Quantitative Genetics - Multiple Loci

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2024-10-11

Two and more Loci

▶ Two loci A and B having an effect on the same quantitative trait.
▶ Additional effect in genetic model: **Interaction** effect (also known as epistasis)
▶ Interaction occurs if effect of one locus can have an influence on the effect of the other locus
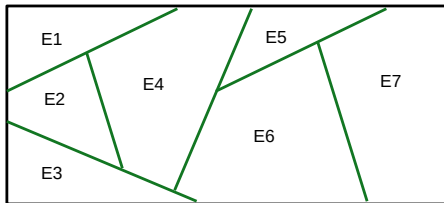▶ Interaction is quantified by

$$I_{AB} = V - V_A - V_B$$

Influence of Two Loci on Quantitative Trait

Two Loci Influencing a Quantitative Trait

Locus A

Locus B

I_{AB}

$V_A = \mu_A + BV_A + D_A$

$V_B = \mu_B + BV_B + D_B$

$V = V_A + V_B + I_{AB}$
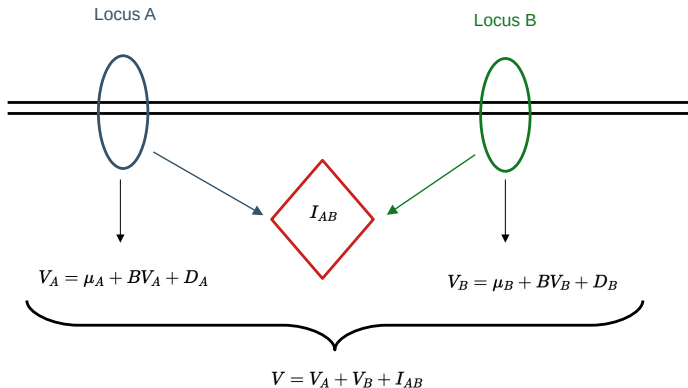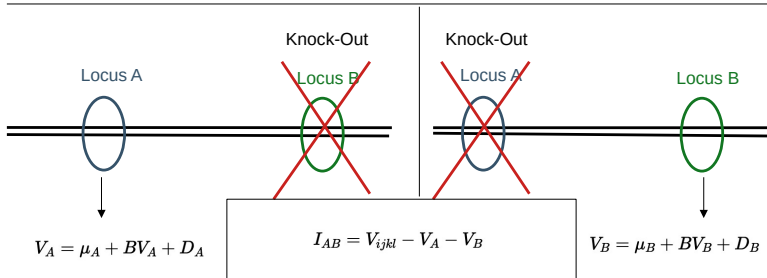
Quantify Interaction Effect

For Animal d with genotype:
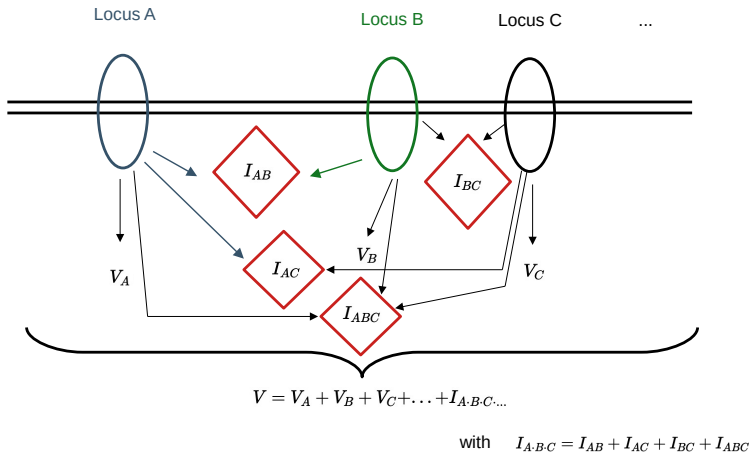$A_i A_j B_k B_l$

Total Genetic Value V_{ijkl}
as mean phenotypic value (Y)
across different environments
(E1 to E7):

$$V_{ijkl} = \frac{1}{N} \sum_{m=1}^{N} Y_{ijklm}$$

Knock-Out Locus B

Knock-Out Locus A

Locus A

Locus B

$V_A = \mu_A + BV_A + D_A$

$I_{AB} = V_{ijkl} - V_A - V_B$

$V_B = \mu_B + BV_B + D_B$

More Than Two Loci

Many Loci Influencing a Quantitative Trait

Summary Genetic Model

▶ Given genetic model

$$V = V_A + V_B + V_C + ... + I_{A \cdot B \cdot C \cdot ...}$$

▶ Decomposition

$$V = \mu_A + BV_A + D_A + \mu_B + BV_B + D_B + \mu_C + BV_C + D_C + ... + I_{A \cdot B \cdot C \cdot ...}$$

▶ Re-group

$$V = \mu_A + \mu_B + \mu_C + ... + BV_A + BV_B + BV_C + ...$$
$$+ D_A + D_B + D_C + ... + I_{A \cdot B \cdot C \cdot ...}$$

▶ Collect

$$V = \mu + BV + D + I_{A \cdot B \cdot C \cdot ...}$$

Extend to Phenotypes

- We know from earlier

$$Y = V + E$$

- Insert decomposition of V

$$Y = \mu + BV + D + I_{A \cdot B \cdot C \cdots} + E$$

- For breeding, only BV is important

$$Y = \mu + BV + E^*$$

with $E^* = D + I_{A \cdot B \cdot C \cdots} + E$

Split of Environment

Non-genetic environment is split into

- known part, corresponding to additional information on animal, like herd, age, sex, ... leads to vector of fixed effects and regression coefficients $\rightarrow b$
- unknown part leads to random resiudal part $\rightarrow e$

Model of Phenotypic Observation

Phenotypic observation (y_i) of an animal i can be modelled as

$$y_i = x_i^T \cdot b + u_i + e_i$$

where

y_i	phenotypic observation of animal i
x_i	vector of regression covariates or indicator values for fixed effects
b	vector of unknown fixed effects and unknown regression coefficients
u_i	random breeding value of animal i
e_i	random environmental effects of animal i

Aggregation over Population

Take all observations from all animals in a given population

$$y = X \cdot b + Z \cdot u + e$$

where

y	vector of phenotypic observations of all animals
b	vector of unknown fixed effects and unknown regression coefficients
u	vector of random breeding values of all animals
e	vector of random environmental effects
X	design matrix with regression covariates or indicator values for fixed effects
Z	design matrix relating breeding values to observations

Example Dataset I

Animal	Sire	Dam	Herd	Weaning Weight	Breast Circumference
12	1	4	1	2.61	1.62
13	1	4	1	2.31	1.96
14	1	5	1	2.44	1.48
15	1	5	1	2.41	1.47
16	1	6	2	2.51	1.50
17	1	6	2	2.55	1.47
18	1	7	2	2.14	1.35
19	1	7	2	2.61	1.41
20	2	8	1	2.34	1.46
21	2	8	1	1.99	1.38
22	2	9	1	3.10	1.70
23	2	9	1	2.81	1.68
24	2	10	2	2.14	1.71
25	2	10	2	2.41	1.36
26	3	11	2	2.54	1.50
27	3	11	2	3.16	1.61

Example Dataset II

- ▶ Weaning weight as response variable y
- ▶ Breast circumference as regression variable
- ▶ Herd as fixed effect
- ▶ Breeding values for
  - ▶ animals with observations: own-performance
  - ▶ sires: sire model
  - ▶ all animals in pedigree: animal model