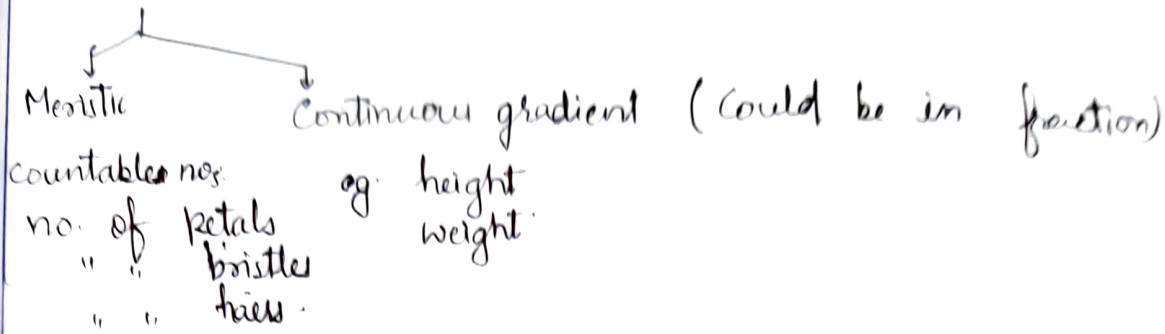


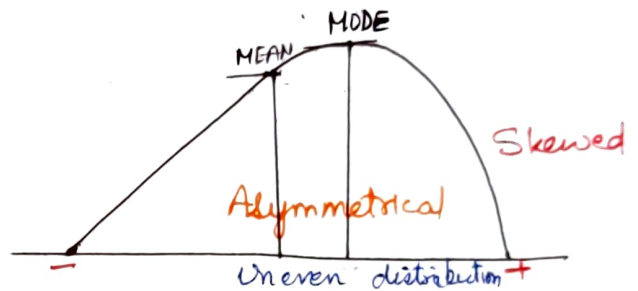
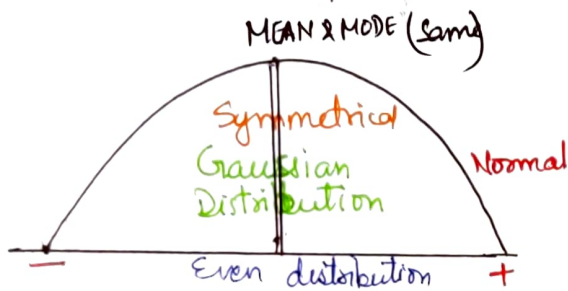
# Quantitative Traits: Quantifiable.

• Metric Trait (measurable)

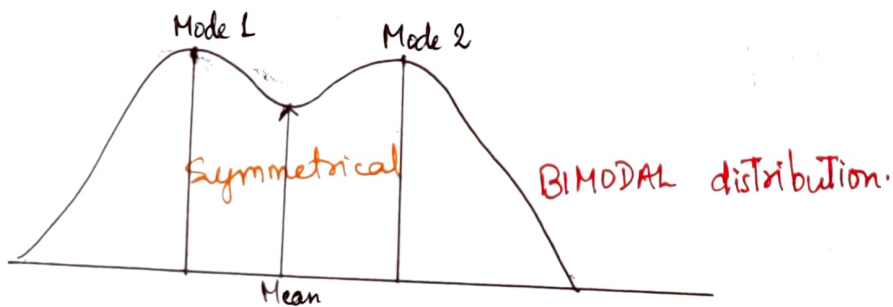


Mean =  $\frac{\text{Sum of the phenotypes}}{\text{Sum of no. of individuals whose values are summed}}$

MODE: Value at the peak of distribution and usually corresponding to the most frequent class of people in distribution.



Mode is peak value always, mean may be equal to mode or may not be.

