# Introduction to Quantitative Genetics

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## In principle:

We can extend **single-locus → multilocus → quantitative models**

**1AA : 2Aa : 1 aa → $(1A_nA_n : 2A_na_n : 1a_na_n)^n$ →** normal distribution

**Genotype / Phenotype correlation →** Heritability
Genotypic expression depends on **environment**
**Heritability** ($h^2$) estimates **proportion of *phenotypic* variation due to *genetic*** variation

***"Is It Genetic?"*** : Genotype / Environmental interaction is variable (& unpredictable)
The **Norm of Reaction** describes this

Heritability is *not* inevitability;
Genetics is *not* destiny

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Variation can be **quantified** (review)

**mean ± standard deviation:** $\bar{X} \pm \sigma$
**variance:** $\sigma^2$

Variation follows "**normal distribution**" (**bell-curve**) **iff**
**Multiple loci** are involved (**quantitative**)
Each locus has about **equal effect** (**additive**)
Each locus acts **independently**
[**interaction variance** (see below) is minimal]
*Ex.:* Suppose a trait is influenced by **5 loci**, each with two alleles **A** & **a**
**A** contributes **2 units** to phenotype, **a** contributes **1 unit**
Range of contributions = (**2**u **aa** : **3**u **Aa**: **4**u **AA**)$^5$
mean = 15 units , range 10 ~ 20 units
(**Aa Bb Cc Dd Ee**) vs (**aa bb cc dd ee ff ~ AA BB CC DD EE FF**)
$3^5$ = **243** genotype classes in **11** phenotype classes → variation continuous

Variation has two sources: **genetic** ($\sigma^2_G$) & **environmental** ($\sigma^2_E$) **variance**

**Variance is additive**: $\sigma^2_{A+B} = \sigma^2 A + \sigma^2 B$

**phenotypic variance** ≡ $\sigma^2_P = \sigma^2 G + \sigma^2_E + \sigma^2_{GxE}$

where $\sigma^2_{GxE}$ is the **interaction variance**, if $\sigma^2 G$ and $\sigma^2_E$ are not independent

*If* $\sigma^2 G$ and $\sigma^2_E$ are *assumed* to be additive, then the interaction variance $\sigma^2_{GxE}$ **~ 0**

**additive variance** ≡ $\sigma^2_A = \sigma^2 G + \sigma^2_E$

**Heritability** ≡ $h^2 = \sigma^2 G / \sigma^2_A = \sigma^2 G / (\sigma^2 G + \sigma^2_E)$

***"heritability** in the **narrow sense"*** ≡ **genetic component** of the **additive variance**
**heritability $h^2$** is the fraction of the (additive) ***phenotypic* variance** due to ***genotypic* variance**
*assuming* genotype / phenotype relationship is ***independent*** of environment

*ignoring* **interaction variance** $\sigma^2_{GxE}$
genotype / phenotype relationship *differs* in different environments.
*Ex*.: same strain of corn produces different yields in different fields

**Artificial breeding** indicates that **phenotypic variation is highly heritable**
**Artificial selection** on agricultural species
Commercially useful traits can be improved by **selective breeding**
**Common Garden** experiments
**Correlation** shows association between variables (cf. **regression** analysis)

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**Mid-parent** value
**Offspring / midparent** correlation estimates heritability

Limits of prediction from **correlation & regression**

For many quantitative traits in many organisms: $h^2 = 0.5 \sim 0.9$

Heritability is typically calculated in a *single* environment.

The **Norm of Reaction** mediates **genotype** through **environment** to produce **phenotype**
**Variation *within* groups**: Is ***variation*** 'genetic' ?
**Variation *among* groups**: Are ***differences*** 'genetic'?

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## Genetics, Heritability, & Society

**"Is it *Genetic*?"**

***Myth 1***: That which is *heritable* is purely *genetic*
**phenotypic variance** ≡ $\sigma^2_P = \sigma^2_G$ [ignore $\sigma^2_E$ & $\sigma^2_{GxE}$]

***Myth 2***: That which is *genetic* is *fixed* & *unchangeable*

*Ex*.:**Heritability, IQ, & Education**
**IQ** test scores in *Homo*: $h^2 = 0.7 \sim 0.8$ *within* groups
Highly heritable traits can be modified by environment if $\sigma^2_{GxE}$ is large

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See also:
Gray & Thompson (2004) [Fig. 3]. Neurobiology of intelligence: ethics and science, *Nature Revs Neurosci* **5**: 471-482.
Foster (2006). Science & Ethics in the Human Genome Project.
American Psychological Association (1995) Intelligence: Knowns and Unknowns
**American Eugenics Archive**

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