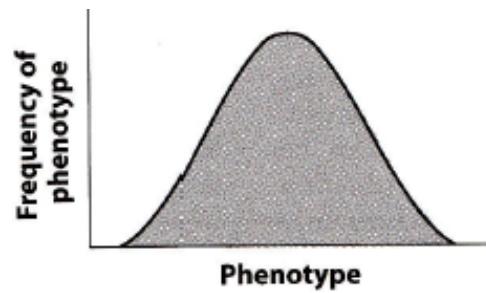
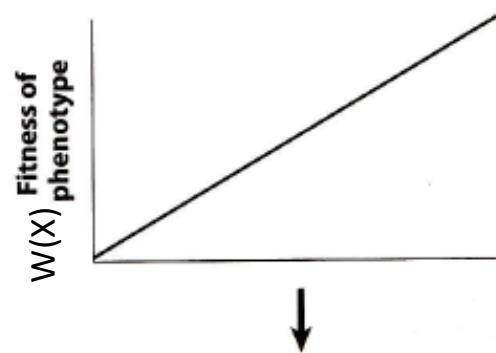


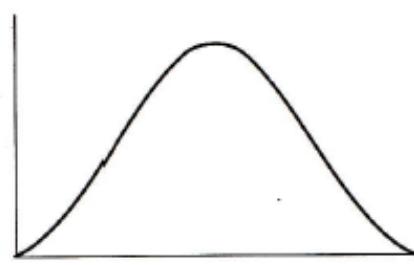
Types of selection



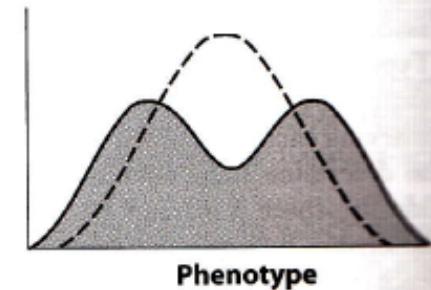
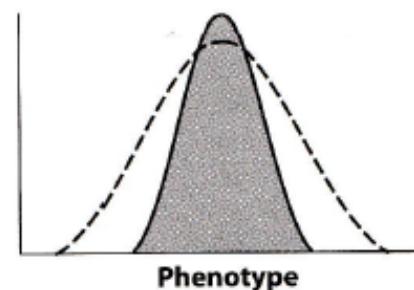
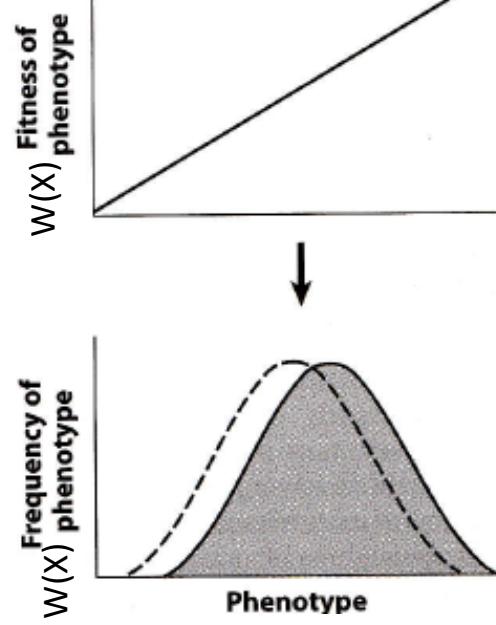
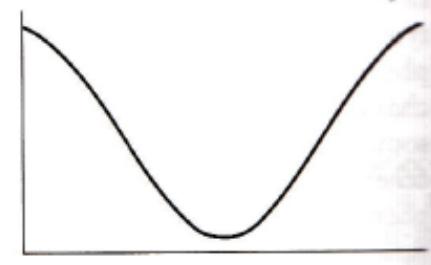
A Directional selection



