

Fixed Linear Effects Models

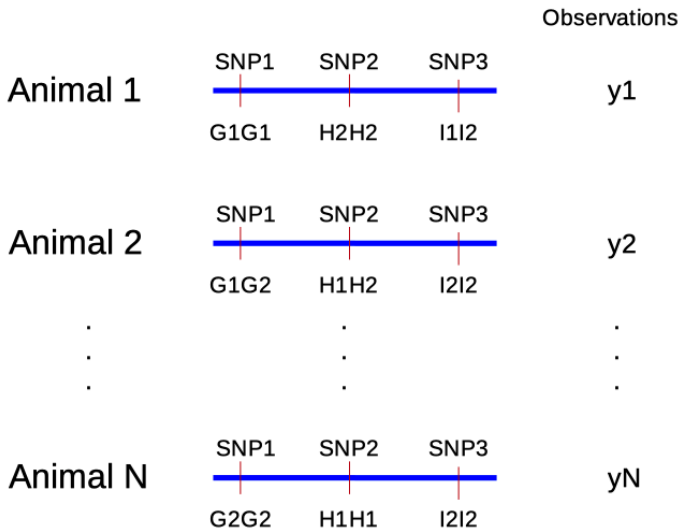
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Background

- ▶ Given a population of N animals
- ▶ Each animal has information on genotypes at loci G , H and I
- ▶ Each animal has an observation for one quantitative trait of interest y
- ▶ **Goal:** Predict genomic breeding values

Data



Two Types Of Models

1. **Genetic** Model: How can we decompose the phenotype into genetic part and non-genetic environmental part
2. **Statistical** Model: How to estimate unknown parameters from a dataset

Goals:

1. Use genetic model to show how observations and genetic information can be used to predict breeding values.
2. Use statistical techniques to do the prediction

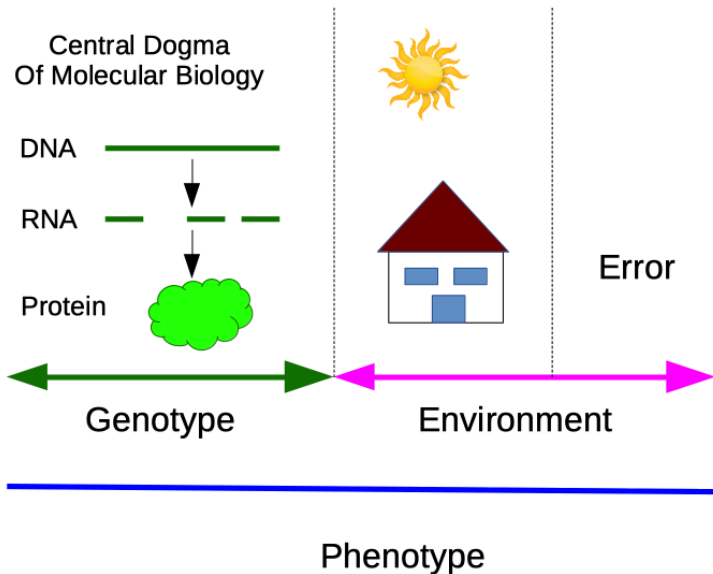
Genetic Model

- ▶ simple model from quantitative genetics to split phenotypic observation into
 - ▶ genetic part g and
 - ▶ environmental part e

$$y = g + e$$

- ▶ environment: split into
 - ▶ known environmental factors: herd, year, ... (β)
 - ▶ unknown random error (ϵ)
- ▶ polygenic model: use a finite number of loci to model genetic part of phenotypic observation

Genetic Model (II)



Polygenic Model

- ▶ Component g can be decomposed into contributions g_j of single loci

$$g = \sum_{j=1}^k g_j$$

- ▶ Assume that loci are additive, hence genotypic values g_j depends on a_j with $d_j = 0$
- ▶ Genotypic values at locus j can either be $-a_j$, 0 or a_j
- ▶ Breeding values based on locus j depends on a_j .

Genotypic Value

- ▶ Genotypic value g_i for animal i over all loci

$$g_i = M_i \cdot a$$

where M_i is a row vector with elements -1 , 0 and 1 and a is the vector of all genotypic values of the positive homozygous genotypes of all loci.

Phenotypic Value

- ▶ Collecting all components for an observation y_i for animal i

$$y_i = W_i \cdot \beta + M_i \cdot a + \epsilon_i$$

- ▶ all animals in the population

$$y = W \cdot \beta + M \cdot a + \epsilon$$

- ▶ combining $b^T = \begin{bmatrix} \beta & a \end{bmatrix}$ and $X = \begin{bmatrix} W & M \end{bmatrix}$

$$y = X \cdot b + \epsilon$$

Statistical Model

- ▶ genetic model from statistics point of view
- ▶ phenotypic observation as response y
- ▶ vector b (known environment and genotypic values) as unknown parameter
- ▶ fixed predictor variables in matrix X
- ▶ vector ϵ as random error terms

→ Fixed Linear Effects Model

Parameter Estimation

- ▶ use regression model
- ▶ regression means both response and predictors are continuous
- ▶ example dataset: body weight on breast circumference

Regression Dataset

Animal	Breast Circumference	Body Weight
1	176	471
2	177	463
3	178	481
4	179	470
5	179	496
6	180	491
7	181	518
8	182	511
9	183	510
10	184	541

Regression Model

- ▶ response y : body weight
- ▶ predictor x : breast circumference
- ▶ model for observation y_i

$$y_i = x_i * b + \epsilon_i$$

- ▶ meaning of b : change x_i by one unit $\rightarrow y_i$ changes on average by b units.
- ▶ use case: measure x_{N+1} for animal $N + 1$ with unknown weight and use b to predict y_{N+1}

Least Squares

- ▶ How to find b such that y is best approximated by x
- ▶ Residuals $r_i = y_i - x_i * b$
- ▶ Minimization of sum of squared residuals (SSQ_R)
- ▶ Use \hat{b} at minimal SSQ_R as estimate

LSQ Diagram

