

# Genetic Evaluation

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# Consequences of Definition of Breeding Value

- ▶ Based on the average of a large number of offspring, because
  - ▶ offspring inherit a random sample of parental alleles
  - ▶ average over a large number of offspring reduces sampling effect
- ▶ The breeding value is defined as a deviation from the population mean
  - ▶ population mean depends on allele frequencies which are specific for each population
  - ▶ hence breeding values can only be compared within one population.
- ▶ Because the breeding value is defined as a deviation its expected value of the breeding value is 0

# The Basic Model

$$y_{ij} = \mu_i + g_i + e_{ij}$$

where

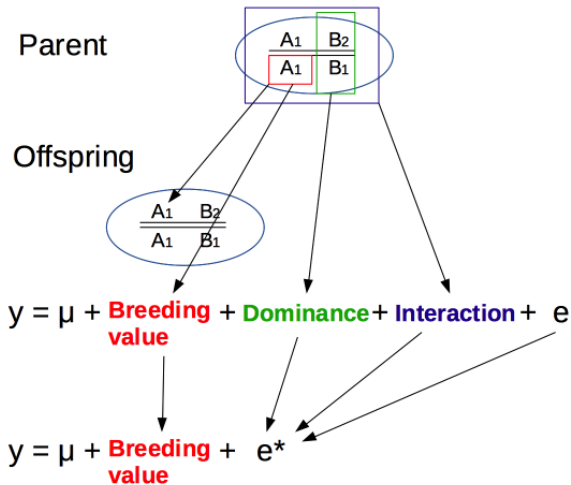
$y_{ij}$   $j^{th}$  record of animal  $i$

$\mu_i$  identifiable fixed environmental effect

$g_i$  sum of all additive ( $a$ ), dominance ( $d$ ) and epistatic effects

$e_{ij}$  random environmental effects of animal  $i$

# Re-arranging Terms



## New Model

$$y_{ij} = \mu_i + a_i + e_{ij}^*$$

where

$y_{ij}$   $j^{th}$  record of animal  $i$

$\mu_i$  identifiable fixed environmental effect

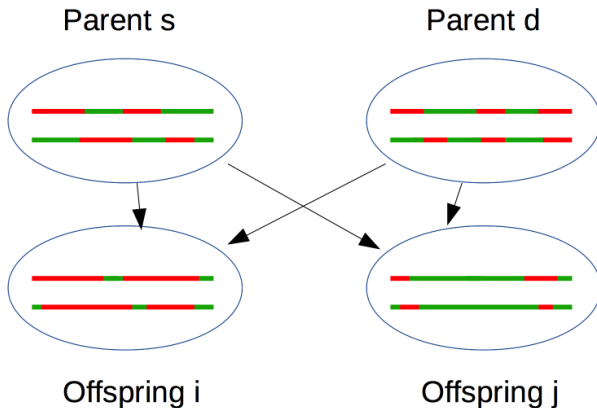
$a_i$  sum of all additive ( $a$ ) genetic effects of the genotype of animal  $i$

$e_{ij}^*$  dominance, epistatic and random environmental effects of animal  $i$  in record  $j$

# Infinitesimal Model

- ▶ Central Limit Theorem for  $a_i$  and  $e_{ij}$  lead to **multivariate normal distributions** with
  - ▶  $E(a) = 0$  and  $E(e) = 0$  and
  - ▶ Known variances and co-variances
  - ▶ No co-variances between  $a_i$  and  $e_{ij}$
- ▶  $\mu$  is assumed to be constant for a given evaluation
- ▶ Phenotypic observation  $y_{ij}$  is the sum of two normally distributed random variables, therefore
  - ▶  $y_{ij}$  also follows a multivariate normal distribution
  - ▶  $E(y) = \mu$

# Decomposition of Breeding Value



$$a_i = 1/2a_s + 1/2a_d + m_i$$

$$a_j = 1/2a_s + 1/2a_d + m_j$$

# Basic Principle of Predicting Breeding Values

Breeding values are predicted according to the following two steps.

1. Observations corrected for the appropriate mean performance values of animals under the same conditions
  - ▶ conditions are described by the effects captured in  $\mu_j$ .
2. The corrected observations are weighted by a certain factor
  - ▶ factor reflects the amount of information available for prediction

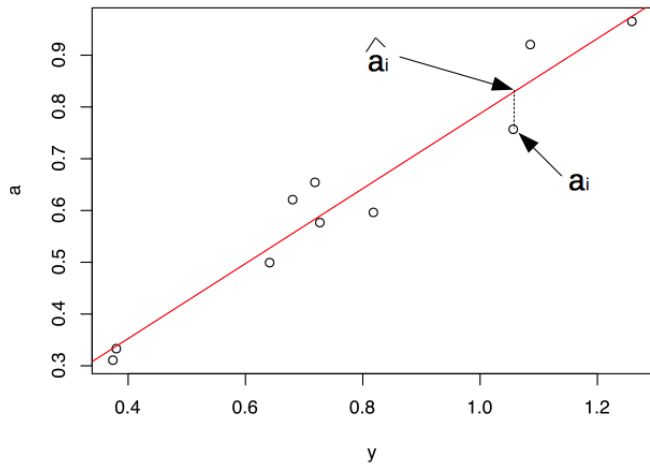


# Animal's Own Performance - Single Record

- ▶ one phenotypic observation per animal
- ▶ search for prediction  $\hat{a}_i$  of the breeding value  $a_i$  of animal  $i$
- ▶ assume  $a_i$  and  $y_i$  known for a certain population

→ plot

## Plot $a$ against $y$



# Regression

- ▶ red line denotes **regression line** from  $a_i$  onto  $y_i$
- ▶ because phenotypes have genetic basis → connection between  $a_i$  and  $y_i$
- ▶ measure for connection: regression coefficient  $b$

$$\begin{aligned} b &= \frac{\text{cov}(a, y)}{\text{var}(y)} \\ &= \frac{\text{cov}(a, \mu + a + e)}{\text{var}(y)} \\ &= \frac{\text{cov}(a, a)}{\text{var}(y)} \\ &= \frac{\text{var}(a)}{\text{var}(y)} = h^2 \end{aligned}$$

where  $h^2$  is called **heritability**

# Prediction

- ▶ Given a new  $y_i$ , what would be the predicted  $a_i$ ?
- ▶ Use regression line and compute  $\hat{a}_i$

$$\begin{aligned}\hat{a}_i &= b * (y_i - \mu) \\ &= h^2 * (y_i - \mu)\end{aligned}$$

# Accuracy

- Measured as correlation between true breeding value  $a$  and selection criterion  $y$

$$\begin{aligned} r_{a,y} &= \frac{\text{cov}(a, y)}{\sigma_a \sigma_y} \\ &= \frac{\sigma_a^2}{\sigma_a \sigma_y} \\ &= \frac{\sigma_a}{\sigma_y} \\ &= h \end{aligned}$$

## Response To Selection

$$R = i * r_{a,y}^2 * \sigma_y = i * h^2 * \sigma_y$$