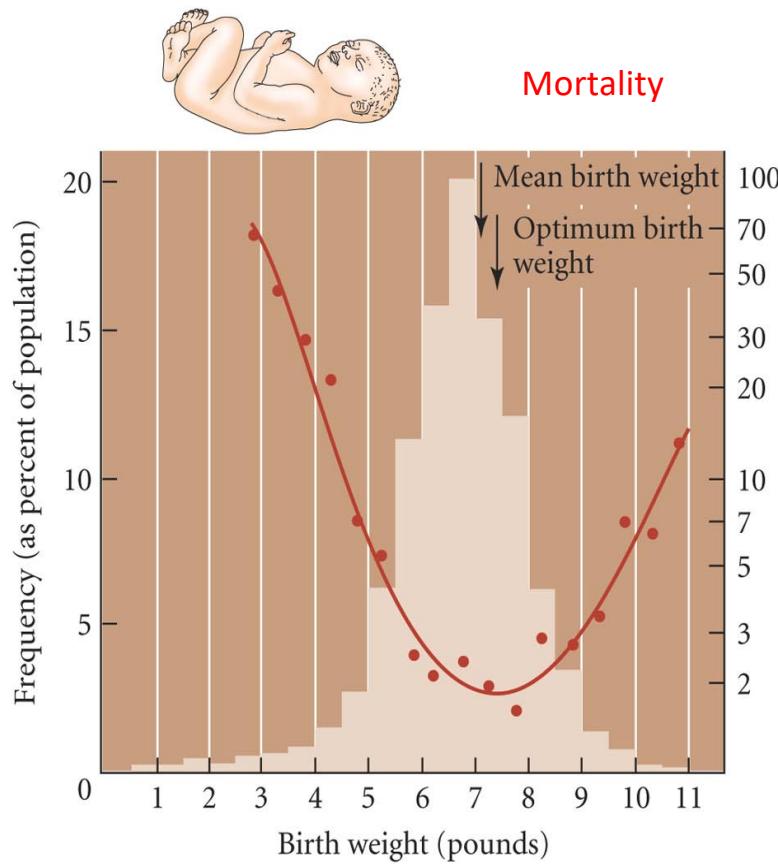
B Stabilizing selection



C Disruptive selection

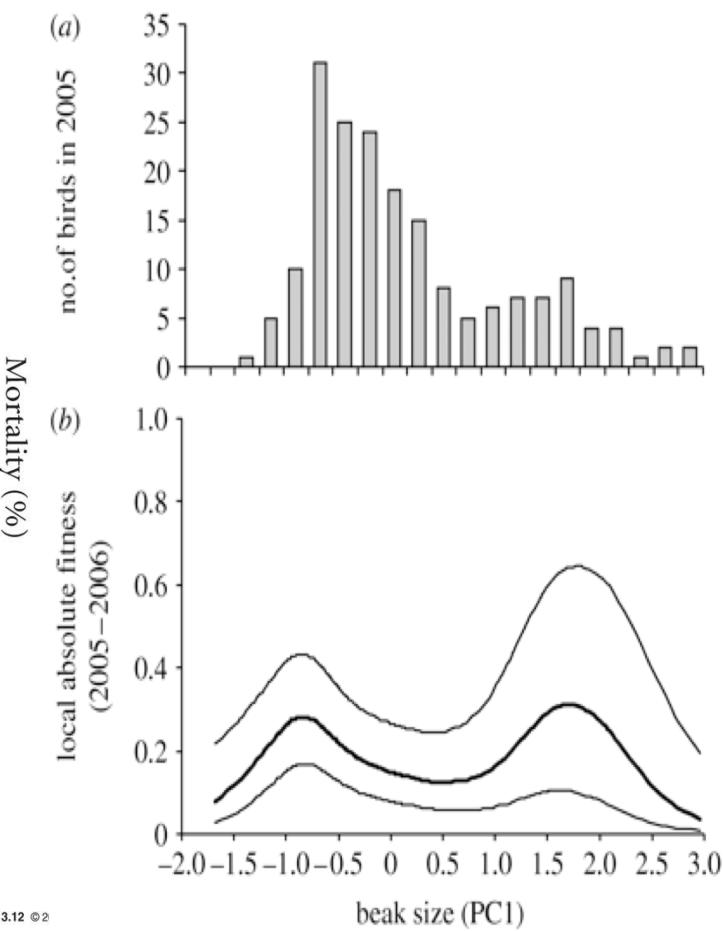


Birth weight in humans: A classic case of stabilizing selection



EVOLUTION, Figure 13.12 © 2

Disruptive selection in a population of Darwin's Finches



Trade-offs

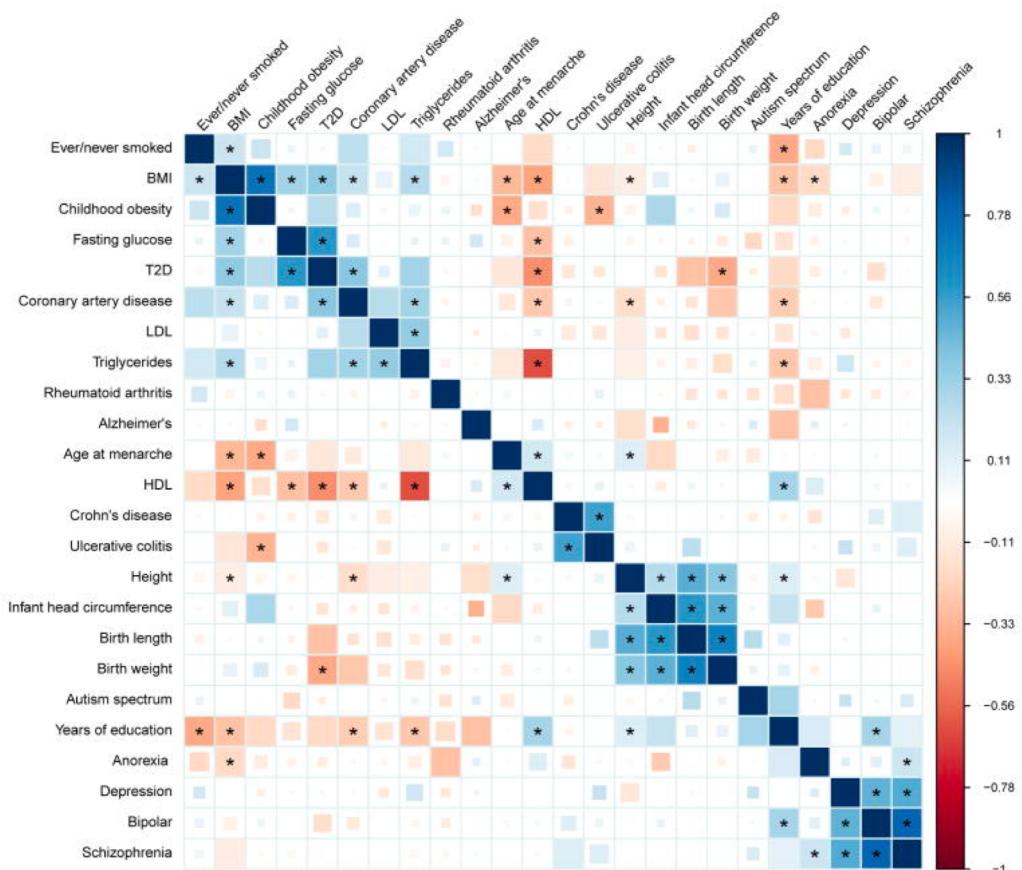
