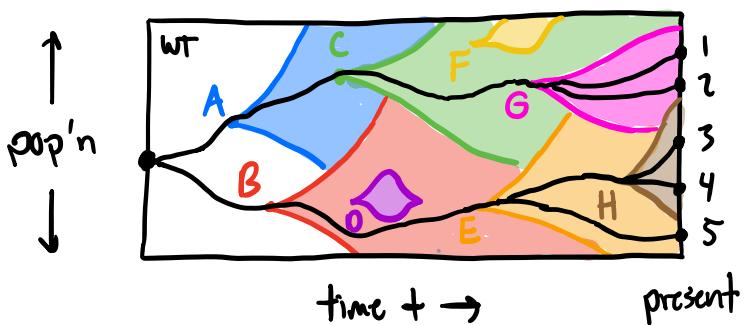


Chapter 15

Linked selection and clonal interference

Linked selection + clonal interference

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



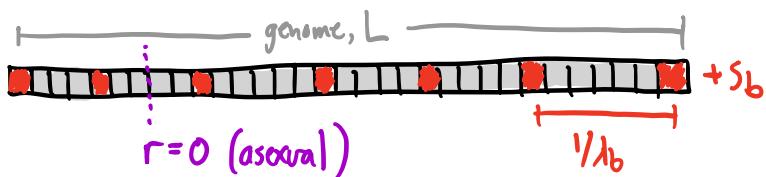
⇒ can't be reduced to $L=1$ or $L=2$ model (collective phase)

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

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

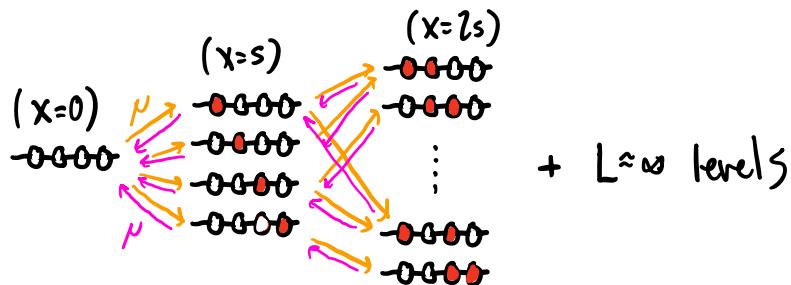
⇒ Analytical progress enabled by starting w/ very simple model:

"Staircase" Model



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

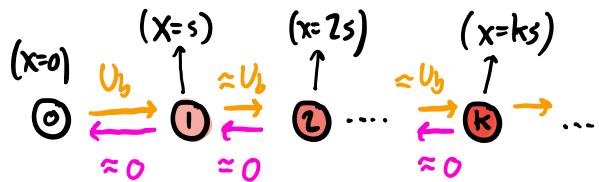
Genotype network:



Key simplification:

"fitness class"

$$f_k \equiv \sum_{|\bar{g}|=k} f(\bar{g})$$



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

$$\frac{df(k)}{dt} = S_b(k - \bar{k}(t))f(k) + U_b[f(k-1) - f(k)]$$

selection (nonlinear) mutation

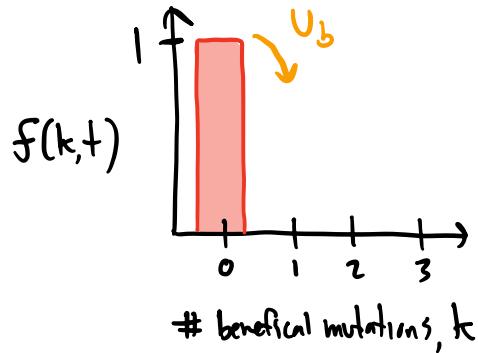
$$+ \sqrt{\frac{f(k)}{N}}\eta(k) - f(k)\sum_{k'} \sqrt{\frac{f(k')}{N}}\eta(k')$$

genetic drift
(stochastic)

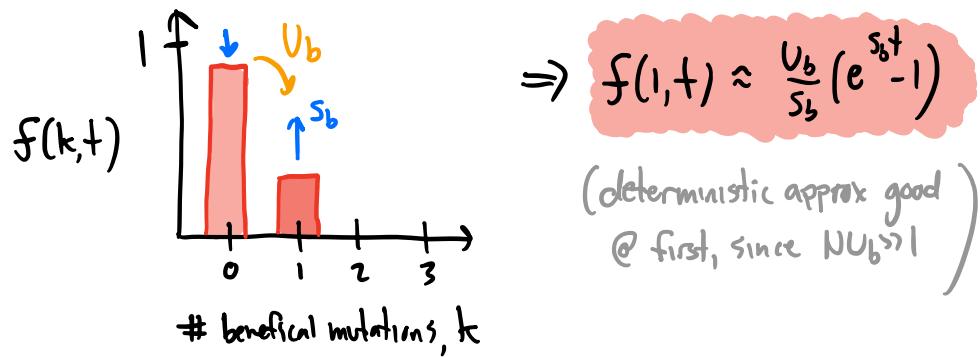
⇒ let's consider behavior when $Ns_b \gg Nu_b \gg 1$

