

Chapter 7

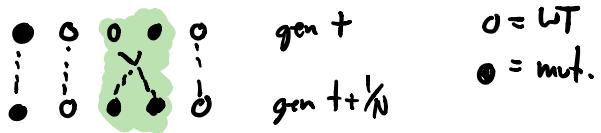
Dynamics of linear branching processes

The previous chapter showed that some of the most interesting dynamics of a new mutation occur while it is still at a low frequency in the population ($f \ll 1$). In this limit, the single-locus model in Eq. (6.1) reduces to the linear SDE,

$$\frac{\partial f}{\partial t} = \underbrace{sf}_{\text{selection}} + \underbrace{\mu - \nu f}_{\text{mutation}} + \underbrace{\sqrt{\frac{f}{N}} \cdot \eta(t)}_{\text{genetic drift}} \quad (7.1)$$

also known as a *linear branching process*.¹ The reasons for this linear behavior can be motivated by revisiting the microscopic Moran model from Chapter 5. When $f \ll 1$, most competitions involving the mutant occur against a wildtype individual, simply because the number of such pairs ($f \cdot 1$) is much larger than the number of mutant-mutant pairs ($f \cdot f \ll f \cdot 1$):

¹Technically, it is a continuous-time, continuous-state branching process. Other versions exist that discretize the time and/or frequency dimensions. You will analyze one such example in Problem X of HW Y.



This suggests that selection and genetic drift can be approximated by assuming that the mutant is growing in an environment consisting *solely* of wildtype individuals. The descendants of any two mutant individuals must be independent in such a scenario, and the only way that this can occur is if the selection and drift terms in the SDE are linear functions of $f(t)$.

The independence assumption will clearly break down when the mutant reaches higher frequencies (e.g. 50%). For example, correlations between individuals are eventually critical for ensuring that the mutant frequency cannot exceed 100%. The linear model in Eq. (7.1), by contrast, allows the “frequency” to diverge to infinity. This unboundedness will not be an important feature for us here — we will always make sure to switch back to the full model in Eq. (6.1) long before the mutation reaches 50% frequency (see Section 7.3).

When the independence assumption is satisfied, the linear nature of Eq. (6.1) is simple enough that we will be able to gain a nearly complete picture of the **temporal dynamics** of mutations, in addition to the long-time limits (e.g. fixation probabilities and stationary distributions) that we explored Chapter 6. Understanding these dynamics will turn out to give us lots of useful intuition for thinking about evolutionary problems, and they will provide a natural starting point when we go on to consider more complicated scenarios later in the course. These temporal dynamics are also increasingly relevant for analyzing longitudinal data (e.g. ancient DNA, genomic surveillance of pathogens, laboratory evolution experiments, etc.), so a detailed understanding of this case will have useful practical benefits as well.

7.1 Dynamics of the mean and variance

For simplicity, we will first consider the case with no mutations ($\mu = \nu = 0$), where Eq. (7.1) reduces to

$$\frac{\partial f}{\partial t} = \underbrace{sf}_{\text{selection}} + \underbrace{\sqrt{\frac{f}{N}} \cdot \eta(t)}_{\text{genetic drift}}. \quad (7.2)$$

Since the selection term is now a linear function of $f(t)$, the moment equations no longer suffer from the “moment hell” that plagued our original model in Chapter 6. The mean frequency now satisfies the deterministic dynamics,

$$\frac{\partial \langle f(t) \rangle}{\partial t} = s \langle f(t) \rangle, \quad (7.3)$$

whose solution is a simple exponential growth function,

$$\langle f(t) \rangle = f_0 e^{st}. \quad (7.4)$$

Similar results can be obtained for higher moments as well. Repeating the steps in Chapter 6, one can show that the second moment now satisfies,

$$\frac{\partial \langle f(t)^2 \rangle}{\partial t} = 2s \langle f(t)^2 \rangle + \frac{\langle f(t) \rangle}{N} \quad (7.5)$$

Since the mean is given by Eq. (7.4), we can integrate this linear ODE to obtain

$$\langle f(t)^2 \rangle = f_0^2 e^{2st} + \frac{f_0 e^{st} (e^{st} - 1)}{Ns}. \quad (7.6)$$

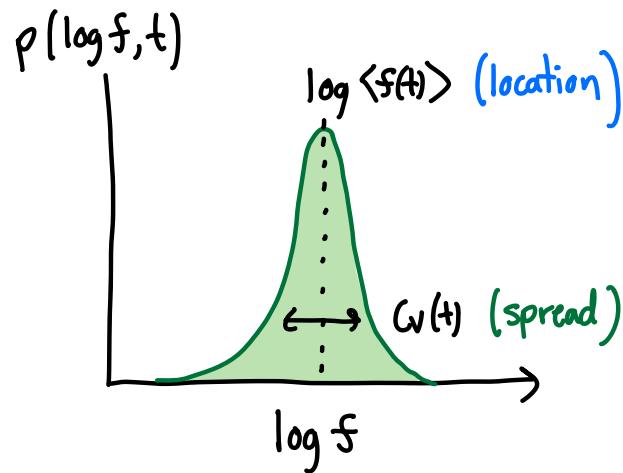
The first term corresponds to the deterministic expectation, $\langle f(t)^2 \rangle \approx \langle f(t) \rangle^2$, while the second term is a new contribution due to genetic drift. It will be useful to express this result in terms of the **coefficient of variation (CV)**,

$$c_V^2(t) \equiv \frac{\text{Var}(f(t))}{\langle f(t) \rangle^2} = \frac{1 - e^{-st}}{Ns f_0}, \quad (7.7)$$

The coefficient of variation is useful for visualizing the spread of a distribution in log space (i.e. how uncertain are we at an order-of-magnitude level). For example, for a “Case 1” distribution with $x = \langle x \rangle \pm \sigma$, we have

$$\log x = \log (\langle x \rangle \pm \sigma) \approx \log \langle x \rangle \pm c_V \quad (7.8)$$

when $c_V \ll 1$. When the coefficient of variation starts to exceed one, the average becomes a poor approximation for actual value of the mutation frequency.



