

Linear models II

Steven Moran & Marco Maiolini

In the previous lecture...

Model	Variables	Distribution	R code
Linear Regression	$Y = b_0 + b_1x$	Normal	<i>lm(formula, data)</i>
General Linear Models	$Y = b_0 + b_1x_1 + b_2x_2 + \dots$	Normal	<i>lm(formula, data)</i>
Generalized Linear Models (GLM)	$Y = b_0 + b_1x_1 + b_2x_2 + \dots$	Any	<i>glm(formula, family, data)</i>

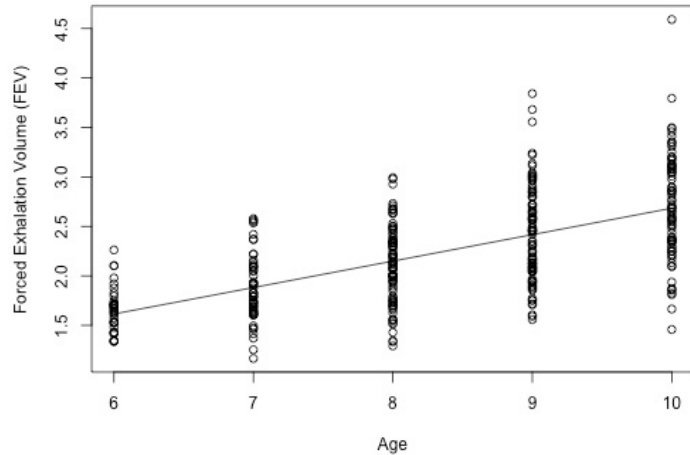
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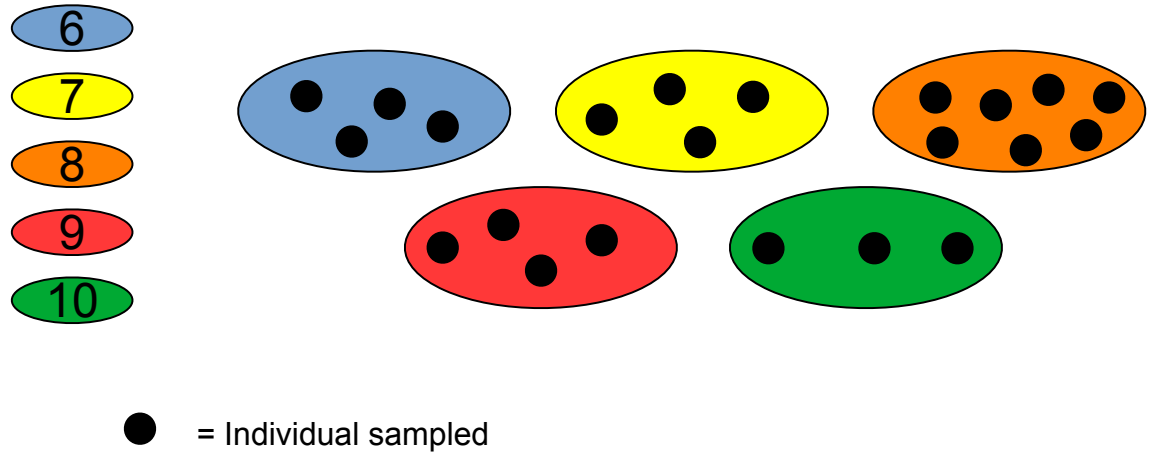
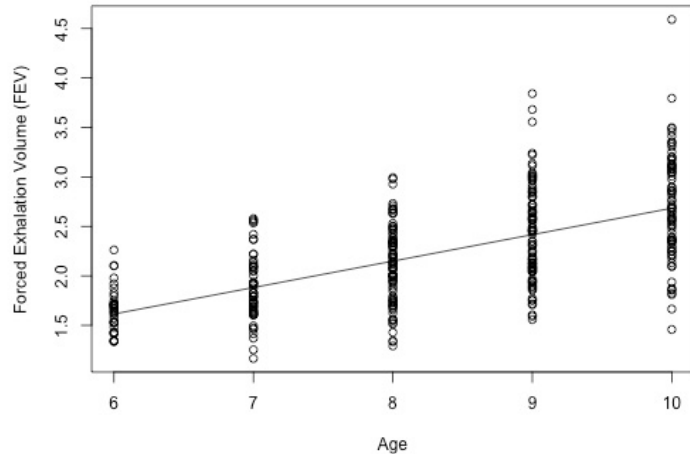
Differences between age of FEV



