

Diffusion theory

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Outline

- Kolmogorov forward equation
- Kolmogorov backward equation
- Fixation probability
- Mean fixation time

Diffusion theory

- Intuitively, selection should dominate large populations, while drift should dominate small populations.
- Diffusion theory combines all evolutionary forces in a single model that is valid for all population sizes:
 - Mutation
 - Selection
 - Drift
 - Recombination
 - Migration
- In particular, diffusion theory considers both deterministic and stochastic processes.

The structure of diffusion theory

- We follow the probability distribution (rather than the deterministic trajectory) of a population over time.
- The probability density that an allele A_1 is at frequency p at time t is

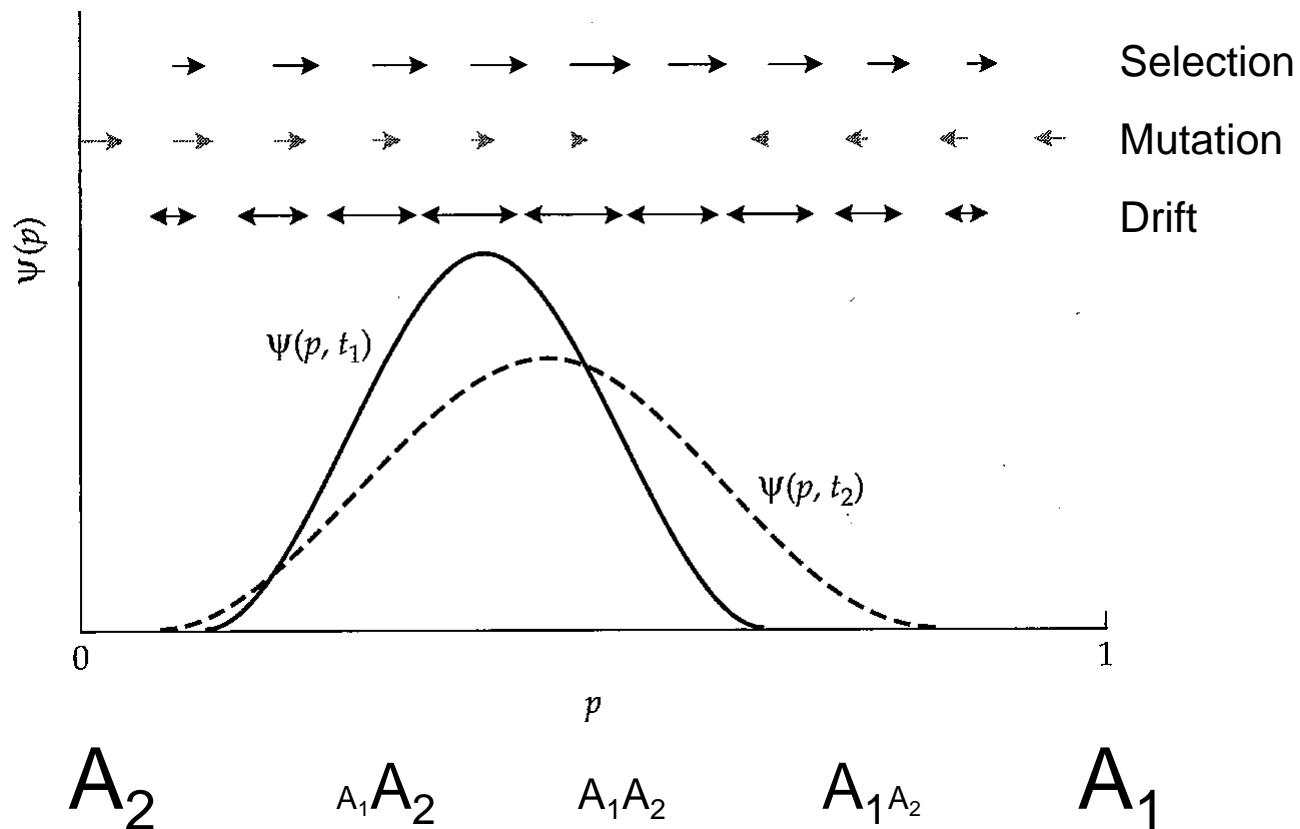
$$\psi(p, t)$$

- The allele frequency distribution $\psi(p) = \psi(p, \cdot)$ changes over time.

