Models in Ecology

"All models are false
but some models are useful"

- Sorts of Models (not exhaustive and not necessarily exclusive):
  - Verbal
  - Descriptive
  - Quantitative
  - Predictive
- Something All Models Share: Simplifying Assumptions
  - Robustness: how many assumptions can you violate before the model becomes seriously inaccurate?
  - Depending on the application of the model, the violations of the assumptions might actually be what you are interested in.
- We will concern ourselves primarily with quantitative/predictive models in this course.
- You should always be asking yourself, "What are the assumptions of this model?"

Evolutionary Fundamentals for Ecology

Principles of Ecology
Biology 472

6/22/99

Objective

Review the basic notions of phenotype, genotype, selection, and evolution. Give an example of the evolution of a simple trait controlled by a single locus (melanism in moths). Then consider quantitative characters influenced by many loci and by environmental factors. This brings us to quantitative genetics. We will try to get through enough of that field to understand what narrow-sense heritability is and we will review heritabilities for the sorts of traits we will be investigating for the first half of the quarter.

Some Review

$$\text{Genotype} \xrightarrow{\text{environment}} \text{Phenotype}$$

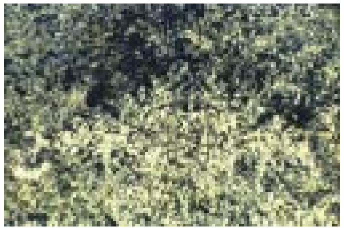
- Genotypes: the genetic "architecture" that the individual carries and which has a chance to be transmitted to offspring
- Phenotype: this is essentially "what you see." The outcome of a melting pot of genetic and environmental factors
- Evolution as change of gene frequencies
- Natural selection operates through fitness differences between different phenotypes
  - Ultimately these are differences in reproductive success
- Differential reproductive success and natural selection "become interesting" when there is a correspondence between phenotype and genotype
- Two situations in which evolution on a trait has a hard time occurring:
  - canalization: many genoytpes $\Longrightarrow$ single phenotype
  - environmental plasticity: when many different phenotypes have the same underlying genotype

A Classic Example of Evolution

- The pepper-moth, *Biston betularia*, and the Industrial Revolution
- Two morphs—dark (melanized) and light
- Melanization controlled by a single autosomal locus (dark = dominant trait)
- Before the Industrial Revolution tree trunks were lighter in color
  - Light-colored morph was better camoflauged
- Dark morphs hide better on soot-covered trees
- Over ≈ 40 generations the freq. of the dark morph increased from about 2% to about 94% in some polluted forests.
- Kettlewell's mark-recapture experiments

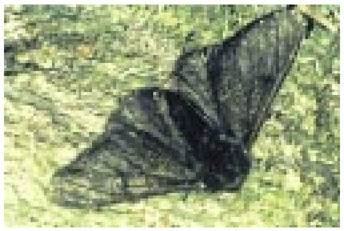
- But this is all very simple!!
- The "one-trait, one-locus" paradigm doesn't apply to more complex traits

Two Morphs of the Pepper-Moth



(a) Light on Unpolluted

(b) Light on Polluted



(c) Dark on Unpolluted

(d) Dark on Polluted

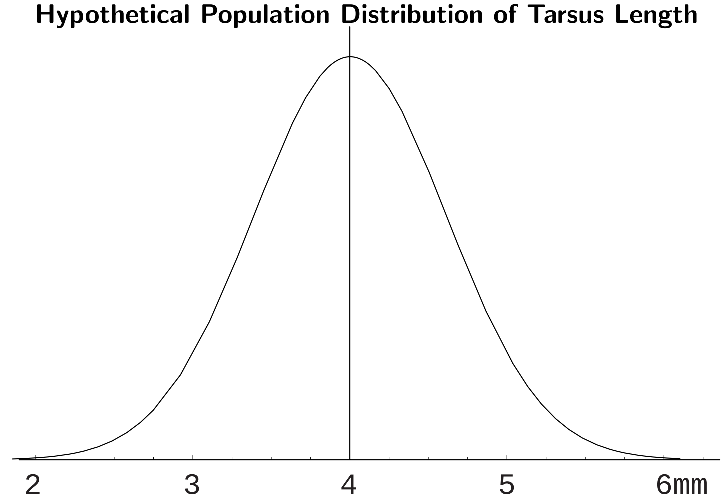
Variation, Fitness, and Heritability in More Complex Traits

- Many traits of interest are controlled by multiple genes
- Traits might be continuous
- *Quantitative genetics* is the field that seeks to understand variation, heritability, and fitness of such traits
  - A spectacular achievement of the 20th century
  - But very complex
  - Eagerly accepted since its inception by animal and plant breeders, but ecologists have been slower to appreciate its utility
  - Recently, however, that trend is changing
- For today we want to take home an understanding of:
  - Breeding Values
  - Heritability
  - Additive Genetic Variance

Consider a Quantitative Trait

- How about tarsus length in red-legged grasshoppers

Hypothetical Population Distribution of Tarsus Length



There is variation from **Genetic** and **Environmental** sources
$\text{Total Phenotypic Variance} = V_G + V_E \ \ (+2\text{Cov}_{G,E})$

The "Breeding Value of an Individual"

- The Breeding Value *of an individual* may be obtained by a thought experiment:
  - Produce many offspring by mating the individual at random with the rest of the population
  - Compute the mean tarsus length of that individual's offspring
  - Multiply by two the difference between that figure and the *population's* mean tarsus length
  - That gives you the individual's breeding value
- Consider doing that with every individual in the population and looking at the distribution of breeding values over all the individuals in the population
- The variance of that distribution of breeding values equals the *additive genetic variance*. This is the most important part of the variance of phenotypes that can be attributed to genetic differences.

$$V_G = V_A + V_D + V_I$$

Additive Genetic Variance

This is the amount of variation in a trait that can be explained by applying to it a very simple model of genetic variation. Namely:

- There are many loci of small effect
- The contribution of each locus to the trait only depends *additively* on the number of alleles (0, 1, or 2) of a particular type at that locus
- Hence this model does not include dominance or epistasis

- The additive genetic variance is, however, that which is most available to alteration by natural selection
- Thus one defines "heritability in the narrow sense," or h^2 as the proportion of the total phenotypic variance accounted for by the additive genetic variance

Estimates of Heritability in Wild Populations

From Mousseau and Roff (1987) as presented in Stearns (1992): Heritability estimates for different types of traits in populations of wild animals.

	Life History	Physiology	Behavior	Morphology
n	341	104	105	570
Mean Heritability	0.262	0.330	0.302	0.461
S.E.	0.012	0.027	0.023	0.004

- In studying evolutionary ecology, we will focus on Behavorial traits and Life-History traits

Using Quantitative Genetics to Study Evolutionary Ecology

In addition to allowing people to estimate heritabilities and selection pressures on traits, a quantitative genetics perspective is available for learning more about the genetic constraints on evolution (genetic correlations between traits that could impede evolutionary progress).

Given this it seems as though it would provide a worthy paradigm for analyzing the evolution of ecological strategies. However, in behavioral ecology the quantitative genetics perspective has been rarely adopted. Rather, people have traditionally used optimality models and game theoretic models. We'll see those starting on Thursday, returning to a more quantitative genetic perspective when we look at the evolution of life-history strategies later in the quarter.