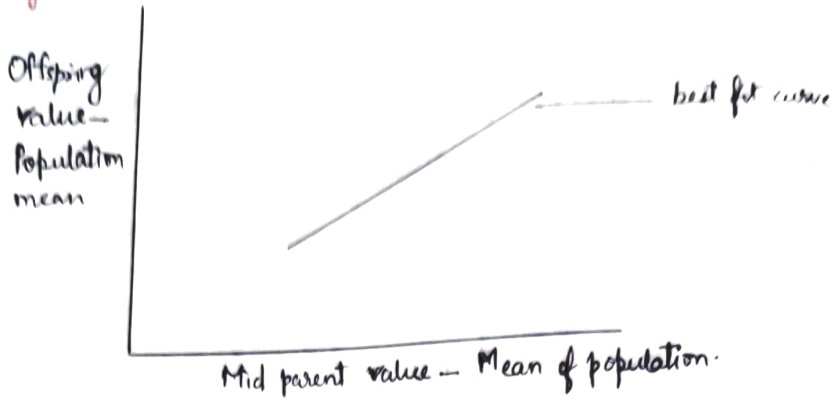


MEDIAN: class that divides the distribution in equal halves by number of individuals.

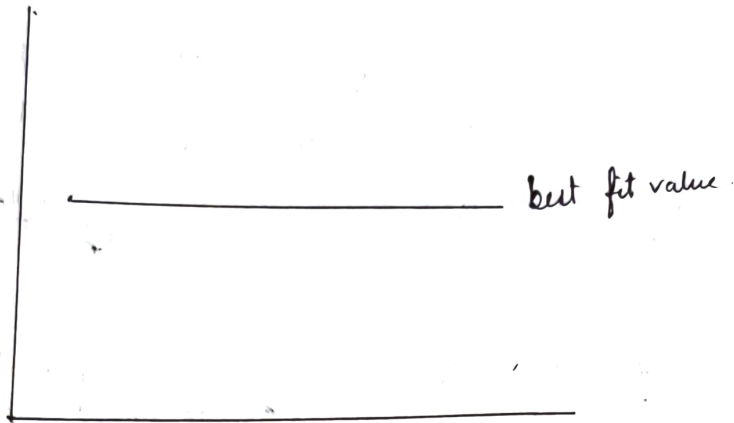
VARIANCE: A measurement of the degree to which individuals within the sample vary from one another.

$$S^2 = \text{Variance (V)} = \frac{\text{Sum of the squared deviation from the mean}}{\text{no. of individuals} - 1} = \frac{\sum (X_i - \bar{X})^2}{n - 1}$$

(1) Height -



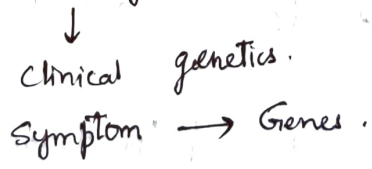
Plot is in an relation with height of offspring vs Mid parent value mean.



Not correlated

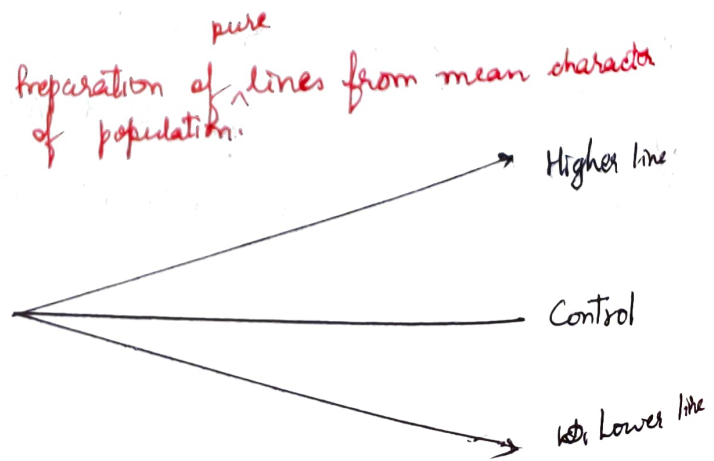
TOOLS FOR ANALYSIS OF INHERITANCE OF POLYGENIC/COMPLEX

- First idea came that - only environment is describing inheritance of traits.
- Environment + Genetics.
- How much genetic (genes??)
- Which are the genes.
- What they do (Molecular pathogenesis)



- ① Family analysis
- ② Twin study.
- ③ Adoption study

↓  
Best strategy to study is Twin - adoption study



Non-Mendelian characters are so called because it doesn't follow pedigree we can't make <sup>pedigree</sup> chart but it follows the <sup>simple</sup> inheritance of trait.