The coefficient of variation in Eq. (7.7) starts out with $c_V(0) \approx 0$, since we have assumed that the mutation begins at a fixed initial frequency. The behavior at later times strongly depends on the relative values of N , s , and f_0 :

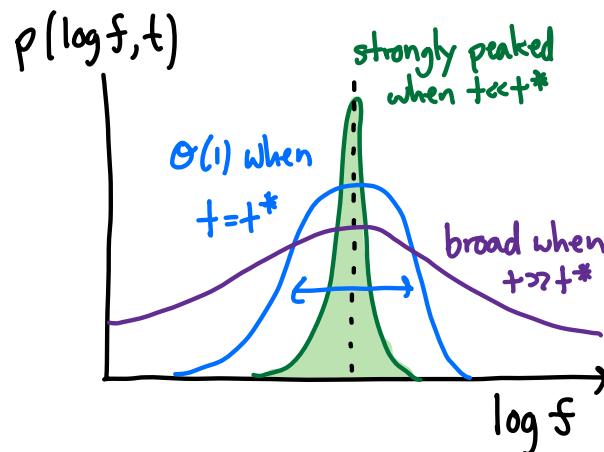
Case 1. For a positively selected mutation ($s > 0$), the coefficient of variation is bounded by its long-term value,

$$c_V^2(t) \leq \frac{1}{Ns f_0} \quad (7.9)$$

Thus, if the mutation starts out in the selection-dominated region of frequency space ($f_0 \gg 1/2Ns$), then coefficient of variation will remain small at all later

times [$c_V(t) \ll 1$]. This implies that the frequency of the mutation will be well-approximated by its average value, $\langle f(t) \rangle = f_0 e^{st}$ (i.e. the distribution will be of the “Case 1” form from Chapter 2). These results are consistent with our fixation probability calculation from Chapter 6, which showed that beneficial mutations are guaranteed to fix when $f_0 \gg 1/2Ns$.

Case 2. In contrast, when a beneficial mutation starts out in the drift-dominated region of frequency space ($f_0 \ll 1/2Ns$), its coefficient of variation will initially be very small [$c_V(t) \ll 1$], but it will eventually reach a point where $c_V(t) \gg 1$. Similar behavior will occur for neutral or deleterious mutations. The location of this transition can be defined by the critical time t^* where $c_V(t^*) \approx 1$.



Solving for t^* yields

$$t^* \approx \begin{cases} Nf_0 & \text{if } f_0 \ll 1/N|s|, \\ \frac{1}{|s|} \log(N|s|f_0) & \text{if } s < 0 \text{ and } f_0 \gg 1/N|s|, \\ \infty & \text{if } s > 0 \text{ and } f_0 \gg 1/Ns. \end{cases} \quad (7.10)$$

When $t \ll t^*$, the coefficient of variation is very small [$c_V(t) \ll 1$], and the frequency of the mutation can be well-approximated by its average value,

$\langle f(t) \rangle = f_0 e^{st}$. In contrast, when $t \gtrsim t^*$, the distribution of $f(t)$ will become extremely broad, and will approach a “Case 2” form whose properties we will derive below.

7.2 Solving for the full distribution

One of the most useful features of the branching process model in Eq. (7.2) is that it allows us to solve for the full distribution of $f(t)$. We could in principle do this by solving the Fokker-Planck equation,

$$\frac{\partial p(f, t)}{\partial t} = -\frac{\partial}{\partial f} [sf p(f, t)] + \frac{\partial^2}{\partial f^2} \left[\frac{f}{N} \cdot p(f, t) \right], \quad (7.11)$$

but the second derivative on the right-hand side makes this a difficult task (see the Appendix of Chapter 6). In this case, it will be much easier to work with the moment generating function of $f(t)$:

$$H(z, t) \equiv \langle e^{-zf(t)} \rangle \equiv \int e^{-zf} p(f, t) df, \quad (7.12)$$

which is governed by an analogous PDE,

$$\frac{\partial H}{\partial t} = \left[sz - \frac{z^2}{2N} \right] \frac{\partial H}{\partial z}. \quad (7.13)$$

subject to the initial condition $H(z, 0) = e^{-zf_0}$. The main difference from our original model in Eq. (6.47) is that the branching process version contains only a single z derivative. PDEs of this form can be solved using a technique known as the *method of characteristics*, which is a generalization of the trick that we used to solve for the fixation probability in Chapter 6. The details of this derivation are presented in the Appendix at the end of the chapter. For now, we will simply quote the final solution,

$$H(z, t) = \exp \left[\frac{-zf_0 e^{st}}{1 + \frac{z}{2Ns} (e^{st} - 1)} \right]. \quad (7.14)$$

Formally, it is possible to invert this expression to obtain the corresponding probability distribution $p(f, t)$. However, the details are somewhat complicated, and the resulting expressions can be difficult to interpret in the general case.² Instead, we will see that one can actually learn a lot about $p(f, t)$ by examining the generating function $H(z, t)$ directly.

For example, using our results for the mean and variance above, we can rewrite $H(z, t)$ in the convenient form,

$$H(z, t) = \exp \left[\frac{-z\langle f(t) \rangle}{1 + z\langle f(t) \rangle \cdot \frac{c_V^2(t)}{2}} \right] \quad (7.15)$$

By comparing this result to the generating function for a Gaussian random variable (Chapter 2),

$$\langle e^{-zx} \rangle = e^{-z\langle x \rangle + z^2\langle x \rangle^2 \cdot \frac{c_V^2}{2}} \quad (7.16)$$

we can see that $f(t)$ is *not* normally distributed in general, but becomes approximately normally distributed in the limit that $c_V(t) \ll 1$. Our results in Eq. (7.7) show that this will be a good approximation at short times, but it will eventually break down for $t \gtrsim t^*$ in Eq. (7.10), when $c_V(t) \gtrsim 1$. What can we say about the distribution of $f(t)$ in these cases?

