

2022-03-07

- mades of nor to 11 way

Extension of Dataset on Body Weight

		response y			predictor)
Animal	ВС	Body Weight	BCS	HEI	Breed Solumn
1	176	471	5.0	161	Angus → ∧
2	177	463	4.2	121	Angus 1
3	178	481	4.9	157	Simmental ₹
4	179	470	3.0	165	Angus 1
5	179	496	6.8	136	Simmental <
6	180	491	4.9	123	Simmental 🕺
7	181	518	4.4	163	Limousin 7
8	182	511	4.4	149	Limousin
9	183	510	3.5	143	Limousin
10	184	541	4.7	130	Limousin ?

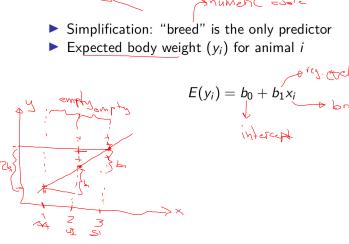
, additional?

Include Breed into Model

- ▶ Breed has an influence on body weight
- Predictor variables must be numeric
- Breed must be converted to numeric code
- Assignment of codes to breeds is rather arbitrary

Code	Breed	
2 🖰	→Angus →Limousin →Simment)
Q Assi	nmenA	arbitrary

Modelling Effect of Breed



Problems

- ► Nothing wrong with previous model
- But the following relations might give a hint to some problems

Expected value for Boly Weight

$$E(BW Angus) = b_0 + 1 \cdot b_1$$

$$E(BW Limousin) = b_0 + 2b_1$$

$$E(BW Simmental) = b_0 + 3b_1$$

This means, for example, that

$$E(BW Limousin) - E(BW Angus) = E(BW Simmental) - E(BW Limousin)$$

$$E(BW Simmental) - E(BW Angus) = 2 [E(BW Limousin) - E(BW Angus)]$$

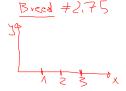
Consequences

Regression - [x] continuous

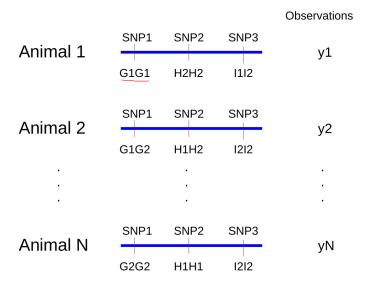
ABC, BC, NEI



- Allocation of numerical codes imposes relations between expected values
- Relations might be unreasonable
- Regression analysis only yields estimates for b_0 and b_1 , effects of other breeds are determined
- ► Conclusion: regression on numerical codes of discrete variables are in most cases unreasonable
- Exception: Estimation of marker effects



Linear Regression Analysis for Genomic Data



For a single SNP: Assuming G1 to be the favorable allele, the numeric code for a given genotype will be the number of G1 alleles