① FAMILY STUDY. Frequency of the trait in individuals of different degrees of relationships.

Degree of genetic relation	Frequency of occurrence
1 <sup>st</sup> Relatives (50%)	40%
2 <sup>nd</sup> " (25%)	20%
3 <sup>rd</sup> " (12.5%)	10%

Frequency of occurrence is decreasing as the degree of relationship is increasing and closeness of relation is decreasing.

Sharing of genes

Directly proportional.

Familial aggregation also called (Familial clustering)

② How much is the co-relation b/w occurrence of trait and genetic relationships → is called a **Familial Risk Ratio (FRR)**. This measurement is calculated in terms of  $\lambda = \frac{\lambda}{\lambda} = FRR$

$\lambda$  value has to be measured.

$$\lambda_R = \frac{\text{Frequency of the disorder in relatives of an affected individual}}{\text{Frequency of the disorder in the population}}$$

These are the polygenic i.e. total gene pool.

~~Total alleles~~

Total no. of genes and alleles in a potentially reproductive gametes is **Gene pool**.

In  $\lambda_R$  R is general denotation of any ~~substance~~ relationship.

$$R = S, P, O, Mz, Dz, 1, 2, 3$$

S - Sibling, P - Parent, O - offspring, Mz - Monozygotic,

Dz - Dizygotic

1, 2, 3 (is degree of relationship)

The degree of relationship remain effective till 3 then after it is not considered.

$$\lambda_R = 1 \text{ (maximum value of } \lambda_R)$$

Chance of developing that trait is not different from general population but equal to any one of the individual

$\lambda_R > 1$  then the disorder is clustered <sup>within</sup> the family.

Familial Risk Ratio =  $\lambda$ .

$\lambda > 1$  then familial clustering.

$\lambda_{MZ} > 1$  for some disorders  
 ↓  
 Twin

Anorexia nervosa - Loss of appetite due to mental disturbances  
 that he/she'll get obese on eating. But if it becomes  
 severe then it is genetic

$\lambda_{MZ} = 710$        $\lambda = 141$   
 General pop<sup>n</sup> = 0.1      11  
 Schizophrenia 48  
 G.P      1

te  
 |10|2018 Degree of family clustering =  $\lambda_R$   
 (Familial Risk Ratio)      calculated in population?      This value is for a particular population. It will vary on changing the

2<sup>nd</sup> relative

	Risk for Relatives <small>observed data</small>	Population incidence	$\lambda_R$
Parents	14.12%	0.8 (For Schizophrenia)	17.65 $(\frac{14.12}{0.8})$
Sibs	8.51%	"	10.6
Childrens	12.31%	"	15.4
Uncle/Aunt	2.01%	"	2.5

O.T.E: In complex trait, population study is essentially required ~~who~~ a  
 familial study may/may not be included. But in Mendel  
 trait only families are studied but not population at all.

Degree of relationship  $\propto$  ~~degree~~ proportion of gene shared

- Whenever incidence level in family matches with population incidence level then it means the disease is not genetically related to particular family.
- A co-relation b/w  $\uparrow$  in degree of relationship with degree of frequency so it is due to genetic component.

## ② TWIN STUDY:

Monozygotic (MZ) ~~1/2~~

One fertilized egg

↓  
split  
↓  
from 2 fetuses

- Either both ♀ or ♂
- Identical twins
- Gene sharing = 100%
- Environmental sharing ~100%

Dizygotic (DZ)

↓  
Two independently fertilized eggs

↓ ↓  
Two fetuses

These are just like siblings but growing together temporarily.

→ ♂ & ♀ both could be in same time

→ Fraternal Twin.

→ Gene sharing 50%

~100%

→ Monozygotic's (MZ) twins

frequency = 3.5/1000 live birth (a globally constant value)

→ Frequency of DZ<sup>twins</sup> → variable worldwide.

East Asia = 1/1000 live birth

Saharan Africa = 12.5/1000 live birth (much high)

Europe = 4.5/1000

→ If both twins are showing (whether they are MZ or DZ) the trait, then it is c/a **Concordance (C)**

If only one twin is showing the trait, then it is c/a **Discordance (D)**

Level of Concordance: It is calculated: