Fixed Linear Effects Models

Peter von Rohr

25.02.2019

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

				Observations
Animal 1	SNP1	SNP2	SNP3	v4
	G1G1	H2H2	1112	y1
Animal 2	SNP1	SNP2	SNP3	y2
	G1G2	H1H2	1212	
•		•		•
Animal N	SNP1	SNP2	SNP3	yN
	G2G2	H1H1	1212	

Two Types Of Models

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

Goals:

- 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

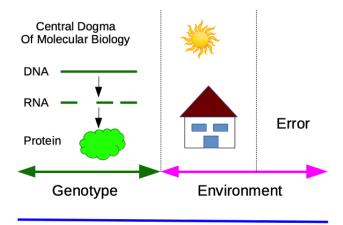
Genetic Model

- 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)



Phenotype