STUDY UNIT 6: QUANTITATIVE GENETICS
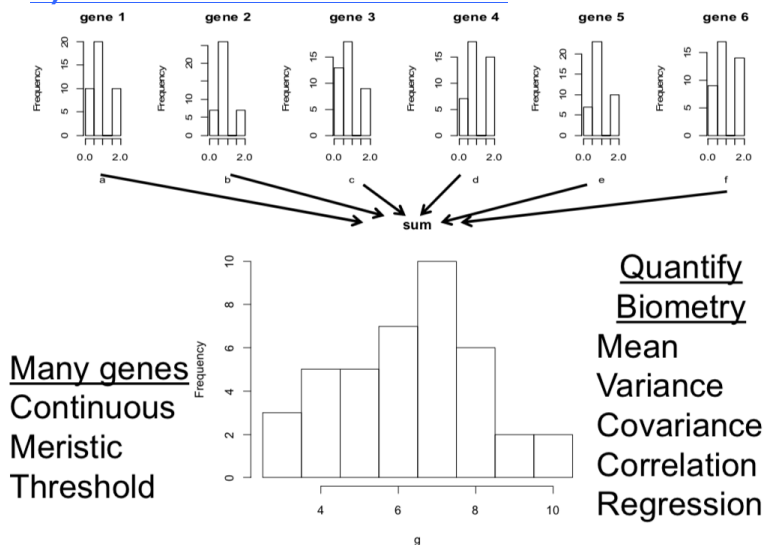
TEXTBOOK CHAPTER 11

LECTURE 18

- Many phenotypic traits (including height , weight , hair and eye colour , blood pressure and serum choleserol levels) are affected by numerous genes : **Quantitative characters**
- **Quantitative Genetics** : The study of the inheritance of quantitative characters
- **Biometrical analysis**: The study of quantitative characters in a population and the similarity of quantitative characters in close relatives
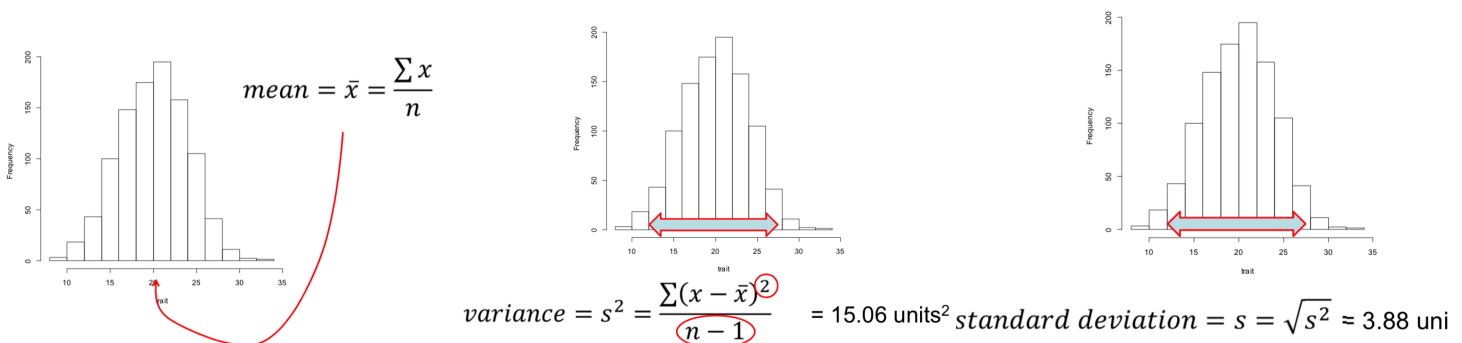
Mendel	Biometrician
• Discrete	• Continuous
• Unchangeable	• Selection
• Jumps	• Slow change
• Offspring are like their parents	• Exceptions
• Dominance	• Blending
• Concerned with single genes	• Concerned with polygenic traits

1)BIOMETRICAL ANALYSIS

Many genes
Continuous
Meristic
Threshold

Quantify
Biometry
Mean
Variance
Covariance
Correlation
Regression

Looking at an example of F.Galton's systematic study of height
- The distribution of the histogram below is a 'bell-shaped' distribution and is typical for most quantitative characters

$$mean = \bar{x} = \frac{\sum x}{n}$$

$$variance = s^2 = \frac{\sum(x-\bar{x})^2}{n-1}$$ = 15.06 units² $standard\ deviation = s = \sqrt{s^2}$ ≈ 3.88 uni

NORMAL DISTRIBUTION
- The probability that an individual has measurement x in a population depends on two parameters:
1. Mean
2. Variance

The distribution has a simple mathematical form:

$$\text{PDF} = f(x|\bar{x}, V) = \frac{1}{\sqrt{2\pi V}} e^{-(x-\bar{x})^2/(2V)}$$ ➔ x is the mean and V is the variance

