Fixed Linear Effects Models

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Extension of Dataset on Body Weight

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

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

Breed Codes

Code	Breed
1	Angus
2	Limousin
3	Simmental

In R: Encoding based on alpha-numeric order of factor names

```
levels(as.factor(tbl_flem$Breed))
```

```
## [1] "Angus"     "Limousin"  "Simmental"
```

```
as.integer(as.factor(tbl_flem$Breed))
```

```
##  [1] 1 1 3 1 3 3 2 2 2 2
```

Dataset with Breed Codes

Animal	Body Weight	Breed	Breed Code
1	471	Angus	1
2	463	Angus	1
3	481	Simmental	3
4	470	Angus	1
5	496	Simmental	3
6	491	Simmental	3
7	518	Limousin	2
8	511	Limousin	2
9	510	Limousin	2
10	541	Limousin	2

Modelling Effect of Breed

- Simplification: “breed” is the only predictor
- Take breed code of animal i as the predictor value x_i
- Expected body weight (y_i) for animal i

$$E(y_i) = b_0 + b_1 x_i$$

Problems

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

$$\left.\begin{array}{l}\text{Animal i of breed Angus}\\ \text{Animal j of breed Limousin}\\ \text{Animal k of breed Simmental}\end{array}\right\} \rightarrow \left\{\begin{array}{l}E(y_i) = b_0 + b_1 * 1\\ E(y_j) = b_0 + b_1 * 2\\ E(y_k) = b_0 + b_1 * 3\end{array}\right.$$

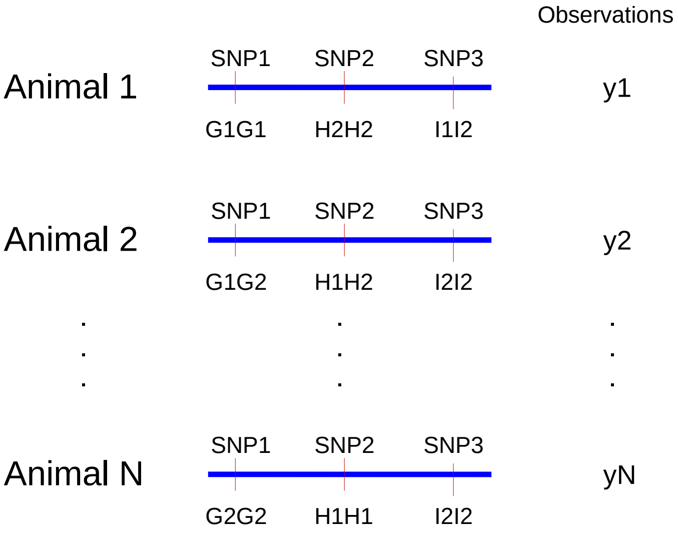
This means, for expected differences between body weights of animals of different breeds

$$E(y_j) - E(y_i) = E(y_k) - E(y_j) = b_1$$
$$E(y_k) - E(y_i) = 2 * b_1$$

Consequences

- 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



Observations

Animal 1 SNP1 SNP2 SNP3 G1G1 H2H2 I1I2 y1

Animal 2 SNP1 SNP2 SNP3 G1G2 H1H2 I2I2 y2

. . .

. . .

. . .

Animal N SNP1 SNP2 SNP3 G2G2 H1H1 I2I2 yN

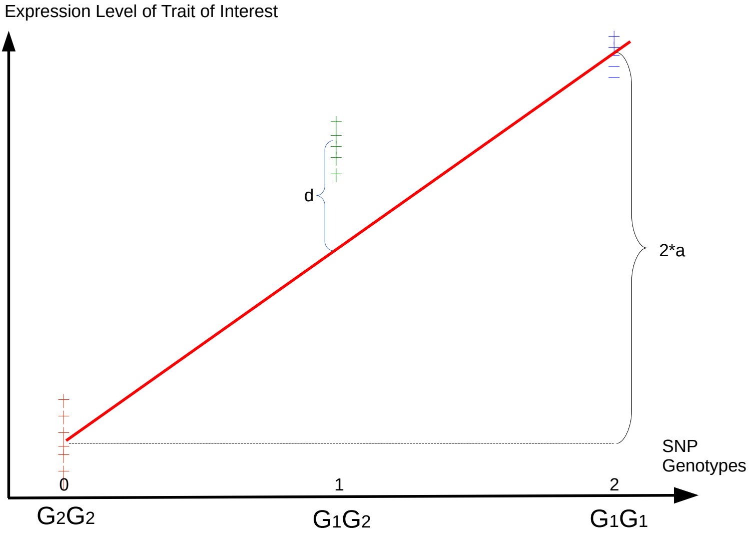
Marker Effect Estimation

- Assume: marker and QTL are very close, such they can no longer be distinguished
- Fit regression of observations (y) on marker genotypes of locus G
- Assume G_1 is the allele with a positive effect on observed trait
- Use the following encoding of marker genotypes to numeric values

Genotype	Code
G_1G_1	2
G_1G_2	1
G_2G_2	0

$\rightarrow$ Biological meaning of genotype code: count number of G_1 alleles

Genomic Regression


Expression Level of Trait of Interest
d
2*a
SNP
Genotypes
G_2G_2
G_1G_2
G_1G_1