



# Linear Mixed Models (LMM)



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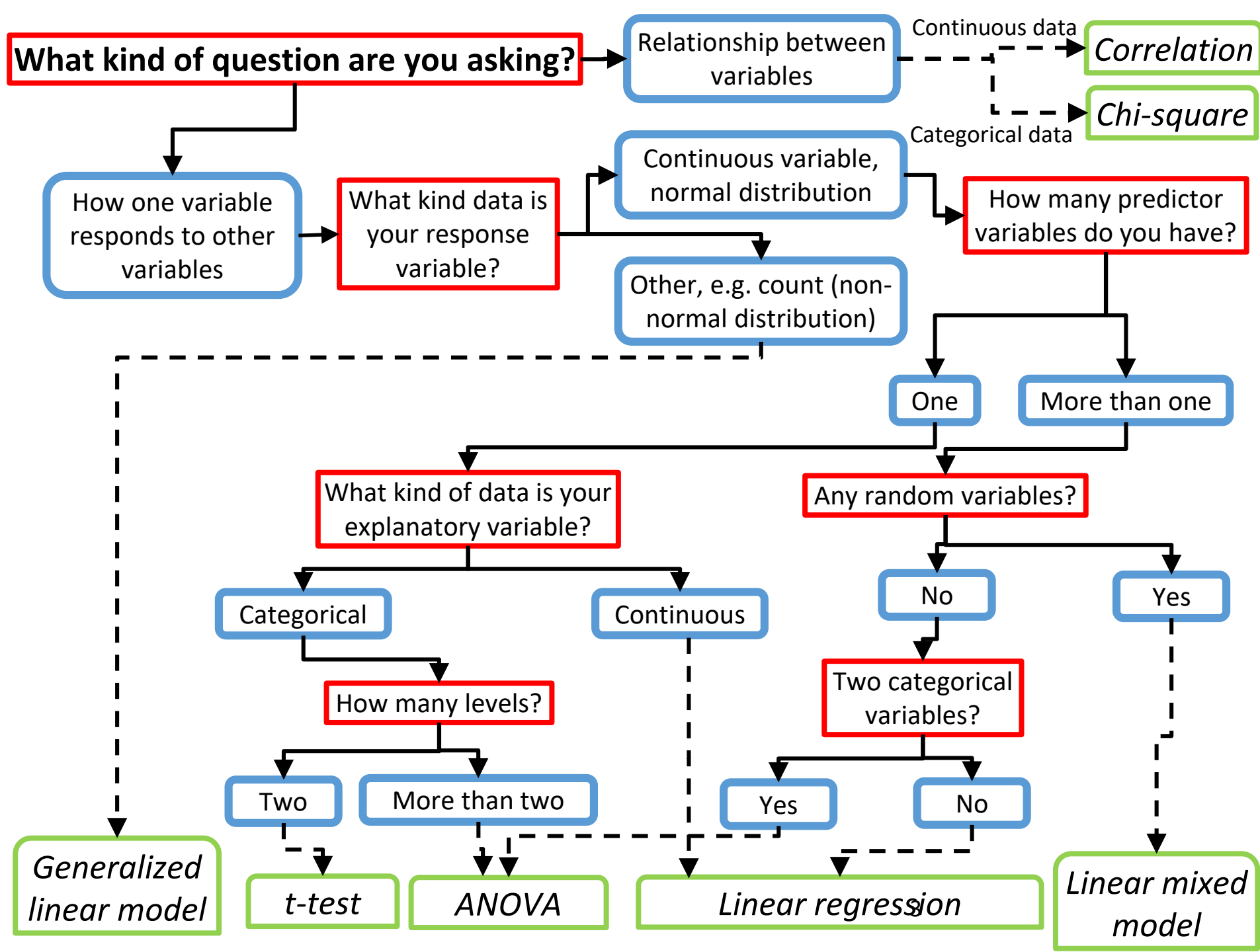


# Overview

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Topics
<b>1</b> – Random Effects
<b>2</b> – How to fit linear mixed-effect models (LMM)
<b>3</b> – Random slope, crossed and nested random effects



**What kind of question are you asking?**

How one variable  
responds to other  
variables

**What kind data is  
your response  
variable?**

Continuous variable,  
normal distribution

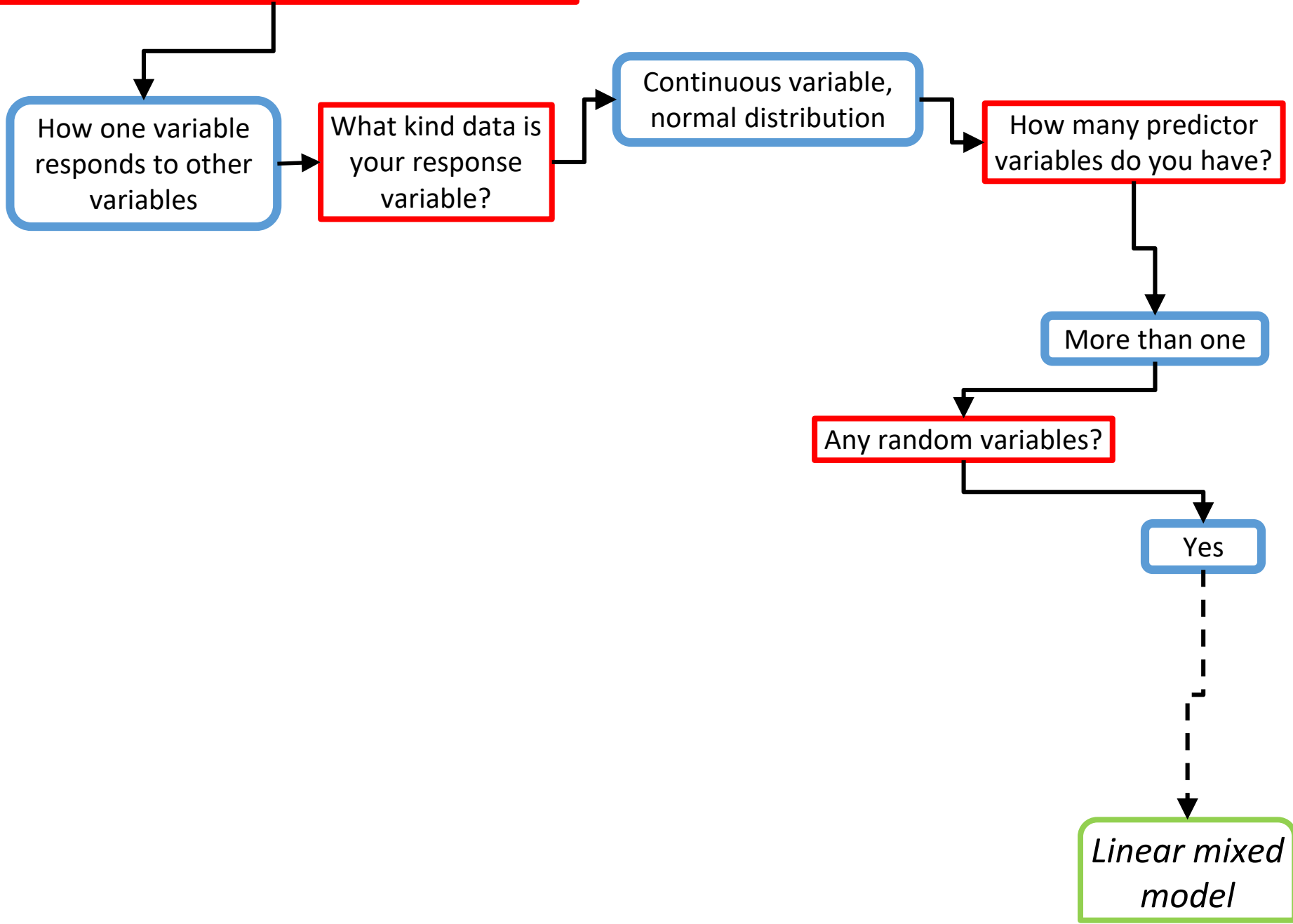
**How many predictor  
variables do you have?**

More than one

**Any random variables?**

Yes

*Linear mixed  
model*





# Random Effects

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In all previous examples, we have treated all **categorical explanatory variables** as if they were the same

There are actually two different sorts of categorical explanatory variables: **fixed effects** and **random effects**.

So-called '**mixed models**' contain both fixed and random effects.

A **factor** is fixed when the levels under study are the only levels of interest.

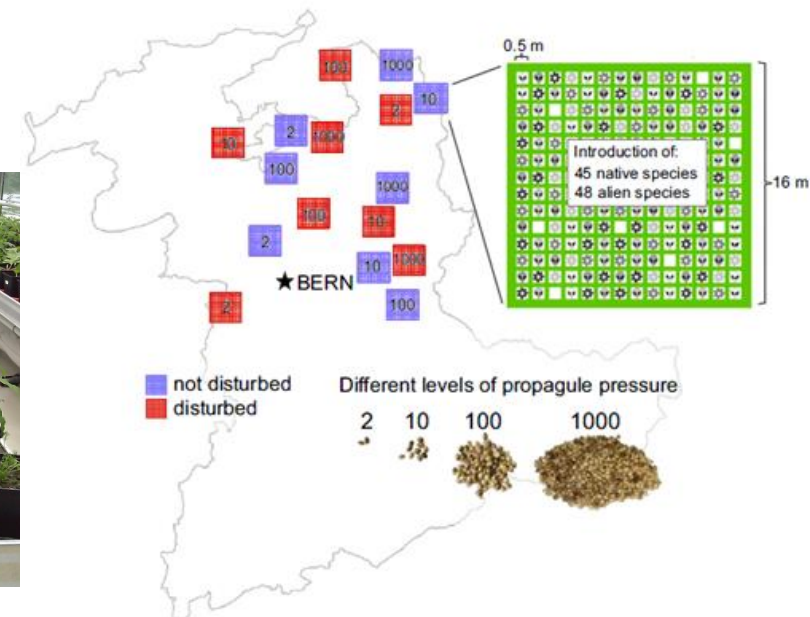
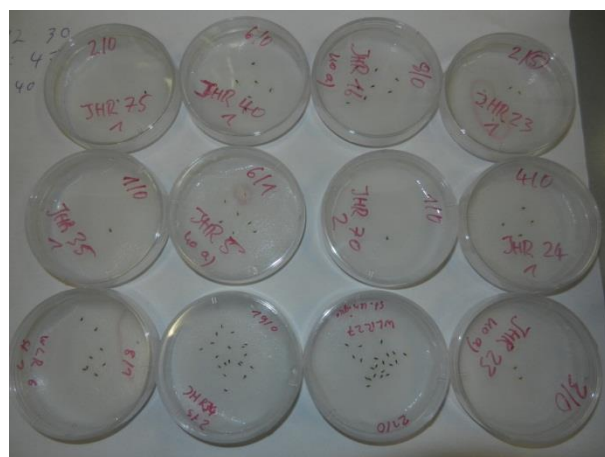
A **factor** is **random** when the levels under study are a **random** sample from a larger population and the goal of the study is to make a statement regarding the larger population.



# Random Effects

## Non independent or grouped data, hierarchical data:

- Lack of independence between data points
  - Repeated measurements on the same individual
- Data may be grouped into experimental blocks
  - Blocks may coincide with some extra, unmeasured variable
  - Some variation in experiment may be explained by block effects
- Data may have a hierarchical structure
  - Block within plot





# Fixed vs Random Effects



**Fixed effects** should:

- be variables for which **we are interested in differences between levels**

*e.g. effects of fertilization level*

- have **levels that are non-random**

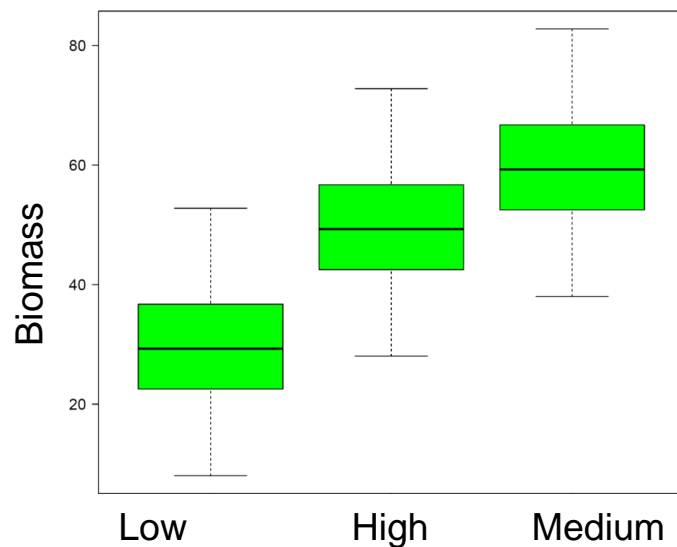
*e.g. levels of fertilization were specifically chosen and set*

- have **few levels**

*e.g. there are only 3 fertilization levels*

- have **levels which are informative**

*e.g. medium fertilization means more fertilizer than low, and less than high*





# Fixed vs Random Effects



- **Random effects** should:
  - be variables for which **we are not interested in effect sizes, but only in variation among levels**

*e.g. if we had 10 genotypes, in order to generalize and account for genotypic variation*

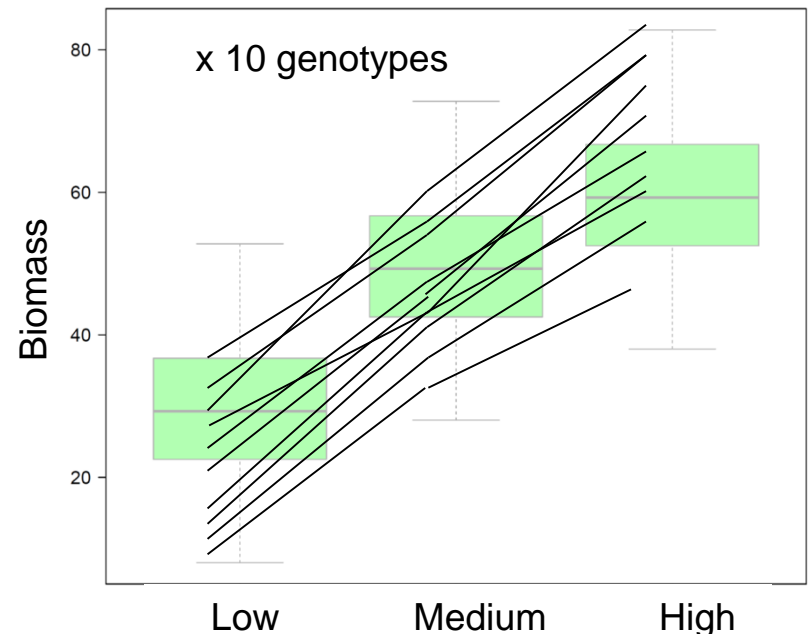
- have **levels that are randomly chosen from a 'population' of levels**

*e.g. there was no a priori reason why these particular genotypes were chosen (= no bias)*

- have **many levels** (a threshold for 'many' is subjective...)

- have **levels which are uninformative**

*e.g. if there is no bias, one genotype should be as different from the others, on average, as the next one, i.e. being one genotype or another informs nothing*







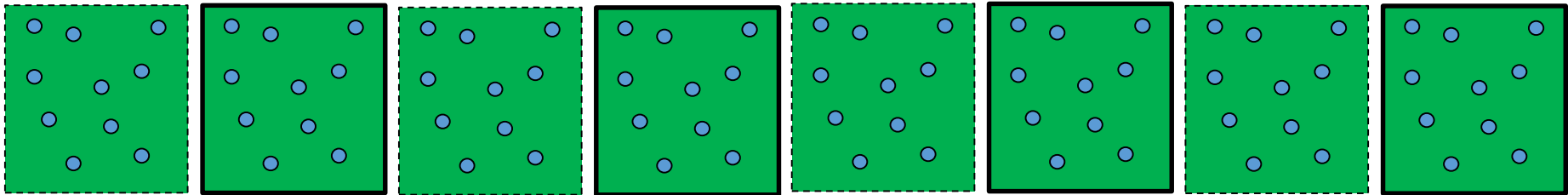
# Examples

## Examples (1/4)



**Question:** influence of herbivory on soil nutrient levels

**Experiment:** We exclude deer from a patch of vegetation, to assess effects of herbivory on soil nutrient levels (x 4 plots of each treatment).  
We take 10 soil cores from each plot.



Our **data points are not independent**, treating them as such is what we call **pseudoreplication**!

Our unit of observation is replicated within units of the treatment replicate: we have a **nested design**.



# Examples

## fixed effects

the levels (not the effects!)  
are fixed

differences between specific  
levels are of interest

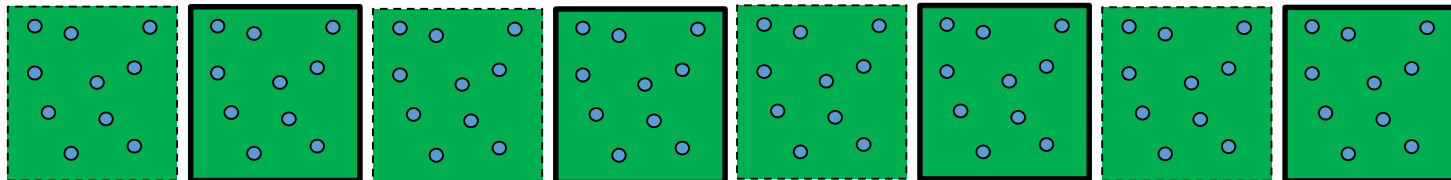
## random effects

the levels are not fixed

variance between the levels  
is of interest (or needs to be  
accounted for in the model)

## Example (1/4)

- Treatment (**herbivory excluded/**  
not excluded)
- Plot



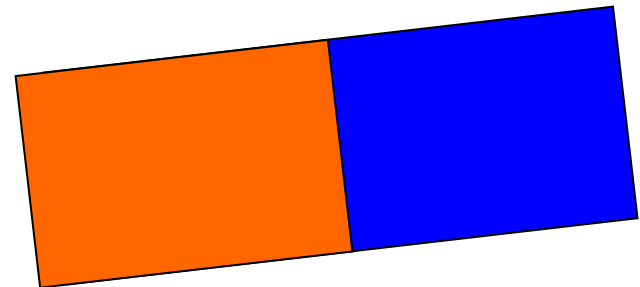
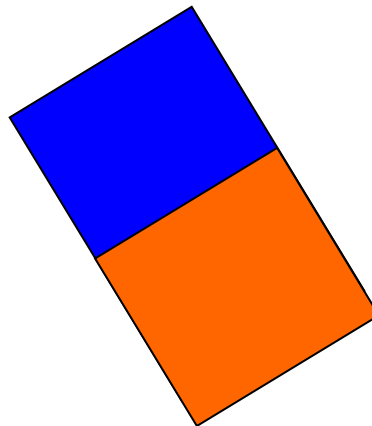
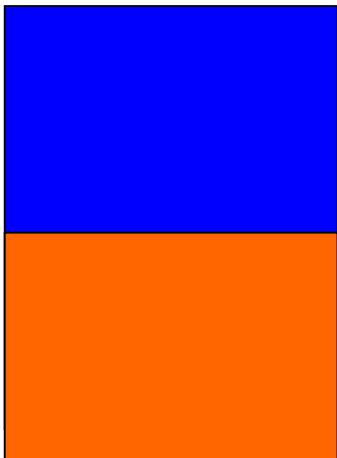


# Examples

## Examples (2/4)

**Question:** difference in biodiversity between different managements in agricultural fields

**Experiment:** apply management **A** and **B** in half of each field





# Examples

## fixed effects

the levels (not the effects!)  
are fixed

differences between specific  
levels are of interest

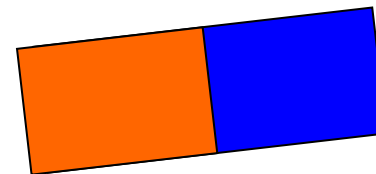
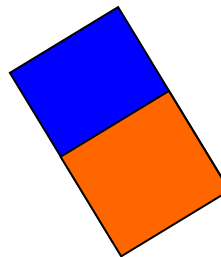
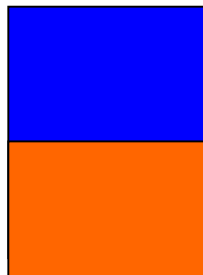
## random effects

the levels are not fixed

variance between the levels  
is of interest (or needs to be  
accounted for in the model)

## Example (2/4)

- Management (A or B)



- Field

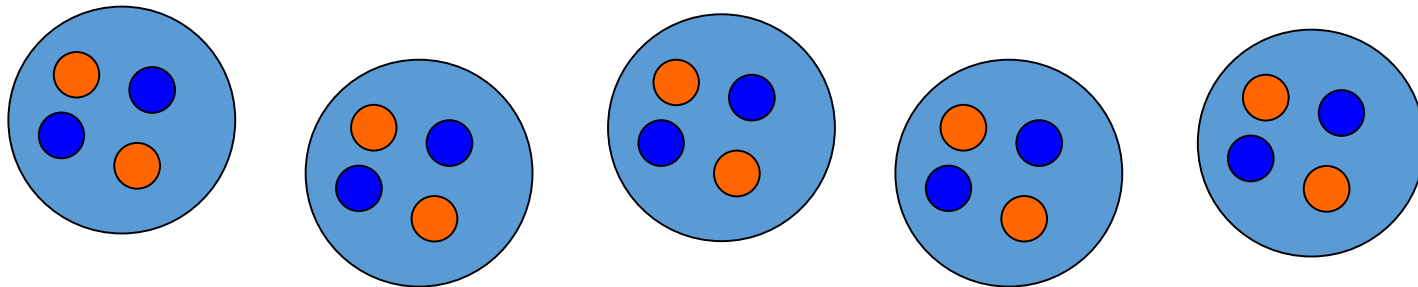


# Examples

## Examples (3/4)

**Question:** influence of corticosterone-implant on barn owl nestling growth rate, measured multiple times on same individual

**Experiment:** in each of  $n$  nests,  
2 nestlings with corticosterone implant  
2 nestlings with a placebo





# Examples

## fixed effects

the levels (not the effects!)  
are fixed

differences between specific  
levels are of interest

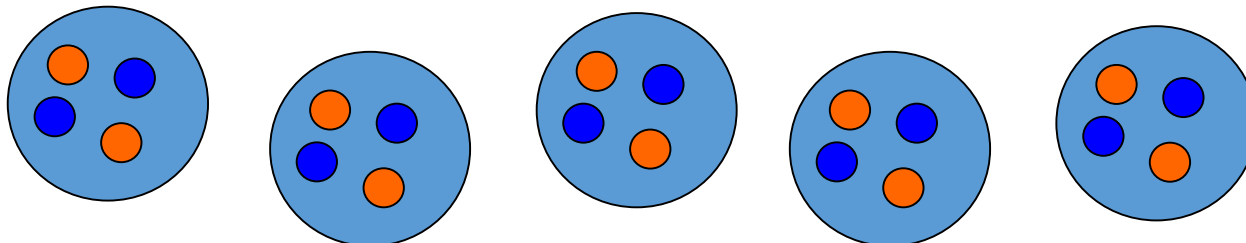
## random effects

the levels are not fixed

variance between the levels  
is of interest (or needs to be  
accounted for in the model)

## Example (3/4)

- Implant (Placebo or Corticosterone)
- Nest
- Individual



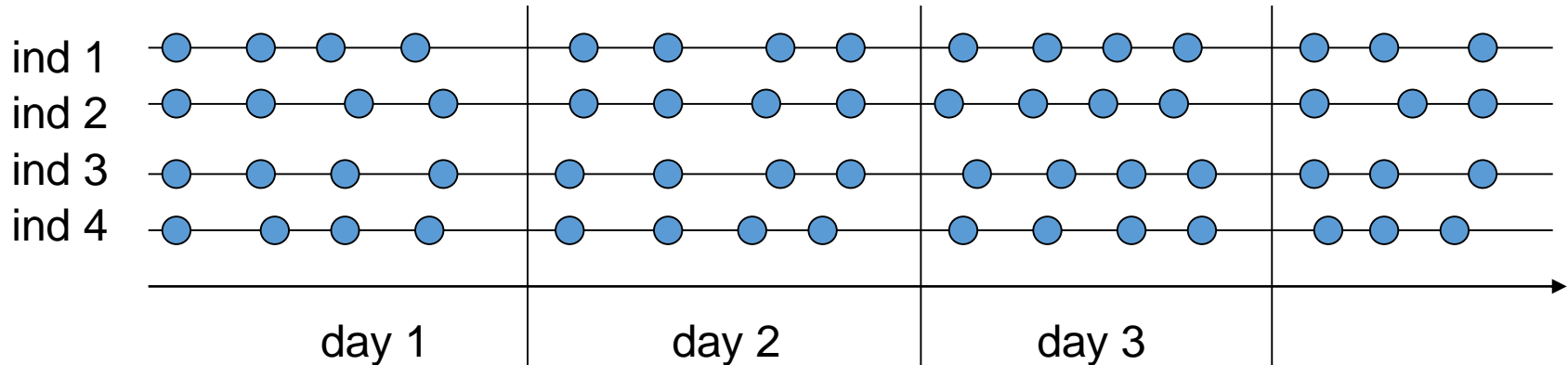


# Examples

## Examples (4/4)

**Question:** is the behaviour of an animal influenced by weather (means per day) and time of day?

**Experiment:** observation of  $n$  individuals four times a day





# Examples

## fixed effects

the levels (not the effects!)  
are fixed

differences between specific  
levels are of interest

## random effects

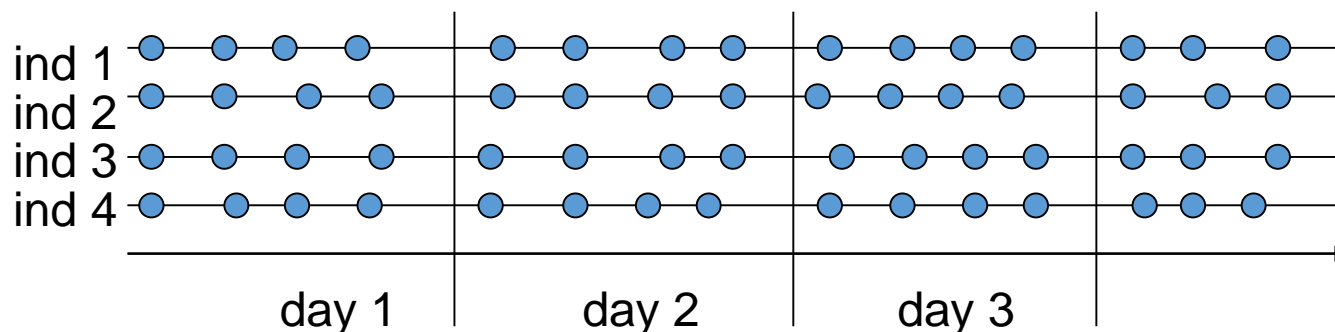
the levels are not fixed

variance between the levels  
is of interest (or needs to be  
accounted for in the model)

## Example (4/4)

- Time of the day
- Mean daily temperature

- Day
- Individual







# Random Effects

- **Random effects** are a way of grouping the data that we are not interested in.
- But the key thing is that **they make our data points non-independent!**
- And remember, **independence between data points is a key assumption** of all the standard statistical tests and models we have seen so far. So, we need to account for those random effects.
- Such lack of independence between data points due to random effects can occur in both **observational and experimental studies**. Hence the **importance of the design** of the field sampling or of the experiment!

## fixed effects

the levels (not the effects!)  
are fixed

differences between specific  
levels are of interest

## random effects

the levels are not fixed

variance between the levels  
is of interest (or needs to be  
accounted for in the model)



# Time for an exercise

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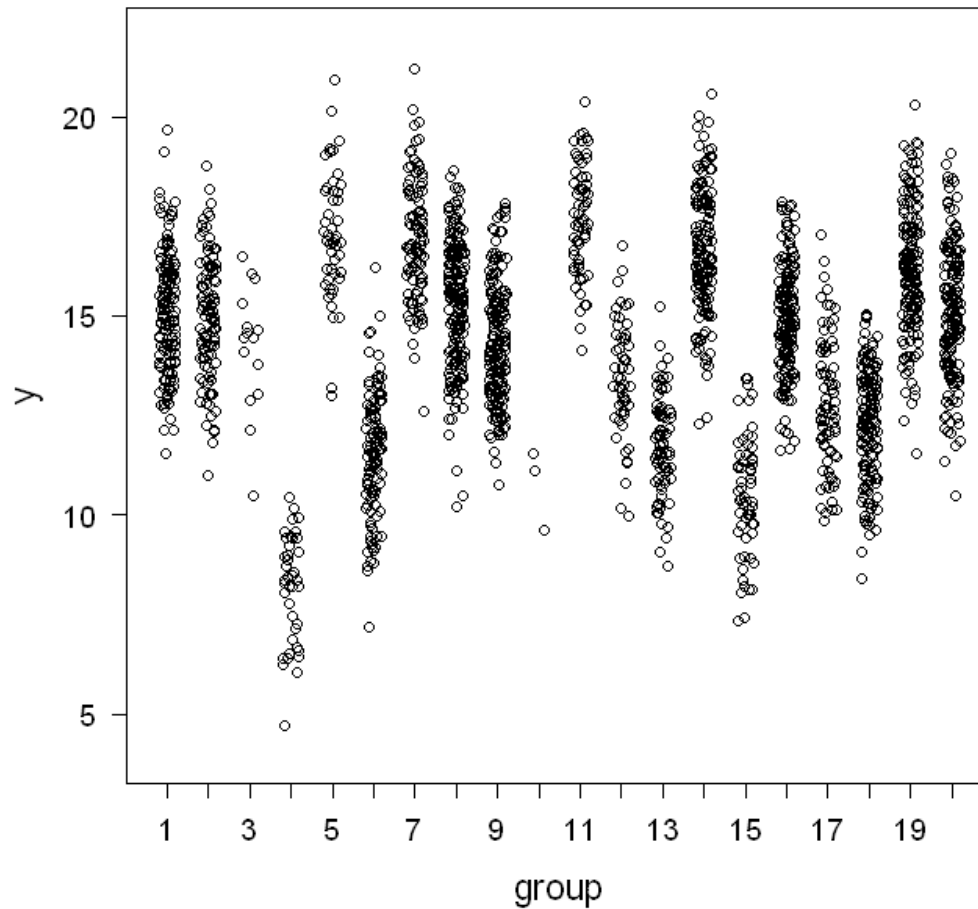
- (1) Take one or more examples of your own study and discuss which of the variables may be treated as „random“ and which ones as „fixed“.



# Complete, partial and no pooling



20 groups with  $n$  between 1 and 200 observations and different means





# Complete, partial and no pooling

complete pooling  
overall mean

$$\hat{y}_i = \beta_o$$

$$y_i \sim \text{Norm}(\hat{y}_i, \sigma^2)$$

partial pooling  
mixed model

$$\hat{y}_i = \beta_o + b_{g_i}$$

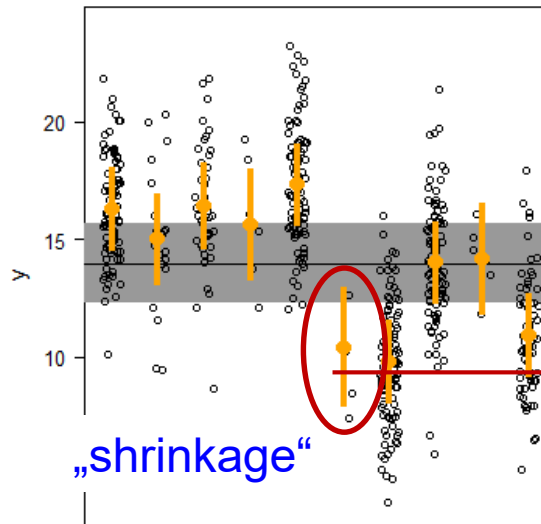
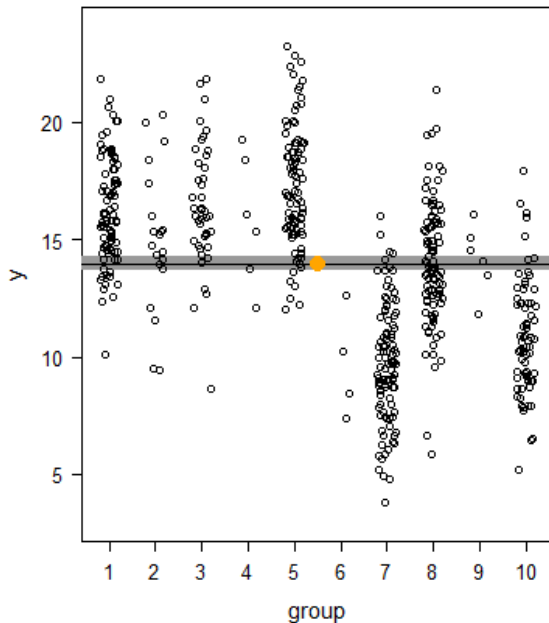
$$y_i \sim \text{Norm}(\hat{y}_i, \sigma^2)$$

$$b_g \sim \text{Norm}(0, \sigma_g^2)$$

no pooling  
groupwise mean

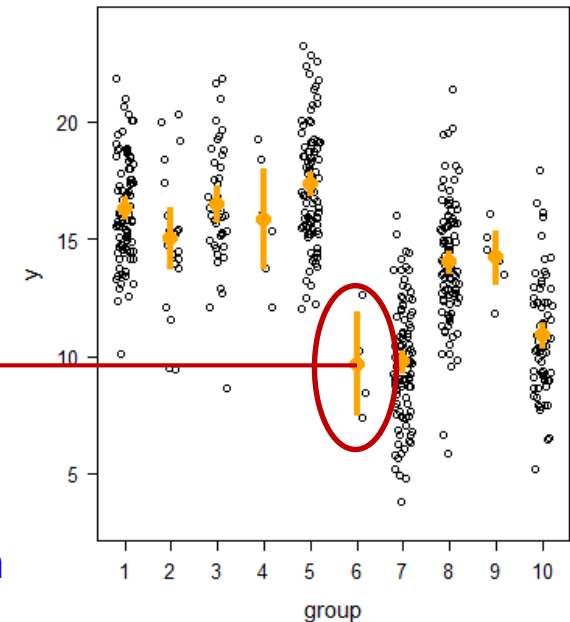
$$\hat{y}_i = \beta_{g_i}$$

$$y_i \sim \text{Norm}(\hat{y}_i, \sigma_{g_i}^2)$$



„shrinkage“

exchange of information  
between the groups





# Complete, partial and no pooling

---



**mixed model** = partial pooling

**group means of a mixed model** = weighted averages of the overall mean and the independent group means

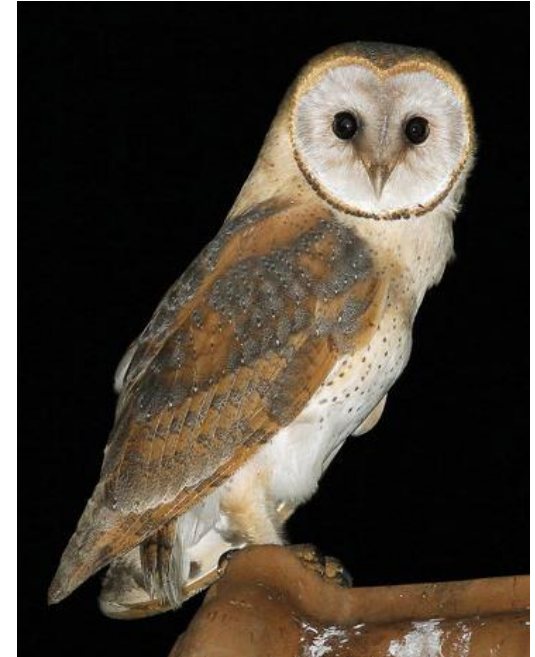
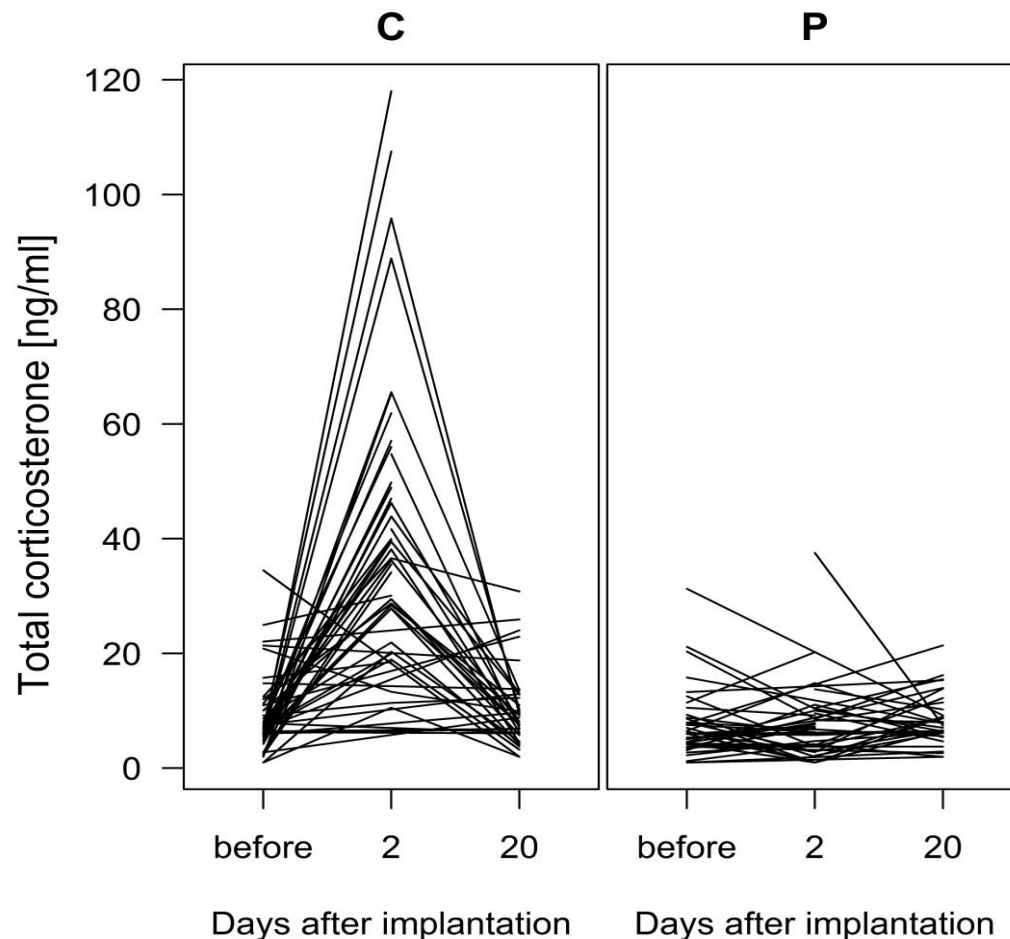
**weights**  $\sim$  sample size and between-group/within-group variance



# Fitting a linear mixed model



Barn owls nestlings and stress hormone:  
How does the **implant** affect **corticosterone concentration**?





# Fitting a linear mixed model

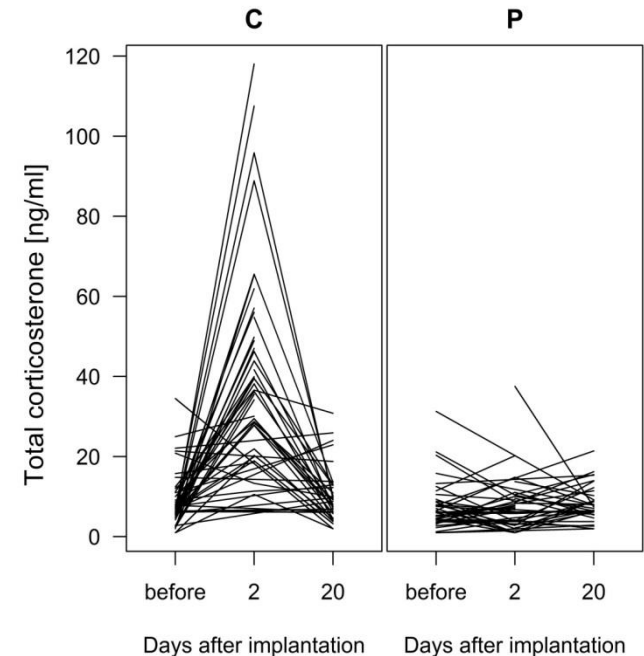


Barn owls nestlings and stress hormone:  
How does the implant affect corticosterone concentration?

$$\hat{y}_i = \beta_o + b_{Ring_i} + \beta_1 I(Implant_i = P) + \beta_2 I(days_i = 3) + \beta_3 I(days_i = 21) + \beta_4 I(Implant_i = P) I(days_i = 3) + \beta_5 I(Implant_i = P) I(days_i = 21)$$

$$y_i \sim Norm(\hat{y}_i, \sigma^2)$$

$$b_{Ring} \sim Norm(0, \sigma_b^2)$$





# Fitting a linear mixed model



```
library(lme4)
```

```
mod.REML=lmer(log(totCort) ~Implant + days
```

```
+ Implant:days
```

```
+ (1|Ring), data=dat, REML=TRUE)
```

Fixed effects

Interaction

random effect





# Fitting a linear mixed model

```
mod.REML=lmer(log(totCort) ~ Implant + days+ Implant:days +  
(1|Ring), data=dat, REML=TRUE)
```

```
summary(mod.REML)
```

```
mod.REML  
Linear mixed model fit by REML ['lmerMod']  
Formula: log(totCort) ~ Implant + days + Implant:days + (1 | Ring)  
Data: dat  
REML criterion at convergence: 611.9053  
Random effects:  
Groups      Name          Std.Dev.  
Ring        (Intercept) 0.3384  
Residual                    0.6134  
Number of obs: 287, groups: Ring, 151
```

```
Fixed Effects:  
(Intercept) ImplantP    days2    days20 ImplantP:days2 ImplantP:days20  
1.91446 -0.08523 1.65307 0.26278          -1.71999          -0.09514
```

restricted maximum likelihood

→ between-individual variance

→ residual variance

fixed effects



# Fitting a linear mixed model

## fixef(mod)

(Intercept)	ImplantP	days2	days20	ImplantP:days2	ImplantP:days20
1.914	-0.084	1.653	0.262	-1.720	-0.095

## ranef(mod)

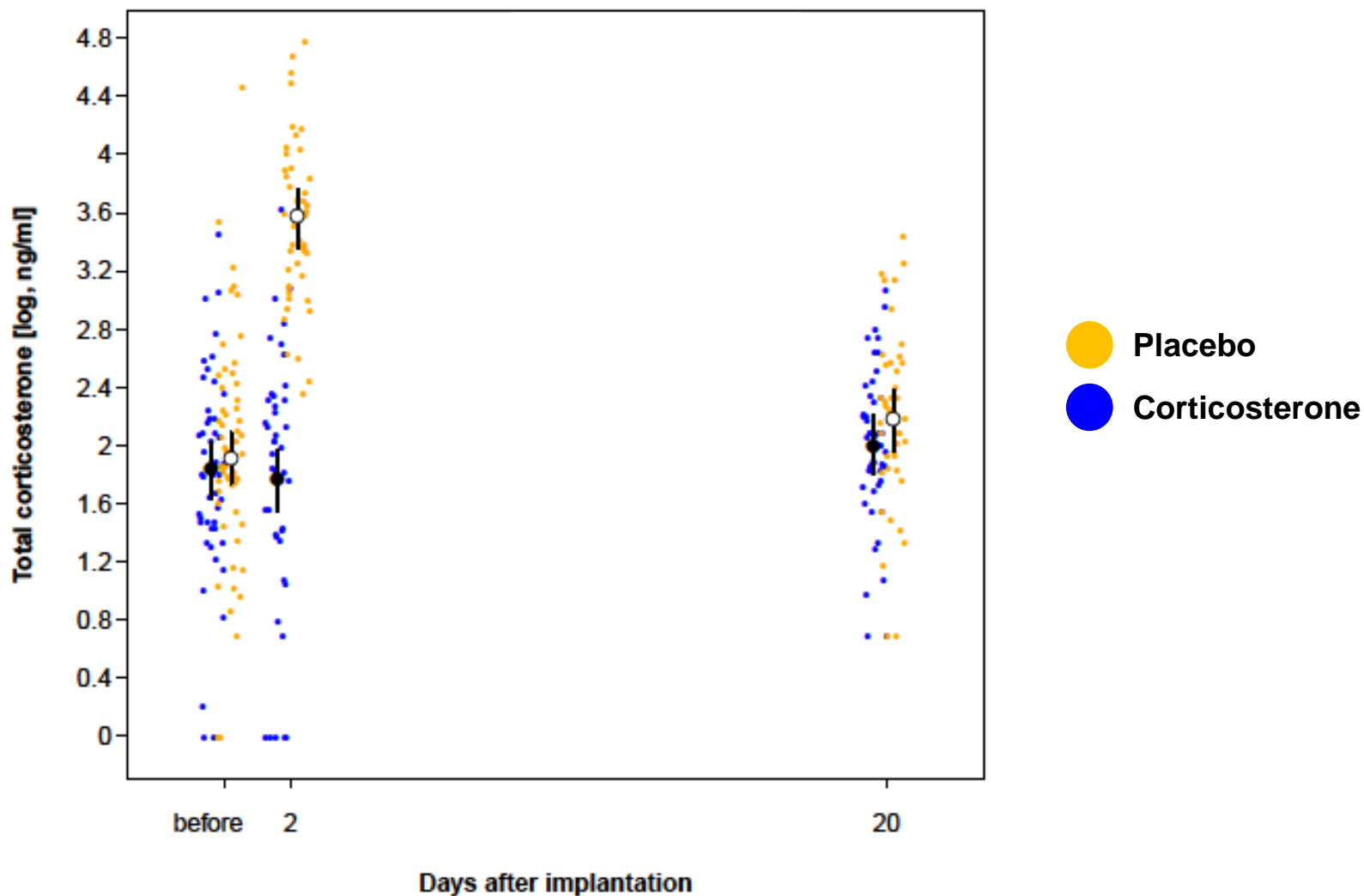
\$Ring	Intercept)
898054	0.250867170
898055	0.119193973
898057	-0.108778053
898058	0.070320591
898059	-0.081330604

## coef(mod)

\$Ring	(Intercept)	ImplantP	days2	days20	ImplantP:days2	ImplantP:days20
898054	2.165247	-0.08488857	1.653434	0.262791	-1.720644	-0.09530968
898055	2.033574	-0.08488857	1.653434	0.262791	-1.720644	-0.09530968
898057	1.805602	-0.08488857	1.653434	0.262791	-1.720644	-0.09530968
898058	1.984700	-0.08488857	1.653434	0.262791	-1.720644	-0.09530968
898059	1.833049	-0.08488857	1.653434	0.262791	-1.720644	-0.09530968



# Fitting a linear mixed model





# REML vs LM

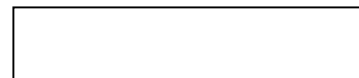
Important: mixed models can be fit by ML or by REML

REML gives unbiased estimates for the variance components  
but are biased in the variance of the fixed effects

## Guideline in fitting mixed models:

1. use REML to analyse the random model structure
2. switch to ML to draw inference about the fixed effect part

```
mod.LM=lmer(log(totCort)~Implant + days + Implant:days  
            +(1|Ring), data=dat, REML=FALSE)
```





# Assesment of model assumptions

# residuals vs. fitted (**homogeneity of variance and distribution**)

```
scatter.smooth(fitted(mod), resid(mod)); abline(h=0, lty=2)
```

```
title("Tukey-Anscombe Plot")
```

→ no pattern

# qq of residuals (**normality**)

```
qqnorm(resid(mod), main="normal QQ-plot, residuals")
```

```
qqline(resid(mod))
```

→ no deviation from the main line

# (squarerooted) residuals vs. fitted (**homogeneity of variance**)

```
scatter.smooth(fitted(mod), sqrt(abs(resid(mod))))
```

→ no pattern

# qq of random effects (**normality of random effects**)

```
qqnorm(ranef(mod)$Ring[,1])
```

```
qqline(ranef(mod)$Ring[,1])
```

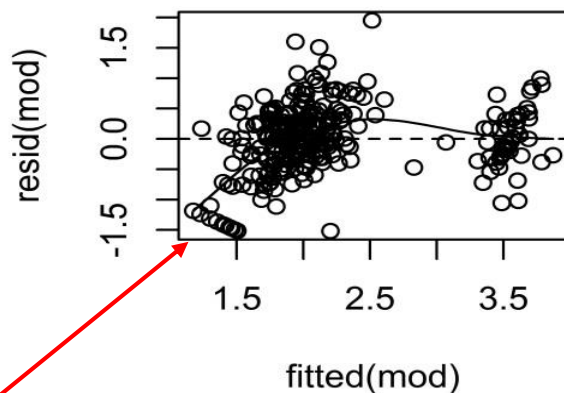
→ no deviation from the main line



# Assesment of model assumptions

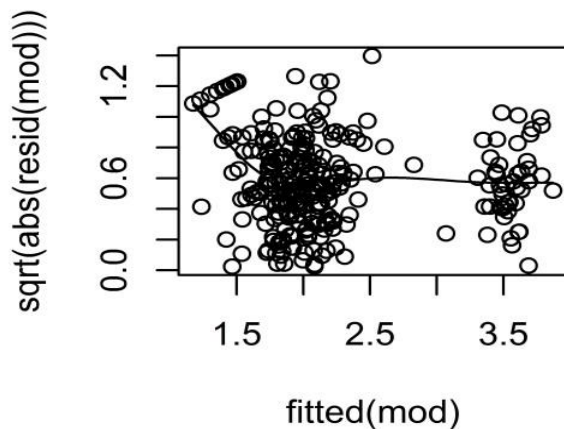
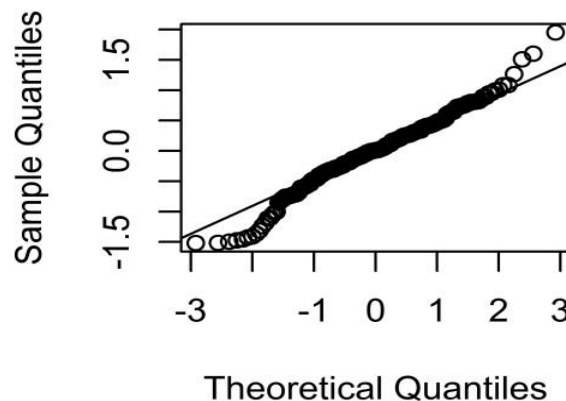


Tukey-Anscombe Plot

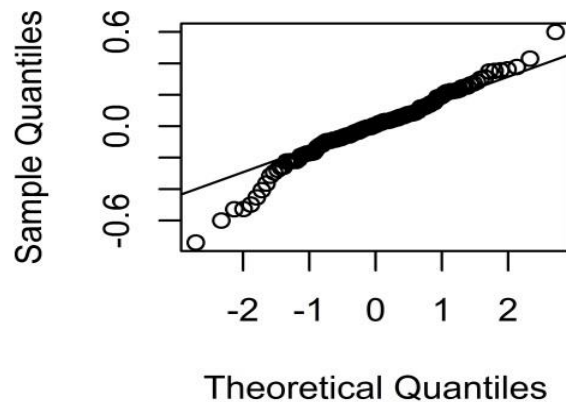


pattern

normal QQ-plot, residuals



normal QQ-plot, random effects





# Time for an exercise

---



Use the dataset “Forest\_data.csv”. Data on individual trees taken on plots along transects in a few sections of a valley in Washington state where trees were encroaching into shrub steppe habitat .

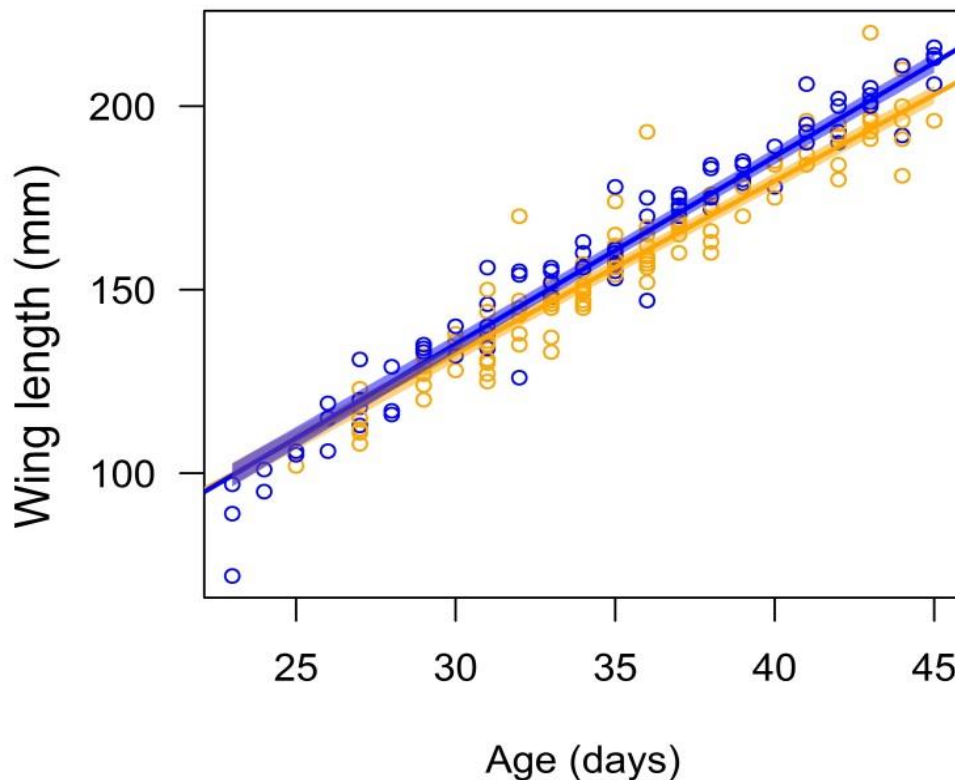
- (1) Input the data into R
- (2) Perform data exploration
- (3) Does **tree height** within each plot depend on the **slope** of the plot? Fit the appropriate model. What do you need to take into account? What could be a problem?
- (4) Perform model validation.
- (5) Think about a question where the random factors you used in (3) become fixed factors.



# Random intercepts and slope

Barn owls nestlings and stress hormone:  
How does **corticosterone** treatment affect **growth rate**?

→ Besides having a different intercept, different individuals are also likely to react slightly differently to the corticosterone treatment



● Placebo  
● Corticosterone







# Random intercepts and slope

**basic model with interaction:**

$$\hat{y}_i = \beta_o + \beta_1 age_i + \beta_2 I(Implant = P) + \beta_3 age_i I(Implant = P)$$

$$y_i \sim Norm(\hat{y}_i, \sigma^2)$$

**plus between-individual variance in growth rate**

$$\hat{y}_i = \beta_o + b_{1, Ring_i} + (\beta_1 + b_{2, Ring_i}) age_i + \beta_2 I(Implant = P) + \beta_3 age_i I(Implant = P)$$

$$y_i \sim Norm(\hat{y}_i, \sigma^2)$$

$$b_{1:2, Ring} \sim MVNorm(\mathbf{0}, \Sigma)$$



# Random intercepts and slope

```
mod = lmer(Wing ~ Age + Implant + Age:Implant  
           + (Age|Ring), data=dat, REML=FALSE)
```

**mod**

Linear mixed model fit by maximum likelihood ['lmerMod']  
Formula: Wing ~ Age + Implant + Age:Implant + (Age | Ring)  
Data: dat

	AIC	BIC	logLik	deviance
	1280.4391	1307.1778	-632.2195	1264.4391

Random effects:

Groups	Name	Std.Dev.	Corr
Ring	(Intercept)	14.6424	
	Age	0.3573	-0.90
Residual		2.5419	

Number of obs: 209, groups: Ring, 86

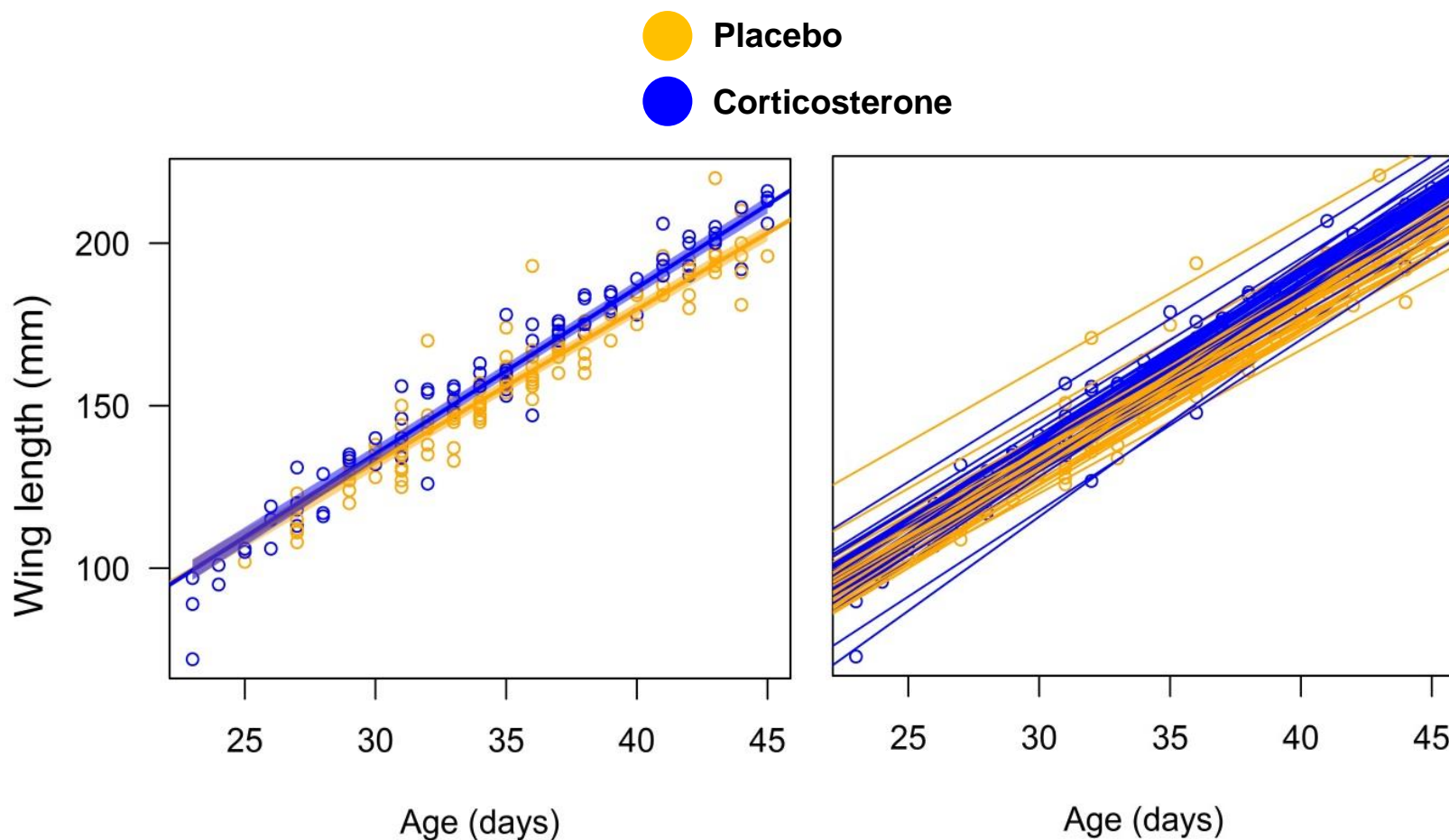
Fixed Effects:

(Intercept)	Age	ImplantP	Age:ImplantP
-8.2887	4.6979	-9.7816	0.4113



# Random intercepts and slope

Barn owls nestlings and stress hormone:  
How does **corticosterone** treatment affect **growth rate**?





# Random intercepts and slope

---

for the corticosterone-treated individuals:

```
abline(fixef(mod) [1] +  
       fixef(mod) [2] +  
       col="orange")
```

```
ranef(mod) $Ring[i,1] ,  
ranef(mod) $Ring[i,2] ,
```

for the placebo-treated individuals:

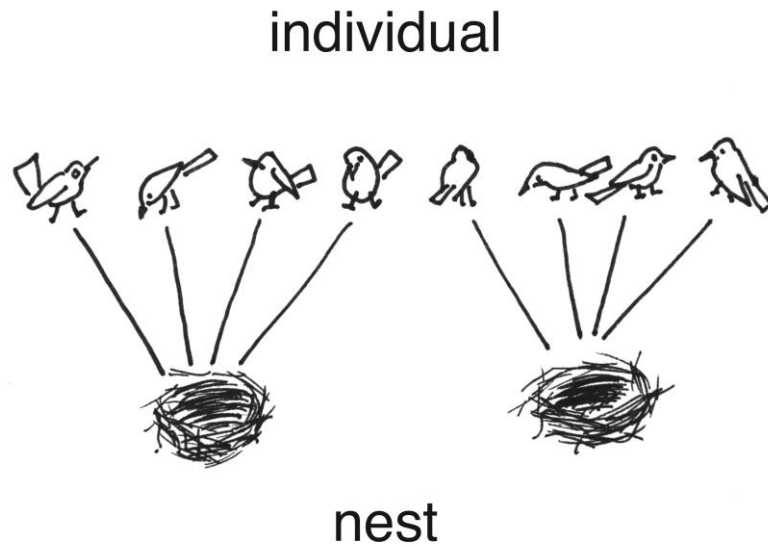
```
abline(fixef(mod) [1] + fixef(mod) [3] + ranef(mod) $Ring[i,1] ,  
       fixef(mod) [2] + fixef(mod) [4] + ranef(mod) $Ring[i,2] ,  
       col="blue")
```



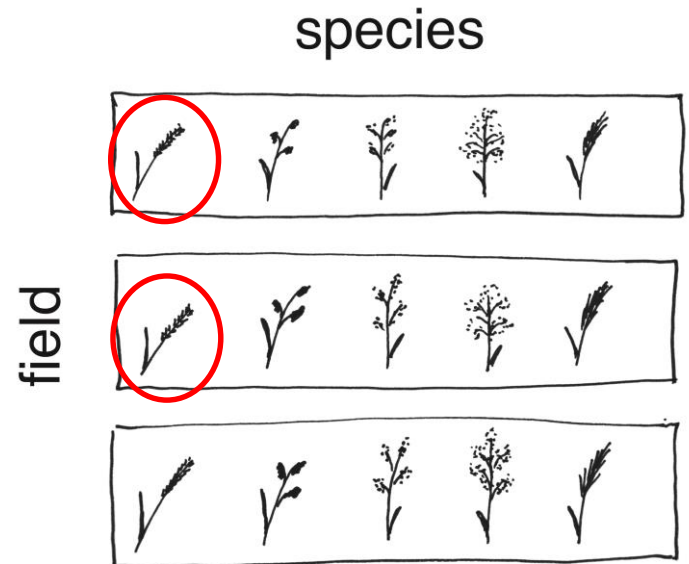
# Nested and crossed random effects



nested



crossed





# Nested and crossed random effects

---

## nested

```
mod <- lmer(log(totCort) ~ Implant + days + Implant:days +  
(1|Brood/Ring), data=cortbowl, REML=FALSE)
```

## crossed

```
mod <- lmer(log(totCort) ~ Implant + days + Implant:days +  
(1|Brood) + (1|Ring), data=cortbowl, REML=FALSE)
```



# What we have learned

- ▶ use REML to analyse **random effects**, use ML to analyse fixed effects
- ▶ mixed models = partial pooling
- ▶ crossed random effects:  $y \sim x + (1 | \text{group1}) + (1 | \text{group2})$
- ▶ nested random effects:  $y \sim x + (1 | \text{group2} / \text{group1})$

$$\begin{aligned} \hat{y}_i &= \beta_o + \beta_1 x_i + b_{g_i} \\ y_i &\sim \text{Norm}(\hat{y}_i, \sigma^2) \\ b_g &\sim \text{Norm}(0, \sigma_b^2) \end{aligned} \quad \left. \vphantom{\begin{aligned} \hat{y}_i &= \beta_o + \beta_1 x_i + b_{g_i} \\ y_i &\sim \text{Norm}(\hat{y}_i, \sigma^2) \\ b_g &\sim \text{Norm}(0, \sigma_b^2) \end{aligned}} \right\} \begin{array}{l} \text{fixed effects} \\ \text{variance} \\ \text{components} \end{array}$$

**random effects**



# Time for an exercise

Use the dataset “Fields.txt”. The dataset contains the number of plant species and soil nitrate levels in 126 plots of vegetation.

- (1) Input the data into R
- (2) Perform data exploration
- (3) Fit a model to look at the relationship between **soil nitrate level** and **species richness**. What do you need to take into account?
- (4) Perform model validation. What do you notice? What is the problem? How can it be solved?







# Practice at home

---



Follow up on the cortbowl.txt dataset we used for the nested model example.

- (1) Draw a graph of the fitted model, specifying a line for each individual.
- (2) Draw a graph of the fitted model, specifying a line for each brood.

# Acknowledgements

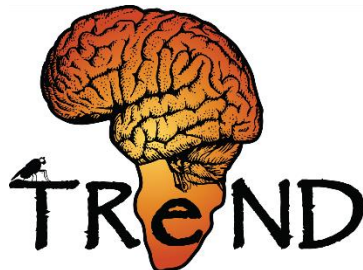
## People:

Noelie Maurel  
Wayne Dawson  
Fränzi Körner

International Max Planck  
Research School  
for Organismal Biology



Institute for  
Health Metrics  
and Evaluation



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Development

Journal of  
**Cell Science**

Journal of  
**Experimental  
Biology**

**Disease Models  
& Mechanisms**

**Biology Open**