Two classes of evolutionary forces

- Directional processes, $M(p)$
 - Non-zero expected change in allele frequency
 - E.g., selection, mutation, migration, recombination
 - $M(p)$ is measured as the expected change per generation
- Nondirectional processes, $V(p)$
 - Zero expected change
 - Increase in the spread of the allele distribution
 - E.g., random variation in survivorship, random gamete success
 - $V(p)$ is measured by the expected variance in the next generation

Directional and non-directional processes



Example: Moran process

- With $p = p(t) = X(t)/N$,

$$\begin{aligned} M(p) &= E[p(t+1) - p(t) \mid p(t)] \\ &= p - p = 0 \end{aligned}$$

$$\begin{aligned} V(p) &= E\{\text{Var}[p(t+1)] \mid p(t)\} \\ &= \frac{1}{N^2} E\{\text{Var}[X(t+1)] \mid X(t)\} \\ &= \frac{2p(1-p)}{N^2} \end{aligned}$$

Change in allele frequency

- We want to predict the change in allele frequency distribution from the current distribution.
- $\psi = \psi(p, t)$
= Probability density of allele frequency p at time t
- $g = g(p, \epsilon; dt)$
= Probability that the allele frequency changes from p to $p + \epsilon$ in time interval dt .
- Any allele frequency p at time $t + dt$ must have evolved from some distribution $p - \epsilon$ at time t ,

$$\psi(p, t + dt) = \int \psi(p - \epsilon, t) g(p - \epsilon, \epsilon; dt) d\epsilon$$

Taylor expansion

- Taylor series expansion of $\psi \cdot g$ around p :

$$\psi(p, t + dt) = \int \left[\psi(p, t) g(p, \epsilon; dt) - \epsilon \frac{\partial(\psi g)}{\partial p} + \frac{\epsilon^2}{2} \frac{\partial^2(\psi g)}{\partial p^2} - \frac{\epsilon^3}{6} \frac{\partial^3(\psi g)}{\partial p^3} + \dots \right] d\epsilon$$

- The *diffusion approximation* is derived by assuming $\epsilon^2 \gg \epsilon^3$. This assumption means that the population does not change too much in any short time interval, i.e., the effects of selection and mutation are relatively weak.

Taylor approximation

- Also, p and ϵ are independent. Thus, approximately,

$$\begin{aligned}\psi(p, t + dt) = & \psi(p, t) \int g(p, \epsilon; dt) d\epsilon - \\ & - \frac{\partial}{\partial p} \psi \int g \epsilon d\epsilon + \frac{1}{2} \frac{\partial^2}{\partial p^2} \psi \int g \epsilon^2 d\epsilon\end{aligned}$$

- Because $\int g(p, \epsilon; dt) d\epsilon = 1$, we have

$$\psi(p, t + dt) = \psi - \frac{\partial}{\partial p} \psi \int g \epsilon d\epsilon + \frac{1}{2} \frac{\partial^2}{\partial p^2} \psi \int g \epsilon^2 d\epsilon$$

What do the integrals mean?

$$\psi(p, t + dt) = \psi - \frac{\partial}{\partial p} \psi \int g \epsilon d\epsilon + \frac{1}{2} \frac{\partial^2}{\partial p^2} \psi \int g \epsilon^2 d\epsilon$$

- $\int g \epsilon d\epsilon = E(\epsilon)$ is the expected change over time dt . With $M(p)$ the rate of directional change, we have

$$\int g(p, \epsilon; dt) \epsilon d\epsilon = M(p) dt$$

- $\int g \epsilon^2 d\epsilon = E(\epsilon^2) = \text{Var}(\epsilon) + E(\epsilon)^2 \approx \text{Var}(\epsilon)$. With $V(p)$ the variance in allele frequency due to nondirectional effects,

$$\int g(p, \epsilon; dt) \epsilon^2 d\epsilon = V(p) dt$$

Integrals substituted

- Substituting we obtain

$$\psi(p, t + dt) = \psi(p, t) - \frac{\partial[\psi(p, t)M(p)]}{\partial p}dt + \frac{1}{2} \frac{\partial^2[\psi(p, t)V(p)]}{\partial p^2}dt$$

- Now subtract $\psi(p, t)$ and divide by dt .
- For $dt \rightarrow 0$, we obtain

The Kolmogorov forward equation

$$\frac{\partial \psi(p, t)}{\partial t} = -\frac{\partial}{\partial p} [\psi(p, t) M(p)] + \frac{1}{2} \frac{\partial^2}{\partial p^2} [\psi(p, t) V(p)]$$

- The equation describes the change in allele frequency in terms of the shape of that distribution and the functions M (directional process) and V (nondirectional process).
- It is also known as the *Fokker-Planck equation* or the *diffusion equation*.