Extinction and survival probabilities

When the variation in $f(t)$ is as large as its mean [$c_V(t) \gtrsim 1$], we must consider the possibility that the mutant has gone extinct [$f(t) = 0$]. The probability of this event can also be easily extracted from the generating function in Eq. (7.14). Recalling the definition of the generating function,

$$H(z, t) \equiv \int e^{-zf} p(f, t) df \quad (7.17)$$

²The details of this inversion are presented in an appendix at the end of this chapter.

we can see that the exponential factor acts like a crude version of a step function, approaching a uniform value for $f \ll 1/z$, and excluding contributions from frequencies with $f \gg 1/z$. In the extreme limit where $z \rightarrow \infty$, the only values of f that will contribute to the generating function integral are those with $f = 0$; all of the nonzero frequencies will have $e^{-zf} \rightarrow 0$. This implies that

$$\lim_{z \rightarrow \infty} H(z, t) = 1 \cdot p_{\text{ext}}(t) + 0 \cdot [1 - p_{\text{ext}}(t)] = p_{\text{ext}}(t) \quad (7.18)$$

where $p_{\text{ext}}(t)$ is the **time-dependent extinction probability** of the mutation (i.e., the probability that it has gone extinct by time t). Using our expression for $H(z, t)$ in Eq. (7.14), we find that

$$p_{\text{ext}}(t) = \exp \left[\frac{-2Ns f_0}{e^{st} - 1} \right] = \exp \left[\frac{-2}{c_V^2(t)} \right]. \quad (7.19)$$

We can also define a corresponding **survival probability**

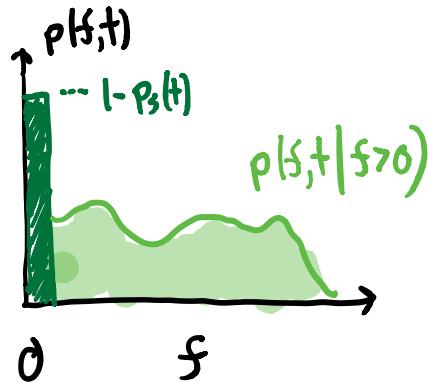
$$p_s(t) = 1 - p_{\text{ext}}(t) = 1 - \exp \left[\frac{-2Ns f_0}{1 - e^{-st}} \right], \quad (7.20)$$

which denotes the probability that the mutant is still alive at time t .

These expressions show that the extinction and survival probabilities are intimately connected to the coefficient of variation in Eq. (7.7). At early times ($t \ll t^*$), the coefficient of variation is very small [$c_V(t) \ll 1$], so there is a negligible chance of extinction (i.e., the survival probability is close to 100%). However, once $c_V(t) \gtrsim 1$, there is a decent chance that the mutant has now gone extinct. This implies that the crossover time t^* in Eq. (7.10) can also be interpreted as a characteristic **extinction time** — i.e. the time at which the survival probability starts to drop below 100%. For a beneficial mutation that starts out in the selection-dominated regime ($f_0 \gg 1/2Ns$), the survival probability in Eq. (7.20) remains close to 100% at all later times. In all other cases, the survival probability will eventually become very small [$p_s(t) \ll 1$], and there is a large chance that the mutant has gone extinct.

Conditioning on non-extinction

Our results above suggest that when $t \gtrsim t^*$, the distribution of $f(t)$ will approach a “Case 2” form that contains a mixture of two different types of mutation trajectories: (i) **extinct paths**, which have $f(t) = 0$, and (ii) **non-extinct paths** where $f(t) > 0$.



We can formalize this idea by writing $p(f, t)$ as a mixture of two components,

$$p(f, t) = \underbrace{[1 - p_s(t)] \delta(f)}_{\text{extinct paths}} + \underbrace{p_s(t) \cdot p(f, t | f > 0)}_{\text{non-extinct paths}} \quad (7.21)$$

where $p(f, t | f > 0)$ denotes the **conditional distribution** of $f(t)$, given that it has survived for a time t . Since $p_s(t)$ is known, this conditional distribution contains all the non-trivial features of the full distribution $p(f, t)$. What can we learn about the frequencies of these surviving lineages?

One of the simplest things we can do is look at the mean of $p(f, t | f > 0)$. Multiplying both sides of Eq. (7.21) by f and integrating, we find that

$$\langle f(t) \rangle = \underbrace{[1 - p_s(t)] \cdot 0}_{\text{extinct paths}} + \underbrace{\langle f(t) | f > 0 \rangle \cdot p_s(t)}_{\text{non-extinct paths}}, \quad (7.22)$$

where $\langle f(t) | f > 0 \rangle$ denotes the **conditional average** of $f(t)$, given that it is alive at time t . We can rearrange this equation to obtain a formula for the

conditional mean as a function of $\langle f(t) \rangle$ and $p_s(t)$:

$$\langle f(t) | f > 0 \rangle = \frac{\langle f(t) \rangle}{p_s(t)} \approx \begin{cases} f_0 e^{st} & \text{if } t \ll t^*, \\ \frac{e^{st}-1}{2Ns} & \text{if } t \gg t^*. \end{cases} \quad (7.23)$$

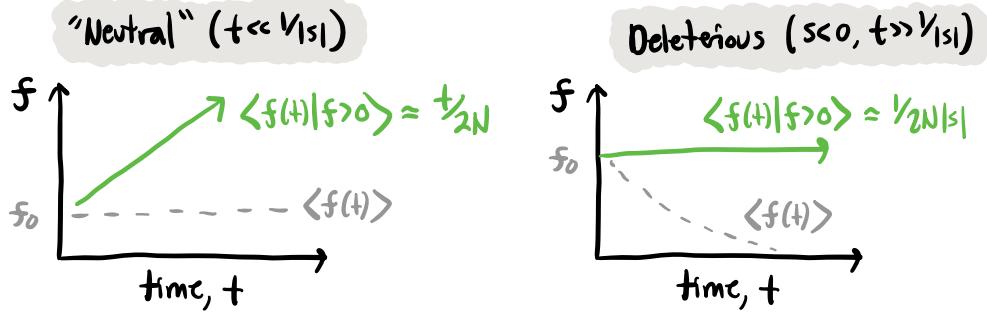
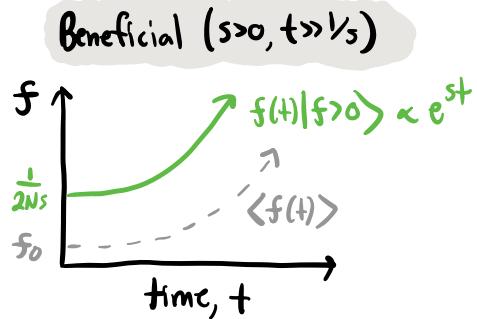
At short times ($t \ll t^*$), the survival probability remains close to 100%, and the conditional mean stays close to the unconditional average, $\langle f(t) \rangle = f_0 e^{st}$. In contrast, when the time starts to exceed the characteristic extinction time ($t \gg t^*$), the average frequency of a surviving lineage becomes much larger than $\langle f(t) \rangle$, since a large fraction of the lineages will have gone extinct.