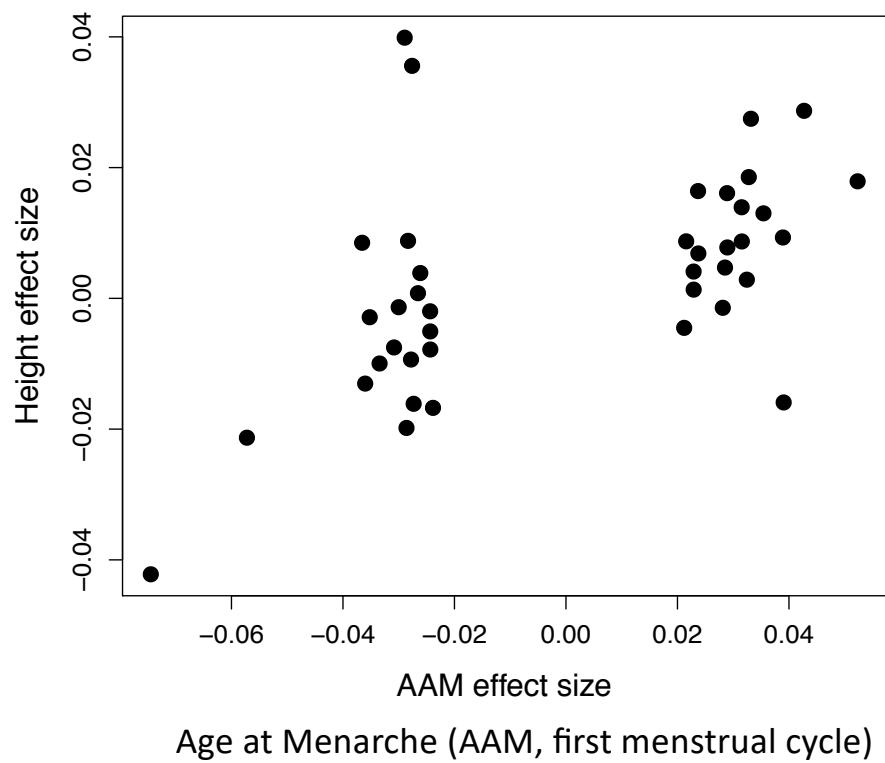
- Why isn't every organism as fast, efficient, attractive as they can be?
- Constraints.
- Evolution is full of trade-offs
 - Given a limited set of resources you have to allocate them.
 - How populations of organisms adapt to these trade-offs, in the face of differences in ecology & environment, generate differences in life histories.

