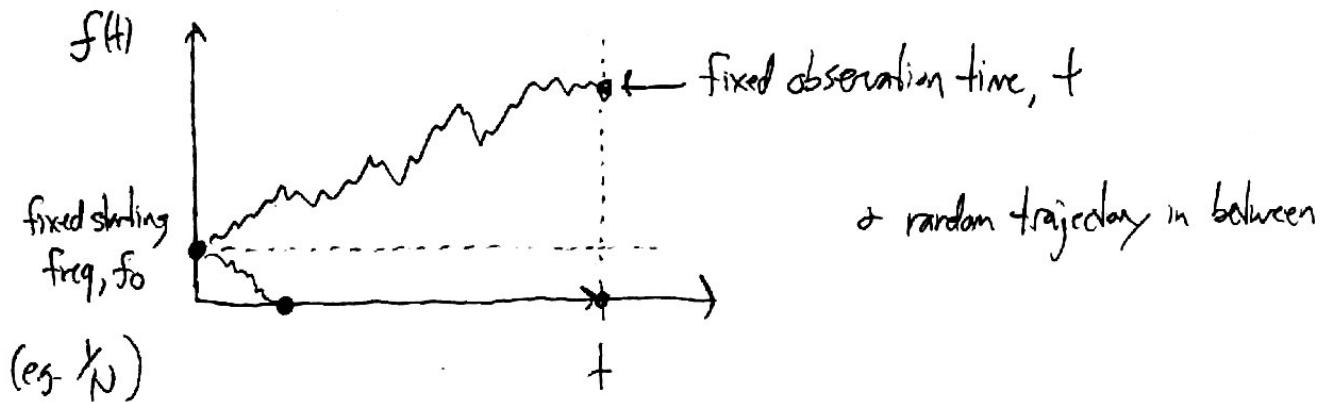


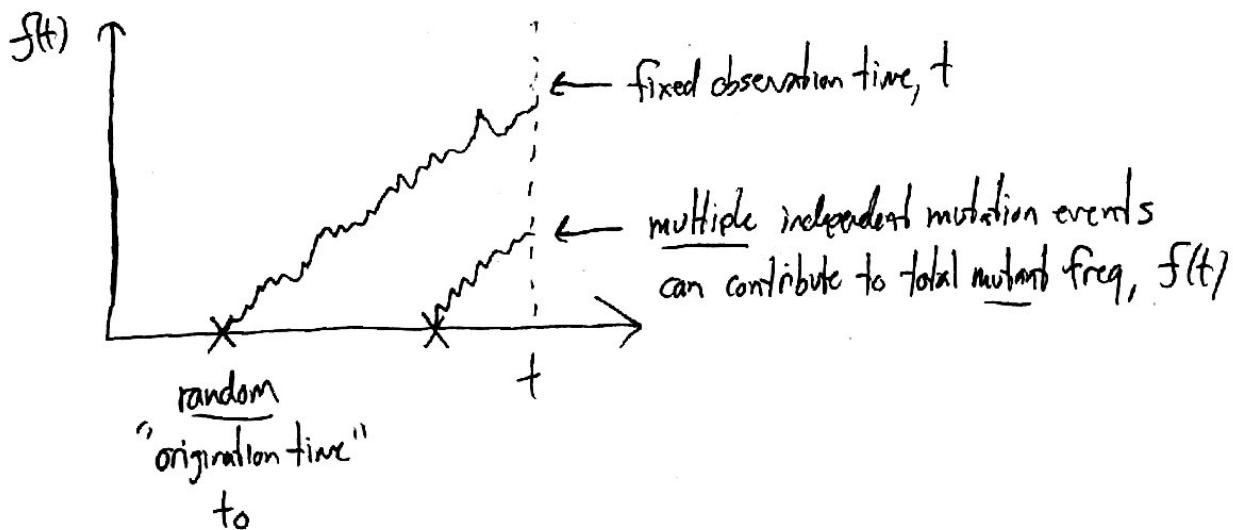
①

Dynamics of Linear Branching Processes II (mutations)