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

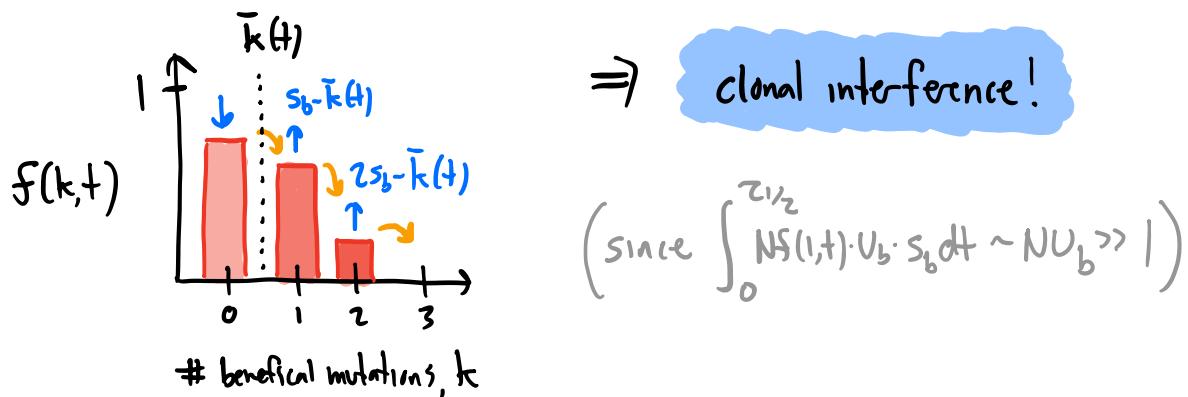
① Start w/ wildtype population @ $t=0$



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



③ Double mutants establish before single mutants take over,



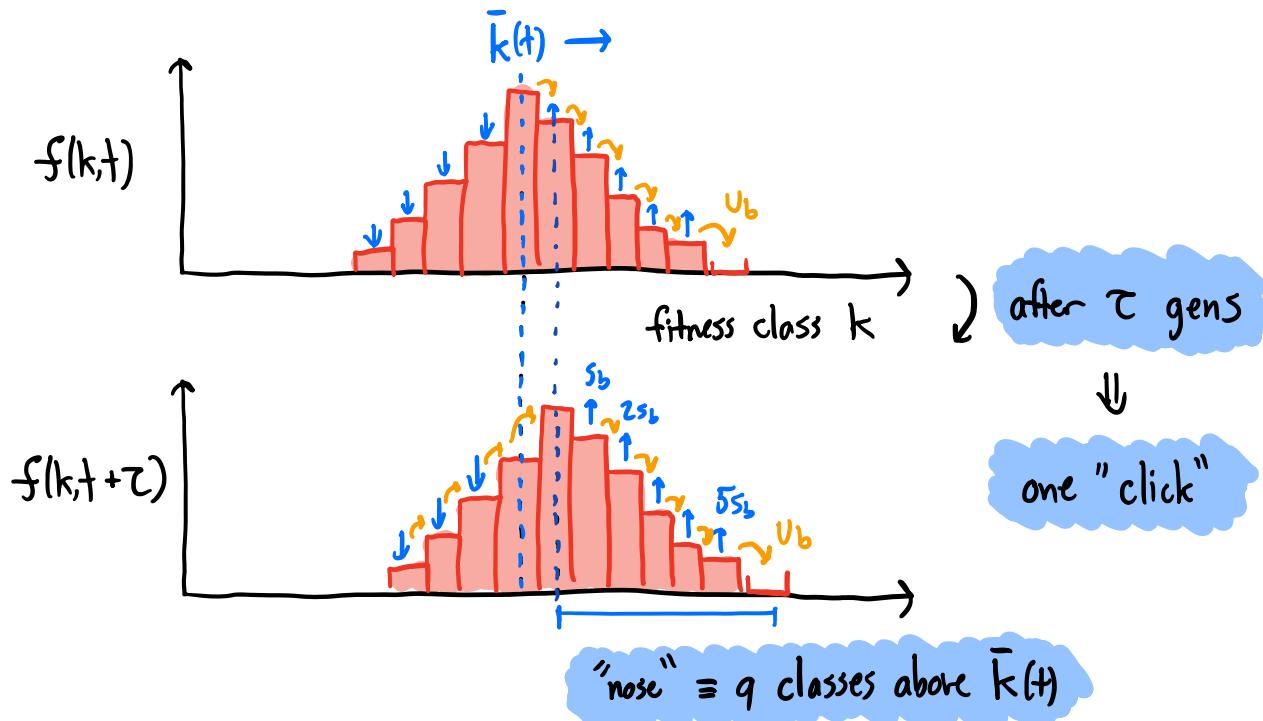
\Rightarrow Is deterministic approx still useful?

$$\frac{df(k)}{dt} = \underbrace{s_b(k - \bar{k}(t))f(k)}_{\text{selection (nonlinear)}} + \underbrace{U_b[f(k-1) - f(k)]}_{\text{mutation}} + \cancel{\underbrace{\sqrt{\frac{f(k)}{N}}\eta(k) - f(k)\sum_k \sqrt{\frac{f(k')}{N}}\eta(k')}}_{\text{genetic drift}} \rightarrow 0$$

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

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

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



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

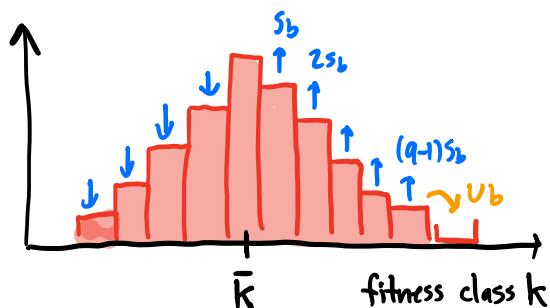
\Rightarrow Today: heuristic analysis [\sim Desai + Fisher 2007]

applies when: $N S_b \gg N U_b \gg 1$ & $q \gg 1$

Leads to simplifications:

① mutations only important for establishing new "nose"

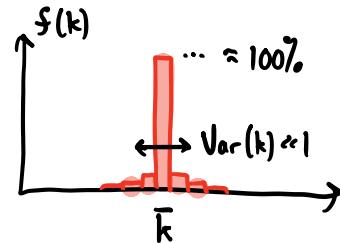
(since $S_b \gg U_b$)



② Genetic drift only important for establishing new noise

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

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

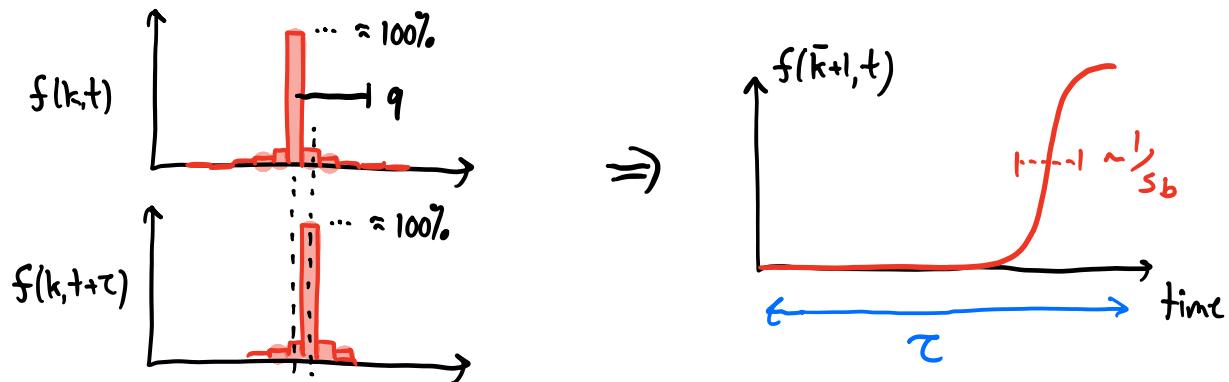


Problem 3 of HW 4:

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

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

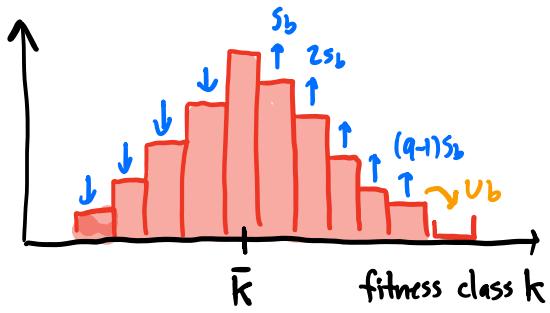
④ Also implies that $\bar{k}(t)$ clicks suddenly:



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

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

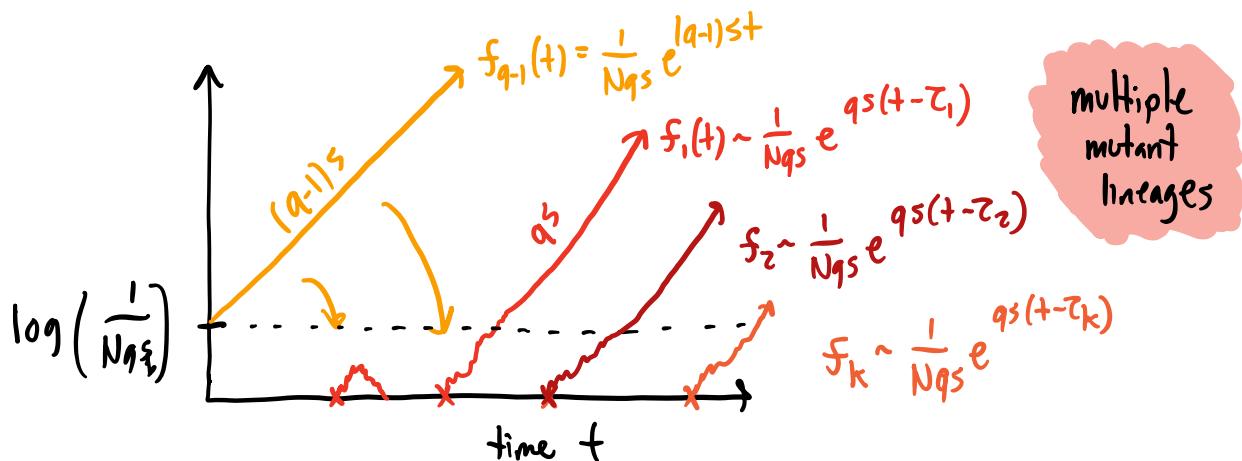
\Rightarrow Now we have all ingredients to understand wave:



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

$$f_q(t) = \frac{1}{Nq_s} e^{qs(t-\tau)}$$

$\Rightarrow \tau \approx \text{establishment time of nose class!}$



$$\Rightarrow f_q(t) = \sum_{k=0}^{K_{\max}} f_k(t) \equiv \frac{1}{Nq^s} e^{qs(t-\tau)}$$

↓
establishment time
for whole class.