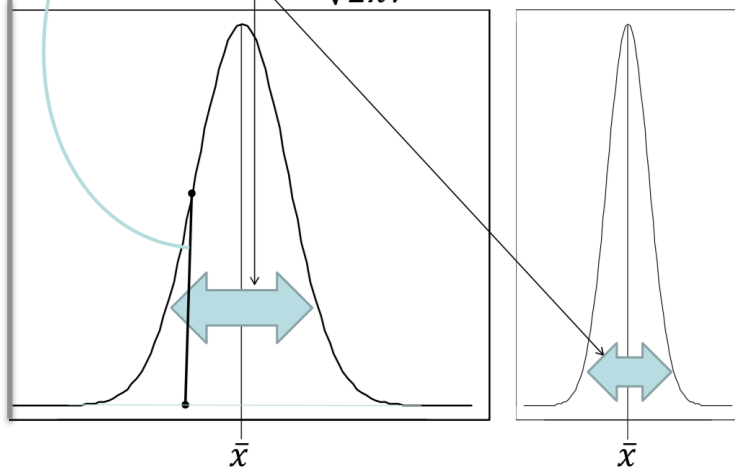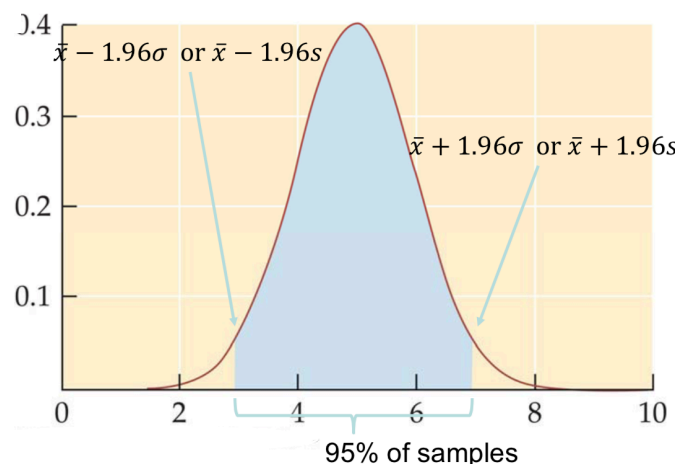*Diagram to the right:* The probability that x is between $\bar{x}$ -1.96σ and $\bar{x}$ + 1.96σ is 0.95
- The reason a normal distribution arises so often is that whenever many random numbers are added, the sum tends to be normally distributed – **The central limit theorem**

We assume that a phenotypic measurement x is the sum of 2 factors:
- X= g + e (where **g** represents net contribution of all geneticc factors to x and **e** represents the net contribution of all environmental factors)
- We assume that genetic and environmental contributions are independent of each other
- V_G: Variance among individuals in all genetic factors that contribute to the trait in question
- V_E: The variance in all environmental factors

BROAD-SENSE HERITABILITY: The fraction of the total variance in x that is attributable to genetic differences

$$H^2 = h_B^2 = \frac{V_G}{V_P} = \frac{V_G}{V_G + V_E}$$

$V_G = V_A + V_I$
- Here the interaction variance includes the effects of interactions between alleles at a locus (dominance) and interactions between alleles at different loci (epistasis)

- The genetic component that is transmitted to each offspring is the **additive genetic component - V_A**
- The genetic component that is not transmitted to each offspring is the **interaction component- V_I**

NARROW-SENSE HERITABILITY:

$$h^2 = \frac{V_A}{V_P}$$

- The total trait variance -VP

To estimate additive genetic variance we compute the covariance between the parental and offspring phenotypes in each set of parent-offspring pairs

$$covariance = Cov_{xy} = \frac{\sum_i (x_i - \bar{x})(y_i - \bar{y})}{n - 1}$$

➔ x is the mean in parents and ȳ is the mean in the offspring
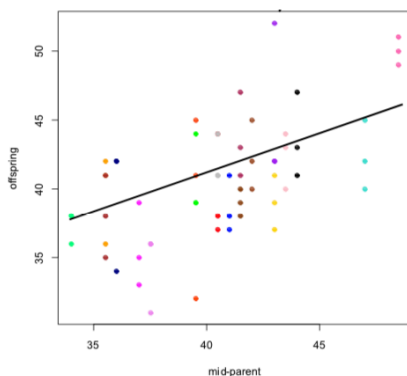
Cov(x,y) = V_A/2
- The factor of ½ is needed because each parent contributes only half of the genes in the offspring

<u>VARIANCE OF THE MID-PARENTAL VALUE</u>
Covariance with the mid-parental value is the same as the covariance with either parent
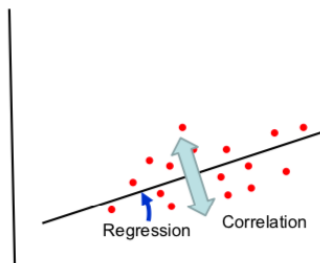
Cov (MP,O) = Cov(P,O) = V_A/2
V_A= 2x Cov(MP,O) = 2 x Cov (P,O)
- MP- Average of the offspring

V_P= V(P)=2V(MP) OR $\sigma_p^2 = 2\sigma_{MP}^2$

$$correlation = \frac{Cov_{xy}}{S_x S_y} \quad \text{Range:-1 to 1}$$

$$regression = b_{yx} = \frac{Cov_{xy}}{S_x^2} \quad s_x^2 = V(x)$$

$$h^2 = \frac{V_A}{V_P} = \frac{2Cov(MP,O)}{2V(MP)} \text{ = regression of offspring on midparents}$$

$$= \frac{V_A}{V_P} = \frac{2Cov(P,O)}{V(P)} \text{ = 2x(regression of offspring on parents)}$$

Regression of y on x = $b_{yx} = \frac{Cov(x,y)}{s_x^2}$