So far, we have focused on scenarios of the form:



in practice, often interested in frequencies of mutant types that arose spontaneously due to random mutation events, whose origination time is not known:



⇒ to understand this case, need to understand B.P. w/ mutations:

$$\frac{df}{dt} = \mu + sf + \sqrt{\frac{f}{N}} \eta(t)$$

(2)

Due to linearity, can also write this process as sum over independent mutation events,

$$f(t) = \int_0^t dt_0 \sum_{i=1}^{\Theta(t_0)} f_i(t | f(t_0) = \frac{1}{N}) = \int_0^t dt_0 \Theta(t_0) \times \left[\frac{1}{\Theta(t_0)} \sum_{i=1}^{\Theta(t_0)} f_i(t | f(t_0) = \frac{1}{N}) \right]$$

where $\Theta(t_0)$ is the (random) # of mutations produced in generation t_0 $[\Theta(t_0) \sim \text{Poisson}(N\nu)]$

and $f_i(t | f(t_0) = \frac{1}{N})$ is random trajectory of mutation event that occurred @ generation t_0 (can predict w/ previous $\nu=0$ results)

e.g. on average,

$$\langle f(t) \rangle = \int_0^t dt_0 \underbrace{\langle \Theta(t_0) \rangle}_{N\nu} \underbrace{\langle f(t | f(t_0) = \frac{1}{N}) \rangle}_{\frac{1}{N} e^{st - 1}} = \frac{\nu}{s} (e^{st} - 1)$$

↓
 same as solving
 $d_t \langle f \rangle = \nu + s \langle f \rangle$

\Rightarrow what about distribution of $f(t)$?

\Rightarrow can again return to generating function, $H(z,t) = \langle e^{-zf(t)} \rangle$

Repeating our derivation for the $\nu=0$ case, we find that $H(z,t)$ satisfies the partial differential equation,

$$\frac{\partial H}{\partial t} = \left[Sz - \frac{z^2}{2\nu} \right] \frac{\partial H}{\partial z} - \underbrace{\nu z H}_{\hookrightarrow \text{new term.}}$$

this time, it will be most interesting to consider an initial condition with no mutant individuals: $H(z,0) = e^{-z \cdot 0} = 1$

this PDE can be solved using the method of characteristics
(actually, a slight variant of what we did before)

can skip to
solution on p. 4
below

In particular, note that if we define the function,

$$\psi(t) \equiv \log H(\underbrace{z^*(t_f-t)}_{\varphi(t)}, t_f - t), \quad \text{where } z^* \text{ is characteristic curve from } \nu=0 \text{ case}$$

then $\psi(t)$ satisfies the ODE

$$\frac{d\psi(t)}{dt} = \nu \varphi(t) \quad \text{w/}$$

$$\begin{aligned}\psi(0) &= \log H(\overbrace{\varphi(0)}^{z_f}, t_f) \\ \psi(t) &= \log H(\varphi(t), 0) = 0\end{aligned}$$

(4)

thus, we have

$$\underline{q}(t) = \underline{q}(0) + \int_0^t \nu \varphi(t') dt' \Rightarrow H(z,t) = e^{-\nu \int_0^t \varphi(t') dt'}$$

or $\log H(z,t)$

plugging in for the characteristic curve, we have:

$$H(z,t) = e^{-\nu \int_0^t \frac{ze^{st'}}{1+\frac{z}{2Ns}(e^{st'}-1)} dt'} = e^{-2N\nu \left[\log \left(1 + \frac{z}{2Ns} (e^{st} - 1) \right) \right]_0^t} = e^{-2N\nu \log \left(1 + \frac{z}{2Ns} (e^{st} - 1) \right)}$$

or

$$H(z,t) = \left(1 + z \cdot \frac{e^{st} - 1}{2Ns} \right)^{-2N\nu}$$

\Rightarrow can recognize as generating function for Gamma distribution w/
shape $\alpha = 2N\nu$ and scale $(e^{st} - 1)/2Ns \equiv s_{\max}$

$$p(s) ds = \frac{1}{\Gamma(2N\nu)} \left(\frac{s}{s_{\max}} \right)^{2N\nu-1} e^{-s/s_{\max}} \left(\frac{ds}{s_{\max}} \right)$$

\hookrightarrow dynamic version of mutation-selection-drift balance

(5)

What does this distribution look like?