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

$$\int_0^{\tau_k} N U_b \cdot f_{q-1}(t) \cdot q s_b dt \sim O(k)$$

Note: extra
info below!

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

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

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

(most time spent waiting for first mut'n)

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

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

$$\Rightarrow f_k(t) = \frac{1}{Nq_s} e^{qs(t-\tau_k)} = \frac{e^{qst}}{Nq_s} \left(\frac{s_b q k}{U_b} \right)^{-1 - \frac{1}{q}}$$

important!

\Rightarrow Size of entire nose class:

$$\Rightarrow f_q(t) = \sum_{k=1}^{K_{\text{nose}}} f_k(t) = \frac{1}{Nq_s} e^{qst} \left(\frac{s_b}{U_b} \right)^{-1 - \frac{1}{q}} \sum_{k=1}^{K_{\text{nose}}} \frac{1}{q} \frac{1}{k^{1 + \frac{1}{q}}}$$

set equal!

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

vs $\tau_k = \frac{1}{q s_b} \log\left(\frac{s_b}{U_b} \cdot q \cdot k\right)$ $\tau < \tau_k$ because
multiple mutations contribute \propto once

\Rightarrow how to determine q ?

\Rightarrow follow new nose over time:

$$f(\bar{k}+q, \tau) \approx \frac{1}{N\varsigma_b} e^{\frac{2S(2-b)}{N\varsigma_b} \tau} \rightarrow \frac{1}{N\varsigma_b} e^{\frac{2S(1-a)}{N\varsigma_b} \tau} \rightarrow \frac{1}{N\varsigma_b} e^{\frac{2S(2-b) + 2S(1-a)}{N\varsigma_b} \tau} \rightarrow \dots$$

(right after est.)

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

$$f(q\tau) \sim \frac{1}{N\varsigma_b} e^{\frac{2S_b + \dots + 2S_b(2-b) + 2S_b(1-a)}{N\varsigma_b} q\tau} \sim \frac{1}{N\varsigma_b} e^{\frac{q^2 \varsigma_b^2}{N} \tau} \sim \mathcal{O}(1)$$

\Rightarrow System of 2 eqs for $\tau + q$:

$$\frac{q^2 \varsigma_b^2 \tau}{2} \approx \log(N\varsigma_b)$$

$$+ \quad \tau = \frac{1}{q\varsigma_b} \log\left(\frac{\varsigma_b}{\varsigma_b}\right)$$

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

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

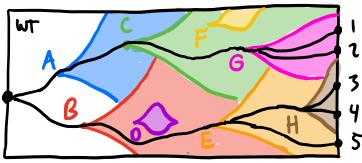
(compare to $\sim N u_b s_b^2$ in **successive mutations regime**)

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

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

Note: used heuristic derivation here...
 for formal analysis (using branching processes)
 see Appendix A and B below

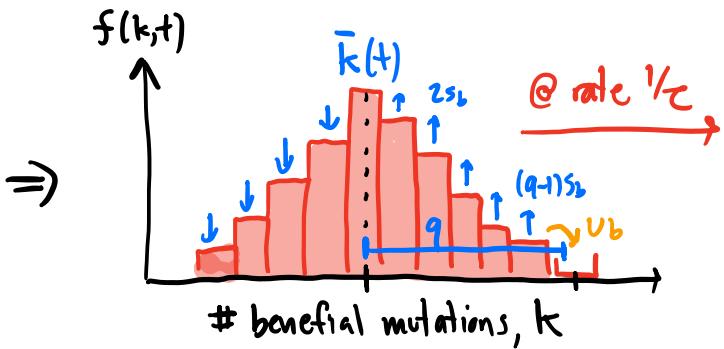
Recap : clonal interference



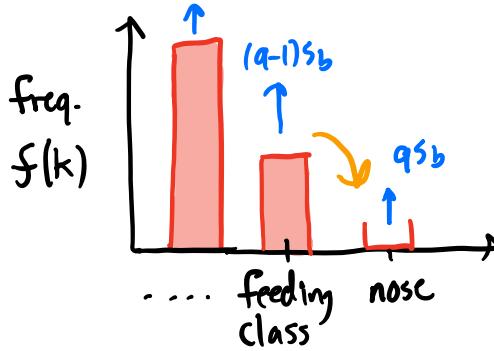
"Staircase" model

← Genome, $L \gg 1$ →

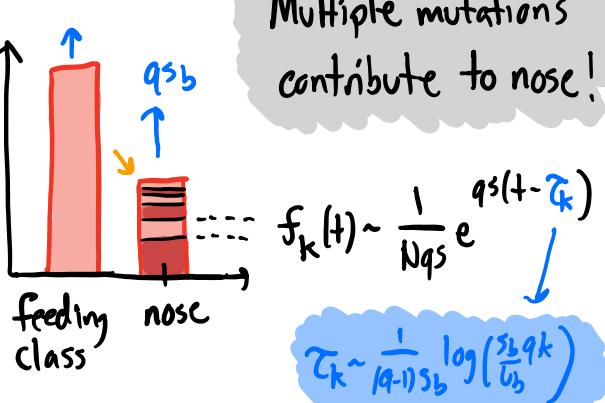
 ↴ selected mut's, + s_b
 total rate $U_b = L\lambda_b N$



key behavior occurs @ "nose":



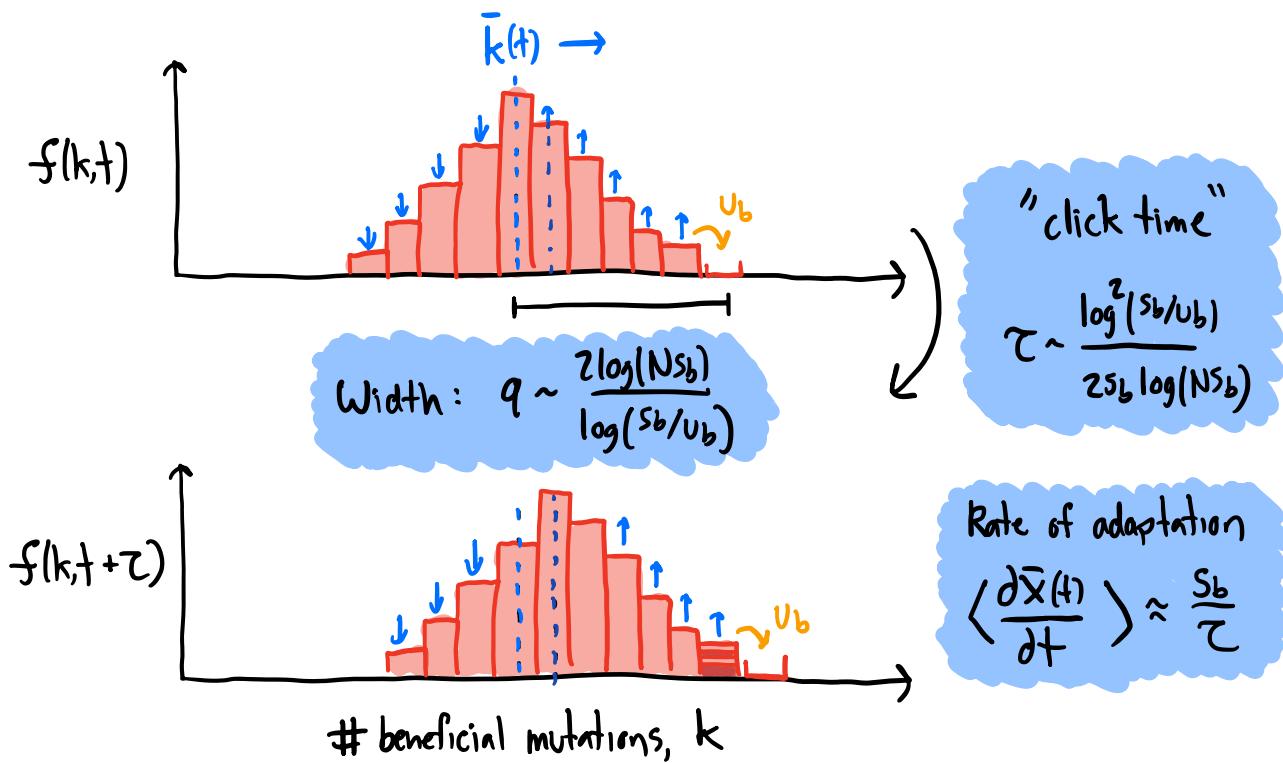
+ τ



Total contribution:

$$f_{\text{nose}}(t) \equiv \sum_{k=1}^{\infty} f_k(t) \equiv \frac{1}{Nqs} e^{qs(t - \tau)} \Rightarrow \tau \sim \frac{1}{(q-1)s_b} \log\left(\frac{s_b}{U_b}\right)$$

\Rightarrow Complete picture of dynamics of fitness dist'n:



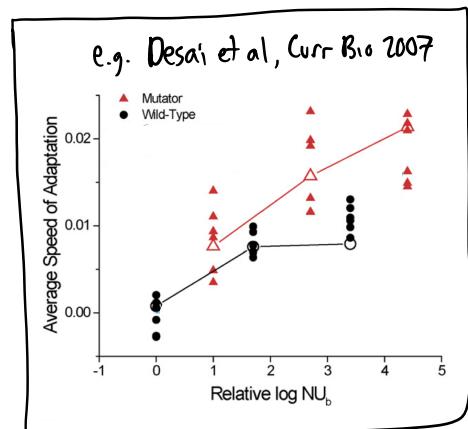
\Rightarrow early tests for clonal interference
in lab evolution experiments:

Successive mutations:

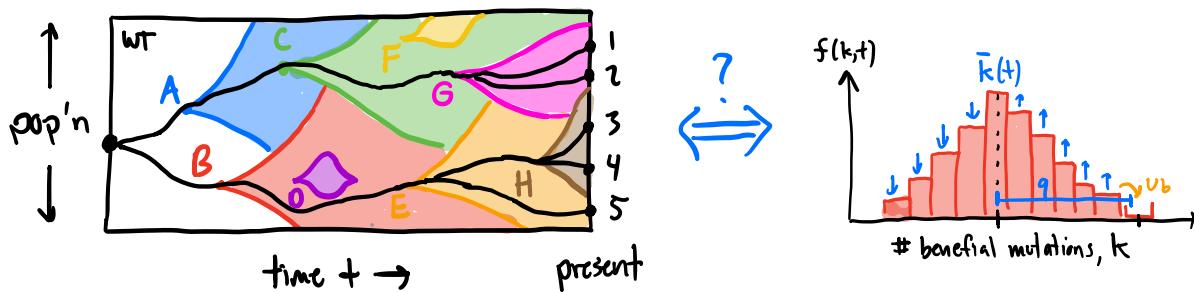
$$\left\langle \frac{d\bar{x}}{dt} \right\rangle \sim s_b^2 \cdot N u_b$$

clonal interference:

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

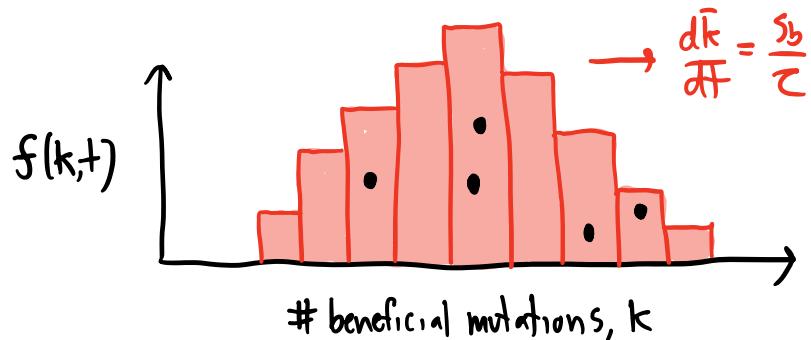


Next: Can we use this picture to understand
genetic diversity backwards in time?

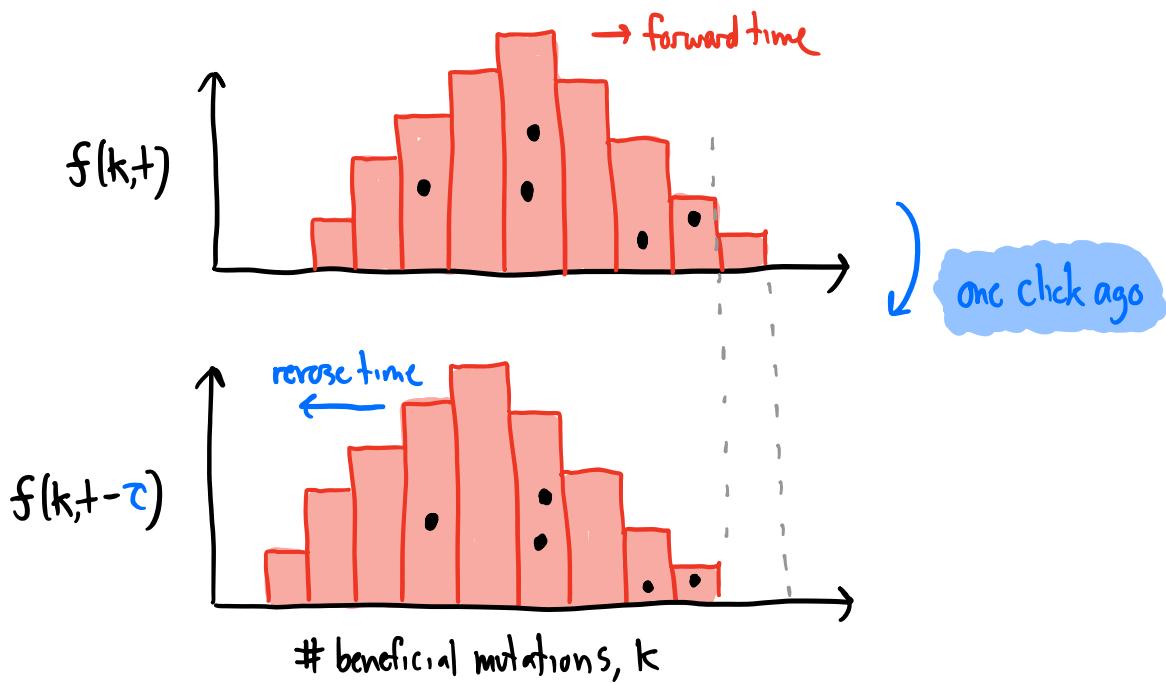


Answer: Yes we can! Let's start w/ some cartoons...

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

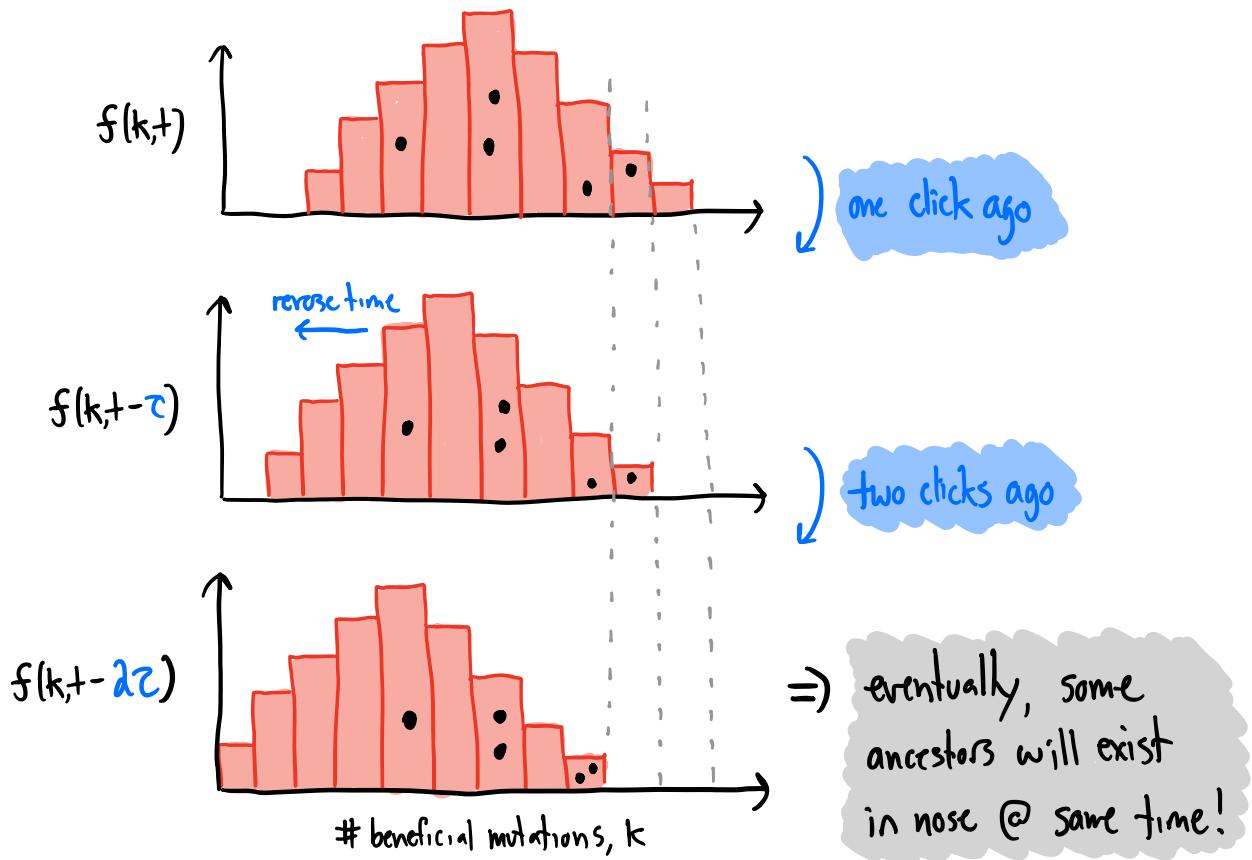


Step 2: where was everyone one click ago?



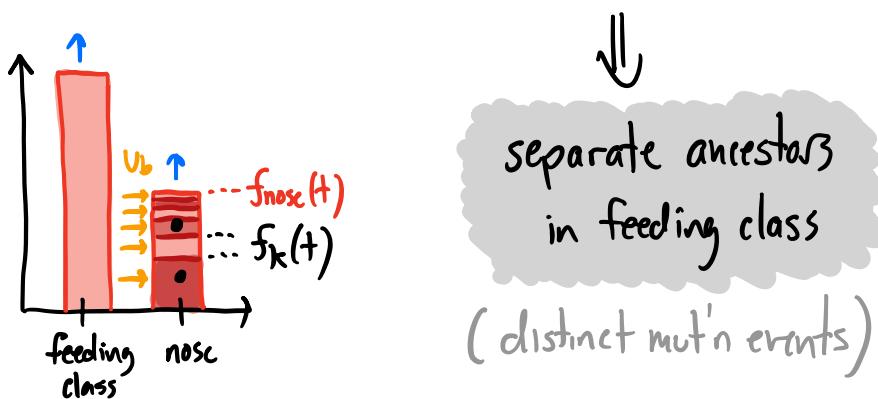
① can only coalesce if in same fitness class

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

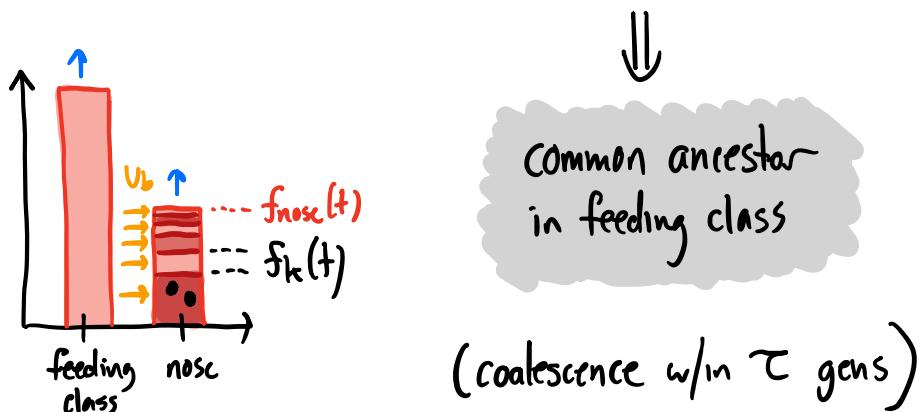


Two possible scenarios:

① Individuals are from separate lineages in the nose



② Individuals from same lineage in nose



$$\Rightarrow \text{Probability: } p_c(\alpha) = \sum_{k=1}^{\infty} \left(\frac{f_k(t)}{f_{\text{nose}}(t)} \right)^2 = \sum_{k=1}^{\infty} \left[\frac{\frac{1}{NqS_b} e^{qS_b(t - \tau_k)}}{\frac{1}{NqS_b} e^{qS_b(t - \tau)}} \right]^2$$

$$= \sum_{k=1}^{\infty} e^{-2qS_b(\tau_k - \tau)}$$



only depends on establishment times τ_k !

\Rightarrow if we plug-in typical values of τ_k & τ from heuristics:

$$\tau_k \sim \frac{1}{(q-1)S_b} \log\left(\frac{S_b q k}{U_b}\right); \quad \tau \sim \frac{1}{(q-1)S_b} \log\left(\frac{S_b}{U_b}\right)$$

$$\Rightarrow P_c(z) = \sum_{k=1}^{\infty} e^{-2qS_b(\tau_k - \tau)} = \sum_{k=1}^{\infty} (qk)^{-\frac{2q}{q-1}} \approx \frac{1}{q^2}$$

\Rightarrow suggests coalescence after $\sim q^2$ clicks ($T_{MRU} \sim q^2 \tau$)

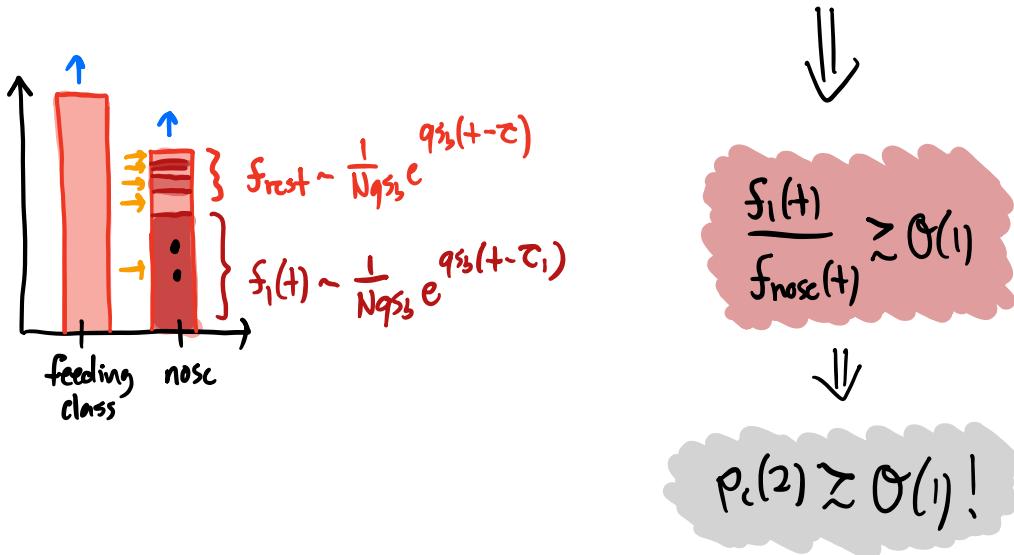
\Rightarrow missing key part of puzzle: fluctuations

\Rightarrow 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 $\tau_1 \leq \tau$:



\Rightarrow not a huge shift: typically, $\tau_1 - \tau \sim \frac{\log(q)}{qS_b} \ll \frac{1}{S_b} \ll \tau$

\Rightarrow occurs w/ total probability:

$$P_{\text{jackpot}} \sim \int_0^\tau d\tau_1 N U_b f_{q-1}(+)\cdot q S_b$$

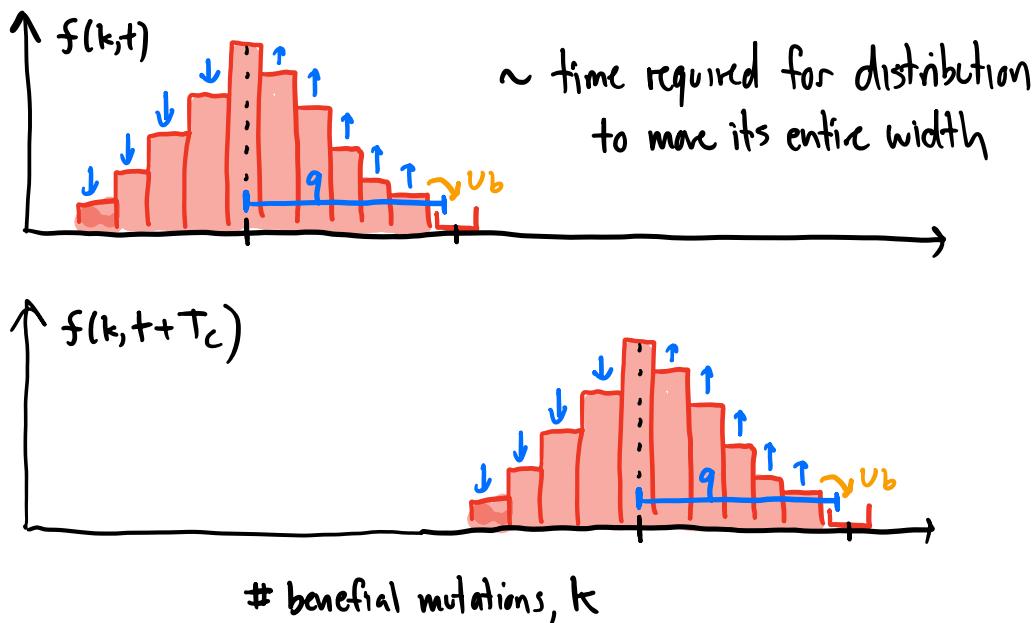
$$\sim \int_0^\tau d\tau_1 N U_b \cdot \frac{e^{(q-1)S_b \tau}}{NqS_b} \cdot \cancel{qS_b} \sim \frac{U_b}{(q-1)S_b} e^{(q-1)S_b \tau}$$

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

$$\Rightarrow P_{\text{jackpot}} \sim \frac{1}{q} \quad (\gg \frac{1}{q^2})$$

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

$$\Rightarrow \text{coalescent timescale} \quad T_c = q \tau - \frac{1}{S_b} \log\left(\frac{S_b}{U_b}\right)$$

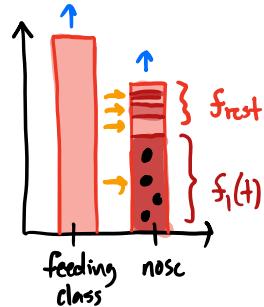


\Rightarrow fluctuations were crucial for determining T_c !

\Rightarrow coalescence is "bursty":

e.g. in larger sample size n :

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



$$\Rightarrow O(1) \text{ if } f_{rest}(t) / f_1(t) \lesssim 1/n$$

$$\Rightarrow P_{\text{jackpot}}(n) = \int_0^{T - \log(n)/qS_b} d\tau_1 N V_b f_{q-1}(t) \cdot q S_b \sim 1/qn$$

\Rightarrow i.e. multiple mergers likely!



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

Another interesting feature of genealogies + travelling wave:

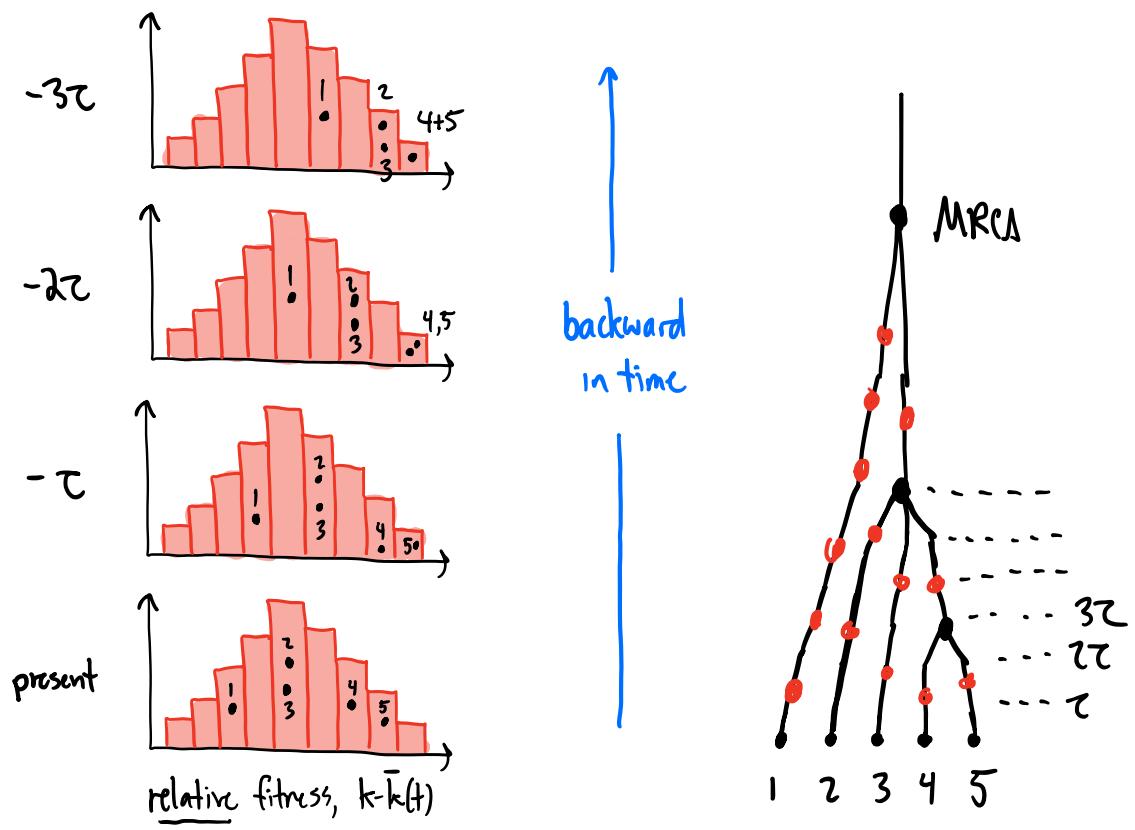
⇒ consider same example:



⇒ which individual's descendants 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...



\Rightarrow time (+burstiness) of coalescence in past

\Rightarrow info about fitness in present

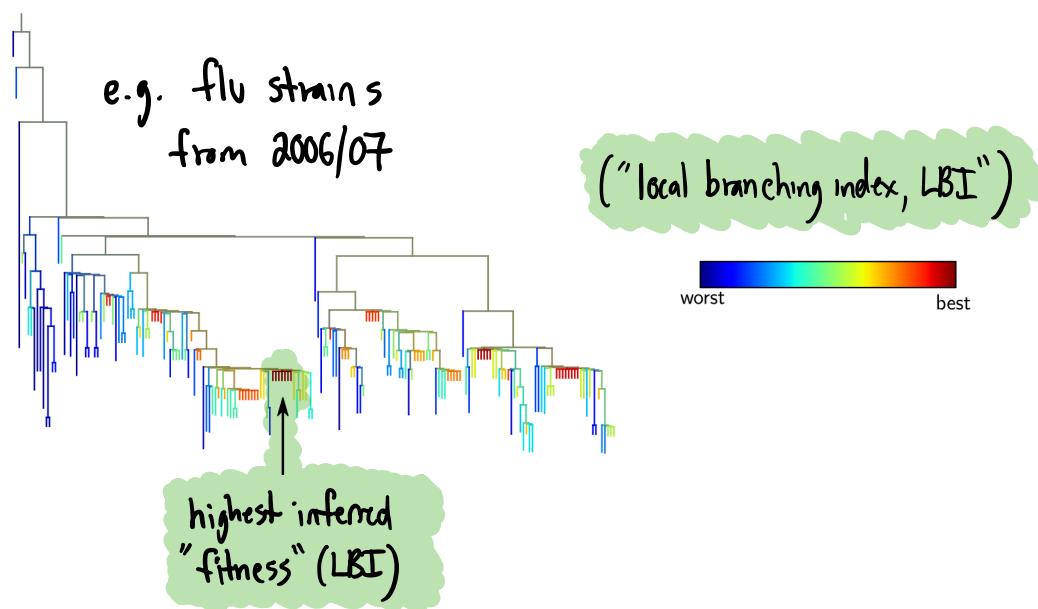
\Rightarrow forecasts about who takes over in future!

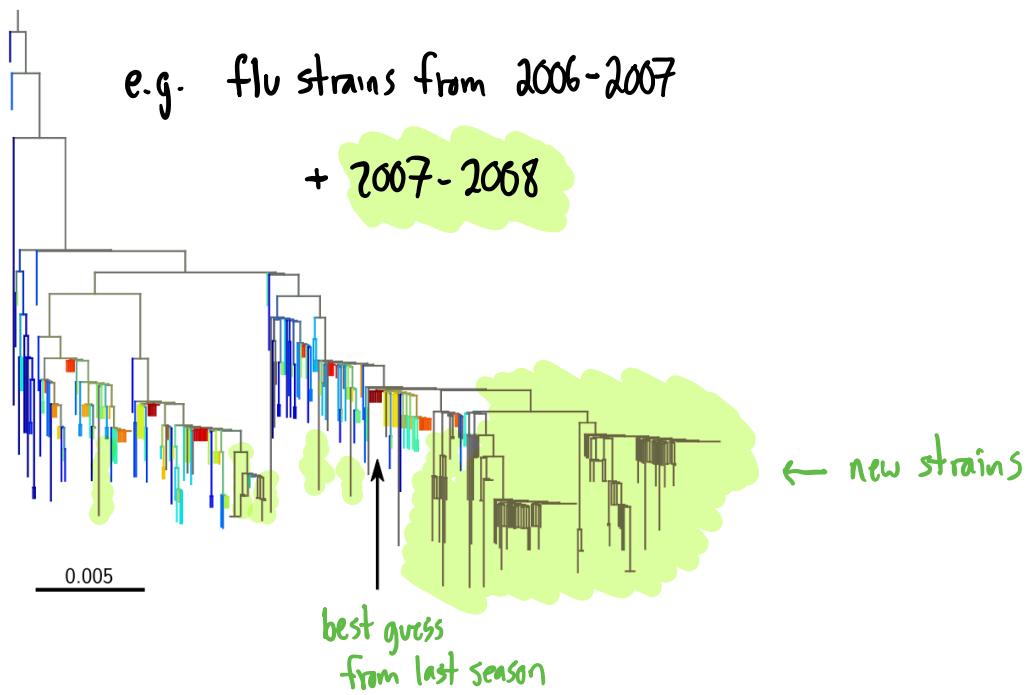
Predicting evolution from the shape of genealogical trees

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

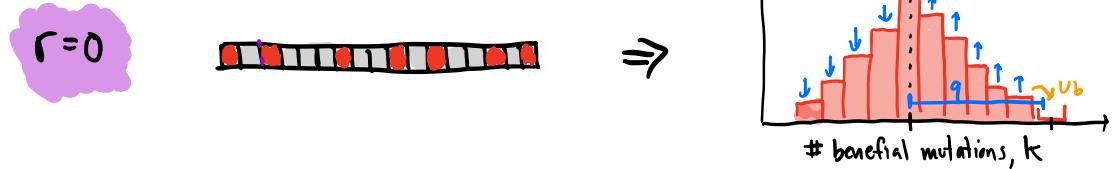
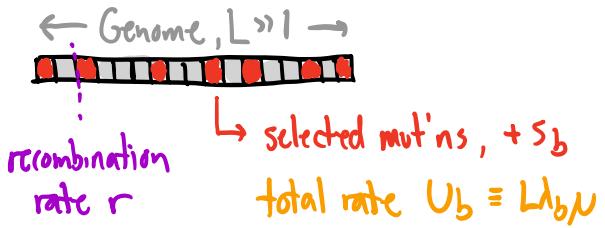
¹Evolutionary Dynamics and Biophysics, Max Planck Institute for Developmental Biology, Tübingen, Germany; ²Department of Veterinary Medicine, University of Cambridge, Cambridge, United Kingdom; ³Kavli Institute for Theoretical Physics, University of California, Santa Barbara, Santa Barbara, United States

\Rightarrow implemented this idea for HA gene in influenza
(data from Problem #1 in Hw1)



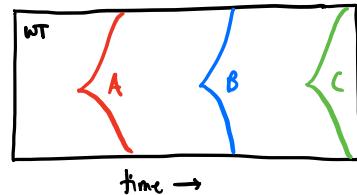


What about recombination?

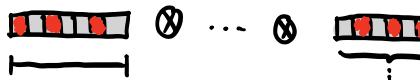


$r \gg N \cdot \mu \lambda_b \cdot s$

$\square \text{---} \square \otimes \cdots \otimes \square \text{---} \square \Rightarrow$



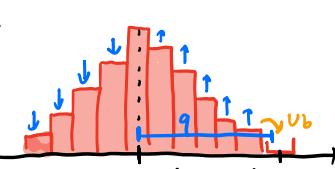
Linkage block ansatz



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

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

\rightarrow



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

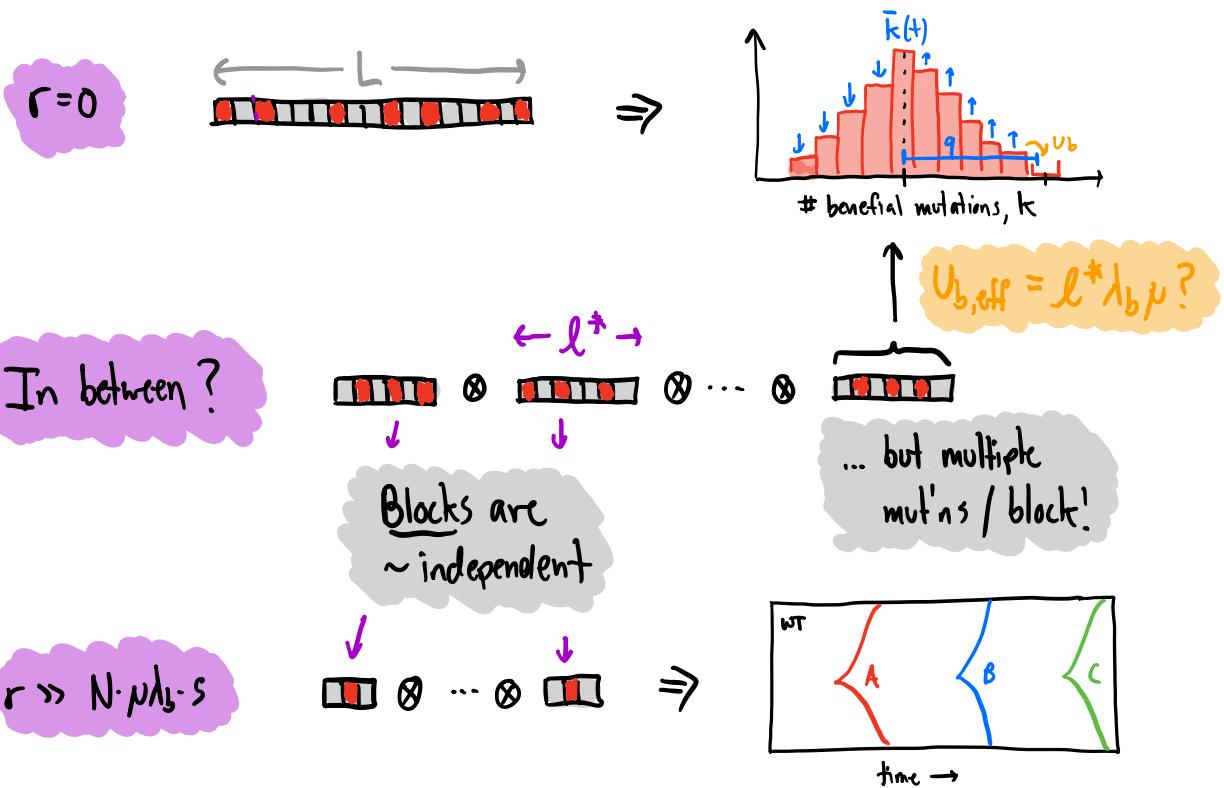
$$\Rightarrow \text{Self consistency: } T_c \sim \frac{1}{S_b} \log\left(\frac{S_b}{\mu \lambda_b} \cdot r T_c\right)$$

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

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

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

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



If true, need:

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

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

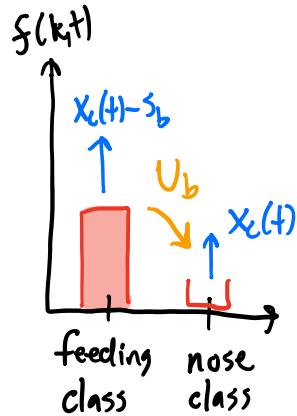
② between blocks, recombination should be frequent!

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

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

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: $U_b f_{q-1}(t) = \frac{U_b}{2Ns_b} e^{\int_0^t (X_c(t') - s_b) dt'}$

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

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

\Rightarrow will be harder because time-varying fitness

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

\Rightarrow 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 $H_f(z, t) = \langle e^{-z \cdot f_1(t)} \rangle$ satisfies the PDE:

$$\frac{\partial H_f}{\partial t} = \left[X_1(t) z - \frac{z^2}{2N} \right] \frac{\partial H_f}{\partial z} - z U_b f_{q-1}(t) H_f$$

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

\Rightarrow can solve w/ method of characteristics:

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

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

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

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

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

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

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

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

where $\frac{dz}{dt} = x_c(t-t')z - \frac{z^2}{2N}, \quad z(0) = z$

\Rightarrow solution for characteristic curve is given by:

(can plug in & check...)

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

$$\text{so } H_f(z, t) = \exp \left[- \int_0^+ \frac{z \cdot u_b f_{q-1}(t-u) e^{\int_0^t x_c(u') du'}}{1 + \frac{z}{2N} \int_u^+ e^{\int_u^{u'} x_c(u'') du''} du'} du \right]$$

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

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

$$\Rightarrow H_v(z, t) \equiv \langle e^{-z \cdot v(t)} \rangle \equiv H_f(2Nq s_b e^{-\int_0^t x_c(t') dt'}, z, t)$$

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

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

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

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

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

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

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

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

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

and hence :

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

(where we have assumed that the click time t_c is $\gg \frac{1}{S_b}$)

\Rightarrow for large q & relevant values of z , this integral will be dominated by times w/in $O(\frac{1}{S_b})$ of τ .

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

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

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

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

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

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

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

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

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

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

\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:

$$f_{\text{nose}}(t) \equiv \sum_{k=1}^{K_{\max}} f_k(t) = \frac{1}{Nqs} e^{qS_b(t-\tau)} \cdot \sum_{k=1}^{K_{\max}} \frac{1}{q} k^{1+\frac{1}{q}}$$

& argued that sum over k converged to ≈ 1 .

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

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

$$\Rightarrow \sum_{k=1}^{K_{\max}} \frac{1}{q} k^{1+\frac{1}{q}} \approx \int_1^{K_{\max}} \frac{dk}{q k^{1+\frac{1}{q}}} = 1 - e^{-\frac{1}{q} \log K_{\max}}$$

Thus, sum converges to 1 provided that

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

\Rightarrow how does this translate to establishment times τ_k ?

recall that $\tau_k - \tau_1 \sim \frac{1}{qS_b} \log(k)$, so condition becomes:

$$\Rightarrow \tau_{k_{\max}} - \tau_1 \sim \frac{1}{qS_b} \log(K_{\max}) \gg \frac{1}{S_b}$$

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

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

\Rightarrow can take $K_{\max} \approx \infty$ 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:

$$f_{\text{nose}}(t) \equiv \frac{\nu}{2Nq_{S_b}} e^{q_{S_b} t} \Rightarrow H_{\nu}(z) \approx e^{-\frac{U_b}{S_b} z^{1-\frac{1}{q}}}$$

(supplement of lecture 19)

Let's fine-grain this further:

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

$$\Rightarrow \text{then } H_{\nu_l}(z) \approx e^{-\frac{U}{S_b} z^{1-\frac{1}{q}}}$$

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

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

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

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

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

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

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

$$\Rightarrow \frac{\partial H_{v_l}}{\partial z} = -\frac{\mu_l}{S_b} (1 - \frac{1}{q}) z^{-\frac{1}{q}} H_{v_l}(z)$$

$$\Rightarrow \frac{\partial^2 H_{V_L}}{\partial z^2} = \frac{1}{q} \frac{N_L}{S_b} \left(1 - \frac{1}{q}\right) z^{-\frac{1}{q}} H_{V_L}(z) + O(N_L^2)$$

so that:

$$\begin{aligned} P_C(z) &= \sum_l \int_0^\infty dz \cdot z \cdot \frac{\partial^2 H_{V_L}(z)}{\partial z^2} \cdot \prod_{l' \neq l} H_{V_{L'}}(z) \\ &= \frac{1}{q} \sum_l \frac{N_L}{S_b} \int_0^\infty dz \frac{N_L}{S_b} \left(1 - \frac{1}{q}\right) z^{-\frac{1}{q}} H_V(z) \stackrel{\text{def}}{=} \prod_l H_{V_L}(z) \\ &= \frac{1}{q} \int_0^\infty -\frac{\partial H_V(z)}{\partial z} = \frac{1}{q} \left[H_V(0) - H_V(\infty) \right] \\ &= \frac{1}{q} \quad \text{as desired} \end{aligned}$$

Can do same thing for larger samples:

$$P_C(n) = \left\langle \sum_l \left(\frac{v_L}{\sum v_L} \right)^n \right\rangle = \sum_l \int_0^\infty dz \cdot \frac{(-1)^n}{\Gamma(n)} \frac{d^n H_{V_L}(z)}{dz^n} \prod_{l' \neq l} H_{V_{L'}}(z)$$

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

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

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

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