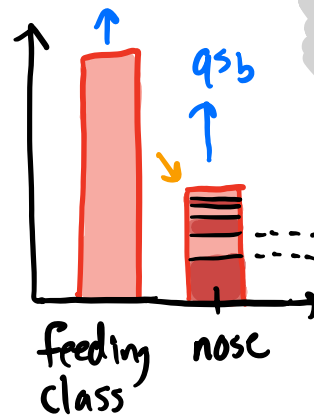
↳ selected mut'ns, $+s_b$
total rate $U_b \equiv L\mu_b$



key behavior occurs @ "nose":



$++\tau$
 \Rightarrow



Multiple mutations contribute to nose!

$$f_j(t) \sim \frac{1}{N_{qs}} e^{qs(t - \tau_j)}$$

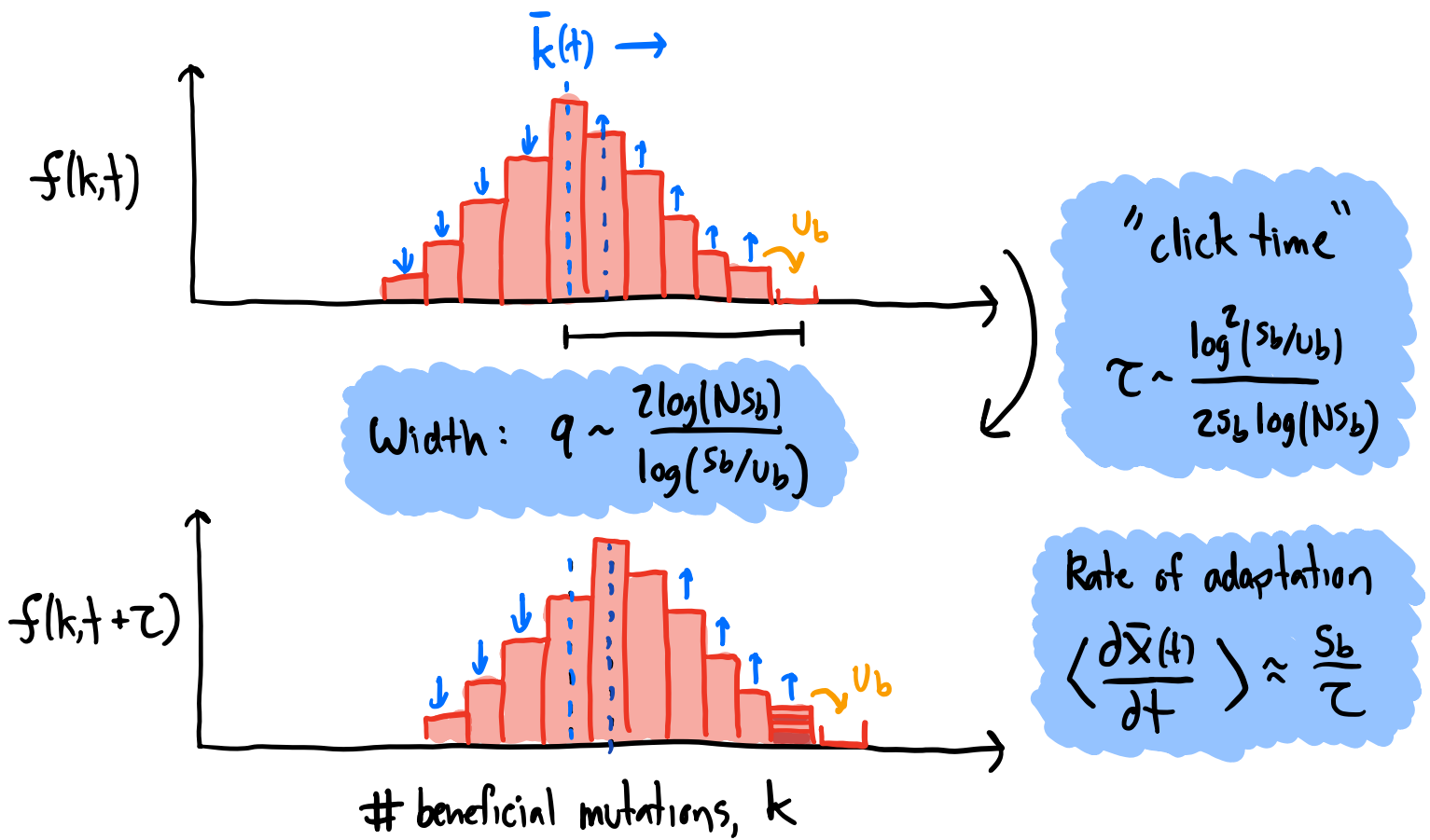
$$\tau_j \sim \frac{1}{(q-1)s_b} \log\left(\frac{s_b q_j}{U_b}\right)$$

Total contribution:

$$f_{\text{nose}}(t) \equiv \sum_{j=1}^{\infty} f_j(t) \equiv \frac{1}{N_{qs}} e^{qs(t - \tau)} \Rightarrow$$

$$\tau \sim \frac{1}{(q-1)s_b} \log\left(\frac{s_b}{U_b}\right)$$

⇒ Complete picture of dynamics of fitness dist'n:



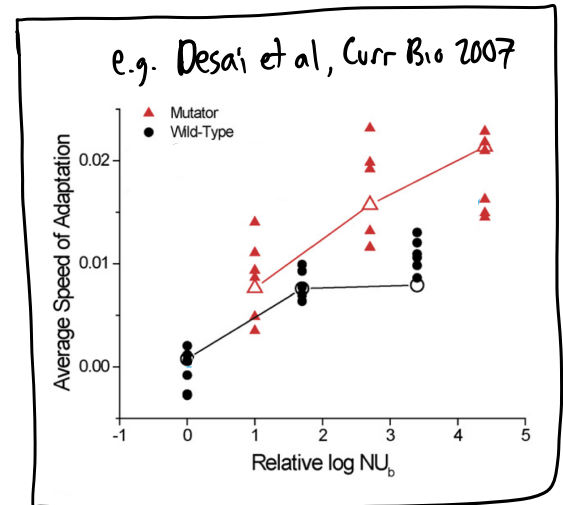
⇒ early tests for clonal interference in lab evolution experiments:

Successive mutations:

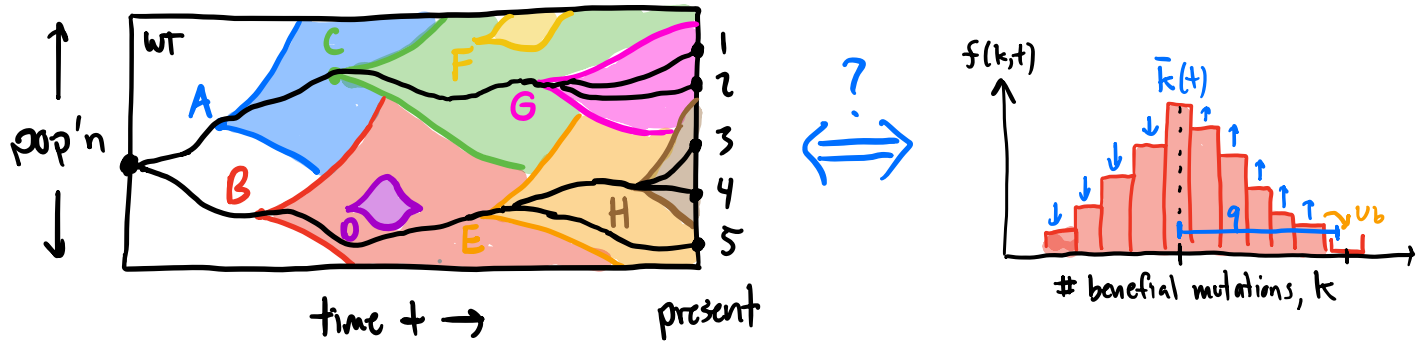
$$\left\langle \frac{d\bar{x}}{dt} \right\rangle \sim s_b^2 \cdot NU_b$$

clonal interference:

$$\left\langle \frac{d\bar{x}}{dt} \right\rangle \sim s_b^2 \cdot \frac{\log(NS_b)}{\log^2(s_b/u_b)}$$