In this latter case, the conditional mean follows a qualitatively different trajectory than the deterministic expectation $f_0 e^{st}$. In particular, the average frequency of a surviving lineage becomes independent of f_0 . This initial frequency plays a crucial role in determining the survival probability of the mutation. But provided that it survives, its average frequency will lose all memory of where it started. We can gain some additional insight into this behavior by splitting Eq. (7.23) into three different cases depending on the relative values of s and t :

$$\langle f(t) | f > 0 \rangle \xrightarrow{t \gg t^*} \begin{cases} \frac{1}{2Ns} \cdot e^{st} & \text{if } s > 0 \text{ and } t \gg 1/s, \\ \frac{t}{2N} & \text{if } t \ll 1/|s|, \\ \frac{1}{2N|s|} & \text{if } s < 0 \text{ and } t \gg 1/|s|. \end{cases} \quad (7.24)$$

These three cases show that

1. Surviving beneficial mutations (eventually) grow exponentially with time, but with a different pre-factor compared to the deterministic expectation:
2. Beneficial and deleterious mutations look like neutral mutations on short timescales ($t^* \ll t \ll 1/|s|$). The frequencies of these mutations grow linearly with time, as opposed to the constant value we would expect in the absence of noise:
3. At longer times, deleterious mutations eventually saturate at a constant value, rather than declining exponentially with time.



The corresponding survival probabilities in each of these three cases are given by

$$p_s(t) \xrightarrow{t \gg t^*} \begin{cases} 2Ns f_0 & \text{if } s > 0 \text{ and } t \gg 1/s, \\ 2N f_0 / t & \text{if } t \ll 1/|s|, \\ 2N|s| f_0 e^{-st} & \text{if } s < 0 \text{ and } t \gg 1/|s|. \end{cases} \quad (7.25)$$

We can see that in each case, the survival probability and conditional mean are perfectly set up so that their product is equal to the unconditioned average $\langle f(t) \rangle$.

We can use a similar argument to calculate the full conditional distribution $p(f, t | f > 0)$. This is easiest to do by going through the generating function $H(z, t)$. Multiplying both sides of Eq. (7.21) by e^{-zf} and integrating, we find that

$$H(z, t) = \underbrace{[1 - p_s(t)] \cdot e^{-z \cdot 0}}_{\text{extinct paths}} + \underbrace{p_s(t) \cdot H(z, t | f > 0)}_{\text{surviving paths}}, \quad (7.26)$$

where we have defined the *conditional generating function*,

$$H(z, t|f > 0) = \int e^{-zf} p(f, t|f > 0) df. \quad (7.27)$$

We can rearrange this equation to obtain a formula for $H(z, t|f > 0)$:

$$H(z, t|f > 0) = \frac{H(z, t) - [1 - p_s(t)]}{p_s(t)} = \frac{e^{\frac{-z\langle f(t) \rangle}{1+z\langle f(t) \rangle c_V^2(t)}} - e^{-\frac{2}{c_V^2(t)}}}{1 - e^{-\frac{2}{c_V^2(t)}}}. \quad (7.28)$$

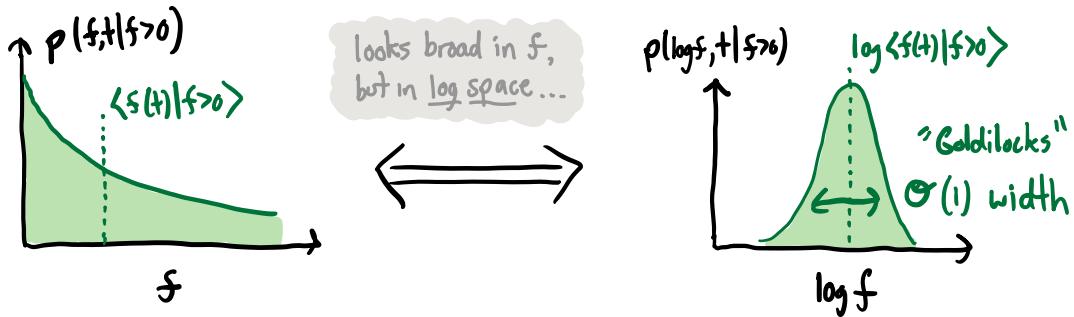
We can simplify this expression by noting that the argument of the first exponential is maximized when $z = \infty$, where $H(z, t) = e^{-2/c_V^2(t)}$. Thus, in the long time limit ($t \gg t^*$) where $c_V(t) \gg 1$, we can Taylor expand each of the exponential terms in Eq. (7.28) to obtain

$$H(z, t|f > 0) \xrightarrow{t \gg t^*} \frac{\left(1 - \frac{z\langle f \rangle}{1+z\langle f \rangle \frac{c_V^2}{2}}\right) - \left(1 - \frac{2}{c_V^2}\right)}{1 - \left(1 - \frac{2}{c_V^2}\right)} = \frac{1}{1 + z \cdot \langle f(t) | f > 0 \rangle}, \quad (7.29)$$

where we have used the fact that $\langle f(t) | f > 0 \rangle \approx 2\langle f(t) \rangle / c_V^2(t)$. By the “*method of Wikipedia*”, we can see that this is the generating function for an exponential distribution with a mean equal to $\langle f(t) | f > 0 \rangle$:

$$p(f, t|f > 0) = \frac{e^{-f/\langle f(t) | f > 0 \rangle}}{\langle f(t) | f > 0 \rangle}. \quad (7.30)$$

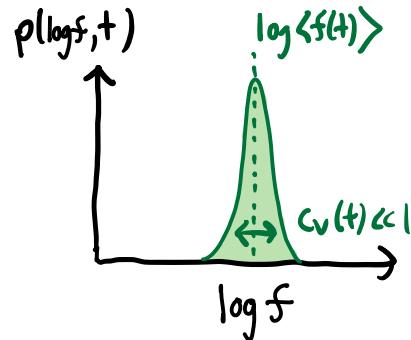
The exponential distribution occupies an intermediate zone between the “Case 1” and “Case 2” distributions in Chapter 2. While it may look broadly distributed when we plot it on a linear scale, if we plot it in terms of $\log f$, we see that most of its probability is concentrated within one order of magnitude of the mean.



We can therefore think of the exponential distribution as a “*Goldilocks case*” where the mean is a *reasonable* summary of the typical behavior [i.e. one that is accurate up to an $\mathcal{O}(1)$ pre-factor].

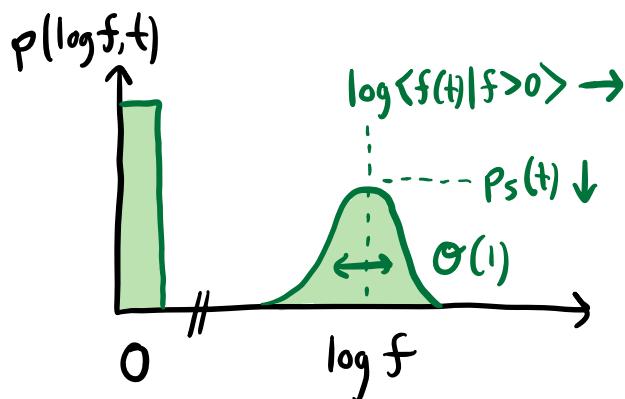
Putting everything together, we can conclude that the temporal dynamics of $p(f, t)$ can be divided into two characteristic regimes:

- **Case I:** At short times ($t \ll t^*$), the distribution of $f(t)$ will be strongly peaked around its deterministic expectation $\langle f(t) \rangle = f_0 e^{st}$, with Gaussian fluctuations of size $\pm \langle f(t) \rangle \cdot c_V(t)$.



For a mutation that starts at a frequency $f_0 \ll 1/2N|s|$, this initial phase will last for $t^* \sim Nf_0$ generations, and the mean and variance are given by $f_0 \pm f_0 t/N$.

- **Case 2:** At longer times ($t \gg t^*$), the distribution of $f(t)$ will split into a bimodal shape, with a large fraction of mutations going extinct ($f = 0$). The surviving mutations will follow an exponential distribution, whose average size marches toward higher frequencies according to the conditional mean $\langle f(t) | f > 0 \rangle$ in Eq. (7.23).



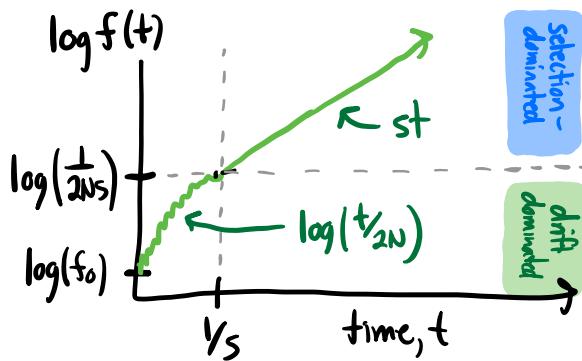
This leads to several interesting conclusions:

1. At intermediate times ($t^* \ll t \ll 1/|s|$), the distribution of $f(t)$ is *indistinguishable* from that of a neutral mutation, even when $N|s| \gg 1$. This shows that our previous deduction from the fixation probability in Chapter 6 extends to the full dynamics of $f(t)$ as well.
2. On these intermediate timescales ($t^* \ll t \ll 1/|s|$), the typical frequencies of the surviving mutations grow linearly in time,

$$\langle f(t) | f > 0 \rangle \approx \frac{t}{2N} \quad (7.31)$$

Since the frequencies are exponentially distributed, this means that we would need to wait for $t \sim Nf$ generations to have an appreciable chance of observing a mutation with $f(t) \sim f$.

3. For a beneficial mutation, the linear growth in Eq. (??) is actually *faster* than the deterministic expectation, $f_0 e^{st}$. If we could measure its frequency trajectory in this early stage, its *apparent* fitness benefit [i.e. the slope of $\log f(t)$] would appear to be much larger than s :

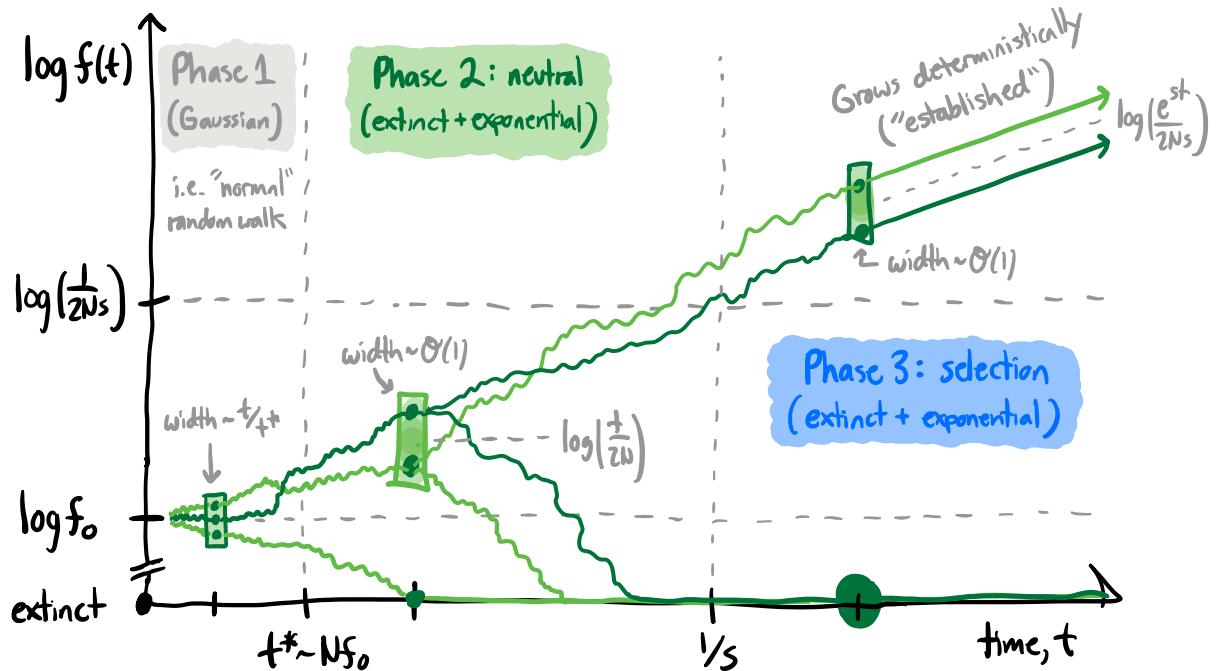


This linear growth is even more counterintuitive for neutral or deleterious mutations, since it implies that the average frequency of a *surviving* mutation tends to increase with time — even though the *overall* average is flat or declining. This paradoxical behavior can be reconciled by remembering that vast majority of the mutations have gone extinct by this point. By restricting our attention to the surviving mutations, we are biasing our observations toward the lucky trajectories that managed to avoid extinction by drifting to anomalously large frequencies.

4. Once $t \gg 1/|s|$, natural selection starts to exert its effect. Deleterious mutations are prevented from rising much higher than $1/2N|s|$, while beneficial mutations start to grow as $\frac{1}{2Ns} e^{st}$, with an overall prefactor set by the exponential distribution.

We can gain some additional insight by examining the whole *ensemble of random paths*, $p[f(t_1), f(t_2), \dots, f(t_n)]$, rather than just the frequency at the final timepoint. We can do this by recursively applying the results above. This

yields an intuitive picture for the trajectory of a mutant lineage that starts at a frequency $f_0 \ll 1/2N|s|$:



The mutation will initially behave like an ordinary random walk, with small fluctuations around its initial frequency. After a time of order $t^* \sim Nf_0$, the mutation will forget its initial frequency and begin to grow linearly as $f(t) \approx t/2N$, while an increasing fraction will drift to extinction ($f = 0$). There will be $\mathcal{O}(1)$ fluctuations around this mean, but these will be forgotten after another $Nf(t)$ generations. In each of these “iterations,” some of the current surviving paths will have a chance of drifting to extinction.

After a time of order $\sim 1/|s|$, the typical surviving frequency reaches $1/N|s|$. Deleterious mutations will get “stuck” at this point, while an increasing fraction are driven to extinction. Beneficial mutations, on the other hand, will begin to grow deterministically at rate e^{st} . In this case, we say that the beneficial mutation has “**established**”, since it will have a negligible probability of going extinct.

The total probability that it reaches this point ($2Ns f_0$) is sometimes known as the *establishment probability*.

At this point, further fluctuations in the frequency will be small from this point forward, so most of the variation in $f(t)$ will come from the last round of fluctuations that occurred when the frequency was close to $\sim 1/Ns$. We can formalize this idea by introducing a new random variable $\nu(t)$ that factors out the expected time-dependence of $f(t)$:

$$f(t) \equiv \frac{\nu(t)}{2Ns} e^{st} \quad (7.32)$$

From the definition of the generating function, we have

$$H_\nu(z, t) = \langle e^{-z \cdot \nu(t)} \rangle = \langle e^{-z \cdot 2Ns e^{-st} f(t)} \rangle = H_f(2Ns e^{-st} \cdot z, t) \quad (7.33)$$

When $t \gg 1/s \gg t^*$, the conditional distribution of ν reduces to

$$H_\nu(z, t | f > 0) \approx \frac{1}{1 + 2Ns z} \implies \nu \sim \text{Exponential}(1) \quad (7.34)$$

This suggests that the randomness in the frequency trajectory when $f(t) \gg 1/2Ns$ can be captured by a single $\mathcal{O}(1)$ pre-factor,

$$f(t) = \frac{\nu}{2Ns} e^{st}. \quad (7.35)$$

which is “frozen in” once $t \gg 1/s$.

7.3 Asymptotic matching at higher frequencies

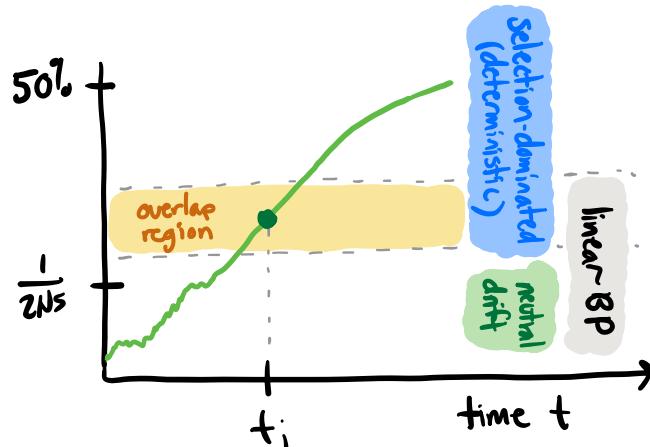
An established beneficial mutation cannot grow exponentially forever. At some point, it will reach a large enough size that $f(t)$ will no longer be small compared to one, and our linear branching process approximation will break down. This will require us to switch back to the full single-locus diffusion model from

Chapter 6. Fortunately, we have already shown that genetic drift will be negligible at these higher frequencies [since $f(t) \gg 1/2Ns$], so we can replace the full model with the deterministic version,

$$\frac{\partial f}{\partial t} = sf(1 - f). \quad (7.36)$$

We can implement the “handoff” between this model and the linear branching process in Eq. (7.2) using a technique known as **asymptotic matching**. The basic idea applies anytime that we have two different approximations that overlap in a smaller region of parameter space. By matching the two approximations in the region where they are both valid, we can find a “global” approximation that is valid across the entire range.

In this case, the overlap region is the part of frequency space where $\frac{1}{2Ns} \ll f \ll 1$. The upper condition ($f \ll 1$) ensures that the linear branching process is a good approximation, while the lower condition ($f \gg 1/2Ns$) ensures that the deterministic approximation in Eq. (7.36) is also valid.



Having identified the relevant overlap region, we can implement our asymptotic matching procedure using the following steps:

- **Step 1.** To make things easier, we will first convert the overlap region from the y-axis (frequency) to the x-axis (time). We can do this by choosing an

intermediate time t_i such that $\frac{1}{2Ns} \ll f(t_i) \ll 1$. When these conditions are satisfied, our results above imply that

$$f(t_i) = \begin{cases} \frac{\nu}{2Ns} e^{st_i} & \text{w/ prob } 2Ns f_0, \\ 0 & \text{else,} \end{cases} \quad (7.37)$$

where ν is an exponential random variable with mean one. The bottom case is easy to extrapolate to later times, since the mutation must remain extinct for all t . This means that we only need to consider the established case. In this case, Eq. (7.37) shows that our assumptions about $f(t_i)$ will be self-consistent if

$$\frac{1}{s} \ll t_i \ll \frac{1}{s} \log(Ns). \quad (7.38)$$

When $Ns \gg 1$, there are (in principle³) many possible t_i values where this will be true. Let's choose one of them.

- **Step 2.** We can then use this intermediate timepoint as the starting point for the deterministic model in Eq. (7.36). This yields the frequency at any later timepoint:

$$f(t) = \frac{f(t_i)e^{s(t-t_i)}}{1 - f(t_i) + f(t_i)e^{s(t-t_i)}} \approx \frac{f(t_i)e^{s(t-t_i)}}{1 + f(t_i)e^{s(t-t_i)}} \quad (7.39)$$

where we have assumed that $f(t_i) \ll 1$.

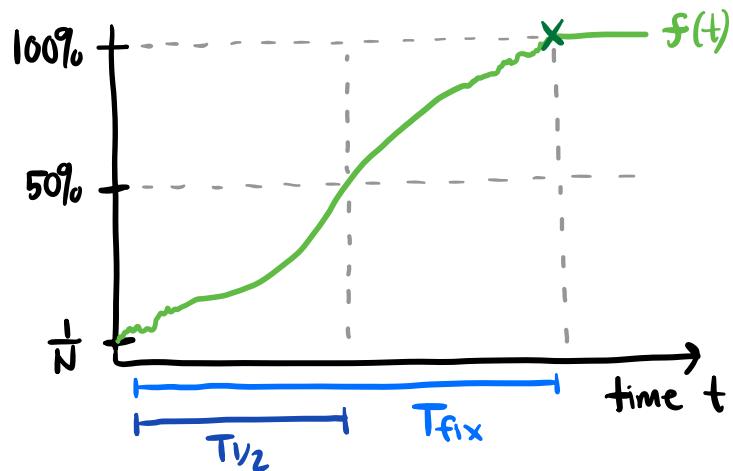
- **Step 3.** We can then substitute our expression for $f(t_i)$ into Eq. (7.39) to obtain a “global” approximation,

$$f(t) = \frac{\left(\frac{\nu}{2Ns} e^{st_i}\right) e^{s(t-t_i)}}{1 + \left(\frac{\nu}{2Ns} e^{st_i}\right) e^{s(t-t_i)}} = \frac{\frac{\nu}{2Ns} e^{st}}{1 + \frac{\nu}{2Ns} e^{st}}, \quad (7.40)$$

³This is the “asymptotic” part of asymptotic matching – it requires us to assume that $Ns \rightarrow \infty$. In practice, since $\log(Ns)$ is a slowly growing function of Ns , the difference between $1/s$ and $\log(Ns)/s$ is never *that* big. Fortunately, like many of other asymptotic approximations we discussed in Chapter 2, we will see that the asymptotic matching approximation remains relatively accurate in practice, even for moderate values of $\log(Ns)$.

that is valid for $t \gg 1/s$. Note that the intermediate time t_i has dropped out of our final answer. This is a good thing, since our choice of t_i was completely arbitrary, and any downstream predictions should not depend on the precise value that we chose.

We can use our global approximation in Eq. (7.40) to calculate an interesting biological quantity: how long does it take for a brand new mutation to take over the population and fix? This is often known as the **fixation time**. We can break this question down into two parts: (i) how long does it take a mutation to go from $f_0 = 1/N$ to $f = 50\%$? and (ii) how long does it take to go from 50% to 100%?



We can answer the first question using our expression in Eq. (7.40). Setting $f(t) = 1/2$ and solving for t yields:

$$T_{1/2} = \frac{1}{s} \log \left(\frac{2Ns}{\nu} \right) = \frac{1}{s} \log(2Ns) + \frac{1}{s} \log \left(\frac{1}{\nu} \right) \quad (7.41)$$

The second half of the trajectory is mirror symmetric with the first if we reverse the direction of time ($t \rightarrow -t$) and focus on the wildtype fraction ($f \rightarrow 1 - f$).

The total *fixation time* is given by

$$T_{\text{fix}} = \frac{2}{s} \log(2Ns) + \frac{1}{s} \left(\frac{1}{\nu_1} \right) + \frac{1}{2} \left(\frac{1}{\nu_2} \right) \quad (7.42)$$

Since $Ns \gg 1$, the first term is much larger than the other two, which yields the leading order approximation,

$$T_{\text{fix}} \approx \frac{2}{s} \log(2Ns). \quad (7.43)$$

It is easy to imagine that evolution might be limited by the time it takes to find the right mutation. Equation (7.43) shows that there is also a fundamental “speed limit” on the time it takes for this newly produced mutation to take over the population and fix.