Correlated evolution of Quantitative traits Through Natural Selection

Genetic correlation

The genetic basis of variation in a phenotype is never independent of some other phenotypes.

Most tradeoffs can be thought of in terms these correlations.



An atlas of genetic correlations across human diseases and traits.

Bulik-Sullivan B^{1,2,3}, Finucane HK⁴, Anttila V^{1,2,3}, Gusev A^{5,6}, Day FR⁷, Loh PR^{1,5}, ReproGen Consortium; Psychiatric Genomics Consortium; Genetic Consortium for Anorexia Nervosa of the Wellcome Trust Case Control Consortium 3, Duncan L^{1,2,3}, Perry JR⁷, Patterson N¹, Robinson EB^{1,2,3}, Daly MJ^{1,2,3}, Price AL^{1,5,6}, Neale BM^{1,2,3}.

Genetic correlations

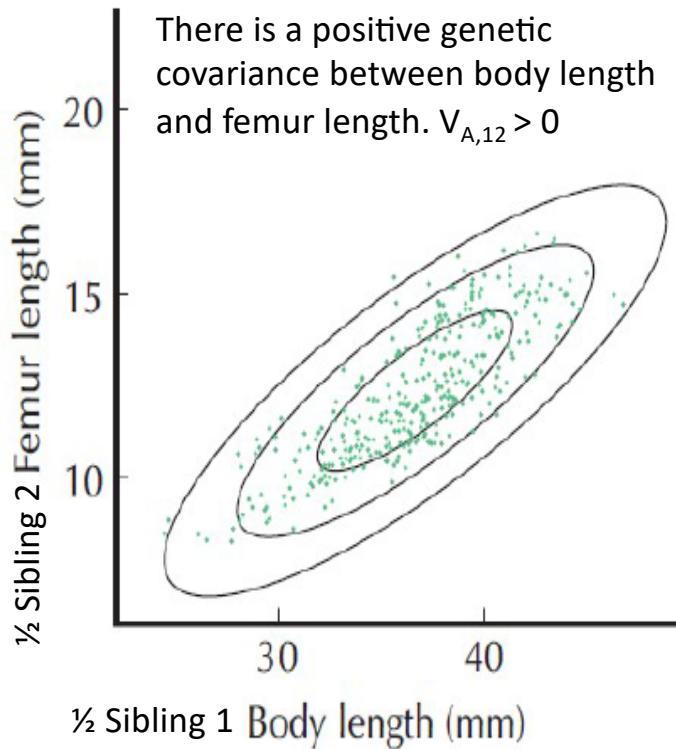
Some pleiotropic effects are more complicated and require a much deep understanding of the organism and/or development/molecular biology of the changes involved.

Also genetic correlations can be driven by linkage:
Alleles responsible for different traits can be physically linked on a chromosome.

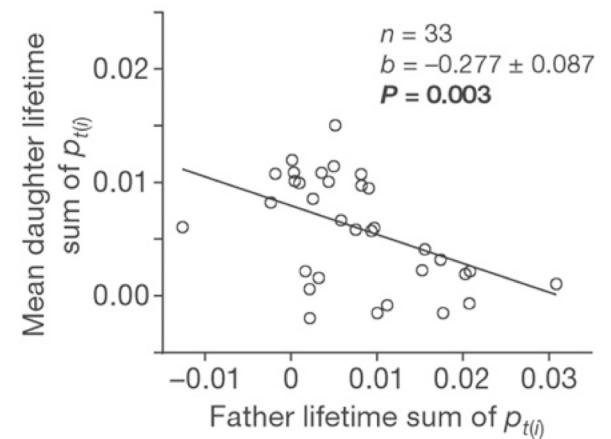
(Also by assortative mating)

--Thus the genetic variance of traits is often partially shared.
i.e. the **genetic covariance** of traits is often not zero.

We can estimate the genetic covariance between traits (1,2) by examining the covariance between traits across relatives, $V_{A,12}$



There is a negative genetic covariance between male fitness And female fitness in red deer $V_{A,12} < 0$



The response to selection on multiple traits

$$R_1 = V_{A,1}\beta_1 + V_{A,12}\beta_2$$

$$R_2 = V_{A,2}\beta_2 + V_{A,12}\beta_1$$

R_1 response to selection (change in mean) across generations for trait 1

R_2 response to selection (change in mean) across generations for trait 2

$V_{A,1}$ and $V_{A,2}$ additive genetic variance for phenotype 1 & 2 respectively

$V_{A,12}$ additive genetic covariance between phenotype 1 & 2

β_1 selection gradient for trait 1

β_2 selection gradient for trait 2

Antagonistic pleiotropy

Selection on traits with non-zero genetic covariance can alter the course taken by adaptation.

Selection on one trait can actively prevent adaptation through another trait due to genetic covariance

Character gradient (S/V_p)	Response	Selection
Character	i	β
Weight	0.28	0.23
Bill length	0.21	-0.17
Bill depth	0.30	0.43