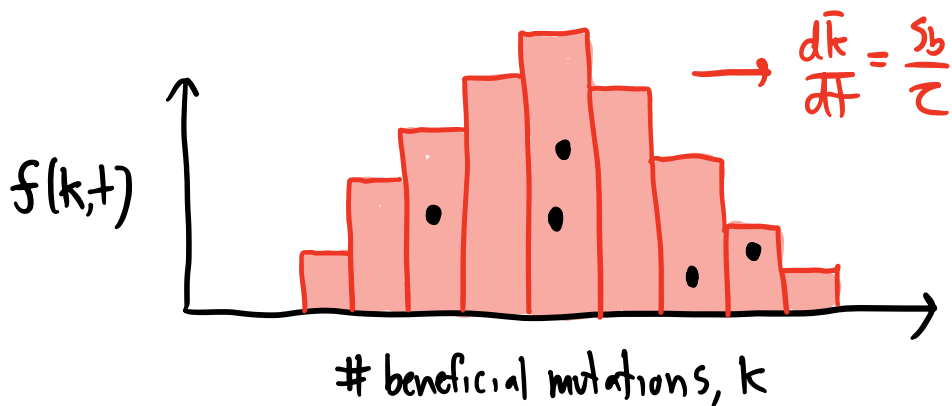


Next: Can we use this picture to understand genetic diversity backwards in time?

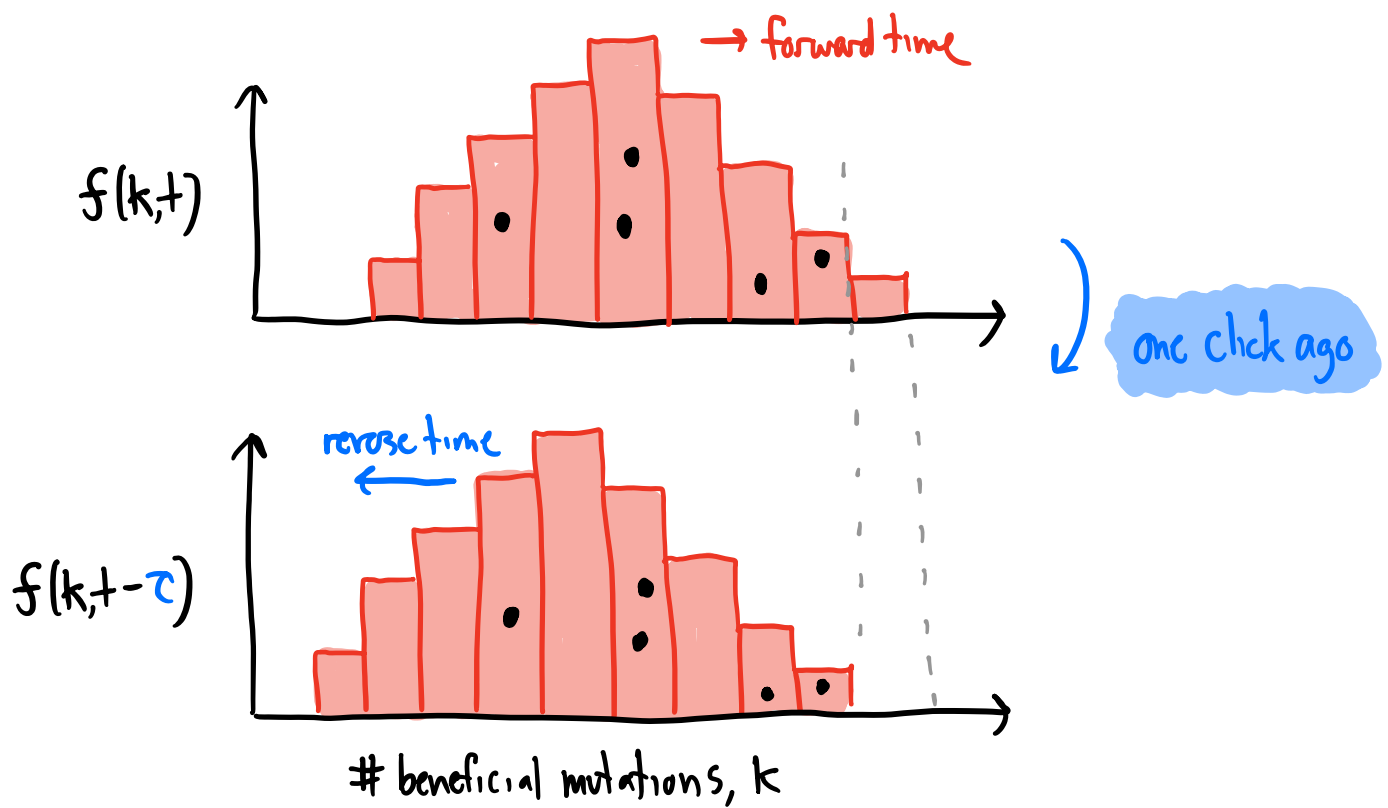


Answer: Yes we can! Let's start w/ some cartoons...

Step 1: draw sample of individuals from pop'n (present day)