Equilibrium

- At equilibrium,

$$-\frac{\partial}{\partial p} [\psi^*(p, t) M(p)] + \frac{1}{2} \frac{\partial^2}{\partial p^2} [\psi^*(p, t) V(p)] = 0$$

- Integrating over p yields

$$\frac{1}{2} \frac{\partial}{\partial p} [\psi^*(p, t) V(p)] - \psi^*(p, t) M(p) = 0$$

- This first order homogeneous ODE can be solved.

Equilibrium distribution

- The equilibrium distribution of the allele frequency is

$$\psi^*(p) = \frac{C}{V(p)} \exp \left[\int_0^p \frac{2M(q)}{V(q)} dq \right]$$

where C is a constant of integration.

Selective competition between two alleles

- Assume two alleles A_1 and A_2 with frequencies p and $1 - p$, and fitness w_1 and w_2 , respectively.
- The average fitness of the population is

$$\bar{w} = pw_1 + (1 - p)w_2 \quad \text{and} \quad \frac{d\bar{w}}{dp} = w_1 - w_2$$

- In the next generation, the allele frequency is

$$p' = (pw_1) / \bar{w}$$

Wright's equation for an adaptive landscape

$$\begin{aligned}\Delta p_{\text{sel}} = p' - p &= \frac{p(w_1 - \bar{w})}{\bar{w}} \\ &= \frac{p(1 - p)(w_1 - w_2)}{\bar{w}} \\ &= \frac{p(1 - p)}{\bar{w}} \frac{d\bar{w}}{dp} \\ &= p(1 - p) \frac{d \log \bar{w}}{dp}\end{aligned}$$

Mutation and selection

- Let u_1 be the A_1 -to- A_2 mutation rate, and u_2 the A_2 -to- A_1 mutation rate.
- The per-generation change due to mutation is $\Delta p_{\text{mut}} = -p u_1 + (1 - p) u_2$.
- Thus, the directional processes of selection and mutation add up to

$$M(p) = \frac{p(1 - p)}{\bar{w}} \frac{d\bar{w}}{dp} - pu_1 + (1 - p)u_2$$

Sampling variance

- Assuming Wright-Fisher dynamics, we have

$$\begin{aligned} V(p) &= E\{\text{Var}[p(t+1)] \mid p(t)\} \\ &= E\{\text{Var}[X(t+1)/N] \mid X(t)/N\} \\ &= \frac{1}{N^2} Np(1-p) \\ &= \frac{p(1-p)}{N} \end{aligned}$$

Mutation, selection, and sampling

$$\frac{M}{V} = N \left[\frac{d \log \bar{w}}{dp} - \frac{u_1}{1-p} + \frac{u_2}{p} \right]$$

$$\Rightarrow$$

$$\int_0^p \frac{M(q)}{V(q)} dq =$$

$$= N [\log \bar{w} + u_1 \log(1-p) + u_2 \log(p)]$$

Wright-Fisher dynamics with mutation and selection at equilibrium

$$\begin{aligned}\psi^*(p) &= \frac{C}{V(p)} \exp \left[\int_0^p \frac{2M(q)}{V(q)} dq \right] \\ &= C \bar{w}^{2N} (1-p)^{2Nu_1-1} p^{2Nu_2-1}\end{aligned}$$

where C is given by the requirement that

$$\int_0^1 \psi^*(p) dp = 1$$

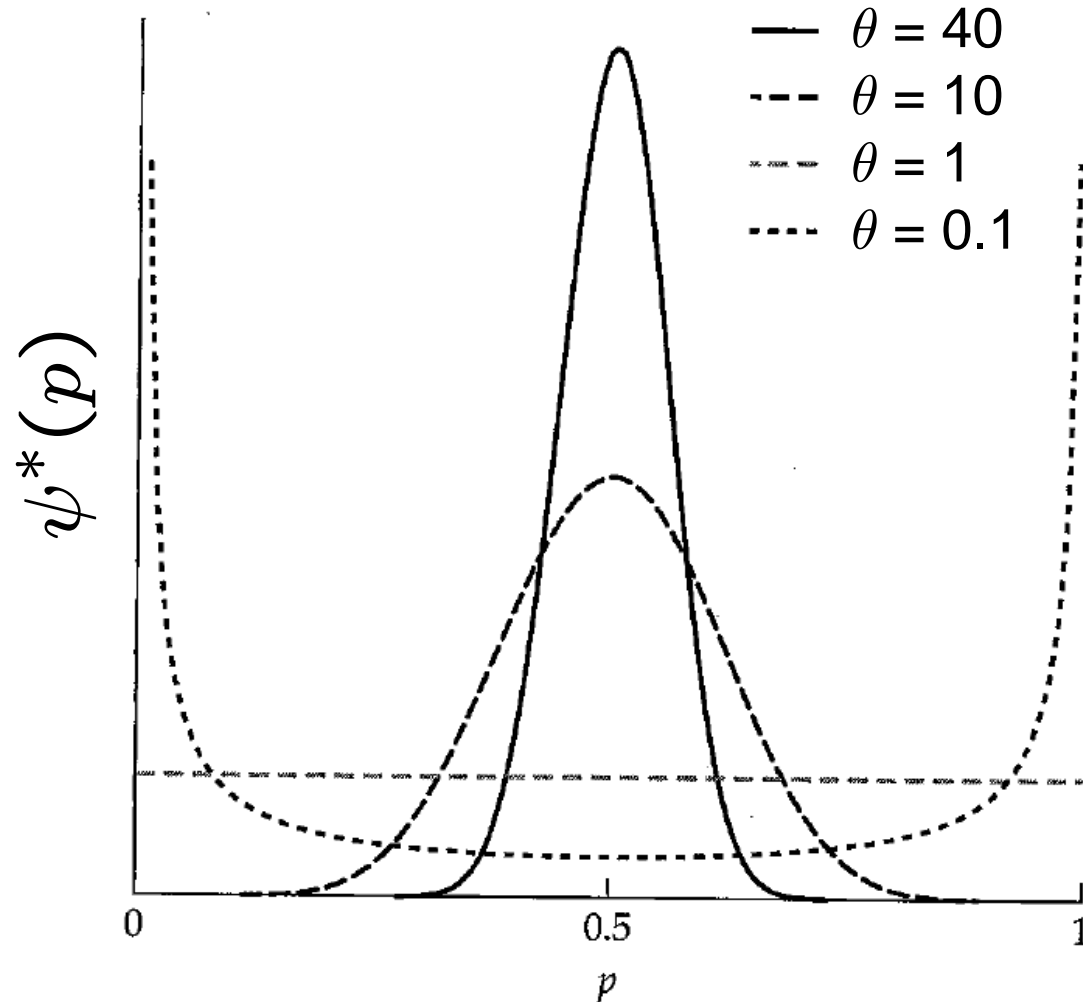
How much neutral variation is maintained under mutation and drift?

For $\bar{w} = 1$ and $u = u_1 = u_2$,

$$\psi^*(p) \propto [p(1 - p)]^{2Nu-1}$$

- We set $\theta = 2 N u$, because this scaled mutation parameter determines the equilibrium distribution.

Mutation-drift dynamics



Selection

- Assume that A_1 has fitness $w_1 = 1 + s$ and A_2 has fitness $w_2 = 1$. Then the average population fitness is

