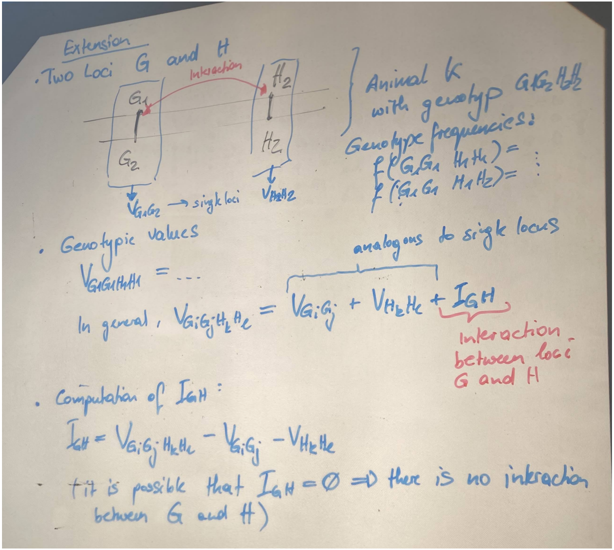
OHP Picture 1



Extension

- Two Loci G and H

Interaction

G_1 G_2 H_2 H_2

$V_{G_1G_2} \rightarrow$ single loci $V_{H_2H_2}$

Animal k with genotyp $G_1G_2H_1H_2$

Genotype frequencies:

$f(G_1G_1\ H_1H_1) = \vdots$

$f(G_1G_1\ H_1H_2) =$

- Genotypic values

$V_{G_1G_1H_1H_1} = \dots$

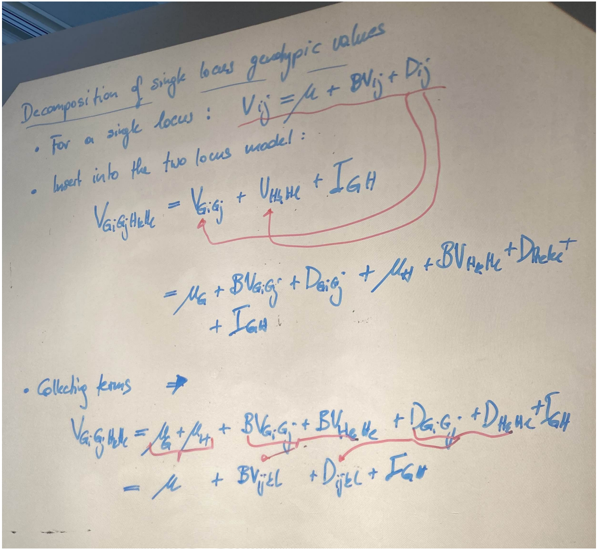
In general, $V_{G_iG_jH_kH_l} = \overbrace{V_{G_iG_j} + V_{H_kH_l}}^{\text{analogous to single locus}} + \underbrace{I_{GH}}_{\text{Interaction between loci G and H}}$

- Computation of I_{GH}:

$I_{GH} = V_{G_iG_jH_kH_l} - V_{G_iG_j} - V_{H_kH_l}$

- (it is possible that $I_{GH} = 0 \Rightarrow$ there is no interaction between G and H)

OHP Picture 2



Decomposition of single locus genotypic values

- For a single locus: $V_{ij} = \mu + BV_{ij} + D_{ij}$
- Insert into the two locus model:

$$V_{G_iG_jH_kH_l} = V_{G_iG_j} + V_{H_kH_l} + I_{GH}$$

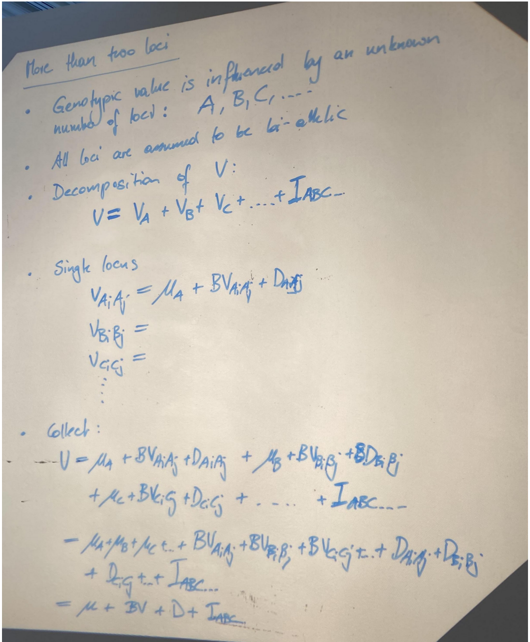
$$= \mu_G + BV_{G_iG_j} + D_{G_iG_j} + \mu_H + BV_{H_kH_l} + D_{H_kH_l} + I_{GH}$$

- Collecting terms ⇒

$$V_{G_iG_jH_kH_l} = \mu_G + \mu_H + BV_{G_iG_j} + BV_{H_kH_l} + D_{G_iG_j} + D_{H_kH_l} + I_{GH}$$

$$= \mu + BV_{ijkl} + D_{ijkl} + I_{GH}$$

OHP Picture 3



More than two loci

- Genotypic value is influenced by an unknown number of loci: $A, B, C, \ldots$
- All loci are assumed to be bi-allelic
- Decomposition of V:

$$V = V_A + V_B + V_C + \ldots + I_{ABC\ldots}$$

- Single locus

$$V_{A_iA_j} = \mu_A + BV_{A_iA_j} + D_{A_iA_j}$$

$$V_{B_iB_j} =$$

$$V_{C_iC_j} =$$

$$\vdots$$

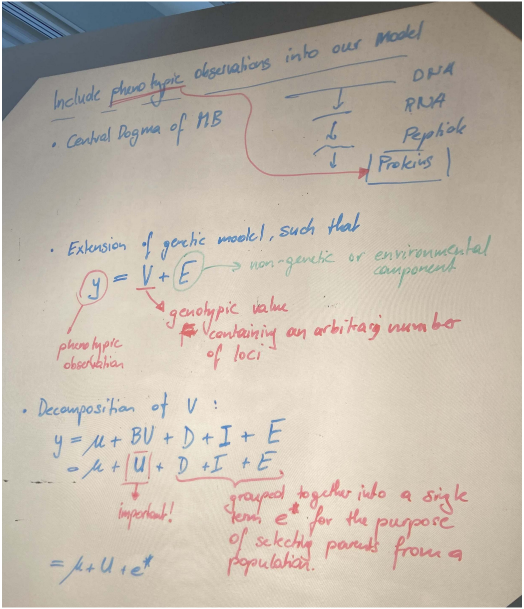
- Collect:

$$V = \mu_A + BV_{A_iA_j} + D_{A_iA_j} + \mu_B + BV_{B_iB_j} + D_{B_iB_j} + \mu_C + BV_{C_iC_j} + D_{C_iC_j} + \ldots + I_{ABC\ldots}$$

$$= \mu_A + \mu_B + \mu_C + \ldots + BV_{A_iA_j} + BV_{B_iB_j} + BV_{C_iC_j} + \ldots + D_{A_iA_j} + D_{B_iB_j} + D_{C_iC_j} + \ldots + I_{ABC\ldots}$$

$$= \mu + BV + D + I_{ABC}$$

OHP Picture 4



Include phenotypic observations into our Model

- Central Dogma of MB

DNA
$\downarrow$
RNA
$\downarrow$
Peptide
$\downarrow$
Proteins

- Extension of genetic model, such that

$$y = V + E$$

non-genetic or environmental component

genotypic value containing an arbitrary number of loci

phenotypic observation

- Decomposition of V:

$$y = \mu + BU + D + I + E$$

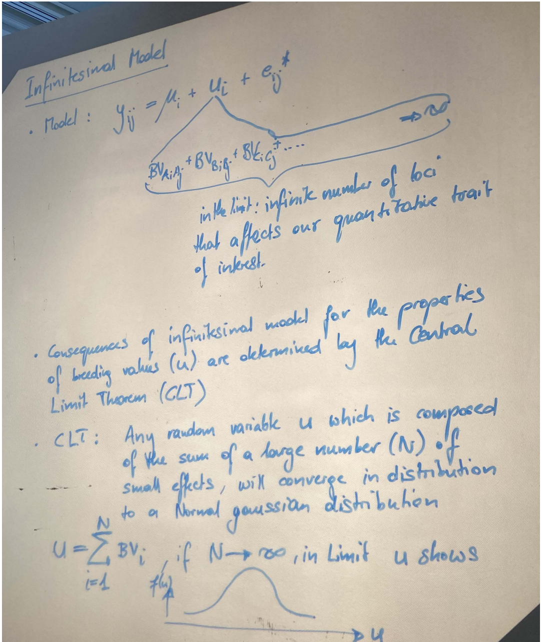
$$= \mu + \boxed{U} + \underbrace{D + I + E}$$

important!

grouped together into a single term e^* for the purpose of selecting parents from a population.

$$= \mu + U + e^*$$

OHP Picture 5



Infinitesimal Model

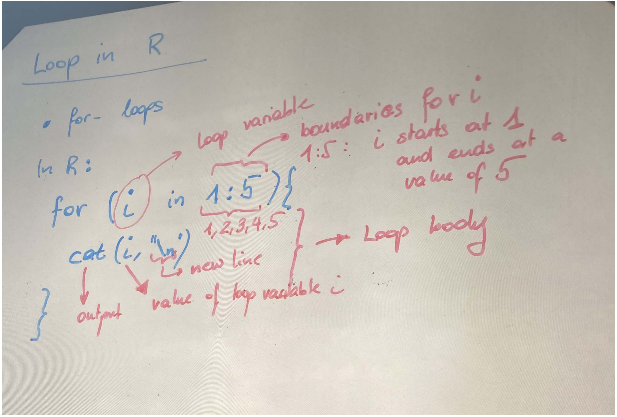
- Model: $$y_{ij} = \mu_i + \underbrace{u_i}_{BV_{A_iA_j} + BV_{B_iB_j} + BV_{C_iC_j} + \dots \to \infty} + e_{ij}^*$$

in the limit: infinite number of loci that affects our quantitative trait of interest.

- Consequences of infinitesimal model for the properties of breeding values (u) are determined by the Central Limit Theorem (CLT)
- CLT: Any random variable u which is composed of the sum of a large number (N) of small effects, will converge in distribution to a Normal gaussian distribution

$u = \sum_{i=1}^{N} BV_i$, if $N \to \infty$, in Limit u shows

OHP Picture 6



Loop in R

- for- loops

In R:

```
for (i in 1:5){
  cat(i, "\n")
}
```

loop variable

boundaries for i

1:5 : i starts at 1 and ends at a value of 5

1,2,3,4,5

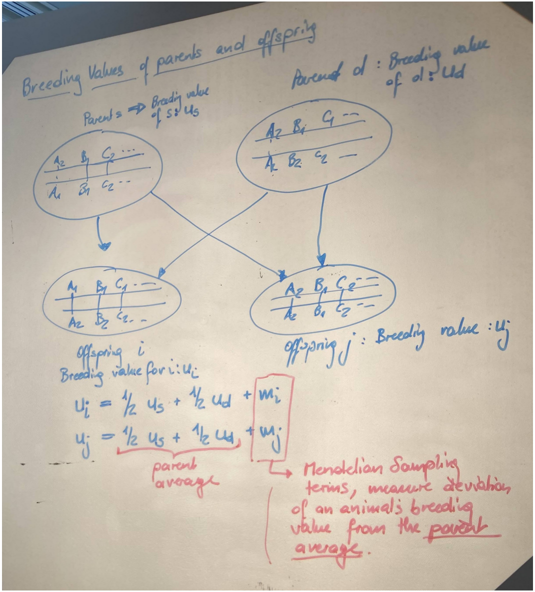
Loop body

new line

output

value of loop variable i

OHP Picture 7



Breeding Values of parents and offspring

Parent s ⇒ Breeding value of s: u_s

Parent d : Breeding value of d: u_d

Offspring i
Breeding value for i: u_i

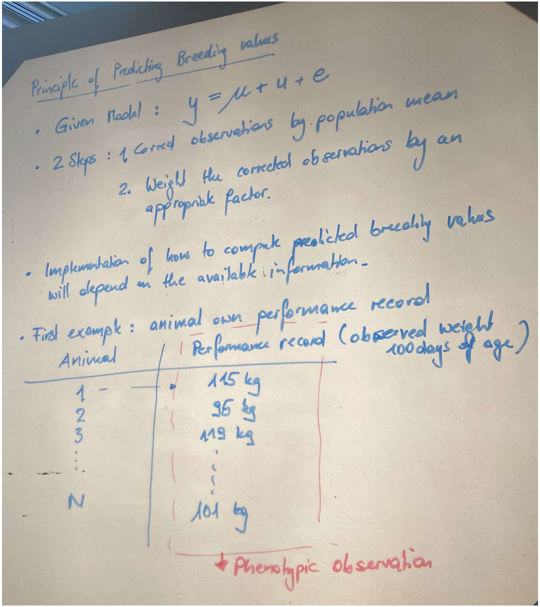
offspring j : Breeding value : u_j

$$u_i = \frac{1}{2} u_s + \frac{1}{2} u_d + \boxed{m_i}$$

$$u_j = \underbrace{\frac{1}{2} u_s + \frac{1}{2} u_d}_{\text{parent average}} + \boxed{m_j}$$

→ Mendelian Sampling terms, measure deviation of an animal's breeding value from the parent average.

OHP Picture 8



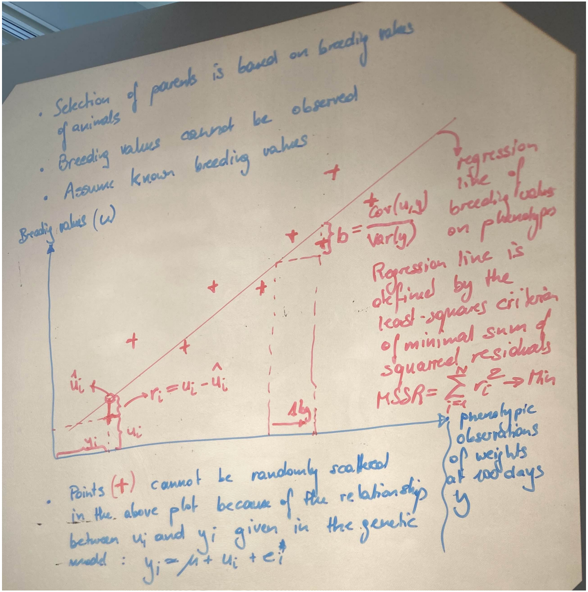
Principle of Predicting Breeding values

- Given Model: $y = \mu + u + e$
- 2 Steps: 1. Correct observations by population mean
  2. Weight the corrected observations by an appropriate factor.
- Implementation of how to compute predicted breeding values will depend on the available information.
- First example: animal own performance record

Animal	Performance record (observed weight 100 days of age)
1	115 kg
2	95 kg
3	119 kg
⋮	⋮
N	101 kg

→ Phenotypic observation

OHP Picture 9



- Selection of parents is based on breeding values of animals
- Breeding values cannot be observed
- Assume known breeding values