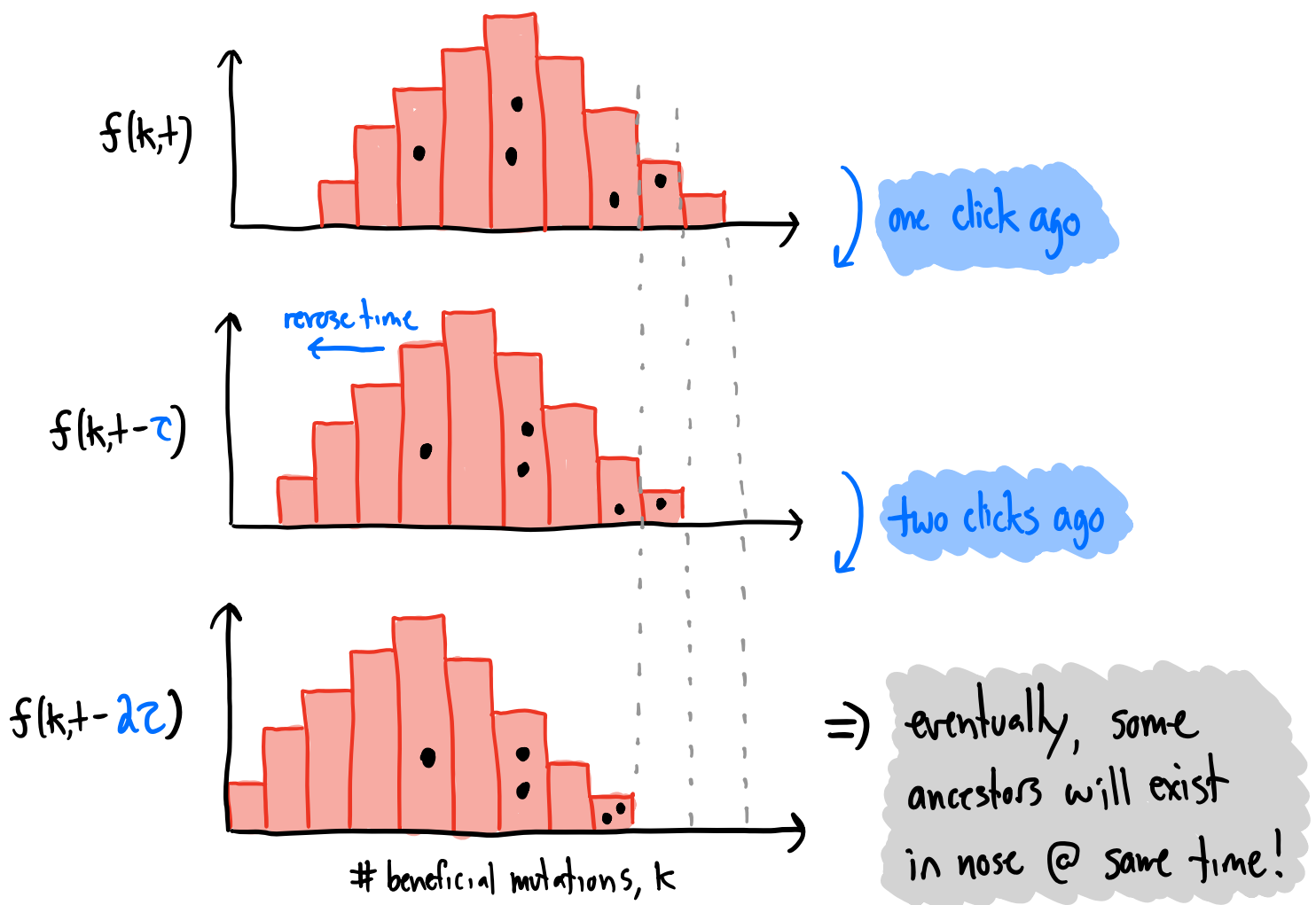


Step 2: where was everyone one click ago?



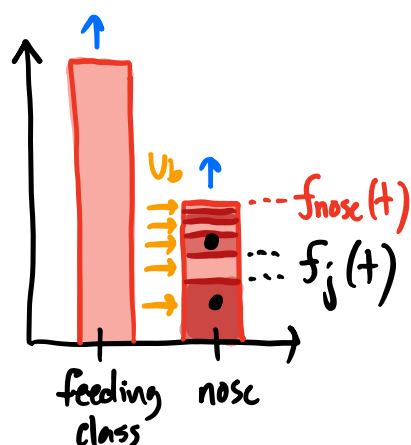
① can only coalesce if in same fitness class

② But little chance of coalescing in "bulk" of dist'n
(since $\tau \ll Nf_{q-1}(\tau), Nf_{q-2}(\tau), \text{etc.}$)



Two possible scenarios:

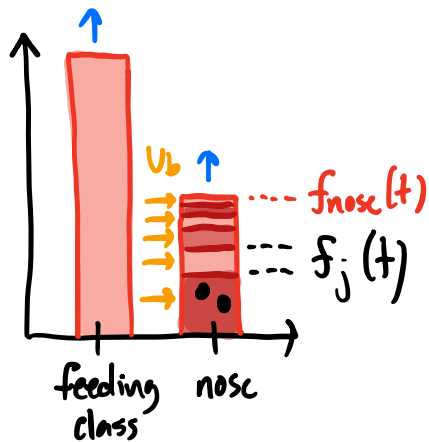
① Individuals are from separate lineages in the nose



\Downarrow

separate ancestors
in feeding class
(distinct mut'n events)

② Individuals from same lineage in nose



common ancestor
in feeding class

(coalescence w/in τ gens)

$$\Rightarrow \text{Probability: } p_c(2) = \sum_{j=1}^{\infty} \left(\frac{f_j(t)}{f_{\text{nose}}(t)} \right)^2 = \sum_{j=1}^{\infty} \left[\frac{\frac{1}{Nq_{sb}} e^{q_{sb}(t-\tau_j)}}{\frac{1}{Nq_{sb}} e^{q_{sb}(t-\tau)}} \right]^2$$

$$= \sum_{j=1}^{\infty} e^{-2q_{sb}(\tau_j - \tau)}$$



only depends on establishment times τ_j !

⇒ if we plug-in typical values of $\tau_j + \tau$ from heuristics:

$$\tau_j \sim \frac{1}{(q-1)s_b} \log\left(\frac{s_b q_j}{u_b}\right); \quad \tau \sim \frac{1}{(q-1)s_b} \log\left(\frac{s_b}{u_b}\right)$$

$$\Rightarrow p_c(z) = \sum_{j=1}^{\infty} e^{-2qs_b(\tau_j - \tau)} = \sum_{j=1}^{\infty} (q_j)^{-\frac{2q}{q-1}} \approx \frac{1}{q^2}$$

~~⇒ suggests coalescence after $\sim q^2$ clicks ($T_{MRCA} \sim q^2 \tau$)~~

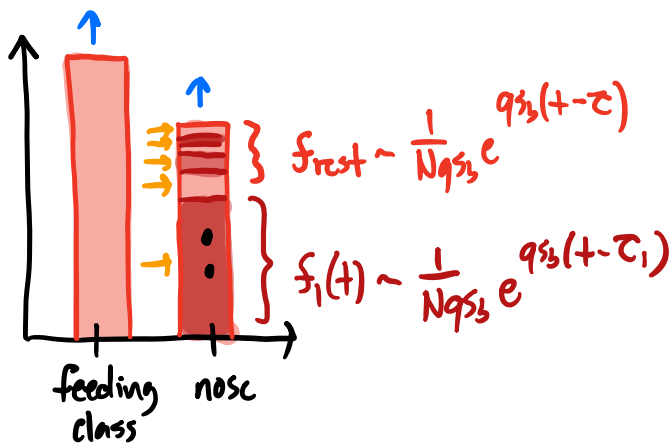
⇒ missing key part of puzzle: fluctuations

⇒ coalescence rare for typical lineage sizes,

but small chance of having anomalously early mutant

where coalescence is much more likely!

e.g. if first successful mutation occurs when $\tau_1 \approx \text{typical } \tau \dots$



$$\frac{f_i(t)}{f_{\text{nose}}(t)} \gtrsim \mathcal{O}(1)$$



$$p_c(2) \sim \mathcal{O}(1)!$$

\Rightarrow not a huge shift in time: typically, $\tau_1 - \tau \sim \frac{\log(q)}{q s_b}$
 so $\Delta\tau_1$ is $\ll 1/s_b \ll \tau$ (i.e. \ll click time)

\Rightarrow occurs w/ total probability:

$$p_{\text{jackpot}} \sim \int_0^\tau d\tau_1 N U_b f_{q-1}(t) \cdot q s_b$$

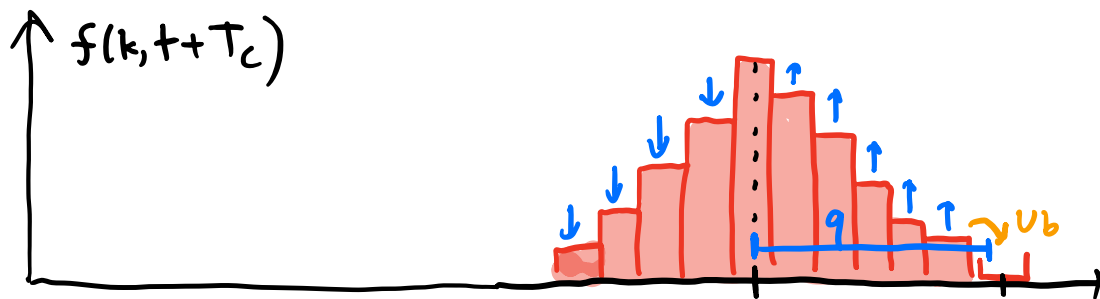
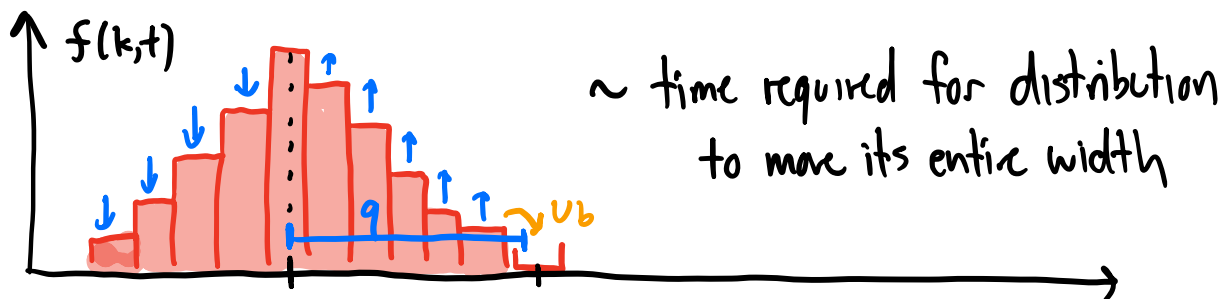
$$\sim \int_0^\tau d\tau_1 \cancel{N U_b} \cdot \frac{e^{(q-1)s_b t}}{\cancel{N q s_b}} \cdot \cancel{q s_b} \sim \frac{U_b}{(q-1)s_b} e^{(q-1)s_b \tau}$$

$$\sim \frac{1}{q}$$

$$\Rightarrow p_{\text{jackpot}} \sim \frac{1}{q} \quad (\gg \frac{1}{q^2} \Rightarrow \text{more likely to coalesce via rare jackpot than normal establishment process})$$

$$\Rightarrow \text{typical coalescence after } \frac{1}{p_{\text{jackpot}}} \sim q \text{ clicks}$$

$$\Rightarrow \text{coalescent timescale } T_c \equiv q\tau \sim \frac{1}{s_b} \log\left(\frac{s_b}{u_b}\right)$$



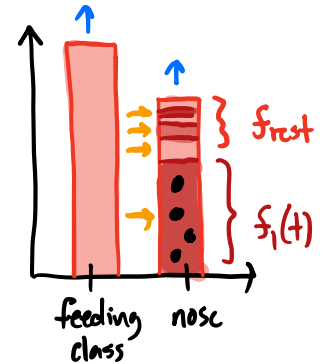
beneficial mutations, k

\Rightarrow fluctuations were crucial for determining T_c !

\Rightarrow coalescence is "bursty":

e.g. in larger sample size n :

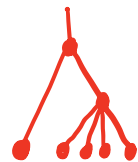
$$P_c(n \rightarrow 1) = \left(\frac{f_1(t)}{f_1(t) + f_{rest}(t)} \right)^n$$



$$\approx \begin{cases} \sim 1 & \text{if } f_1(t) \gtrsim n \cdot f_{rest}(t) \\ \ll 1 & \text{else} \end{cases}$$

$$\Rightarrow P_{\text{jackpot}}(n) = \int_0^{\tau - \log(n)/q s_b} d\tau, N V_b f_{q-1}(t) \cdot q s_b \sim 1/qn$$

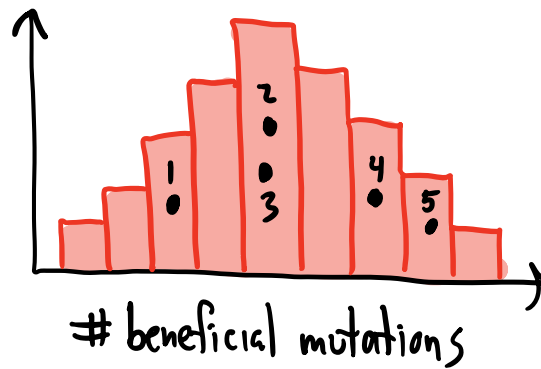
\Rightarrow i.e. multiple mergers likely!



* For "formal" treatment, see Appendix C...

Another interesting feature of genealogies + travelling wave:

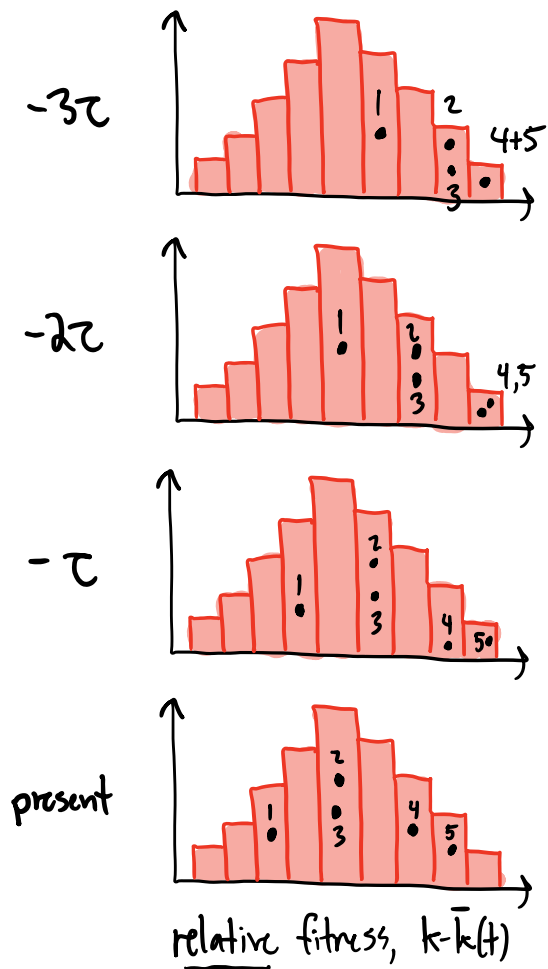
⇒ consider same example:



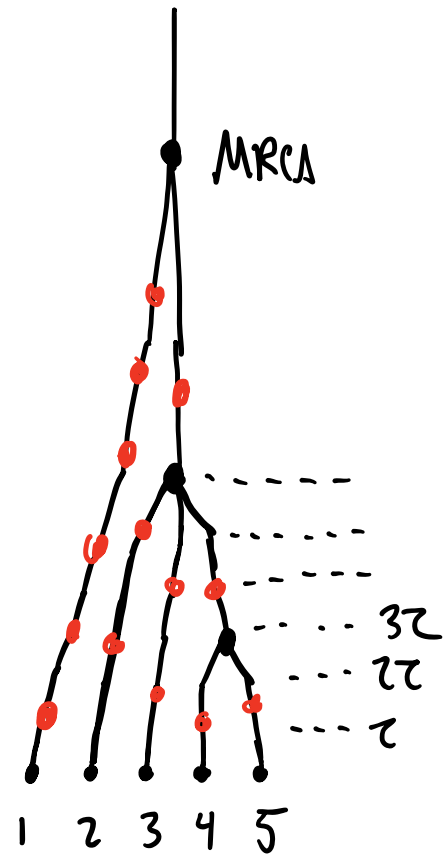
⇒ which individual's descendents are more likely to take over pop'n in future?

⇒ e.g. $5 \rightarrow 4 \rightarrow 2, 3 \rightarrow 1$

⇒ now let's try to "simulate" genealogy...



backward
in time



\Rightarrow time (+burstiness) of coalescence in past

\Rightarrow info about fitness in present

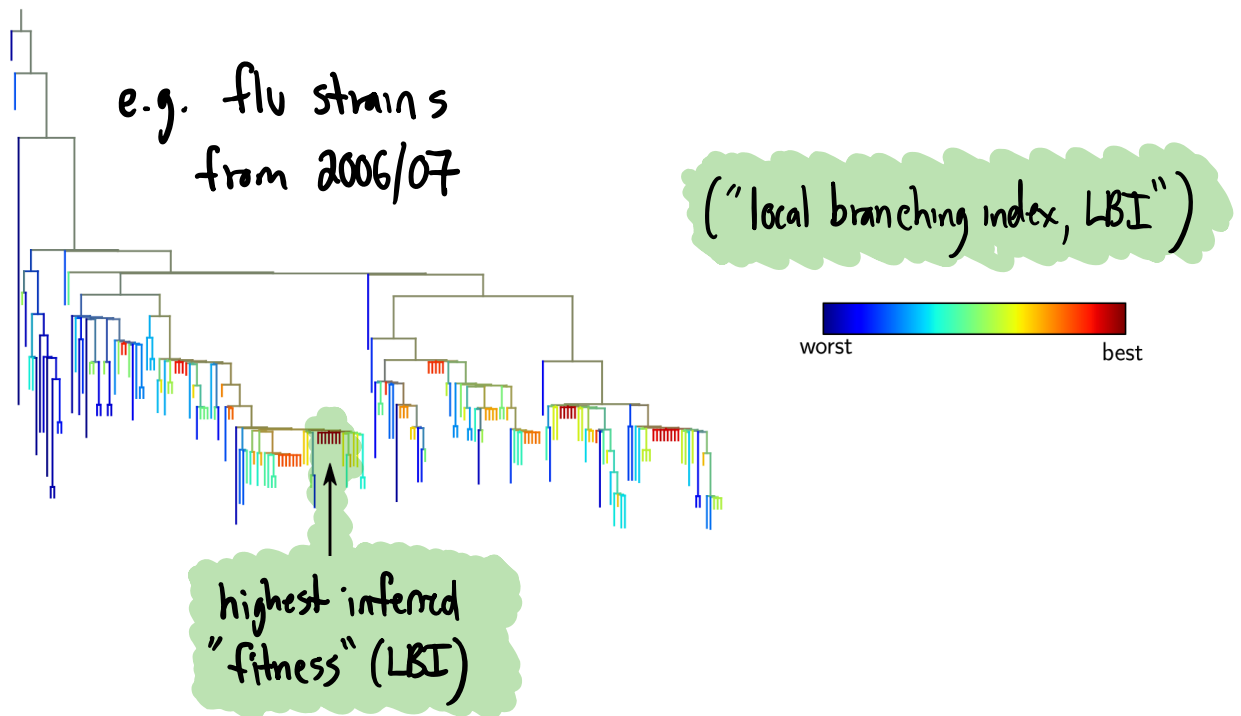
\Rightarrow forecasts about who takes over in future!

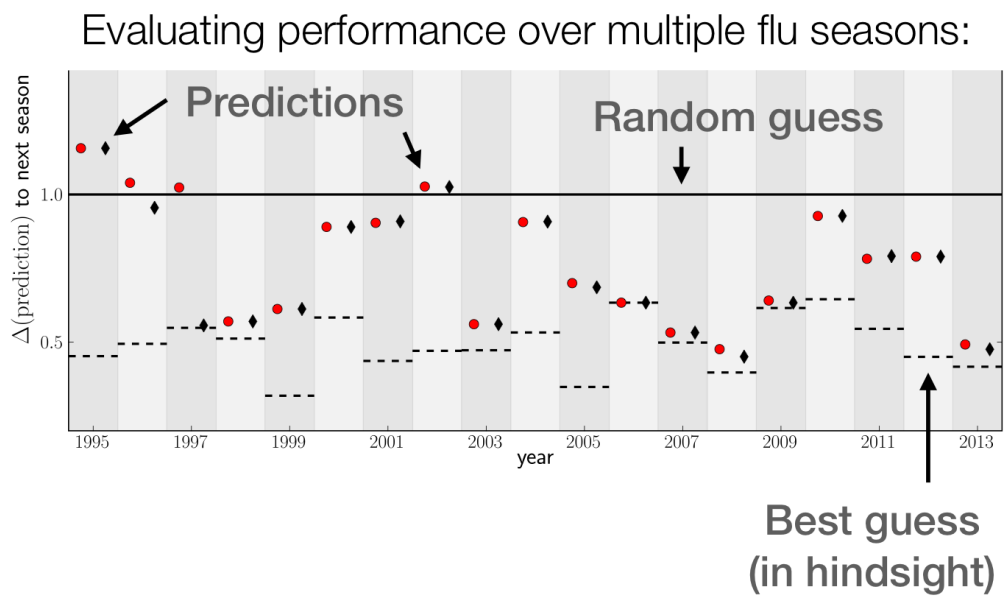
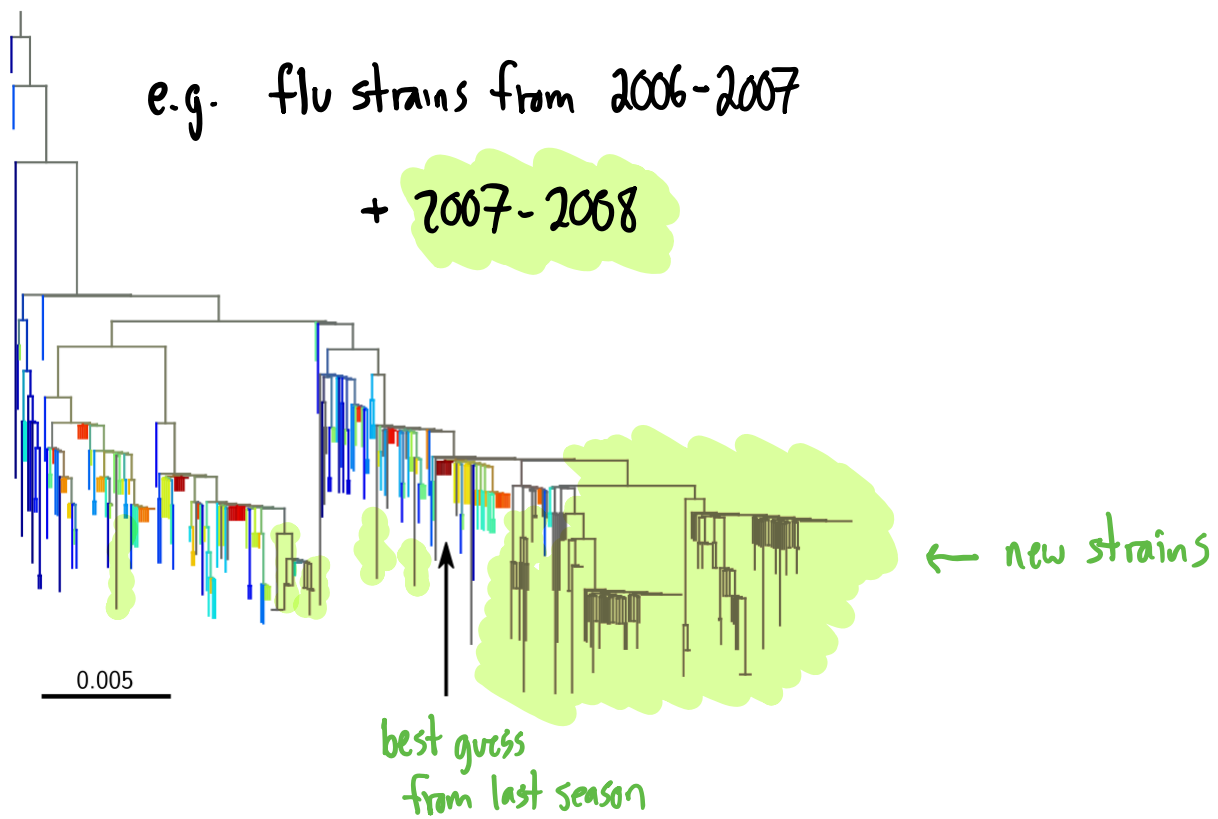
Predicting evolution from the shape of genealogical trees

Richard A Neher^{1*}, Colin A Russell², Boris I Shraiman^{3*}

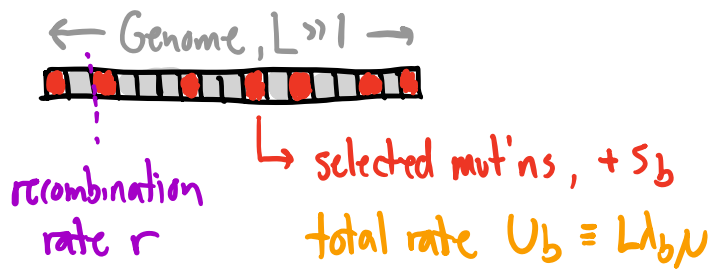
¹Evolutionary Dynamics and Biophysics, Max Planck Institute for Developmental Biology, Tübingen, Germany; ²Department of Veterinary Medicine, University of Cambridge, Cambridge, United Kingdom; ³Kavli Institute for Theoretical Physics, University of California, Santa Barbara, Santa Barbara, United States

⇒ implemented this idea for HA gene in influenza
(data from Problem #1 in HW1)





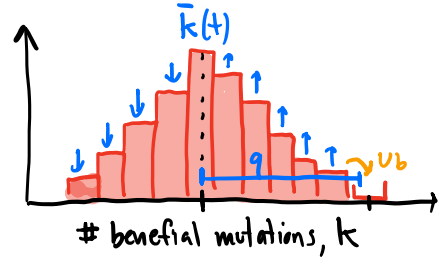
What about recombination?



$$r=0$$



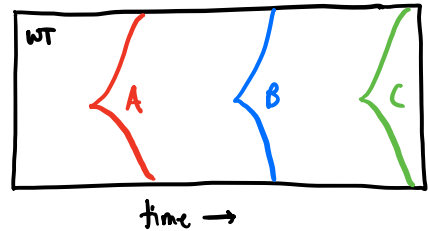
⇒



$$r \gg N \cdot \mu \lambda_b \cdot s$$



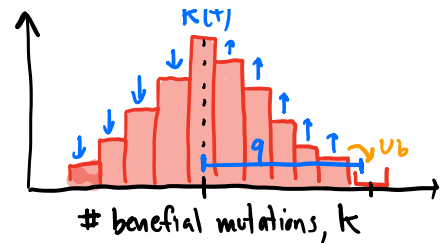
⇒



$r=0$

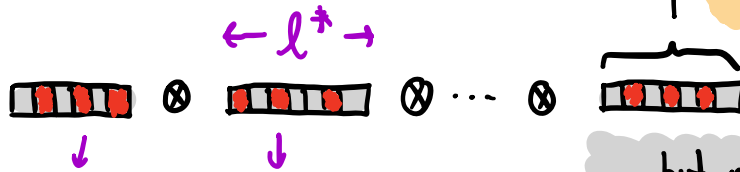


\Rightarrow



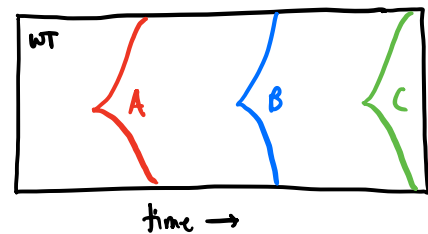
$U_{b,eff} = \ell^* \lambda_b \mu?$

In between?



Blocks are ~ independent

... but multiple mut's / block!



$r \gg N \cdot \mu_b \cdot s$



\Rightarrow

If true, need:

① w/in blocks, recombination should be rare! ($r \approx 0$)

$\Rightarrow r \ell^* \cdot T_c(N, s_b, U_{eff}(\ell^*)) \ll 1$

② between blocks, recombination should be frequent!

$\Rightarrow r \ell^* \cdot T_c \gg 1$

\Rightarrow can we (almost) satisfy both w/ $r \ell^* \cdot T_c \sim \mathcal{O}(1)$?

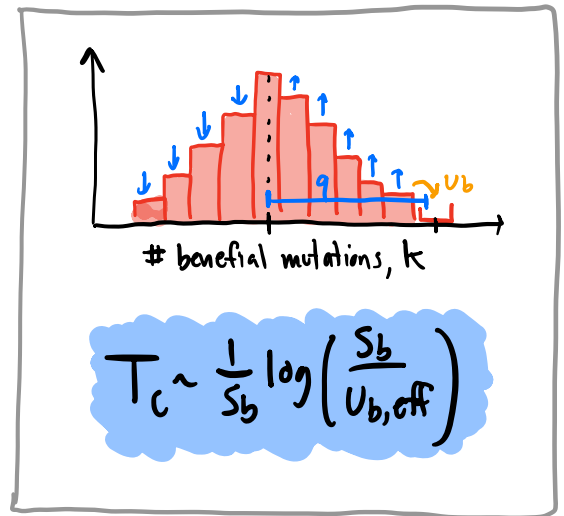
Linkage block ansatz



$$l^* \sim 1/r T_c$$

$$U_{b, \text{eff}} = l^* \lambda_b \mu$$

→



$$T_c \sim \frac{1}{S_b} \log \left(\frac{S_b}{U_{b, \text{eff}}} \right)$$

$$\Rightarrow \text{Self consistency: } T_c \sim \frac{1}{S_b} \log \left(\frac{S_b}{\mu \lambda_b} \cdot r T_c \right)$$

$$\Rightarrow \text{solution: } T_c \sim \frac{1}{S_b} \log \left(\frac{r}{\mu \lambda_b} \right)$$

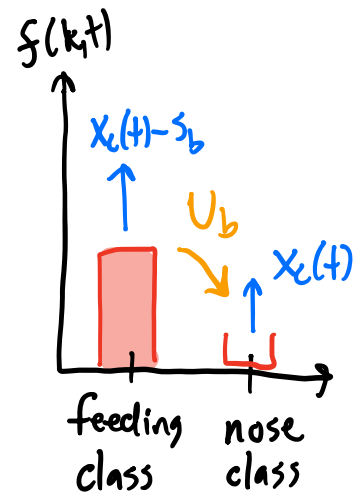
$$\Rightarrow l^* \sim \frac{S_b}{r} \log^{-1} \left(\frac{r}{\mu \lambda_b} \right)$$

$$\Rightarrow \text{self consistent if } N U_{b, \text{eff}} \log(N \lambda_b) \gg 1 \quad \& \quad U_{\text{eff}, b} \ll S_b$$

$$\Rightarrow N \cdot \mu \lambda_b \cdot S_b \gg r \gg \mu \lambda_b$$

Appendix A: Formal analysis of the nose class

⇒ we can understand the establishment of the nose class more formally using the branching process framework that we studied in the 1st half of the course



⇒ Under our assumptions, nose can be described by LBP model:

$$\frac{df_q}{dt} = x_c(t)f_q + U_b f_{q-1}(t) + \sqrt{\frac{f_q}{N}} \eta(t)$$

w/ $f_q(0) = 0$ & time-varying:

selection: $x_c(t) = [q - \bar{k}(t)]s_b$

+
mutation: $U_b f_{q-1}(t) = \frac{U_b}{2Nqs_b} e^{\int_0^t (x_c(t) - s_b) dt}$

⇒ In their analysis, Desai & Fisher (2007) assumed that $\bar{K}(t) \approx 0$ throughout the establishment period, so that $X_c(t) \equiv q s_b$ & $f_{q-1}(t) = \frac{1}{N q s} e^{(q-1)s_b t}$

⇒ Let's see how far we can get by relaxing this approx & explicitly modeling the "click" of $\bar{K}(t)$...

