I. Last lecture we showed that:

$$\Delta \bar{z} = h^2 Cov[z, w] = \frac{G}{V[z]} \beta V[z] = G\beta$$
⁽¹⁾

Where β is the slope of the linear regression of relative fitness on individual phenotype.



II. What do these expressions tell us about evolution by natural selection?

- Q1: What determines the rate of evolution?
- Q2: What determines the direction of evolution?
- Q3: What role does phenotypic variation play?

III. How does adaptation influence ecology?

We saw in section two that phenotypic variation for a trait influencing fitness causes the population mean phenotype to evolve. Can we also predict how population size will change in a phenotypically variable and evolving population?

The total population size in the next generation is:

$$N' = \int W(z)N(z)\,dz$$

Doing some simple algebra:

$$N' = N \int \frac{W(z)N(z)}{N} dz$$
$$N' = N \int W(z)f(z) dz$$
$$N' = N\overline{W}$$
(2)

 \rightarrow The change in population size depends on the mean ***absolute*** fitness of the population.

How does mean fitness change over time?

Equation (1) is valid for any trait. What if the trait of interest were absolute fitness?

$$\begin{split} \Delta \bar{z} &= h^2 Cov[W,w] \\ = h^2 (E[W*w] - E[W]E[w]) \\ &= h^2 \left(E\left[W*\frac{W}{\overline{W}}\right] - E[W] \right) \\ &= h^2 \left(\frac{1}{\overline{W}} E[W*W] - E[W] \right) \\ &= h^2 \left(\frac{1}{\overline{W}} \overline{W^2} - \overline{W} \right) \\ &= h^2 \left(\frac{1}{\overline{W}} (V[W] + \overline{W}^2) - \overline{W} \right) \\ &= h^2 \left(\frac{1}{\overline{W}} (V[W] + \overline{W}^2) - \overline{W} \right) \end{split}$$

$$= h^{2} \left(\frac{V[W]}{\overline{W}} \right)$$
$$= \frac{G}{V[W]} \left(\frac{V[W]}{\overline{W}} \right)$$

 \rightarrow The change in the population mean ***absolute*** fitness over a generation is:

$$\Delta \overline{W} = \frac{G}{\overline{W}} \qquad \text{or} \qquad \overline{W}' = \overline{W} + \frac{G}{\overline{W}} \tag{3}$$

This is essentially Fisher's fundamental theorem of natural selection: the change in population mean fitness is proportional to the additive genetic variance for fitness.







IV. How can we use the theory to predict/understand adaptation in the real world?

What quantities would we want to measure?

How could we measure them?

What assumptions must we make?

How could we standardize the data so that selection could be compared across studies?

Total fitness vs. Fitness components and the realities of studying NS in natural pops

A. Measuring heritability

The heritability of a population, h^2 , can be estimated by calculating the slope of the linear regression of mid-parent phenotype on offspring phenotype. Although sufficient for the purposes of this class, this is a crude approach and much more sophisticated methods exist.

B. Estimating the strength and form of selection

Directional Selection

i. Binary fitness data (e.g., survived vs. died) can be easily analyzed by simply estimating the difference between the mean of the surviving individuals and the mean of the entire population prior to selection. The result is an estimate of the *selection differential S*. Multiplying the selection differential by the heritability yields a prediction for the change in the trait mean over a single generation.

ii. Continuous fitness data (e.g., fertility, seed set, growth rate, etc) can be analyzed by calculating the slope of the regression of relative fitness (or a component of fitness) on trait value. This slope is equal to the selection gradient β . Multiplying this selection gradient by the additive genetic variance *G*, yields a prediction for the change in the trait mean over a single generation.

Warnings and conventions

i. *Warning:* Fitness data rarely conforms to the assumptions of linear regression. Thus, it is often tempting to transform the fitness data. DO NOT do this. Transforming the fitness data yields incorrect prediction. The only adjustment you should make to fitness is to transform absolute fitness into relative fitness.

ii. *Convention:* Trait values are generally transformed into units of phenotypic standard deviations. Although this does not influence the accuracy of prediction, it facilitates comparison across studies where traits may have very different units of measurement.