From properties of Gamma dist'n, know that

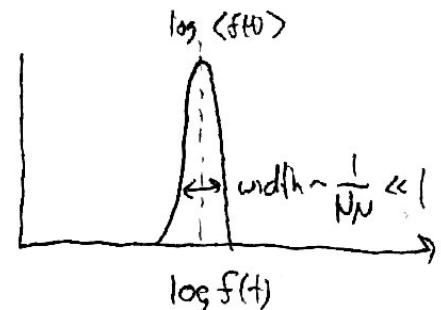
$$\langle f(t) \rangle = \alpha f_{\max} = 2N\mu \cdot \left(\frac{e^{st} - 1}{2Ns} \right) = \frac{\mu}{s} (e^{st} - 1) \quad \begin{bmatrix} \text{same as from} \\ \text{SOE} \end{bmatrix}$$

$$\text{Var}(f(t)) = \alpha f_{\max}^2 = \frac{1}{2N\mu} \langle f(t) \rangle^2 \Rightarrow \boxed{C_V(t) = \frac{1}{2N\mu}} \quad \textcircled{B}$$

\Rightarrow unlike single trajectory, no longer a transition w/ t.

Instead, like equilibrium mut-sel-drift balance, 2 very diff behaviors depend on Nμ

case 1: when $N\mu \gg 1$, dist'n strongly peaked around characteristic value, $\langle f(t) \rangle$:



e.g. for deleterious mutations ($s < 0$)

$$\langle f(t) \rangle = \cancel{\Theta(t_0)} \frac{\mu}{|s|} (1 - e^{-|s|t}) \rightarrow \bar{f} = \frac{\mu}{|s|} \quad \text{"deterministic mut-sel balance"}$$

can understand from integral eq'n:

$$f(t) = \int_0^t dt_0 \Theta(t_0) \times \underbrace{\left[\frac{1}{\Theta(t_0)} \sum_{i=1}^{S(t_0)} f_i(t | f_i(t_0) = 1/N) \right]}_{\{ \}}$$

law of large #s: $\langle S(t_0) \rangle \times \langle f_i(t | f_i(t_0) = 1/N) \rangle = \text{deterministic value}$

$$= N\mu \quad = \frac{1}{N} e^{s(t-t_0)}$$

(6)

can calculate spread w/ perturbative approach:

let $f(t) = \bar{f} + \delta f(t)$ w/ $\delta f(t) \ll \bar{f}$. then plugging into SDE, obtain:

$$\frac{d(\delta f)}{dt} = -|s| \cdot \delta f(t) + \sqrt{\frac{\bar{f}}{N}} \eta(t) \Rightarrow \begin{array}{l} \text{classic physics problem} \\ (\text{Brownian particle in quadratic potential}) \\ \text{w/ } r=|s|, D=\bar{f}/N. \end{array}$$

$$\Rightarrow \text{Var}(\delta f) \sim \sqrt{D} \sim \frac{\bar{f}^2}{N\mu} \quad \checkmark,$$

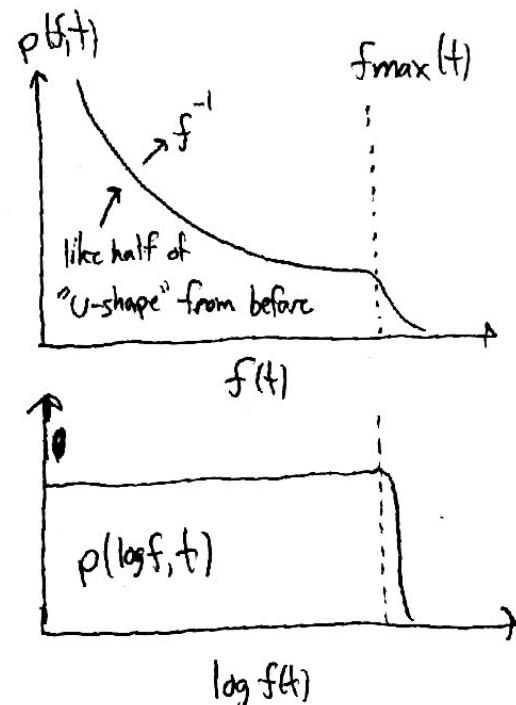
\Rightarrow Note: this general approach (almost) always works when f is close to avg value.
 (might recognize as mean-field theory from stat phys.)

case 2 : In opposite extreme ($N\mu \ll 1$)
 dist'n of f becomes very broad:

$$p(f,t) \approx 2N\mu f^{-1} e^{-f/f_{\max}}$$

\Downarrow or, in log space

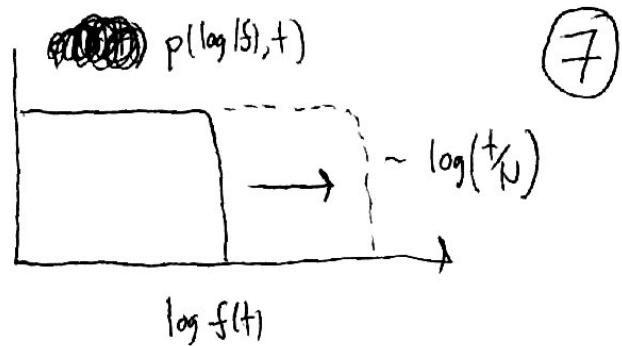
$$p(\log f, t) \approx 2N\mu e^{-e^{\log f/f_{\max}}} \approx 2N\mu \Theta(f_{\max} - f)$$



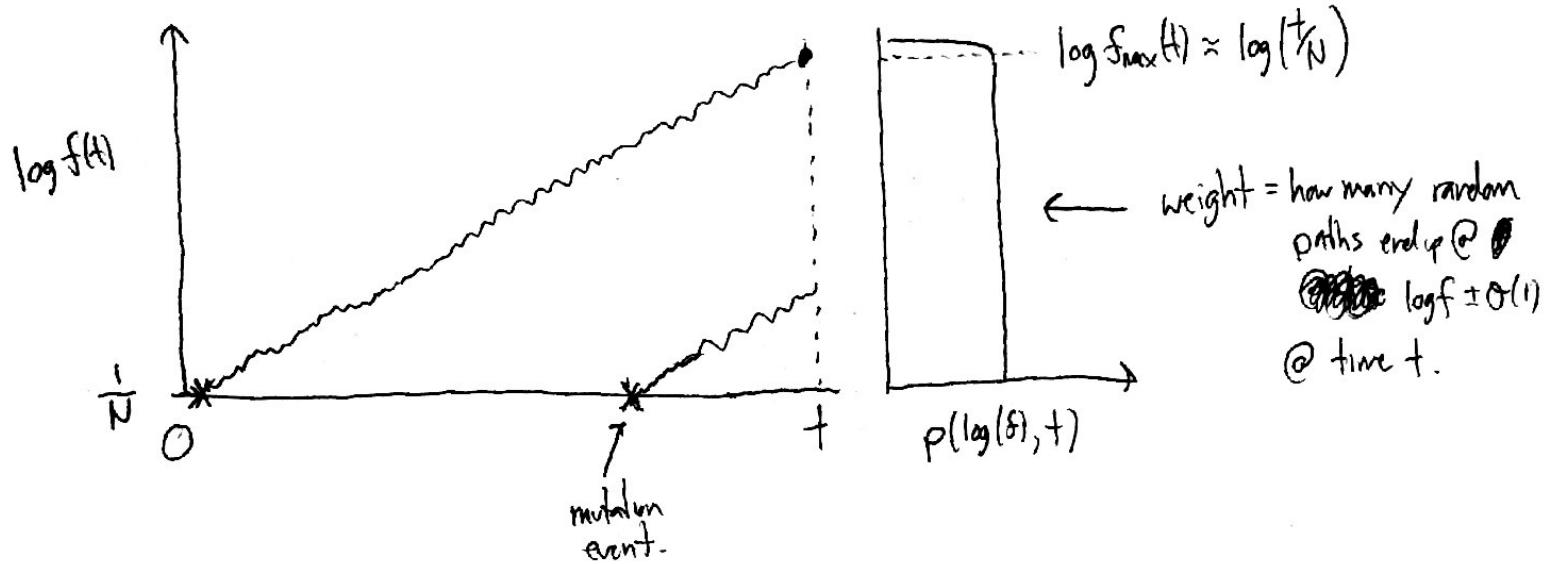
Interpretation: most weight near $f=0$, but w/ prob $\sim N\mu$ considerable chance of observing any order of magnitude between $0 \approx f_{\max}$
 (little chance of $f > f_{\max}$)

e.g. for neutral mutation, $f_{\max}(t) = t/2N$

$$\Rightarrow p(f, t) = \frac{2Nf}{f} e^{-\frac{2Nf}{t}}$$



* can understand dist'n as contribution from @ most 1 random mutation event between 0 and t . Helps to visualize as:



\Rightarrow can see that $f_{\max} \sim t/N$ is largest size mutation could have reached if it occurred @ earliest possible time ($t=0$).

\Rightarrow hence, little probability of seeing $f > f_{\max}$.

\Rightarrow for $f \ll f_{\max}$, we see that to contribute to $\log f \pm \Theta(1)$, must have arisen at least $\sim Nf$ generations earlier, so that there is time to drift from $1/N \rightarrow f$.

~~so for large f, probability of being near f is small, but for small f, probability of being near f is large.~~

what range of times contribute?

\Rightarrow since $f \sim \frac{t}{N} \Rightarrow \log f \pm \Theta(1) \Leftrightarrow \Delta t \sim Nf$

probability of surviving until $t: \sim \frac{1}{Nf}$

\Rightarrow mutations w/ $t_0 < t - Nf$ are much less likely to be alive to contribute to $\log f \pm \Theta(1)$ @ time t .

Putting everything together, have:

$$p(\log f, t) \Delta \log f \approx N\mu \times Nf \times \left(\frac{1}{Nf}\right) = N\mu \checkmark.$$

prob that mutation occurs per gen. prob that mutation occurs in right time window to contribute $t - \log(f) \pm \Theta(1)$ prob that mutation survives long enough to reach $\log f \pm \Theta(1)$ at time t .

\Rightarrow thus, "U"-shape in $p(f, t)$ arises because probability of surviving until $\log f(t) \approx \log f \pm \Theta(1)$ is balanced by larger # of times that can contribute.
origin.

what about selected mutations?

\Rightarrow just like single trajectory, selected mutations indistinguishable from neutral mutations when $t \ll s_1$ (since $s_{\max}(t) \sim \frac{t}{N}$)

(9)

