UNIVERSITÉ DE NEUCHÂTEL

Master of Cognitive Science

Data Science Course

Linear model II

Professor: Moran Steven

Lecturer: Maiolini Marco

Lecture 9: 27/April/2022

Outline

- Part 1: Book report & discussion (15 minutes)
- Part 2: Mixed linear models (45 minutes)

Break (15 minutes)

- Part 3: Practical

On the previous lecture...

Model	Variables	Distribution	R code
Linear Regression	**$Y = b_0 + b_1x$**	Normal	*lm(formula, data)*
General Linear Models	**$Y = b_0 + b_1x_1 + b_2x_2 + ...$**	Normal	*lm(formula, data)*
Generalized Linear Models (GLM)	**$Y = b_0 + b_1x_1 + b_2x_2 + ...$**	Any	*glm(formula, family, data)*

Linear Models (LMs)

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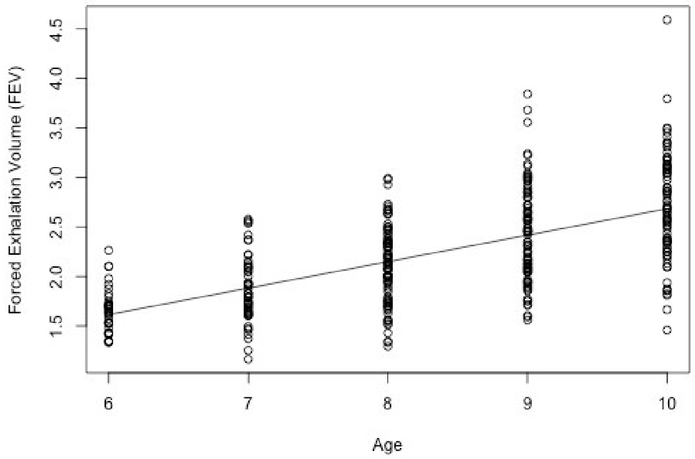
Differences between age of FEV



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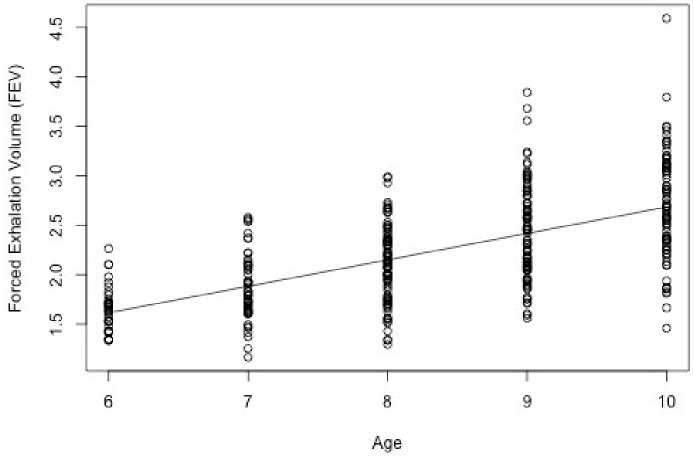

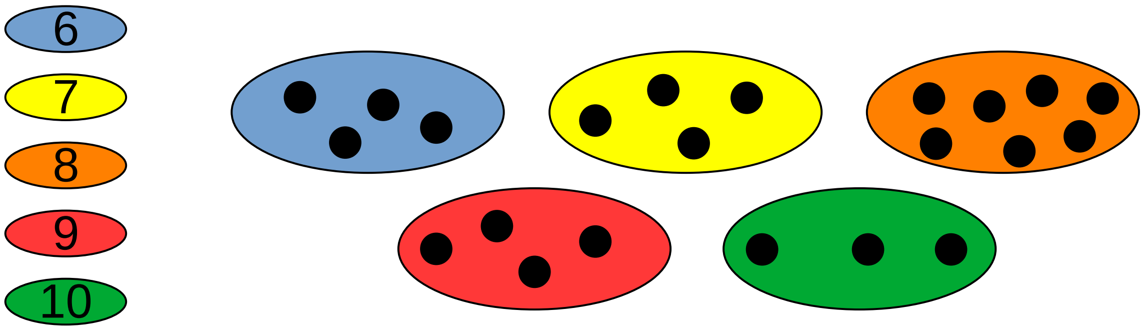

● = Individual sampled

<u>The samples of each level are selected randomly, but the levels (Age) of X are not randomly chosen</u>

Linear Models (LMs)

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Differences between sex in tool use acquisition in Bonobos

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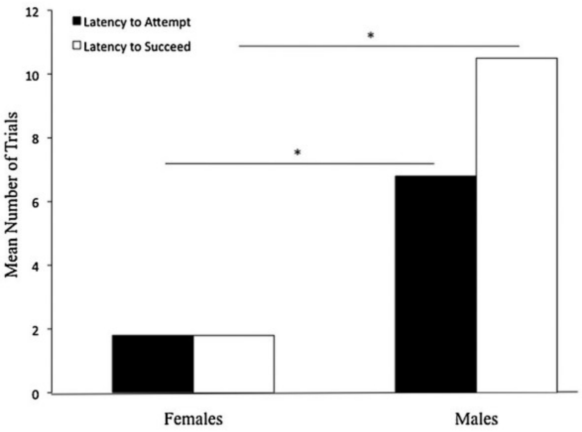

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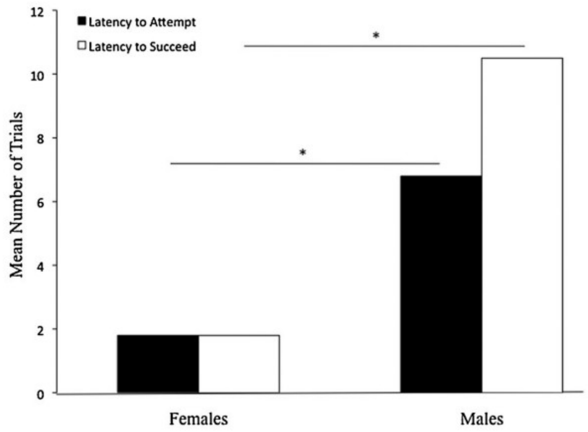

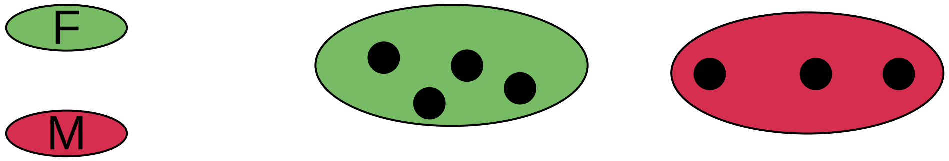

● = Individual sampled

<u>The samples of each level are selected randomly, but the levels (Sex) of X are not randomly chosen</u>

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Linear Models (LMs)

The levels of our study (Age, Sex) are called FIXED EFFECT.

- Each level of Fixed Factor is not derived randomly among infinite possibilities

- In my experiment, I took all the possible levels of Fixed Factor

- If I change the levels of Fixed Factor, I have to change the Hypothesis and repeat the experiment

Linear Mixed Models (GLMMs)

Most of Biological and Behavioural data involves RANDOM EFFECTS, whose purpose is instead to quantify the variation among units.

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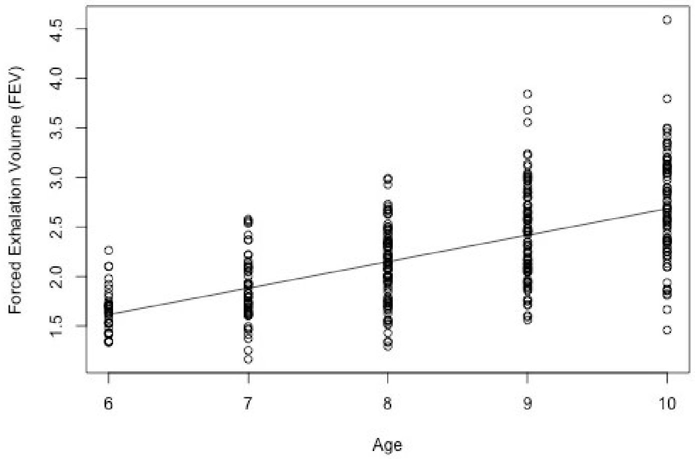
Differences between age of FAV, recorded in 2 schools.



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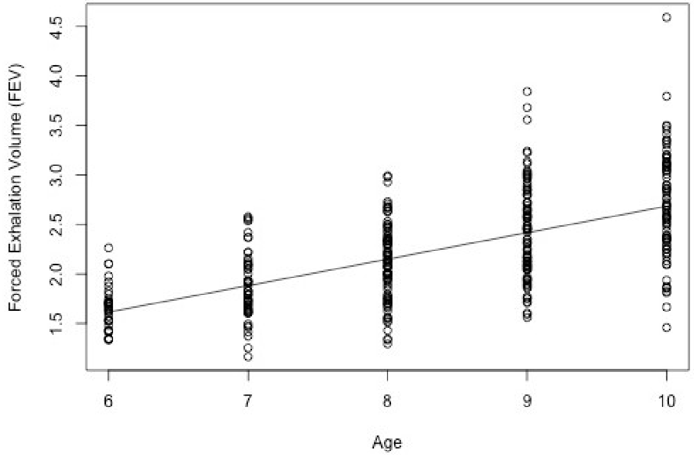

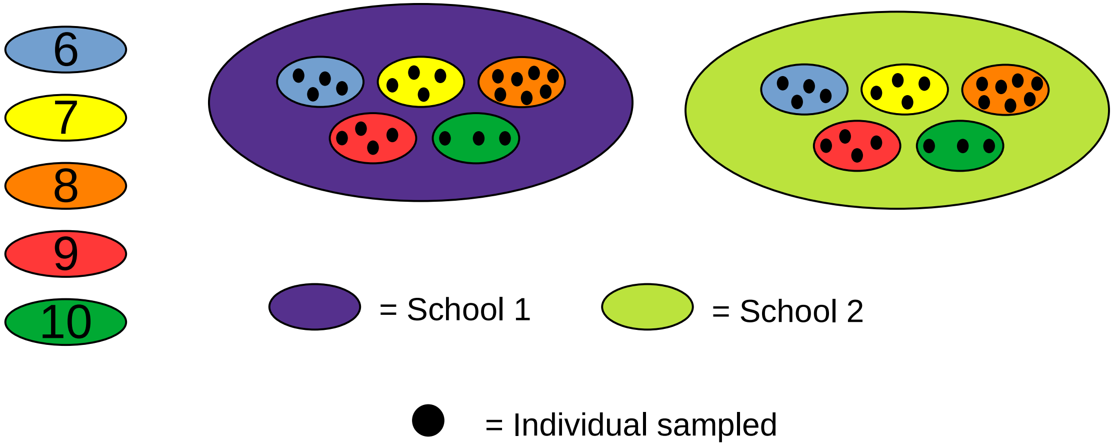

= School 1

= School 2

● = Individual sampled

<u>The samples of each level are selected randomly, as the Schools</u>

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Most of Biological and Behavioural data involves RANDOM EFFECTS, whose purpose is instead to quantify the variation among units.

Differences between sex in tool use acquisition in Bonobos, in 3 different groups

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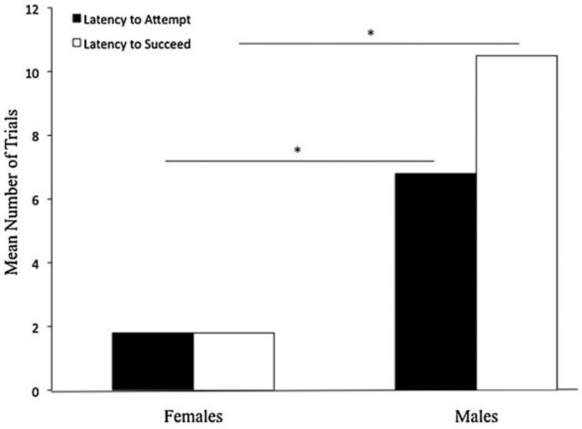

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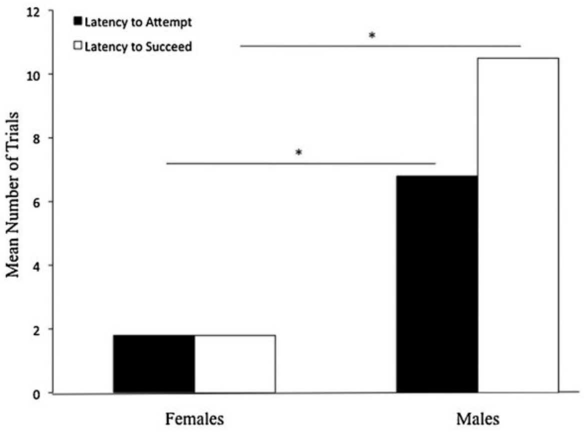
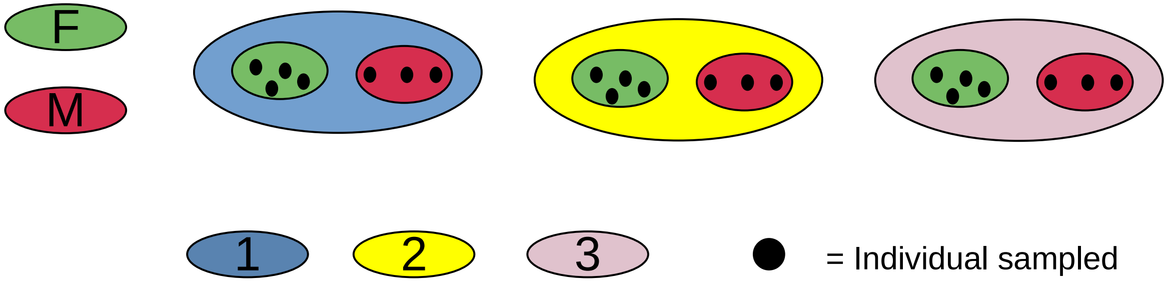




<u>The samples of each level are selected randomly, as the groups</u>

Boose et al., 2013; "Sex differences in tool use acquisition in bonobos (pan paniscus)", American Journal of Primatology.

Linear Mixed Models (GLMMs)

The levels that quantify our variance are called RANDOM EFFECT.

- Each level of Random Effect is collected randomly among infinite possibilities

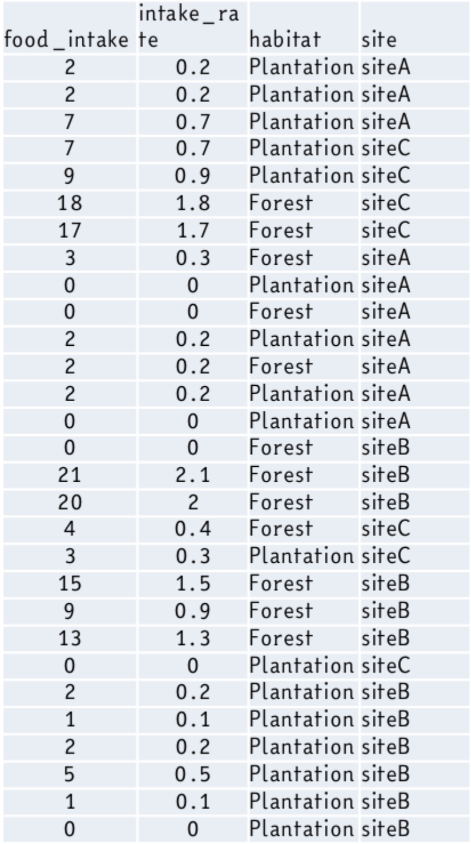
- In my experiment, I could not take all the possible levels of Random Effect

- If I change the levels of Random Effect, I have not to change the Hypothesis.

Linear Mixed Models (LMMs)

Example

You want to measure how much it is the food intake for a species in two habitat types (Forest and Plantation), measured in three different sites.



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2	0.2	Plantation	siteA
2	0.2	Plantation	siteA
7	0.7	Plantation	siteA
7	0.7	Plantation	siteC
9	0.9	Plantation	siteC
18	1.8	Forest	siteC
17	1.7	Forest	siteC
3	0.3	Forest	siteA
0	0	Plantation	siteA
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2	0.2	Plantation	siteA
2	0.2	Forest	siteA
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21	2.1	Forest	siteB
20	2	Forest	siteB
4	0.4	Forest	siteC
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2	0.2	Plantation	siteB
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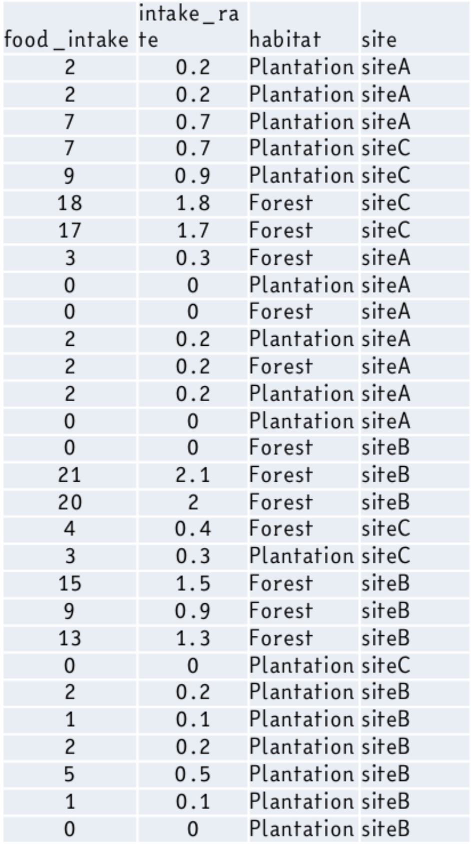

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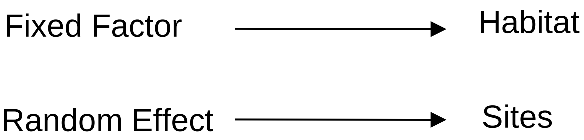
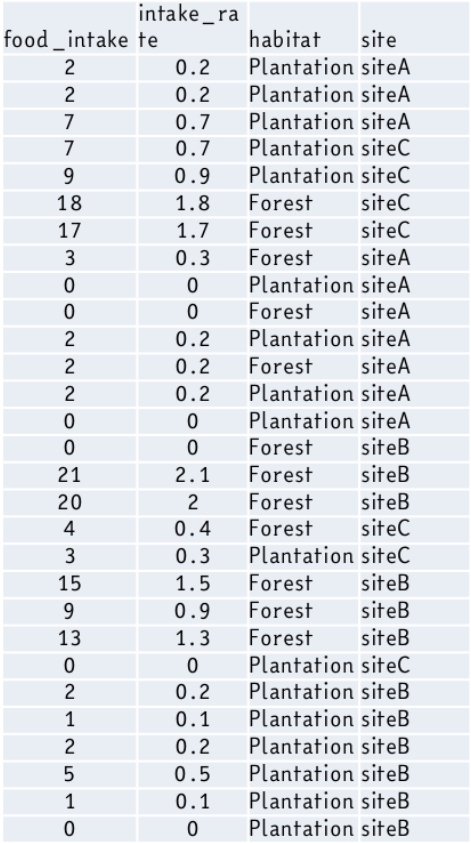

Fixed Factor → Habitat

Random Effect → Sites



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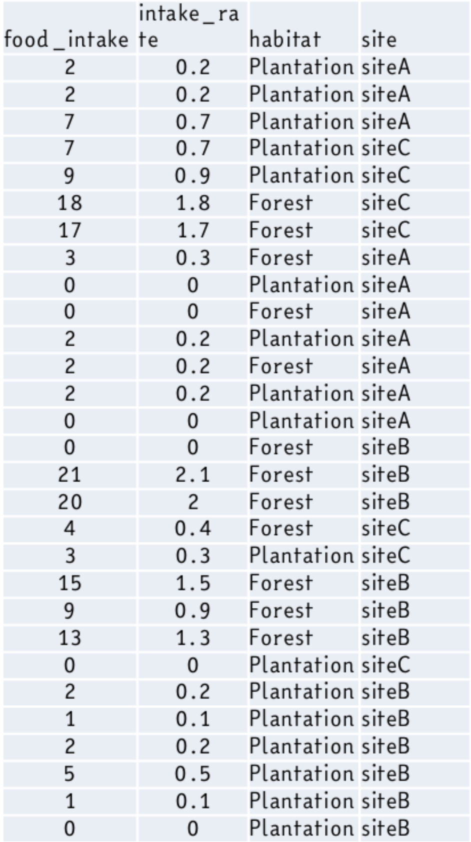

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In R:

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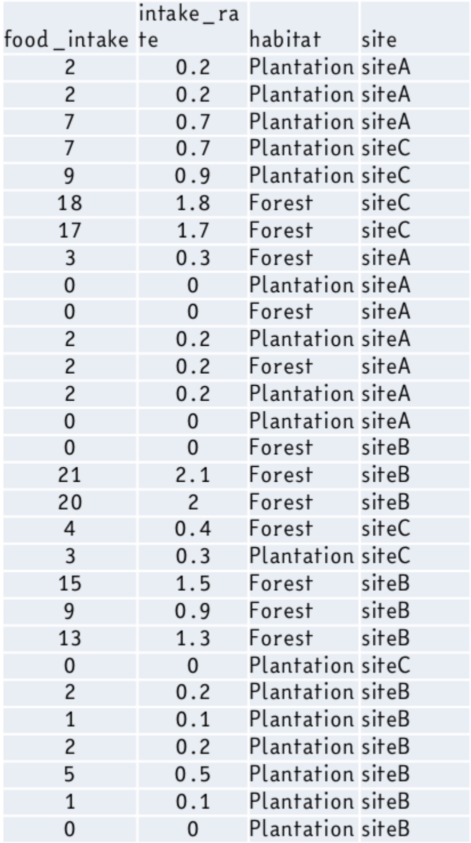

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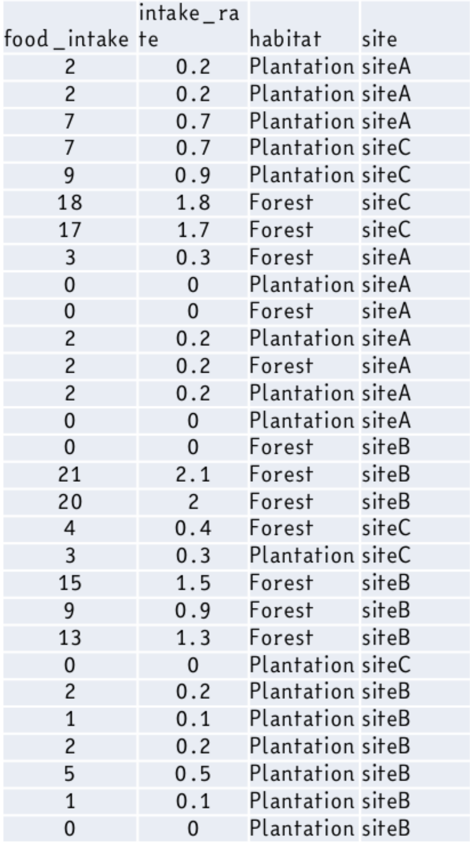
lmer(intake_rate ~ habitat + (1|site), data = …)

Remember to check if the residuals are normally distributed

A ← residuals(lmer(intake_rate ~ habitat + (1|site), data = …))
Shapiro.test(A)

In R:

lmer(Response variable ~ Fixed Factor + (1|Random), data = dataset)



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Generalized Linear Mixed Models (GLMMs)

GLMMs combine the proprieties of Linear Mixed Models (LMM) and Generalized Linear Models (GLM), which handle non normal data.

- Have Random Effect

- Can handle data with poisson, binomial or normal distribution

- Can handle interactions and additive effects

Generalized Linear Mixed Models (GLMMs)

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You take the data from different individuals, groups and songs.

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Fixed Factor → Context

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Example

You want to check if there is a rhythmic difference among context in the indris’ song.
You take the data from different individuals, groups and songs.

Response → Rhythm

Fixed Factor → Context

Random Effect → Individuals, groups and songs

In R:

lmer(Response variable ~ Fixed Factor + (1|RE1) + (1|RE2), family = …, data = dataset)

Generalized Linear Mixed Models (GLMMs)

Example

You want to check if there is a rhythmic difference among context in the indris' song.
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lmer(rhythm ~ context + (1|individual) + (1|group) + (1|song), family = …, data = …)

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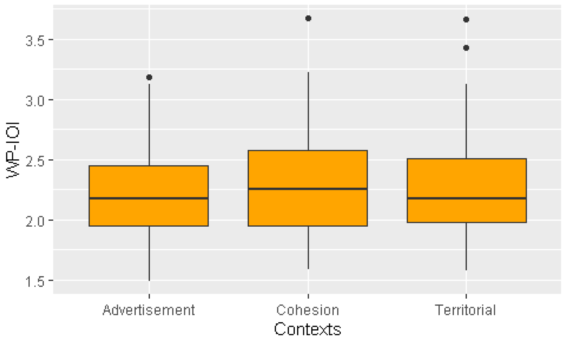

lmer(rhythm ~ context + (1|individual) + (1|group) + (1|song), family = …, data = …)

In R:

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Model Selection

Ockham razor

Model Selection

Ockham's razor → *"Pluralitas non est ponenda sine neccesitate"*

Between two theories that have same predictions, the simpler the better.

Model Selection

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Between two theories that have same predictions, the simpler the better.

When comparing different models we want to find out which model explain better my data regardless the **Individual independent variables** in the model.

❗ It doesn’t mean that there is a right and a wrong model!

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Akaike's information criteria (AIC):

AIC estimates model complexity. It works estimating the expected performance of model's predictions, for that scope it use observed data and hypothetical sample generated by the same model.

The best model show the smallest value; a difference within **4 - 7** units indicate less support, a difference over **10** indicate that the worse model can be omitted

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In R:

AIC(model)

Model Selection

Example

You want to check if there is a difference in water infection difference depending on the river tract sampled.
You sample different rivers.

Model Selection

Example

You want to check if there is a difference in water infection difference depending on the river tract sampled.
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```
Model1 ← lmer(water_infection ~ river_tract + (1|id_rivers), data = ... )

Summary(Model1)

AIC(Model1)
```

Model Selection

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```
AIC BIC logLik deviance df. Resid

4838 4920 -2410 4820 900
```

AIC = 4838

Model Selection

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AIC(Model1)
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```
AIC BIC logLik deviance df. Resid

4838 4920 -2410 4820 900
```

AIC = 4838

```
Model2 ← lmer(water_infection ~ river_tract + slope + (1|id_rivers), data = ... )

Summary(Model2)

AIC(Model2)
```

Model Selection

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You want to check if there is a difference in water infection difference depending on the river tract sampled.
You sample different rivers.

```
Model1 ← lmer(water_infection ~ river_tract + (1|id_rivers), data = ... )
Summary(Model1)
AIC(Model1)
```

```
AIC BIC logLik deviance df. Resid
4838 4920 -2410 4820 900
```

AIC = 4838

```
Model2 ← lmer(water_infection ~ river_tract + slope + (1|id_rivers), data = ... )
Summary(Model2)
AIC(Model2)
```

```
AIC BIC logLik deviance df. Resid
4810 4911 -2287 4780 899
```

AIC = 4810

Model Selection

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You sample different rivers.

```
Model1 ← lmer(water_infection ~ river_tract + (1|id_rivers), data = ... )

Summary(Model1)

AIC(Model1)
```

```
AIC BIC logLik deviance df. Resid

4838 4920 -2410 4820 900
```

AIC = 4838

```
Model2 ← lmer(water_infection ~ river_tract + slope + (1|id_rivers), data = ... )

Summary(Model2)

AIC(Model2)
```

```
AIC BIC logLik deviance df. Resid

4810 4911 -2287 4780 899
```

AIC = 4810

4838 – 4810 = 28

Model Selection

Example

You want to check if there is a difference in water infection difference depending on the river tract sampled.
You sample different rivers.

```
Model1 ← lmer(water_infection ~ river_tract + (1|id_rivers), data = ... )
Summary(Model1)
AIC(Model1)
```

AIC BIC logLik deviance df. Resid

4838 4920 -2410 4820 900

AIC = 4838

```
Model2 ← lmer(water_infection ~ river_tract + slope + (1|id_rivers), data = ... )
Summary(Model2)
AIC(Model2)
```

AIC BIC logLik deviance df. Resid

4810 4911 -2287 4780 899

AIC = 4810

4838 – 4810 = <u>28</u>

Model2 is better

datacamp

R