

Mixed Linear Effects Models

Peter von Rohr

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Repeated Measurements

- ▶ Same characteristics (Body Weight, BC, ...) measured multiple times for the same animal

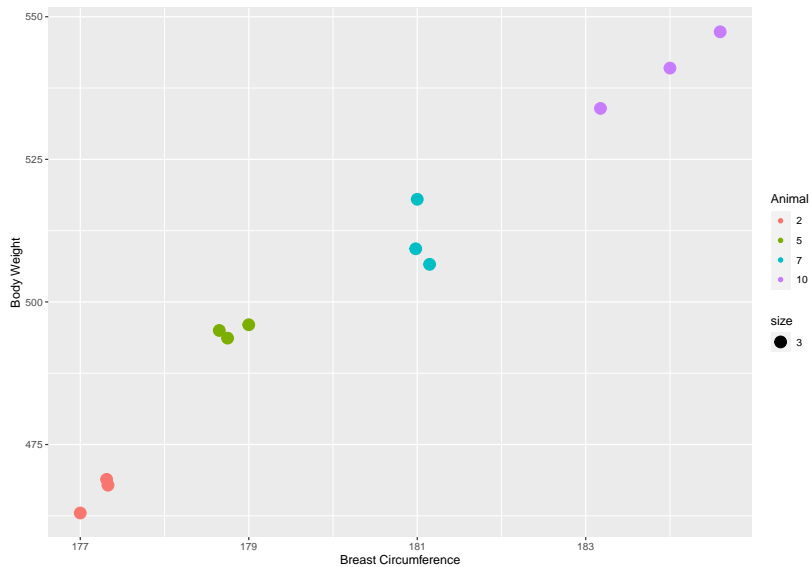
Animal	Breast Circumference	Body Weight
2	177.0000	463.0000
2	177.3129	468.8940
2	177.3292	467.8753
5	179.0000	496.0000
5	178.6501	495.0033
5	178.7485	493.6563
7	181.0000	518.0000
7	180.9819	509.3221

- ▶ Column `Animal` no longer just a counter, it becomes a model factor

Properties

- ▶ What is the benefit of repeated measurements?
- ▶ Equivalent to more animals in the dataset?
- ▶ Assumption: repeated observations of the same animal are more “similar”
- ▶ No longer independence of observations

Data Scatterplot



Statistical Analysis

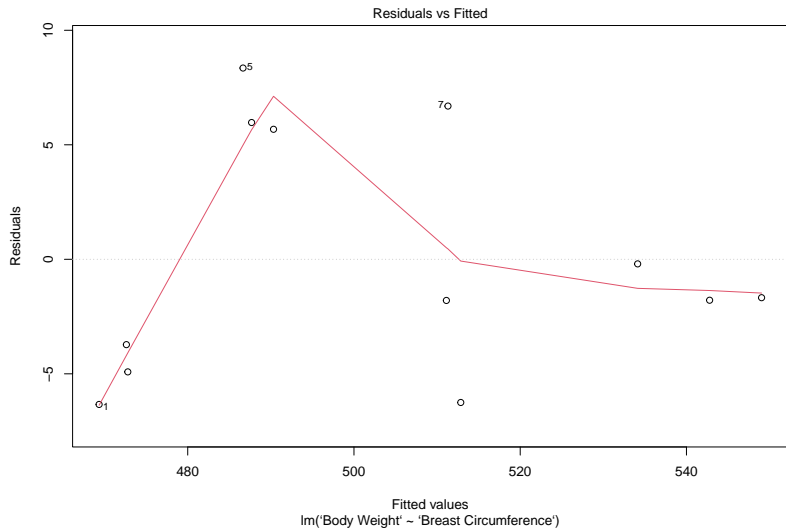
- ▶ Technically, same regression analysis is possible
- ▶ But assumption of independence is violated
- ▶ Consequence of independence

$$\text{var}(\mathbf{e}) = \mathbf{I} * \sigma_e^2$$

* Check residuals plot

Diagnostics Plot

```
plot(lm_rep_obs)
```



ANOVA

```
aov_bw_breed <- aov(`Body Weight` ~ Breed,  
                    data = tbl_rep_obs_breed)  
summary(aov_bw_breed)
```

```
##              Df Sum Sq Mean Sq F value    Pr(>F)  
## Breed          2   7356    3678    22.29 0.000327 ***  
## Residuals     9   1485     165  
## ---  
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1
```

ANOVA I: Breed and Animal

```
aov_bw_breed_animal <- aov(`Body Weight` ~ Breed + Animal,  
                             data = tbl_rep_obs_breed)  
summary(aov_bw_breed_animal)
```

```
##           Df Sum Sq Mean Sq F value    Pr(>F)  
## Breed      2   7356    3678  160.06 3.53e-07 ***  
## Animal     1   1302    1302   56.64 6.76e-05 ***  
## Residuals  8    184      23  
## ---  
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1
```


ANOVA II

```
aov_bw_no_breed_rep <- aov(`Body Weight` ~ Error(Animal),  
                           data = tbl_rep_obs_no_breed)  
summary(aov_bw_no_breed_rep)
```

```
##
```

```
## Error: Animal
```

```
##           Df Sum Sq Mean Sq F value Pr(>F)
```

```
## Residuals  3   8658     2886
```

```
##
```

```
## Error: Within
```

```
##           Df Sum Sq Mean Sq F value Pr(>F)
```

```
## Residuals  8  183.8     22.98
```

ANOVA III

```
aov_bw_breed_rep <- aov(`Body Weight` ~ Breed +  
                        Error(Animal),  
                        data = tbl_rep_obs_breed)  
summary(aov_bw_breed_rep)
```

```
##  
## Error: Animal  
##           Df Sum Sq Mean Sq F value Pr(>F)  
## Breed      2   7356    3678   2.826  0.388  
## Residuals  1   1302    1302  
##  
## Error: Within  
##           Df Sum Sq Mean Sq F value Pr(>F)  
## Residuals  8  183.8    22.98
```

lme4

```
lme_bw_no_breed_rep <- lme4::lmer(`Body Weight` ~  
                                (1|Animal),  
                                data = tbl_rep_obs_no_breed)  
summary(lme_bw_no_breed_rep)
```

```
## Linear mixed model fit by REML ['lmerMod']  
## Formula: 'Body Weight' ~ (1 | Animal)  
## Data: tbl_rep_obs_no_breed  
##  
## REML criterion at convergence: 82.7  
##  
## Scaled residuals:  
##      Min      1Q   Median      3Q      Max  
## -1.36360 -0.50301  0.06086  0.26850  1.43838  
##  
## Random effects:  
##  Groups      Name      Variance Std.Dev.  
##  Animal      (Intercept) 954.34   30.892
```

With Breed

Animal	Body Weight	Breed
2	463.0000	Angus
2	468.8940	Angus
2	467.8753	Angus
5	496.0000	Simmental
5	495.0033	Simmental
5	493.6563	Simmental
7	518.0000	Limousin
7	509.3221	Limousin
7	506.5958	Limousin
10	541.0000	Limousin
10	547.3609	Limousin
10	533.9288	Limousin

ANOVA

```
aov_bw_breed_rep <- aov(`Body Weight` ~ Breed +  
                        Error(Animal),  
                        data = tbl_rep_obs_breed)  
summary(aov_bw_breed_rep)
```

```
##  
## Error: Animal  
##           Df Sum Sq Mean Sq F value Pr(>F)  
## Breed      2   7356    3678   2.826  0.388  
## Residuals  1   1302    1302  
##  
## Error: Within  
##           Df Sum Sq Mean Sq F value Pr(>F)  
## Residuals  8  183.8    22.98
```

lme4

```
lme_bw_breed_rep <- lme4::lmer(`Body Weight` ~ Breed +  
                               (1|Animal),  
                               data = tbl_rep_obs_breed)
```

```
summary(lme_bw_breed_rep)
```

```
## Linear mixed model fit by REML ['lmerMod']  
## Formula: 'Body Weight' ~ Breed + (1 | Animal)  
## Data: tbl_rep_obs_breed  
##  
## REML criterion at convergence: 61.8  
##  
## Scaled residuals:  
##      Min      1Q  Median      3Q      Max  
## -1.3714 -0.5383  0.0640  0.3213  1.4305  
##  
## Random effects:  
##  Groups      Name      Variance Std.Dev.  
##  Animal  (Intercept) 426.21   20.645
```