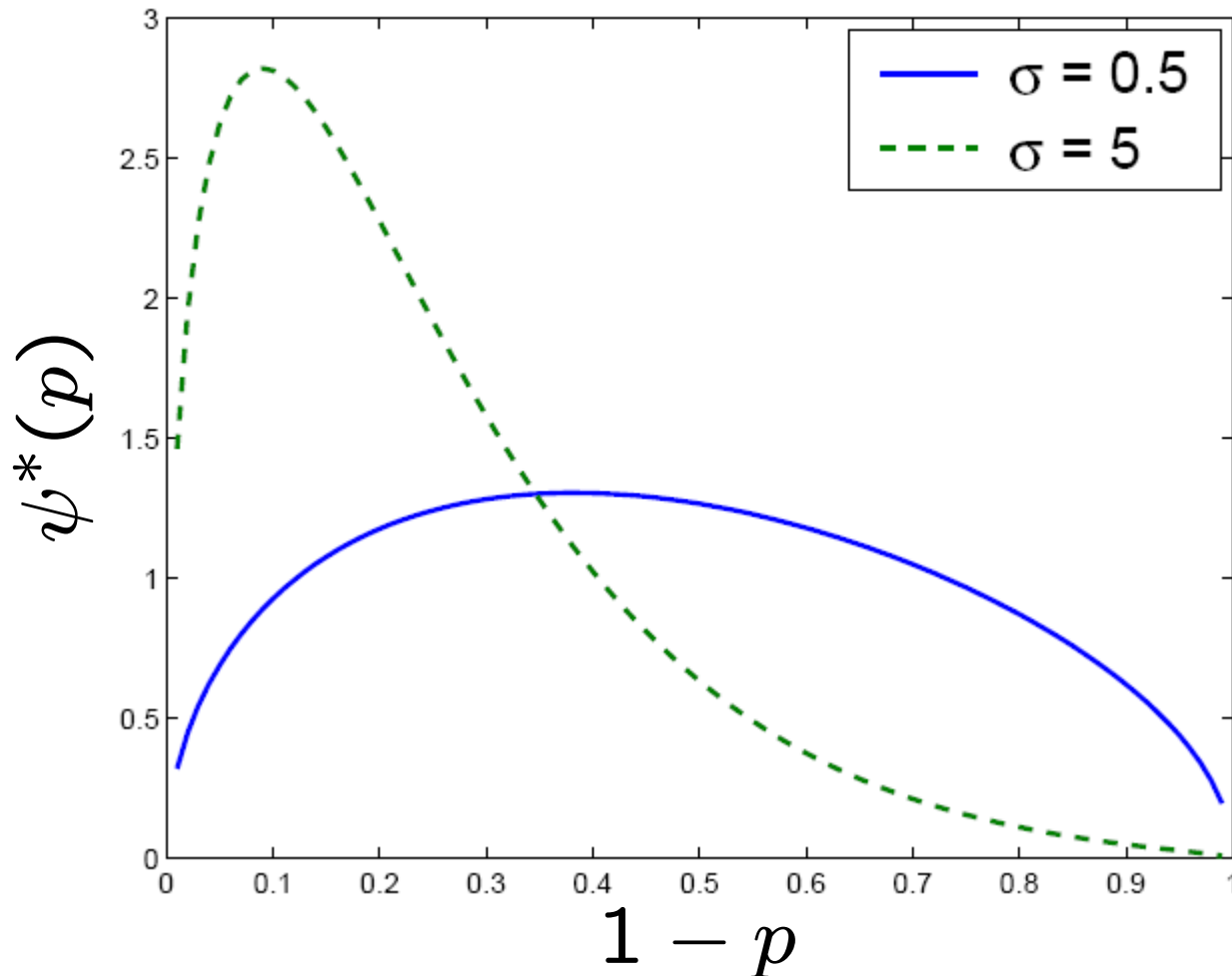
$$\begin{aligned}\bar{w} &= p(1 + s) + (1 - p) \\ &= 1 + sp \approx e^{sp}\end{aligned}$$

$$\Rightarrow \bar{w}^{2N} = e^{2Nsp}$$

- We set $\sigma = 2 N s$, because this scaled selection parameter determines the equilibrium dynamics.
- Ignoring mutation, we have

$$\psi^*(p) \propto e^{\sigma p} / p(1 - p)$$

Selection-drift dynamics



Summary

- The equilibrium allele frequency distribution in the diffusion approximation of the Wright-Fisher process (for haploids) reads

$$\psi^*(p) \propto (1 - p)^{\theta-1} p^{\theta-1} e^{\sigma p}$$

with scaled mutation parameter $\theta = 2Nu$ and scaled selection parameter $\sigma = 2Ns$.

What about fixation?

- We need to study $\psi(p, t \mid p_0)$, the density of a population having allele frequency p at time t *given that the allele frequency was p_0 at time 0*.
- Consider all ways to go from p_0 to $p_0 + \epsilon$ in time dt :

$$\psi(p, t + dt \mid p_0) = \int \psi(p, t \mid p_0 + \epsilon) g(p_0, \epsilon; dt) d\epsilon$$

Taylor expansion

- Taylor series expansion of $\psi(p, t \mid p_0 + \epsilon)$ around p_0 :

$$\begin{aligned} \psi(p, t \mid p_0 + \epsilon) = & \psi(p, t \mid p_0) + \\ & + \frac{\partial \psi}{\partial p_0} \epsilon + \frac{\epsilon^2}{2} \frac{\partial^2 \psi}{\partial p_0^2} + \frac{\epsilon^3}{6} \frac{\partial^3 \psi}{\partial p_0^3} + \dots \end{aligned}$$

- Write $\psi = \psi(p, t, \mid p_0)$, $g = g(p_0, \epsilon, dt)$ and approximate to

$$\begin{aligned} \psi(p, t + dt \mid p_0) = & \psi \int g d\epsilon + \\ & + \frac{\partial \psi}{\partial p_0} \int g \epsilon d\epsilon + \frac{1}{2} \frac{\partial^2 \psi}{\partial p_0^2} \int g \epsilon^2 d\epsilon \end{aligned}$$

The Kolmogorov backward equation

- The integrals have the same meaning as before.
- Subtract $\psi(p, t \mid p_0)$, divide by dt , and let $dt \rightarrow 0$ to obtain

$$\begin{aligned} \frac{\partial \psi(p, t \mid p_0)}{\partial t} &= \\ &= M(p_0) \frac{\partial \psi(p, t \mid p_0)}{\partial p_0} + \frac{1}{2} V(p_0) \frac{\partial^2 \psi(p, t \mid p_0)}{\partial p_0^2} \end{aligned}$$