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Differences between age of FEV



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

Linear Models (LMs)

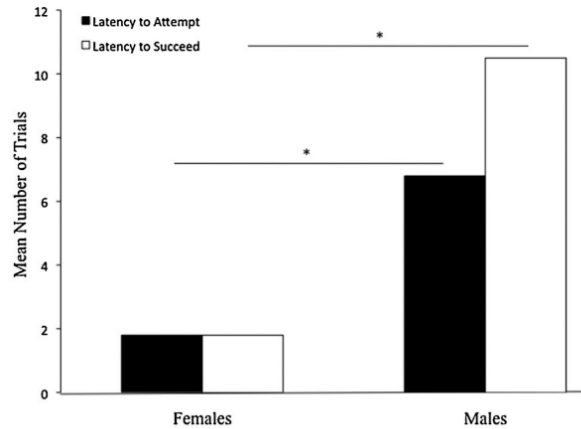
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Differences between sex in tool use acquisition in Bonobos

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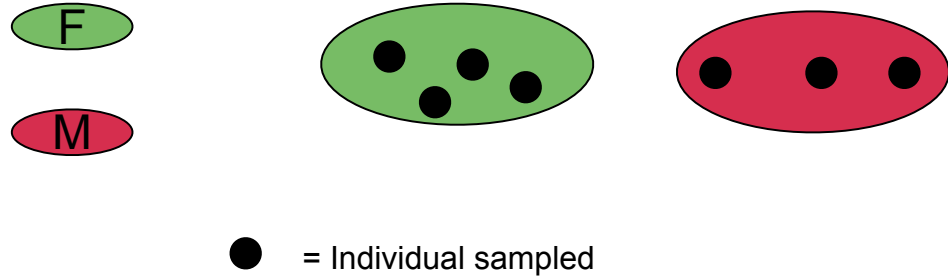
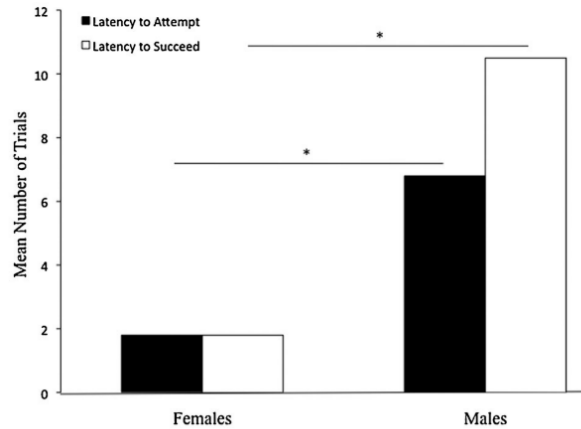
Differences between sex in tool use acquisition in Bonobos



Linear Models (LMs)

In most models that we have seen (LM or GLM) we were interested in quantifying the exact effect of each explanatory variable.

Differences between sex in tool use acquisition in Bonobos



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

Linear Models (LMs)

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

- Each level of a Fixed Factor is not derived randomly among infinite possibilities
- In an experiment, we look at all the possible levels of a Fixed Factor
- If we change the levels of a Fixed Factor, we have to change the hypothesis and repeat the experiment

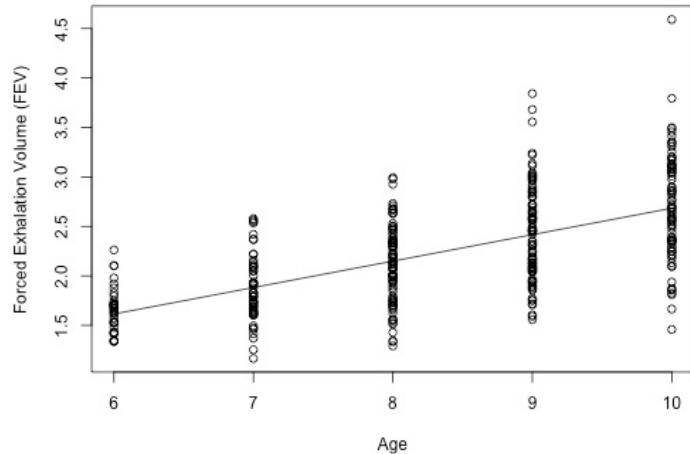
Linear Mixed Models (GLMMs)

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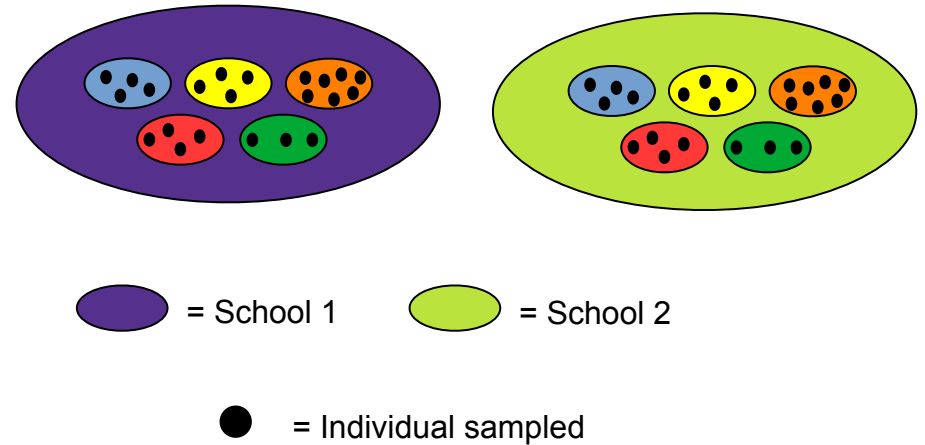
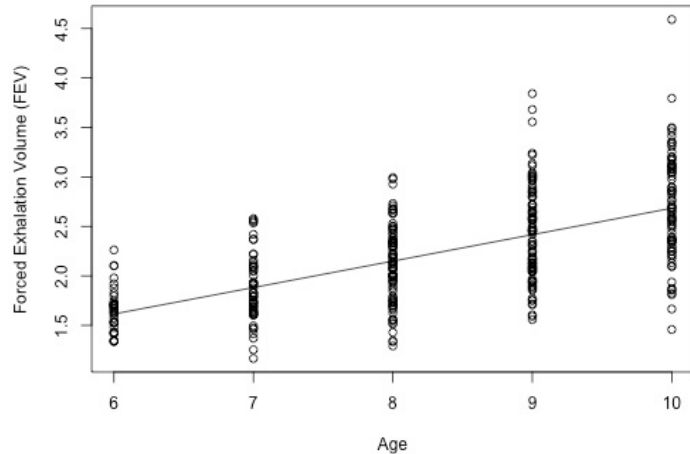
Differences between age of FAV, recorded in 2 schools.



Linear Mixed Models (GLMMs)

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Differences between age of FAV, recorded in 2 schools.



The samples of each level are selected randomly within each school

Linear Mixed Models (GLMMs)

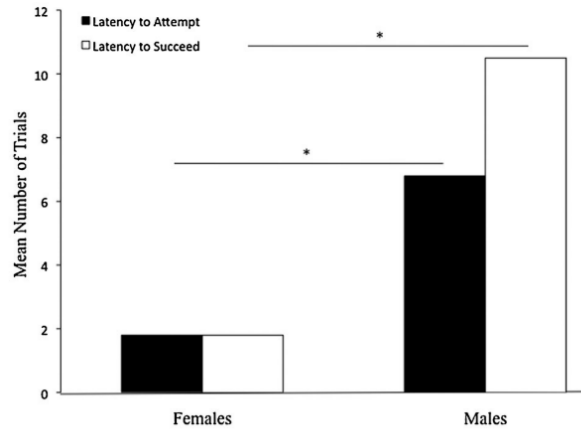
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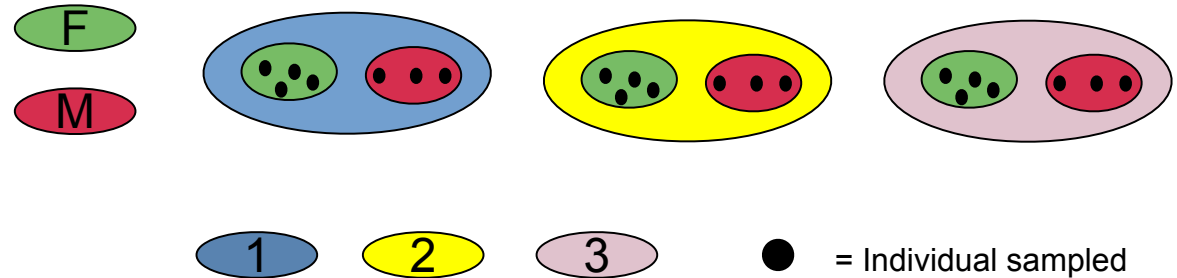
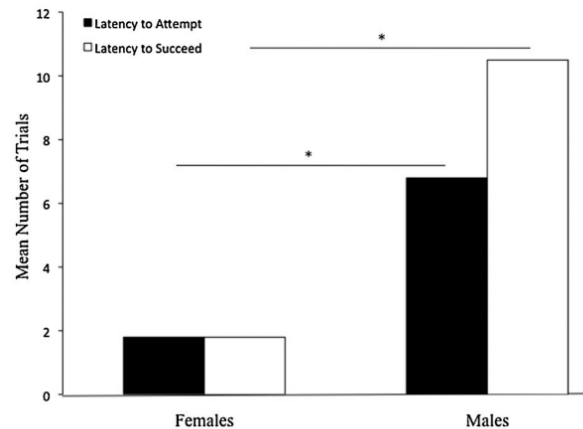
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Linear Mixed Models (GLMMs)

Most of biological and behavioral 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



The samples of each level are selected randomly within each group

Linear Mixed Models (GLMMs)

The levels that quantify our variance are called RANDOM EFFECT.

- Each level of a Random Effect is collected randomly among infinite possibilities
- In an experiment, we cannot take all the possible levels of a Random Effect
- If we change the levels of a Random Effect, we do not have to change our hypothesis.

Linear Mixed Models (LMMs)

Example

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

food_intake	intake_rate	habitat	site
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
0	0	Forest	siteA
2	0.2	Plantation	siteA
2	0.2	Forest	siteA
2	0.2	Plantation	siteA
0	0	Plantation	siteA
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21	2.1	Forest	siteB
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Linear Mixed Models (LMMs)

Example

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

Fixed Factor \longrightarrow Habitat

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In R:

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

Linear Mixed Models (LMMs)

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

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Fixed Factor \longrightarrow Habitat

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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)
```

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Generalized Linear Mixed Models (GLMMs)

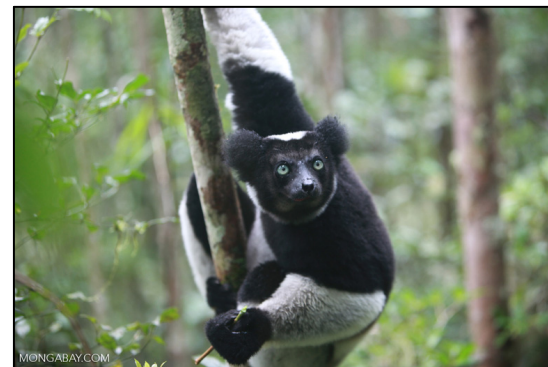
GLMMs combine the proprieties of Linear Mixed Models (LMM) and Generalized Linear Models (GLM), which handle non normal data.

- You have a Random Effect
- It can handle data with poisson, binomial or normal distribution
- It can handle interactions and additive effects

Generalized Linear Mixed Models (GLMMs)

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.

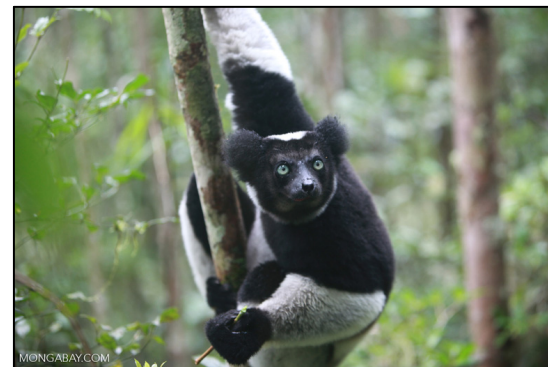


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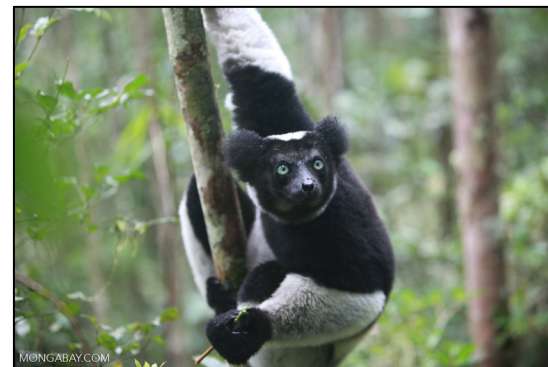
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Response \longrightarrow Rhythm

Fixed Factor \longrightarrow Context



Generalized Linear Mixed Models (GLMMs)

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Response	→	Rhythm
Fixed Factor	→	Context
Random Effect	→	Individuals, groups and songs



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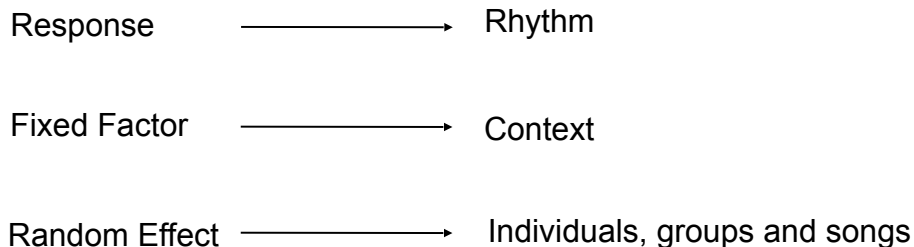
In R:

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

Generalized Linear Mixed Models (GLMMs)

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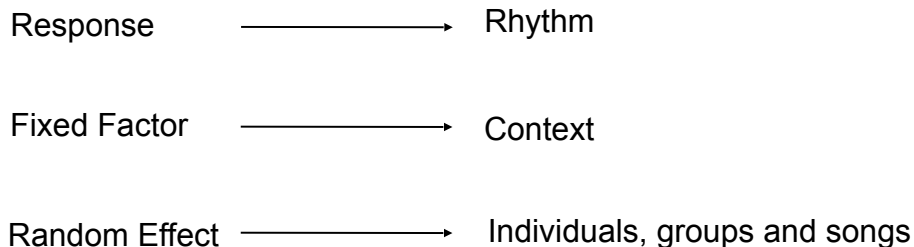
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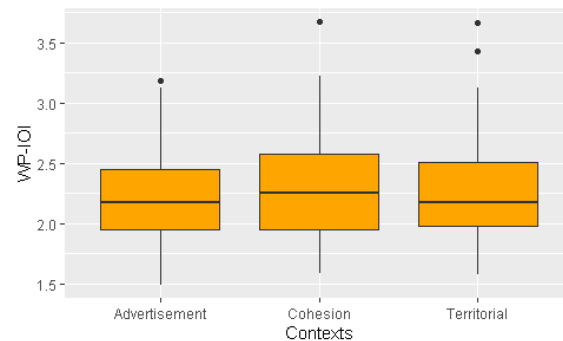
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Model Selection

Ockham's razor

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Ockham's razor —————→ *“Pluralitas non est ponenda sine neccesitate”*

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

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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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Akaike's information criteria (AIC):

In R:

AIC(model)

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.

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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

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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)
```

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.

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AIC BIC logLik deviance df. Resid

4838 4920 -2410 4820 900

AIC = 4838

Model Selection

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4838 4920 -2410 4820 900

AIC = 4838

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

```
Summary(Model2)
```

```
AIC(Model2)
```

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)
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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

Example

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

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```
Summary(Model1)
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```
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AIC = 4838

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```

```
Summary(Model2)
```

```
AIC(Model2)
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$$4838 - 4810 = \underline{28}$$

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Model Selection

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```
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```
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$$4838 - 4810 = \underline{28}$$

Model2 is better