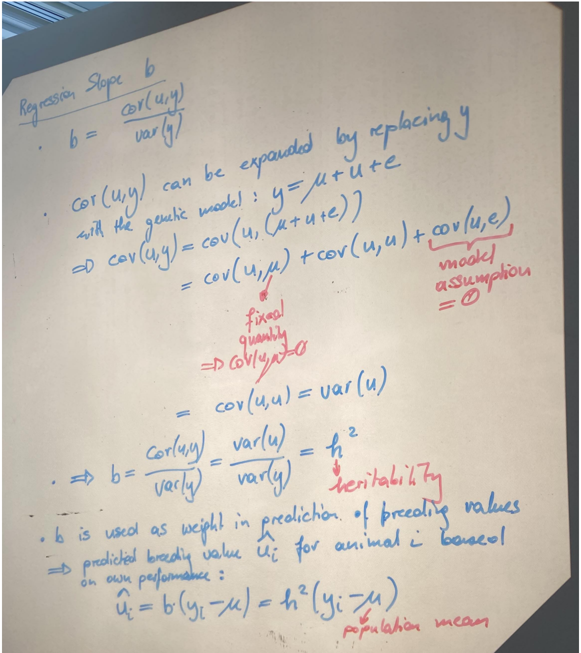
$b = \frac{cov(u,y)}{var(y)}$

Regression line is defined by the least-squares criterion of minimal sum of squared residuals

$MSSR = \sum_{i=1}^{N} r_i^2 \rightarrow Min$

- Points (+) cannot be randomly scattered in the above plot because of the relationship between u_i and y_i given in the genetic model : $y_i = \mu + u_i + e_i$

OHP Picture 10



Regression Slope b

- $b = \frac{\mathrm{cov}(u,y)}{\mathrm{var}(y)}$
- $\mathrm{cor}(u,y)$ can be expanded by replacing y with the genetic model: $y = \mu + u + e$

$$\Rightarrow \mathrm{cov}(u,y) = \mathrm{cov}(u, (\mu + u + e))$$

$$= \mathrm{cov}(u,\mu) + \mathrm{cov}(u,u) + \underbrace{\mathrm{cov}(u,e)}_{\text{model assumption } = 0}$$

fixed quantity

$\Rightarrow \mathrm{cov}(u,\mu) = 0$

$$= \mathrm{cov}(u,u) = \mathrm{var}(u)$$

- $\Rightarrow b = \frac{\mathrm{Cor}(u,y)}{\mathrm{var}(y)} = \frac{\mathrm{var}(u)}{\mathrm{var}(y)} = h^2$

heritability

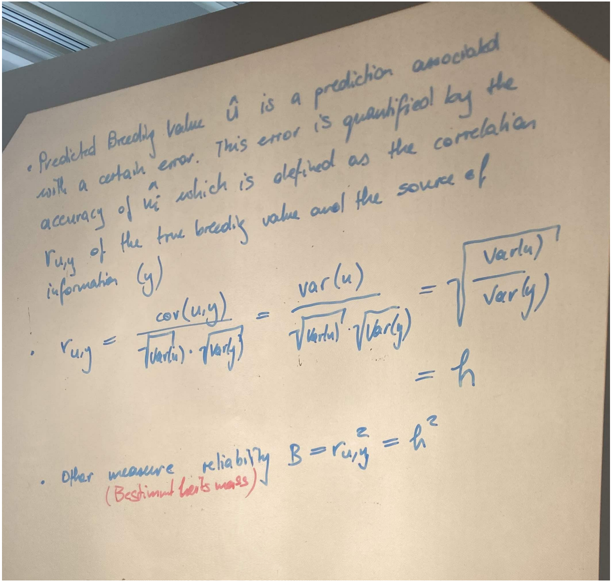
- b is used as weight in prediction of breeding values

$\Rightarrow$ predicted breeding value $\hat{u}_i$ for animal i based on own performance:

$$\hat{u}_i = b \cdot (y_i - \mu) = h^2 (y_i - \mu)$$

population mean

OHP Picture 11



- Predicted Breeding Value $\hat{u}$ is a prediction associated with a certain error. This error is quantified by the accuracy of $\hat{u}_i$ which is defined as the correlation $r_{u,y}$ of the true breeding value and the source of information (y)

- $$r_{u,y} = \frac{cov(u,y)}{\sqrt{Var(u)} \cdot \sqrt{Var(y)}} = \frac{var(u)}{\sqrt{Var(u)} \cdot \sqrt{Var(y)}} = \sqrt{\frac{Var(u)}{Var(y)}}$$
$$= h$$

- Other measure reliability (Bestimmtheitsmass) $B = r_{u,y}^2 = h^2$