In large populations, the total fixation time can be much larger than the time it takes for a mutation to go from 10% \rightarrow 90%, or even 1% \rightarrow 99%. Our decomposition shows that most of this time elapses in the deterministic phase of the mutation’s lifetime [$f(t) \gtrsim 1/2Ns$], while it is still at a low frequency in the population [$f(t) \ll 1$]. You will have the chance to work through some concrete examples in Problem 5 of Homework 3. This speed limit on the fixation time of a new mutation will be very important when we consider longer genomes later in the course.

7.4 Heuristic picture

Because the linear branching process spans both the drift-dominated and selection-dominated regions of frequency space, it is able to *quantitatively* capture the complex transition between stochastic and deterministic growth. This transition is critical for understanding how new mutations take over a population. At the same time, we saw that obtaining these analytical results required some complex mathematical machinery (e.g., moment equations, generating functions,

asymptotic matching) which can obscure some of the underlying physical intuition.

In this section, we will present a powerful *heuristic approach* for re-deriving many of the exact results we have obtained so far. This approach may seem sloppy or arbitrary at first, but it can be done in a way that keeps track of the approximations in a controlled manner, while highlighting some of the key physical intuition...

7.5 Incorporating spontaneous mutations

7.6 Appendix

7.6.1 Exact solution using the method of characteristics

In this section, we show how to solve the partial differential equation for the generating function of the linear branching process using the *method of characteristics*.

No mutations ($\mu = \nu = 0$)

We will start by considering the case without mutations ($\mu = \nu = 0$), where the mutant starts at an initial frequency $f(0) = f_0$. The generating function satisfies the PDE in Eq. (7.13),

$$\frac{\partial H}{\partial t} = \left[sz - \frac{z^2}{2N} \right] \frac{\partial H}{\partial t}, \quad (7.44)$$

subject to the initial condition $H(z, 0) = e^{-zf_0}$.

The method of characteristics is a generalization of the trick that we used to solve for the fixation probability of the full single-locus model in Chapter 6. Recall that in that case, we found a special value of $z^* = 2Ns$ for which

$\partial_t H(z^*, t) = 0$. This allowed us to relate the values of $H(z^*, t)$ at long times (where $f = 0, 1$) with the initial value $H(z^*, 0)e^{-z^* f}$.

We can generalize this idea by searching for a **family of curves**, $z^*(t)$, along which

$$\frac{d}{dt} [H(z^*(t), t)] = 0. \quad (7.45)$$

When this condition is satisfied, we can again relate the values of $H(z, t)$ between the initial timepoint and any later time,

$$H(z^*(t), t) = H(z^*(0), 0) = e^{-z^*(0)f_0} \quad (7.46)$$

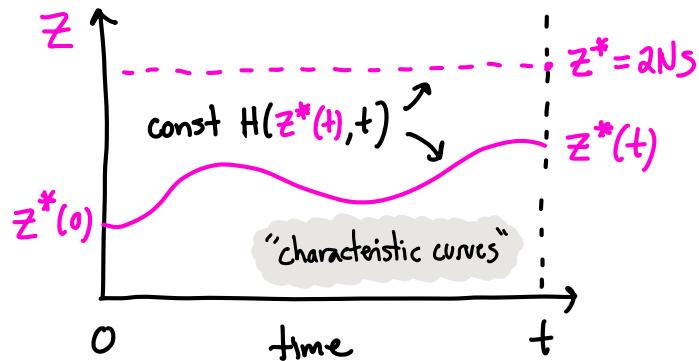
The line $z^*(t) = 2Ns$ is one such **characteristic curve**, but there are infinitely many others. Using the chain rule on Eq. (7.45), we can write the total derivative as

$$\frac{dH(z^*(t), t)}{dt} = \frac{\partial H}{\partial t} + \frac{\partial H}{\partial z} \frac{dz^*}{dt} = \frac{\partial H}{\partial z} \left[sz^* - \frac{z^{*2}}{2N} + \frac{dz^*}{dt} \right], \quad (7.47)$$

where we have used the equation of motion in Eq. (7.44) to replace $\partial H/\partial t$. This shows that if $z^*(t)$ satisfies the first order ODE,

$$\frac{dz^*}{dt} = -sz^* + \frac{z^{*2}}{2N} \quad (7.48)$$

then Eq. (7.46) will be satisfied. We can visualize this the following diagram:



The curve $z^*(t) = 2Ns$ is one possible solution Eq. (7.48) corresponding to the initial condition $z^*(0) = 2Ns$. However, Eq. (7.46) shows that this only allows us to evaluate the generating function at a special value of $z = z^*$. To obtain the full generating function $H(z, t)$, we want to be able to choose the value of z that we will use to evaluate $H(z, t)$ in the present. In other words, we need to find the initial value $z^*(0)$ that produces a characteristic curve with $z^*(t) = z$.

This is easiest to accomplish by defining a corresponding curve in **reverse time** (i.e. working back from the final time t). In particular, if we define a function,

$$\phi(t') = z^*(t - t') \quad (7.49)$$

then $\phi(t')$ must satisfy the initial value problem

$$\frac{\partial \phi}{\partial t'} = s\phi - \frac{\phi^2}{2N}, \quad (7.50)$$

with $\phi(0) = z$, and the generating function is given by

$$H(z, t) = e^{-\phi(t)f_0}. \quad (7.51)$$

In this case, the solution to Eq. (7.50) is a simple logistic function,

$$\phi(t) = \frac{ze^{st}}{1 + \frac{z}{2Ns}(e^{st} - 1)}, \quad (7.52)$$

so the generating function is given by

$$H(z, t) = \exp \left[\frac{-zf_0e^{st}}{1 + \frac{z}{2Ns}(e^{st} - 1)} \right]. \quad (7.53)$$

Incorporating new mutations

TODO.