Equilibrium distribution

- At equilibrium,

$$M(p_0) \frac{\partial \psi^*}{\partial p_0} + \frac{1}{2} V(p_0) \frac{\partial^2 \psi^*}{\partial p_0^2} = 0$$

- We find

$$\frac{\partial \psi^*}{\partial p_0} = C \exp \left(- \int_0^p \frac{2M(q)}{V(q)} dq \right)$$

- Integration w.r.t. p_0 does not yield a unique solution.

Probability of fixation

- We are interested in the probability of fixation of the first allele, A_1 , ($p = 1$) given its initial allele frequency p_0 , i.e., in

$$\rho(p_0) = \psi(1, \infty \mid p_0)$$

- Clearly,

$$\rho(1) = \psi(1, \infty \mid 1) = 1$$

$$\rho(0) = \psi(1, \infty \mid 0) = 0$$

- With these boundary conditions, we can solve for ψ^* .

Fixation probability

$$\rho(p_0) = \frac{\int_0^{p_0} \exp \left(- \int_0^p \frac{2M(q)}{V(q)} dq \right) dp}{\int_0^1 \exp \left(- \int_0^p \frac{2M(q)}{V(q)} dq \right) dp}$$

Selection

- Recall that

$$\bar{w} = 1 + ps, \quad \frac{d\bar{w}}{dp} = s,$$

$$M(p) = \frac{p(1-p)}{\bar{w}} \frac{d\bar{w}}{dp} = \frac{p(1-p)s}{1+ps}$$

- For $p \ll 1$,

$$\frac{2M(p)}{V(p)} = \frac{2Ns}{1+ps} \approx 2Ns$$

because s is also small.

Fixation probability in a haploid population

- Now,

$$\int_0^p \frac{2M(q)}{V(q)} dq = 2Ns p$$

and hence

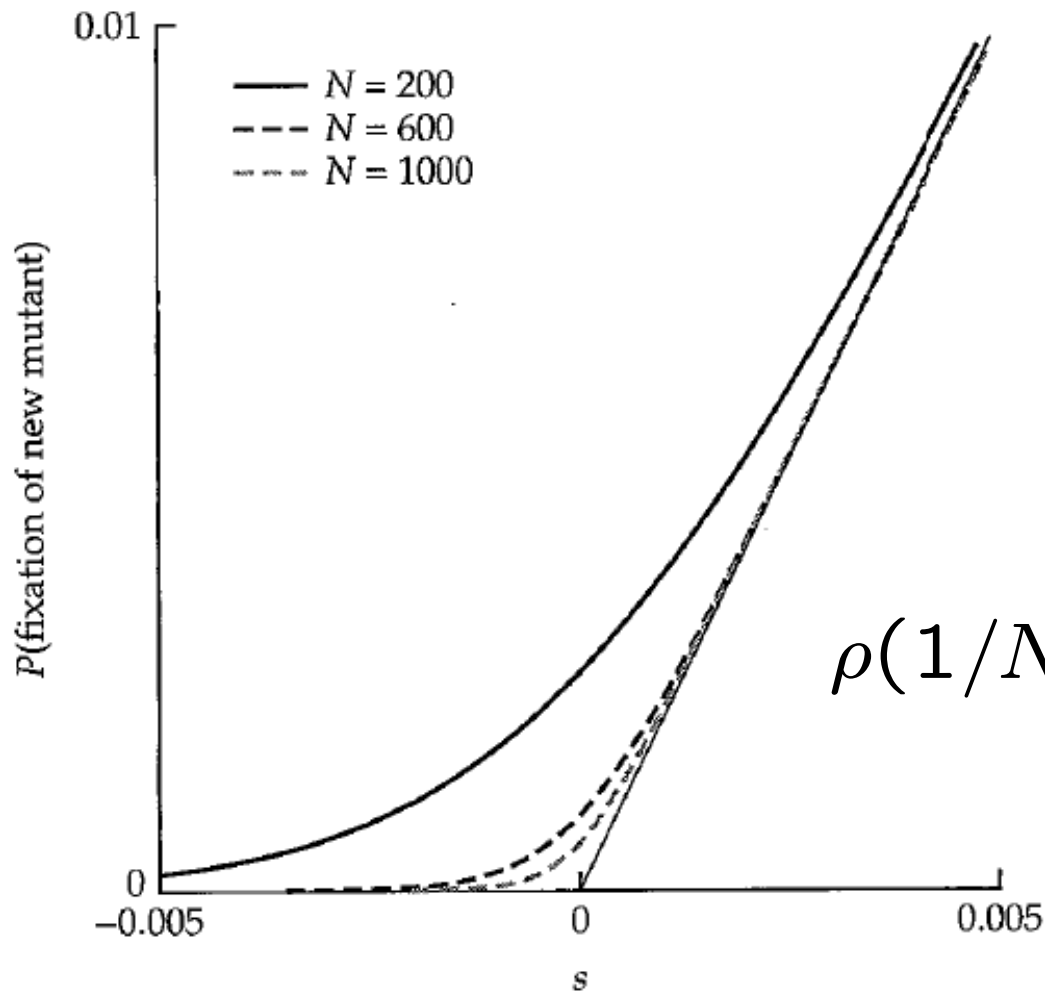
$$\rho(p_0) = \frac{1 - e^{-2Ns p_0}}{1 - e^{-2Ns}}$$

Neutral case

- For $s = 0$, $\rho(p_0)$ is undefined. However,

$$\lim_{s \rightarrow 0} \rho(p_0) = \frac{-2Nsp_0}{-2Ns} = p_0$$

Fixation probability of a new mutant



$$\rho(1/N) = \frac{1 - e^{-2s}}{1 - e^{-2Ns}}$$

A new mutant in a large population

$$\rho(1/N) = \frac{1 - e^{-2s}}{1 - e^{-2Ns}}$$

- If N is large, $2Ns \gg 1$, then the denominator is one.
- If s is small, $s \ll 1$, then $\exp(-2s) \approx 1 - 2s$
- In this situation, we recover a classical result due to Haldane (1927):

$$\rho(\text{new mutant}) \approx 2s$$

Mean fixation time

- Let $\tau(p_0)$ be the expected waiting time until A_1 becomes fixed, given its fixation and the initial allele frequency p_0 .
- Define

$$A(p) = \int_0^p \frac{2M(q)}{V(q)} dq$$

$$S(p_0) = \int_0^{p_0} \exp(-A(p)) dp$$

such that $S(0) = 0$ and $\rho(p_0) = S(p_0)/S(1)$

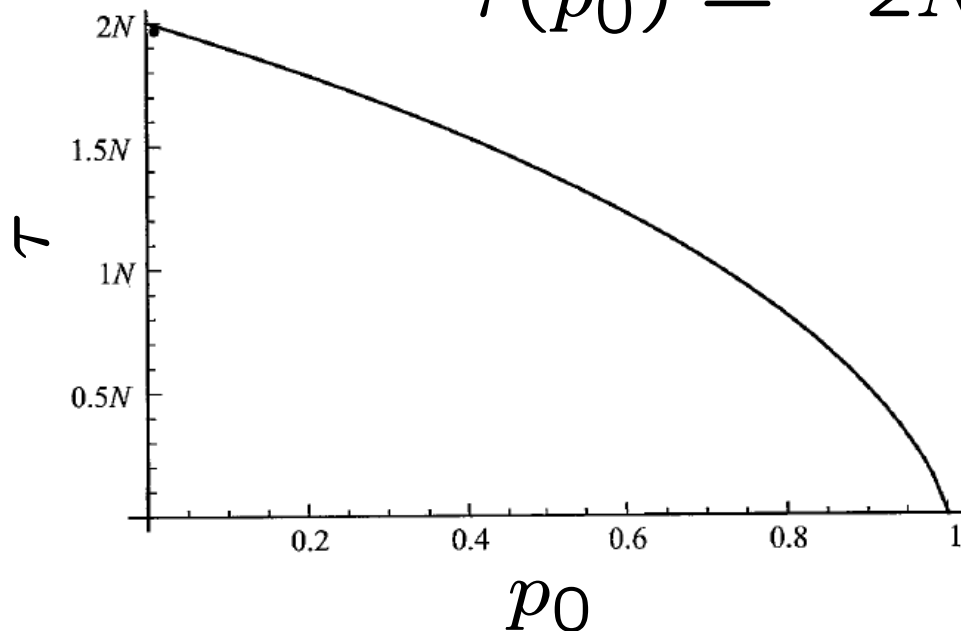
Waiting time to fixation

- Using the Kolmogorov backward equation, one can derive an analytical expression for $\tau(p_0)$.

$$\tau(p_0) = 2S(1) \left[\int_{p_0}^1 \frac{\rho(y)(1 - \rho(y))}{\exp(-A(y))V(y)} dy + \frac{1 - \rho(p_0)}{\rho(p_0)} \int_0^{p_0} \frac{\rho(y)^2}{\exp(-A(y))V(y)} dy \right]$$

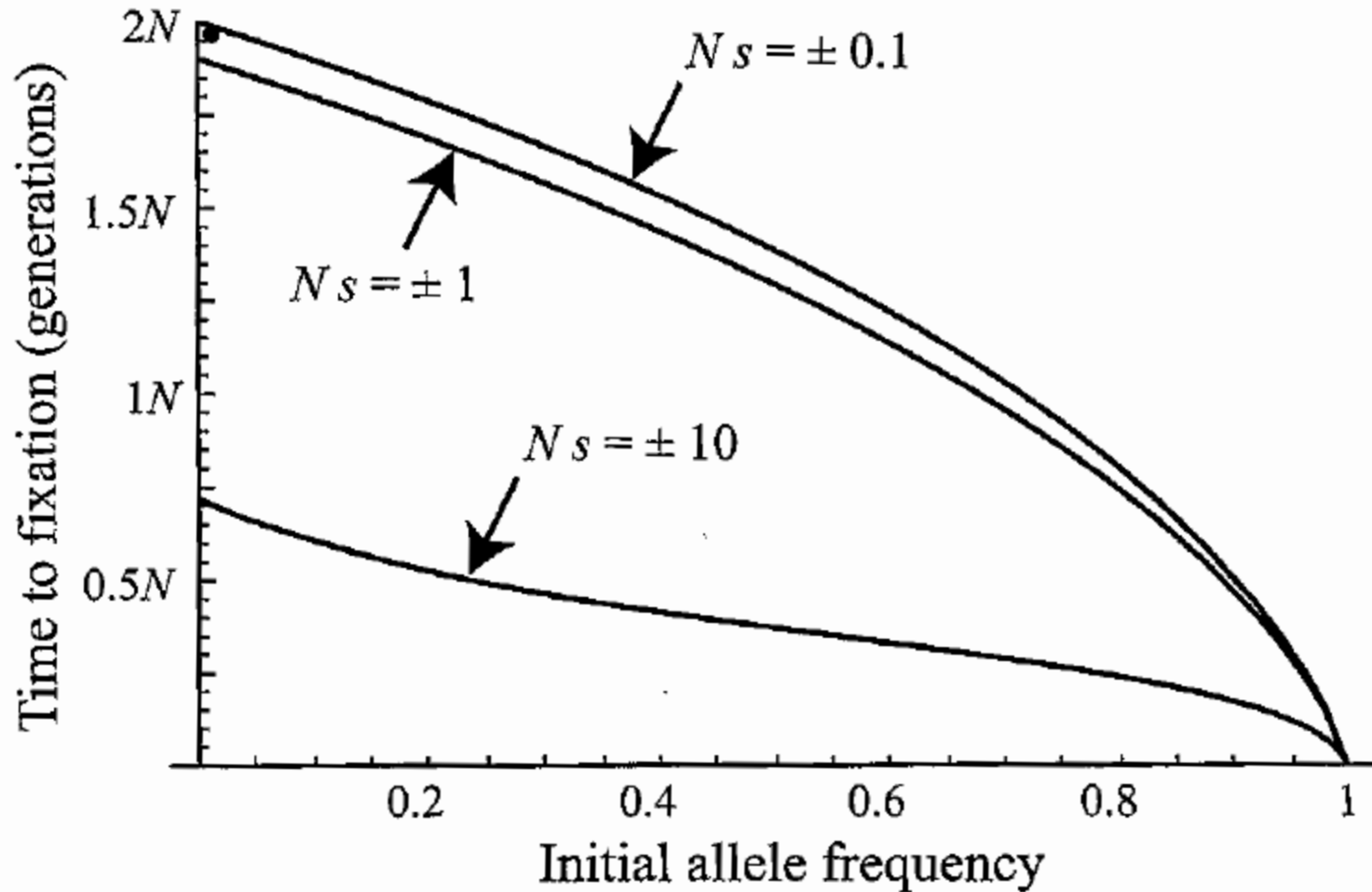
Fixation time for the neutral Wright-Fisher model

$$\tau(p_0) = -2N \frac{1 - p_0}{p_0} \log(1 - p_0)$$



- For $p_0 = 1 / N$, we have approximately $\tau(1/N) = 2N$

Waiting time for a selected mutant to fix



Further reading

- Rice SH. *Evolutionary Theory*, Chapter 5
- Otto SP, Day T. *A Biologist's Guide to Mathematical Modeling in Ecology and Evolution*, Chapter 15