For deleterious mutations ($s < 0$), $f_{\max}(t) \rightarrow \frac{1}{2Ns}$

$$\Rightarrow p(f, t) \rightarrow p(f) = \frac{2Ns}{f} e^{-2Ns/f}$$

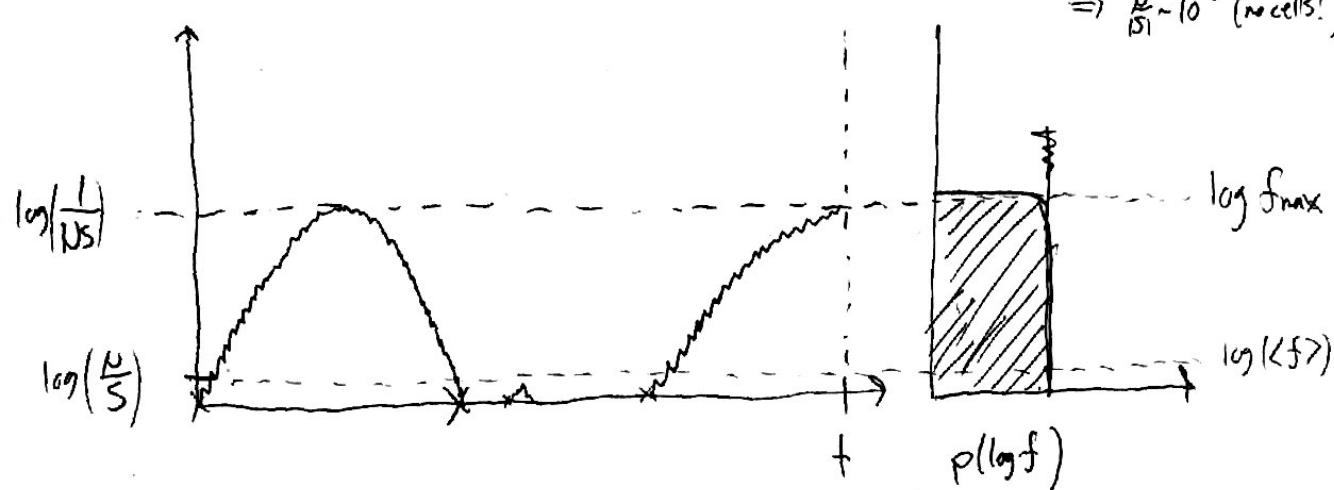
\Rightarrow i.e. mostly zero, but w/ prob $\sim Ns$ chance to grow as large as $\sim 1/2Ns$

\Rightarrow very different than avg!

e.g. ABX resistance mut w/
 $1s \sim 10^2$, $N \sim 10^6$, $Ns \sim 10^{-10}$

$$\Rightarrow \frac{1}{2Ns} \sim 10^{-8} \text{ (no cells!)} \quad \frac{1}{Ns} \sim \frac{1}{10^4} \text{ (100 cells!)}$$

can again visualize w/ paths:

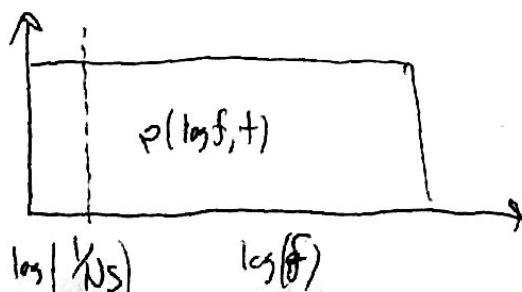


Now mutations can't get much larger than $\frac{1}{2Ns}$, can't survive much larger than \sqrt{Ns}

\Rightarrow mutations can only contribute if they arose in last $\sim \sqrt{Ns}$ gens.

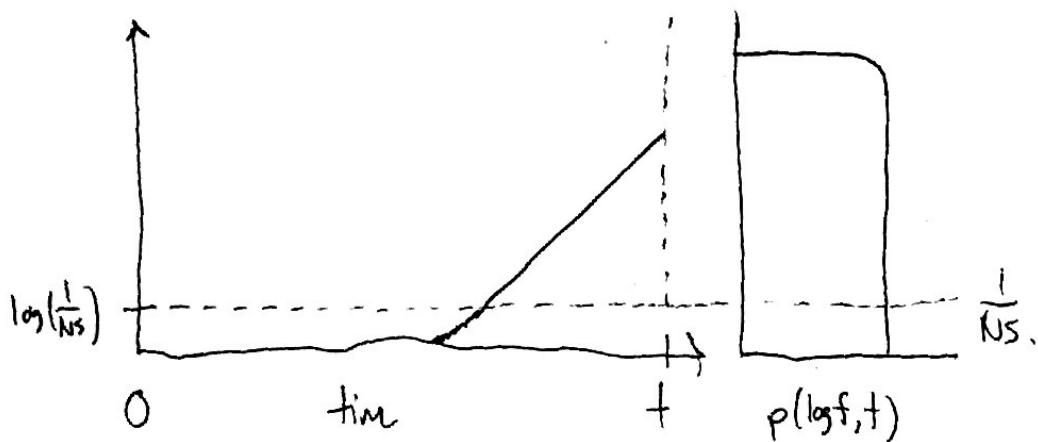
$$\Rightarrow$$
 hence like neutral case w/ $t_{eff} \sim \sqrt{Ns}$

Finally, for beneficial mutations s , $f_{\max}(t) \rightarrow \frac{e^{st}}{2Ns} \gg \frac{1}{Ns}$



\Rightarrow weird... knew that $f(t)$ not drifting when $f \gg 1/Ns$.

can again understand from picture:



mutations grow as $f(t) \sim \frac{1}{NS} e^{S(t-t_0)}$ $\Rightarrow \log f \pm \Theta(1) \Leftrightarrow \Delta t = \frac{1}{S}$

Putting it together: $p(\log f, t) \Delta \log f = N \nu \times (\frac{1}{S}) \times (S) = N \nu \checkmark$

prob that mutation
occurs in right time
window to contribute
to $\log f \pm \Theta(1)$

prob that mutation
survives drift to
reach $\log f \pm \Theta(1)$

\Rightarrow same as neutral dist'n, but very different reason underneath.

\Rightarrow differences become important when considering full path, $f(t)$.

\Rightarrow path of beneficial mutation \approx deterministic once $f(t) \gg \frac{1}{NS}$ -

i.e. for large t , expect to capture all randomness in single #,

$$f(t) = \nu e^{St} \quad (\text{just like } \mu=0 \text{ case})$$

\Rightarrow Find $\nu \sim \text{Gamma}(2N\nu, \frac{1}{2NS})$ for $t \gg 1/S$. (^{independent} of time ✓)

Often helpful to rewrite ν as a time, $f(t) = \frac{1}{2Ns} e^{s(t-\tau_{\text{est}})}$

$$\text{or } \tau_{\text{est}} = \frac{1}{s} \log\left(\frac{1}{2Ns\nu}\right)$$

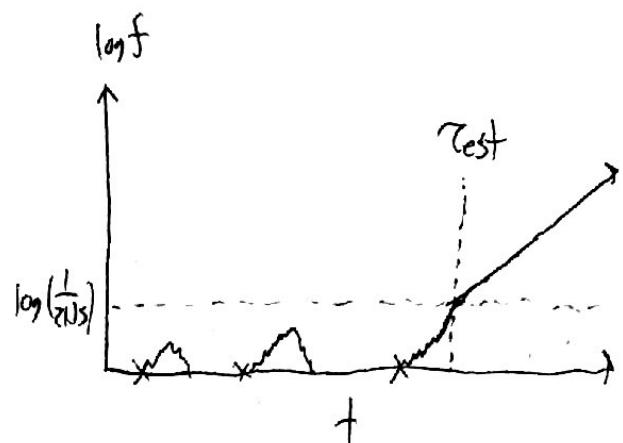
* this is known as establishment time.

\Rightarrow intuitively, it's the time that

$$f(t) \text{ would have reached } \frac{1}{2Ns} \text{ if it}$$

grew deterministically the whole time.

(i.e. roughly time that mutation arose + survived drift)



\Rightarrow can show that when $N\nu \ll 1 \Rightarrow \tau_{\text{est}} \sim \text{Exponential}\left(\frac{1}{2N\nu s}\right) \pm O\left(\frac{1}{s}\right)$

Has simple interpretation: mutations occur @ rate $N\nu$ per gen
+ survive drift w/ prob $\sim s$.

\Rightarrow successful mutations occur as Poisson process
w/ rate $\sim N\nu s$.

\Rightarrow "limited by supply of new mutations" (i.e. increasing N or ν by const factor)
decreases τ_{est} by same amount

\Rightarrow same picture also helps us understand behavior when $N\nu \gg 1$. \downarrow rate \checkmark time window to contribute

\Rightarrow in this case, $\sim N\nu$ establishment events contribute to ν^* ($2Ns \times \frac{1}{s} = 2Ns$)

each w/ typical size $\sim \frac{1}{Ns} e^{\tau_{\text{est}}}$.

(17)

in this case, have $T_{\text{est}} = -\frac{1}{S} \log(N\nu) \pm O\left(\frac{1}{\sqrt{N\nu}}\right)$
 (deterministic and negative)

\Rightarrow negative because multiple mutation events contribute. initially grows much faster than e^s

\Rightarrow time it takes mutation to reach $f=1/2$ is $t_{1/2} \sim \frac{1}{S} \log\left(\frac{N}{\nu}\right)$

(independent of N , weakly dependent on $\nu \Rightarrow$ limited mainly by strength of selection)

compare to $N\nu \ll 1$ case:

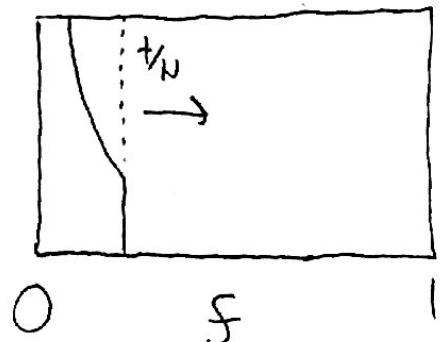
$$t_{1/2} \sim \text{Exponential}\left(\frac{1}{N\nu s}\right) + \frac{1}{S} \log(Ns) \sim \frac{1}{N\nu s} \quad (N\nu \ll 1/\log(Ns))$$

Finally, can use our new found knowledge to understand what was going on w/ "U"-shaped stationary dist'n from full single-locus model:

$$p(f) \propto f^{2N\nu-1} (1-f)^{2N\nu-1} e^{-2NsF} \xrightarrow{s=0} f^{N\nu-1} (1-f)^{N\nu-1}$$

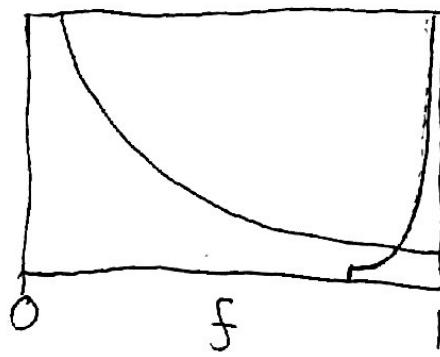
so far neutral mutations ($s=0$), movie is following: (13)

(1)



Need $t \sim N$ generations for left ~~left~~ half ~~right~~ of "U-shape" to form from forward mutations from $f=0$.

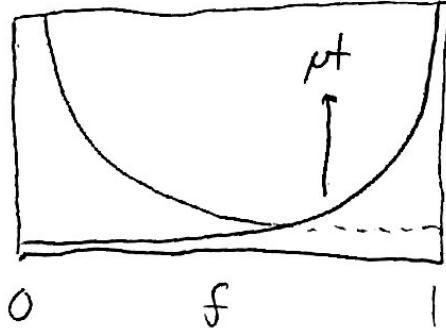
(2)



Now chance for ~~left~~ right half of "U-shape" to form from back-mutations from $f=1$

↳ but initially, ~~is~~ height of right half is small
(since low probability to reach $f=1$)

(3)



Rate that mutations reach $f=1$ from $f=0$ is

$$N\mu \times \left(\frac{1}{N}\right) = \mu \Rightarrow \text{need } t_{eq} \sim \frac{1}{\mu} \text{ generations}$$

before $f=0$ & $f=1$ are equally likely.

* this time scale is super long! e.g. humans $\sim \mu = 10^{-8}$

so $t_{eq} \sim 10^8$ generations \Rightarrow ~~>~~ > 1 billion years (way longer than time since human-chimp split)

~~most recent common ancestor~~

most recent common ancestor of humans lived $< 10^6$ years ago
so not enough time for human pop to reach stationary dist'n.

Later we will see that this is true more generally:

when $N \ll \tau$, never enough time for neutral stationary dist'n to equilibrate in time since common ancestor of population.

\Rightarrow instead, more relevant dist'n is quasi-stationary dist'n:

$$p(f) \approx \frac{2N\mu}{f} \quad (\text{valid for } s=0, \tau \gg N, \mu \ll \gamma_\mu)$$

compare to strongly deleterious case,

$$p(f) \approx \frac{2N\mu}{f} e^{-2Ns/f} \quad \text{valid for } Ns \gg 1, \tau \gg \gamma_{|s|}$$