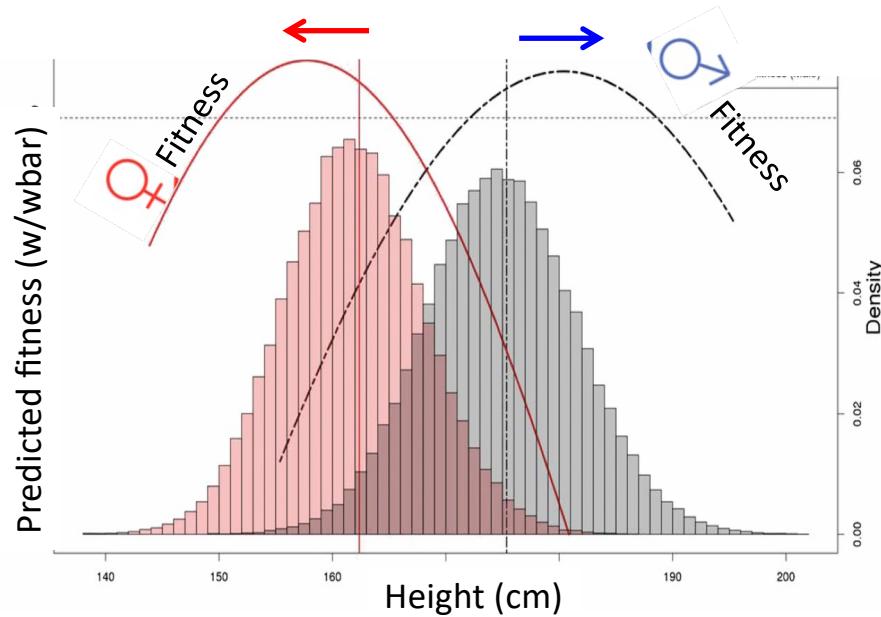
Beak length increased despite shorter beaks being selected for because it has a positive genetic covariance with beak depth and weight.

sexually antagonistic pleiotropy

Sexual antagonism selection on height

$$\beta_{HT,F} = -0.028 \pm 0.0021 (P < 10^{-39})$$

$$\beta_{HT,M} = 0.022 \pm 0.0025$$



+ve genetic corr. between sexes
inhibits optimum solution for both
sexes

Evidence of directional and stabilizing selection in contemporary humans

Jaleal S. Sanjak, Julia Sidorenko, Matthew R. Robinson,
Kevin R. Thornton, and Peter M. Visscher

Haploid model of selection

Consider alleles A_1 and A_2 at frequency p_t and $q_t = 1 - p_t$ at time t , and assume that the population size N is so large that we can ignore genetic drift.

Diploid model of selection

Consider alleles A_1 and A_2 at frequency p_t and $q_t = 1 - p_t$ at time t , and assume that the population size N is so large that we can ignore genetic drift.

Genotype	A_1A_1	A_1A_2	A_2A_2
Absolute fitness	w_{11}	w_{12}	w_{22}

Change in allele frequencies due to viability selection

$$p_{t+1} = f_{11} + \frac{1}{2} f_{12} = \frac{w_{11}p_t + w_{12}q_t}{\bar{w}} p_t$$

$$\Delta p_t = p_{t+1} - p = \frac{w_{11}p_t + w_{12}q_t}{\bar{w}} p_t - p_t$$

$$\bar{w}_1 = w_{11}p_t + w_{12}q_t$$

$$\bar{w}_2 = w_{12}p_t + w_{22}q_t$$

Marginal fitnesses of A_i : weighted mean fitness across genotypes carrying A_i

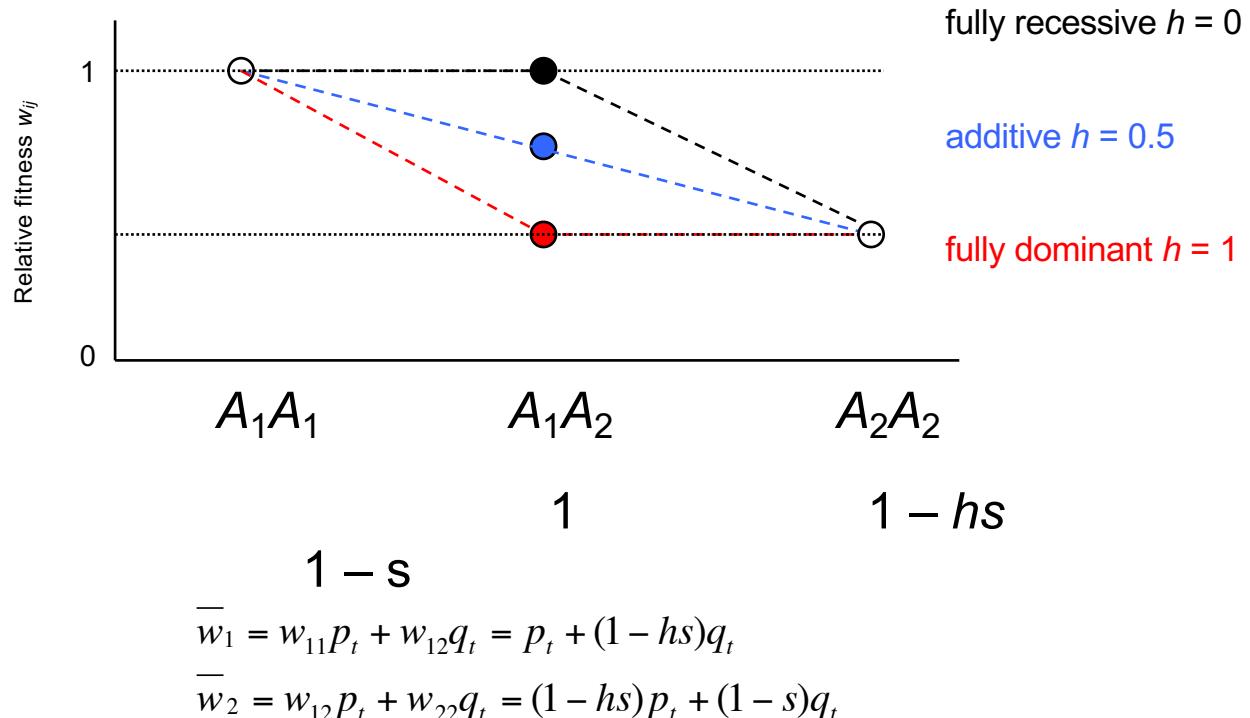
$$\Delta p_t = \frac{\bar{w}_1 - \bar{w}_2}{\bar{w}} p_t q_t, \quad \Delta q_t = -\Delta p_t$$

Frequency of A_1 is expected to increase if the marginal fitness of A_1 is higher than A_2 , regardless of how small the difference

$$\Delta p_t = \frac{1}{2} p_t q_t \frac{dw}{dp_t}$$

Alternative formulation by Haldane (1924). Frequency of A_1 increases if mean fitness is an increasing function of frequency of A_1 .

Directional selection

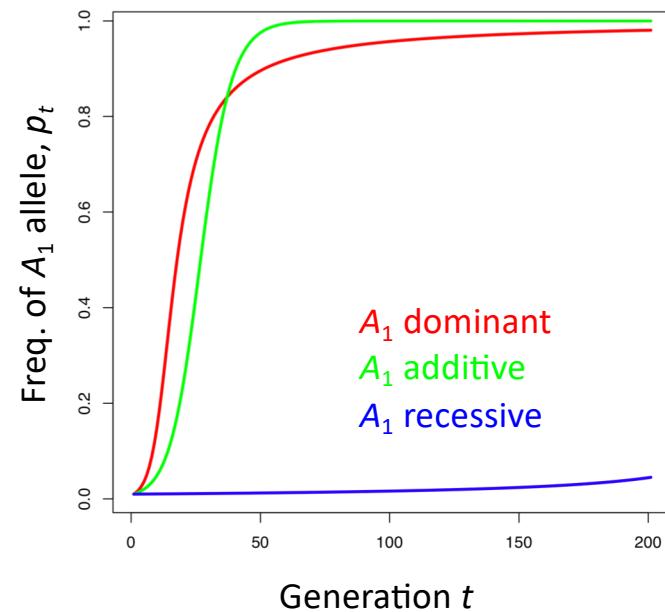
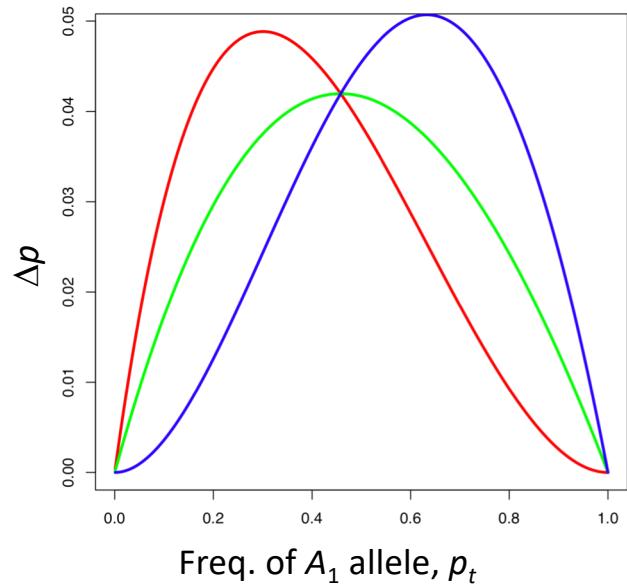