⇒ will be harder because time-varying fitness

$$X_c(t) = q s_b - s_b \bar{K}(t)$$

⇒ From our discussion in class, can take

$$\bar{K}(t) \equiv \frac{e^{s_b(t-t_c)}}{1 + e^{s_b(t-t_c)}}$$

where t_c is the time that $\bar{K}(t)$ clicks.

(later we will imagine that t_c is close to τ ...)

\Rightarrow From SDE, the generating function $H_f(z, t) = \langle e^{-z \cdot f_q(t)} \rangle$
satisfies the PDE:

$$\frac{\partial H_f}{\partial t} = \left[x_c(t) z - \frac{z^2}{2N} \right] \frac{\partial H_f}{\partial z} - z v_b f_{q-1}(t) H_f$$

w/ initial condition $H_f(z, 0) = 1$

\Rightarrow can solve w/ method of characteristics:

$$\text{define: } \psi(t_R) = \log \left[H_f(z(t_R), t - t_R) \right]$$

$$\text{w/ } \psi(t) = 0, \quad z(0) = z,$$

$$\psi(0) \equiv \log H_f(z, t)$$

$$\Rightarrow \psi \text{ satisfies: } \frac{d\psi}{dt_R} = - \frac{\frac{\partial H_f}{\partial t}}{H_f} + \frac{\frac{\partial H_f}{\partial z}}{H_f} \left(\frac{dz}{dt_R} \right)$$

$$\Rightarrow \frac{d\psi}{dt_R} = \left\{ \frac{dz}{dt_R} - \left[x_c(t-t_R)z - \frac{z^2}{2N} \right] \right\} \frac{d \log H_f}{dz} + z(t_R) U_b f_{q-1}(t-t_R)$$

$$\Rightarrow \text{if } \frac{dz}{dt_R} = x_c(t-t_R)z - \frac{z^2}{2N} \quad \& \quad z(0) = z$$

$$\Rightarrow \psi(t_R) = \psi(0) + \int_0^{t_R} z(t'_R) U_b f_{q-1}(t-t'_R) dt'_R$$

$$\Rightarrow \log H_f(z, t) = - \int_0^t z(\tau) U_b f_{q-1}(t-\tau) d\tau$$

where

$$\frac{dz}{d\tau} = x_c(t-\tau)z - \frac{z^2}{2N}, \quad z(0) = z$$

\Rightarrow solution for characteristic curve is given by:

$$z(\tau) = \frac{z e^{\int_0^\tau x_c(t-\tau') d\tau'}}{1 + \frac{z}{2N} \int_0^\tau e^{\int_0^{\tau'} x_c(t-\tau'') d\tau''} d\tau'}$$

(can plug in & check...)

$$\text{so } H_f(\bar{z}, t) = \exp \left[- \int_0^+ \frac{\bar{z} U_b f_{q-1}(t-\tau) e^{\int_0^\tau x_c(t-\tau') d\tau'}}{1 + \frac{\bar{z}}{2N} \int_0^\tau e^{\int_0^{\tau'} x_c(t-\tau'') d\tau''} d\tau'} d\tau \right]$$

$$= \exp \left[- \int_0^+ \frac{\bar{z} \cdot U_b f_{q-1}(u) e^{\int_u^+ x_c(u') du'}}{1 + \frac{\bar{z}}{2N} \int_u^+ e^{\int_{u'}^+ x_c(u'') du''} du'} du \right]$$

$$\Rightarrow \text{again, helpful to define } v(t) \text{ s.t. } f_q(t) \equiv \frac{v(t)}{2NqS_b} e^{\int_0^+ x_c(t') dt'}$$

$$\Rightarrow H_v(\bar{z}, t) \equiv \langle e^{-\bar{z} \cdot v(t)} \rangle \equiv H_f \left(2NqS_b e^{-\int_0^+ x_c(t') dt'} \bar{z}, t \right)$$

$$\Rightarrow H_v(\bar{z}, t) = \exp \left[- \int_0^+ \frac{\bar{z} U_b f_{q-1}(u) 2NqS_b e^{-\int_0^u x_c(u') du'}}{1 + qS\bar{z} \cdot \int_u^+ du' e^{-\int_0^{u'} x_c(u'') du''}} du \right]$$

\Rightarrow similar to single-locus case, we expect $v(t)$ to approach constant value v @ long times

$$\Rightarrow H_v(z) \equiv \lim_{t \rightarrow \infty} H_v(z, t)$$

$$\Rightarrow \log H_v(z) = - \int_0^{\infty} \frac{z \cdot U_b e^{-s_b t} dt}{1 + z \cdot q s_b \int_t^{\infty} dt' e^{-\int_0^{t'} x_c(t'') dt''}}$$

\Rightarrow Now we have to plug in our expression for $X_c(t)$:

$$X_c(t) = q s_b - \frac{s_b e^{s_b(t-t_c)}}{1 + e^{s_b(t-t_c)}}$$

$$\Rightarrow \int_0^t x_c(t') dt' = q s_b t - \log \left[\frac{1 + e^{s_b(t-t_c)}}{1 + e^{-s_b t_c}} \right]$$

$$\Rightarrow e^{-\int_0^t x_c(t') dt'} = e^{-q s_b t} \left[\frac{1 + e^{s_b(t-t_c)}}{1 + e^{-s_b t_c}} \right]$$

$$\Rightarrow q s_b \int_t^{\infty} dt' e^{-\int_0^{t'} x_c(t'') dt''} = \frac{e^{-q s_b t}}{1 + e^{-s_b t_c}} + \left(\frac{q}{q-1} \right) \frac{e^{-q s_b t} e^{s_b(t-t_c)}}{1 + e^{-s_b t_c}}$$

and hence:

$$\log H_V(z) = - \int_0^{\infty} \frac{z \cdot U_b e^{-s_b t} dt}{1 + z \cdot e^{-q s_b t} \left[1 + e^{s_b(t-t_c)} \left(\frac{q}{q-1} \right) \right]}$$

(where we have assumed that the click time t_c is $\gg 1/s_b$)

\Rightarrow for large q + relevant values of z , this integral will be dominated by times w/in $O(1/s_b)$ of τ .

\Rightarrow can extend lower limit of integral to $t = -\infty$
w/o much error...

\Rightarrow if t_c is also w/in $O(1/s_b)$ of τ , we can expand $e^{s_b(t-t_c)}$ term in denominator, so that

$$\log H_V(z) \approx - \int_{-\infty}^{\infty} \frac{z \cdot U_b e^{-s_b t} dt}{1 + 2 \cdot z \cdot e^{-q s_b t}}$$

changing variables to $\xi = (2z)^{1/q} e^{-s_b t}$,

$$\log H_\nu(z) = \exp \left[-\frac{U_b}{S_b} \cdot z^{1-1/q} \cdot \left(2^{-1/q} \int_0^\infty \frac{\xi d\xi}{1+\xi^q} \right) \right] \xrightarrow{1+O(1/q)}$$

$$\Rightarrow H_\nu(z) = e^{-\frac{U_b}{S_b} z^{1-1/q}}$$

\Rightarrow typical value of ν occurs when $H_\nu(z = \frac{1}{\nu^*}) = e^{-1}$

$$\Rightarrow \nu^* = \left(\frac{S_b}{U_b} \right)^{\frac{q}{q-1}}$$

$$\Rightarrow \text{substituting into } f_q(t) = \frac{\nu}{2NqS} e^{qs t} = \frac{e^{qs(t-\tau)}}{2NqS}$$

$$\Rightarrow \text{typical value of } f_q^*(t) = \frac{e^{s_b t}}{NqS_b} \left(\frac{S_b}{U_b} \right)^{\frac{q}{q-1}}$$

\Rightarrow typical value of establishment time:

$$\tau^* = \frac{1}{(q-1)s_b} \log\left(\frac{s_b}{u_b}\right)$$

\Rightarrow consistent w/ results from
simpler heuristic argument!

