

**Quantitative characters I: polygenes and environment**

Most ecologically important quantitative traits (QTs) vary. Distributions are often *unimodal* and approximately *normal*. Offspring and parents are *correlated*. What's the explanation?

Independent contributions by genotypes at *many loci*, and by *random environmental influences*.

Number of individuals vs Height (in) for Men and Women. Photograph of corn cobs labeled with numbers.

**A QT is anything you can measure on a scale (with units of some kind).**

Some examples:  
 Morphology (size, shape)  
 Physiology (pressure, temp., rate)  
 Performance (speed, puzzle-solving)  
 Fitness! (seeds, surviving offspring)

Number of individuals vs Swimming speed (m/s) for Men and Women. Histograms of Beak depth (mm) and PC general cognitive ability.

**Most quantitative traits are distributed approximately normally.**

A normal distribution is fully described by its *mean* and *variance* (or *standard deviation*). The variance is the *average squared deviation from the mean*. The standard deviation is the *square root of the variance*.

Dermal ridges

Frequency of occurrence vs Total number of dermal ridges.  $N = 825$ . Mean  $\approx 145$  ridges, s.d.  $\approx 40$  ridges.

Normal distributions are easy because they're all the *same!* Just *subtract the mean* from every observation (so the mean becomes 0). Then *divide every observation by the standard deviation* (so it and the variance become 1).

And you get the "standard normal" Upshot: the units of measurement are always arbitrary!

Standard normal distribution curve showing 68% of area between  $-\sigma$  and  $\sigma$ , 96% between  $-2\sigma$  and  $2\sigma$ , and 99.7% between  $-3\sigma$  and  $3\sigma$ .

**The simplest QT model: independent loci with "+" and "-" alleles**

Assume each individual's trait value is the *sum* of its "+" alleles at all loci. That is, a "+" allele at locus A has the *same* effect as a "+" at locus B. Then with random mating and free recombination, we get *binomial* distributions. As the number of loci increases, these distributions become *smooth* and *normal*.

Parents Short (aa) and Tall (AA) leading to F1 (Aa) and F2 binomial distribution. Parents Short (aabb) and Tall (AABB) leading to F1 (AaBb) and F2 binomial distribution. Parents Short (aabbccddeeff) and Tall (AABBCCDDEEFF) leading to F1 (AaBbCcDdEeFf) and F2 normal distribution.

**The general model: genomic and environmental "causes" add up**

Mom makes a genomic contribution  $X_m$ . Its variance (over moms) is  $V(X_m)$ . Dad makes a genomic contribution  $X_p$ . Its variance (over dads) is  $V(X_p)$ . The environment makes a contribution  $\epsilon$ . Its variance (over offspring) is  $V(\epsilon)$ .

$P = X_m + X_p + \epsilon$

For any given offspring, its **phenotype** (quantitative character state) is the **sum** of these three contributions. And over the **population** as a whole, the **variance** of the phenotypic values is the **sum of the variances** of the three contributions:

$V(P) = V(X_m) + V(X_p) + V(\epsilon) = V_G + V_E$

(This assumes that the parents are uncorrelated with each other, and with the environment, which is often *roughly* true.)