$$\Delta p_t = \frac{\bar{w}_1 - \bar{w}_2}{\bar{w}} p_t q_t = \frac{p_t hs + q_t s(1-h)}{\bar{w}} p_t \underset{s \ll 1}{\approx} \frac{1}{2} s p_t q_t$$

$$\bar{w}_1 = w_{11}p_t + w_{12}q_t = p_t + (1-hs)q_t$$

$$\bar{w}_2 = w_{12}p_t + w_{22}q_t = (1-hs)p_t + (1-s)q_t$$

$$\Delta q_t = \frac{\bar{w}_2 - \bar{w}_1}{\bar{w}} p_t q_t = \frac{-p_t hs - q_t s(1-h)}{w} q_t$$



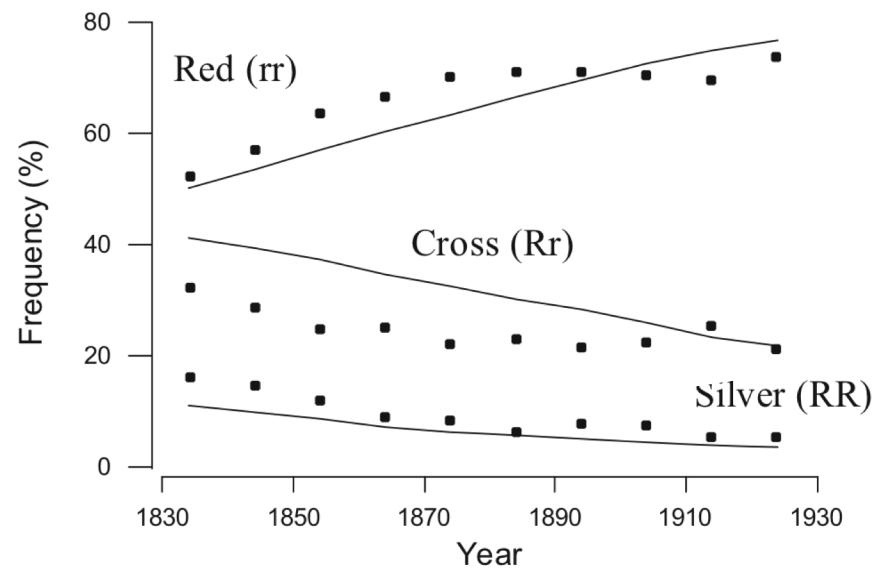
Beneficial dominant alleles are quick to spread but slow to fix.



Red Morph:
Homozygotes rr and heterozygotes rR



Silver fox morph :RR homozygote



Silver fox pelts were particularly valuable to hunters