Appendix B: How many lineages contribute to new nose?

Recall in heuristic argument, we had:

$$f_{\text{nose}}(t) \equiv \sum_{j=1}^{J_{\max}} f_j(t) = \frac{1}{Nq_s} e^{qs_b(t-\tau)} \cdot \sum_{j=1}^{J_{\max}} \frac{1}{q_j^{1+1/q}}$$

+ argued that sum over k converged to ≈ 1 .

\Rightarrow Let's look @ this more carefully...

\Rightarrow if $J_{\max} \gg 1$ (will revisit below)

$$\Rightarrow \sum_{j=1}^{J_{\max}} \frac{1}{q_j^{1+1/q}} \approx \int_1^{\max} \frac{dk}{q_j^{1+1/q}} = 1 - e^{-\frac{1}{q} \log J_{\max}}$$

Thus, sum converges to 1 provided that

$\log J_{\max}$ is large compared to q

\Rightarrow how does this translate to establishment times τ_j ?

recall that $\tau_j - \tau_1 \sim \frac{1}{qs_b} \log(j)$, so condition becomes:

$$\Rightarrow \tau_{j_{\max}} - \tau_1 \sim \frac{1}{qs_b} \log(J_{\max}) \gg \frac{1}{s_b}$$

Thus, mutations that establish $\gg \frac{1}{s_b}$ after τ_1
have negligible contribution to $s_{\text{nose}}(t)$, τ , etc

\Rightarrow since $\frac{1}{s_b} \ll \tau$, this happens long before next click.

\Rightarrow can take $J_{\max} \approx \infty$ w/o losing any accuracy

i.e., can pretend that infinite # of muts
contribute to establishment of new nose.

Appendix C: formal analysis of coalescence in the nose

Recall: main result for stochastic size of nose:

$$f_{\text{nose}}(t) \equiv \frac{\nu}{2Nq s_b} e^{q s_b t} \Rightarrow H_\nu(z) \approx e^{-\frac{\nu}{s_b} z^{1-1/q}}$$

(supplement of lecture 19)

Let's fine-grain this further:

\Rightarrow let $f_\ell(t) \equiv$ freq of lineage in nose founded by beneficial mutation @ site ℓ

$$\Rightarrow \text{then } H_{\nu_\ell}(z) \approx e^{-\frac{\nu}{s_b} z^{1-1/q}}$$

\Rightarrow Probability that 2 individuals coalesce =
probability that they came from same lineage:

$$\Rightarrow \rho_c(z) = \left\langle \sum_{l=1}^{L_b} \left(\frac{f_l(t)}{\sum_{e'} f_{e'}(t)} \right)^2 \right\rangle = \left\langle \sum_{l=1}^{L_b} \left(\frac{v_l}{\sum_{e'} v_{e'}} \right)^2 \right\rangle$$

\Rightarrow Trick: using $\int_0^\infty \frac{\lambda^\alpha}{\Gamma(\alpha)} z^{\alpha-1} e^{-\lambda z} dz = 1$, can write as

$$\rho_c(z) = \left\langle \sum_l \left(\frac{v_l}{\sum_{e'} v_{e'}} \right)^2 \right\rangle = \left\langle \sum_l v_l^2 \int_0^\infty dz z e^{-\left(\sum_{e'} v_{e'}\right) z} \right\rangle$$

$$= \sum_l \left\langle \int_0^\infty dz z \cdot \left(v_l^2 e^{-z v_l} \right) \cdot \prod_{e' \neq l} e^{-v_{e'} z} \right\rangle$$

$$= \sum_l \int_0^\infty dz z \cdot \frac{\partial^2 H_{v_l}(z)}{\partial z^2} \cdot \prod_{e' \neq l} H_{v_{e'}}(z)$$

\Rightarrow using results above for $H_{v_l}(z)$ and $H_v(z)$,

$$\Rightarrow \frac{\partial H_{v_l}}{\partial z} = -\frac{\nu_l}{s_b} \left(1 - \frac{1}{q}\right) z^{-\frac{1}{q}} H_{v_l}(z)$$

$$\Rightarrow \frac{\partial^2 H_{\nu_\ell}}{\partial z^2} = \frac{1}{q} \frac{\nu_\ell}{s_b} \left(1 - \frac{1}{q}\right) z^{-1-\frac{1}{q}} H_{\nu_\ell}(z) + \mathcal{O}(\nu_\ell^2)$$

so that:

$$\begin{aligned} p_c(z) &= \sum_{\ell} \int_0^{\infty} dz \cdot z \cdot \frac{\partial^2 H_{\nu_\ell}(z)}{\partial z^2} \cdot \prod_{\ell' \neq \ell} H_{\nu_{\ell'}}(z) \\ &= \frac{1}{q} \sum_{\ell} \frac{\nu_\ell}{\nu_b} \int_0^{\infty} dz \frac{\nu_b}{s_b} \left(1 - \frac{1}{q}\right) z^{-\frac{1}{q}} H_{\nu}(z) = \prod_{\ell} H_{\nu_\ell}(z) \\ &= \frac{1}{q} \int_0^{\infty} - \frac{\partial H_{\nu}(z)}{\partial z} = \frac{1}{q} \left[H(\overset{\uparrow}{0}) - H(\overset{\uparrow}{\infty}) \right] \\ &= \frac{1}{q} \quad \text{as desired} \end{aligned}$$

Can do same thing for larger samples:

$$p_c(n) = \left\langle \sum_{\ell} \left(\frac{\nu_\ell}{\sum_{\ell'} \nu_{\ell'}} \right)^n \right\rangle = \sum_{\ell} \int_0^{\infty} dz \cdot \frac{(-1)^n z}{\Gamma(n)} \frac{\partial^n H_{\nu_\ell}(z)}{\partial z^n} \prod_{\ell' \neq \ell} H_{\nu_{\ell'}}(z)$$

$$\Rightarrow \frac{\partial^n H_{\nu_e}(z)}{\partial z^n} = \frac{\mu_e}{S_b} \frac{(-1)^n}{q} \left(1 - \frac{1}{q}\right) \prod_{k=1}^{n-2} \left(k + \frac{1}{q}\right) z^{-n+1-\frac{1}{q}} H_{\nu_e}(z) + \mathcal{O}(\mu_e^2)$$

$$\approx \frac{\mu_e}{S_b} \frac{(-1)^n (n-2)!}{q} z^{-n+1-\frac{1}{q}} H_{\nu_e}(z)$$

$$\Rightarrow p_c(n) = \frac{1}{q} \frac{\Gamma(n-1)}{\Gamma(n)} \cdot \sum_e \frac{\mu_e}{U_b} \cdot \int_0^\infty dz \cdot \frac{-\partial H_{\nu_e}(z)}{\partial z}$$

$$\approx \frac{1}{q(n-1)}$$

$$\Rightarrow p_c(n) = \frac{p_c(2)}{n-1} \leftarrow \text{also known as Boltzhausen-Sznitman coalescent (BSC)}$$