

# Linear and Hierarchical Linear Models

Mixed Models, and Multilevel Models, GLMMs, etc...

AUTHORS

Camila Pacheco

Katrín Björnsdóttir

## Today

---

- Linear Models
- What are hierarchical linear models
- Identify situations in which the use of mixed effects is appropriate
- Implement basic linear mixed models (LMM) with [R](#)
- Break 😊
- Practice



## Required Material

---

<https://github.com/lacapary/BIO503/>

## Required Material

---

You are required to have downloaded and installed

```
install.packages(c("lme4",
                  "ggeffects",
```

```
    "stargazer"  
  ))
```

## Required Material

Do not hesitate to ask questions!

## Linear models

### Linear models

Now we want to test if there is a relationship between petal length and petal width. For that we run a simple linear model.

```
— Attaching core tidyverse packages ————— tidyverse 2.0.0 —  
✓ dplyr     1.1.4      ✓ readr     2.1.5  
✓ forcats   1.0.0      ✓ stringr   1.5.1  
✓ ggplot2   3.5.0      ✓ tibble    3.2.1  
✓ lubridate 1.9.3      ✓ tidyr    1.3.1  
✓ purrr    1.0.2  
— Conflicts ————— tidyverse_conflicts() —  
✖ dplyr::filter() masks stats::filter()  
✖ dplyr::lag()   masks stats::lag()  
ℹ Use the conflicted package (<http://conflicted.r-lib.org/>) to force all conflicts to become  
errors  
New names:  
Rows: 150 Columns: 6  
— Column specification —————  
Delimiter: ","  
chr (1): Species  
dbl (5): ...1, Sepal.Length, Sepal.Width, Petal.Length, Petal.Width  
  
ℹ Use `spec()` to retrieve the full column specification for this data.  
ℹ Specify the column types or set `show_col_types = FALSE` to quiet this message.
```

```
iris.m1 <- lm(Petal.Length ~ Petal.Width, data = iris)  
summary(iris.m1)
```

Call:

```
lm(formula = Petal.Length ~ Petal.Width, data = iris)
```

Residuals:

	Min	1Q	Median	3Q	Max
-1.33542	-0.30347	-0.02955	0.25776	1.39453	

```

Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept) 1.08356   0.07297 14.85 <2e-16 ***
Petal.Width 2.22994   0.05140 43.39 <2e-16 ***
---
Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```

Residual standard error: 0.4782 on 148 degrees of freedom  
 Multiple R-squared: 0.9271, Adjusted R-squared: 0.9266  
 F-statistic: 1882 on 1 and 148 DF, p-value: < 2.2e-16

The summary function gives you the output from the model. We can see that petal width significantly effects petal length (as you might have expected). Our model did very good, explaining about 93% of the variation in petal length.

## Linear models

---

Do we expect there to be a difference between species? Lets add species as an interaction to make it a bit more complicated.

```

iris.m2 <- lm(Petal.Length ~ Petal.Width * Species, data = iris)
summary(iris.m2)

```

Call:

```
lm(formula = Petal.Length ~ Petal.Width * Species, data = iris)
```

Residuals:

Min	1Q	Median	3Q	Max
-0.84099	-0.19343	-0.03686	0.16314	1.17065

Coefficients:

	Estimate	Std. Error	t value	Pr(> t )
(Intercept)	1.3276	0.1309	10.139	< 2e-16 ***
Petal.Width	0.5465	0.4900	1.115	0.2666
Speciesversicolor	0.4537	0.3737	1.214	0.2267
Speciesvirginica	2.9131	0.4060	7.175	3.53e-11 ***
Petal.Width:Speciesversicolor	1.3228	0.5552	2.382	0.0185 *
Petal.Width:Speciesvirginica	0.1008	0.5248	0.192	0.8480

---

Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 0.3615 on 144 degrees of freedom  
 Multiple R-squared: 0.9595, Adjusted R-squared: 0.9581  
 F-statistic: 681.9 on 5 and 144 DF, p-value: < 2.2e-16

## Linear models

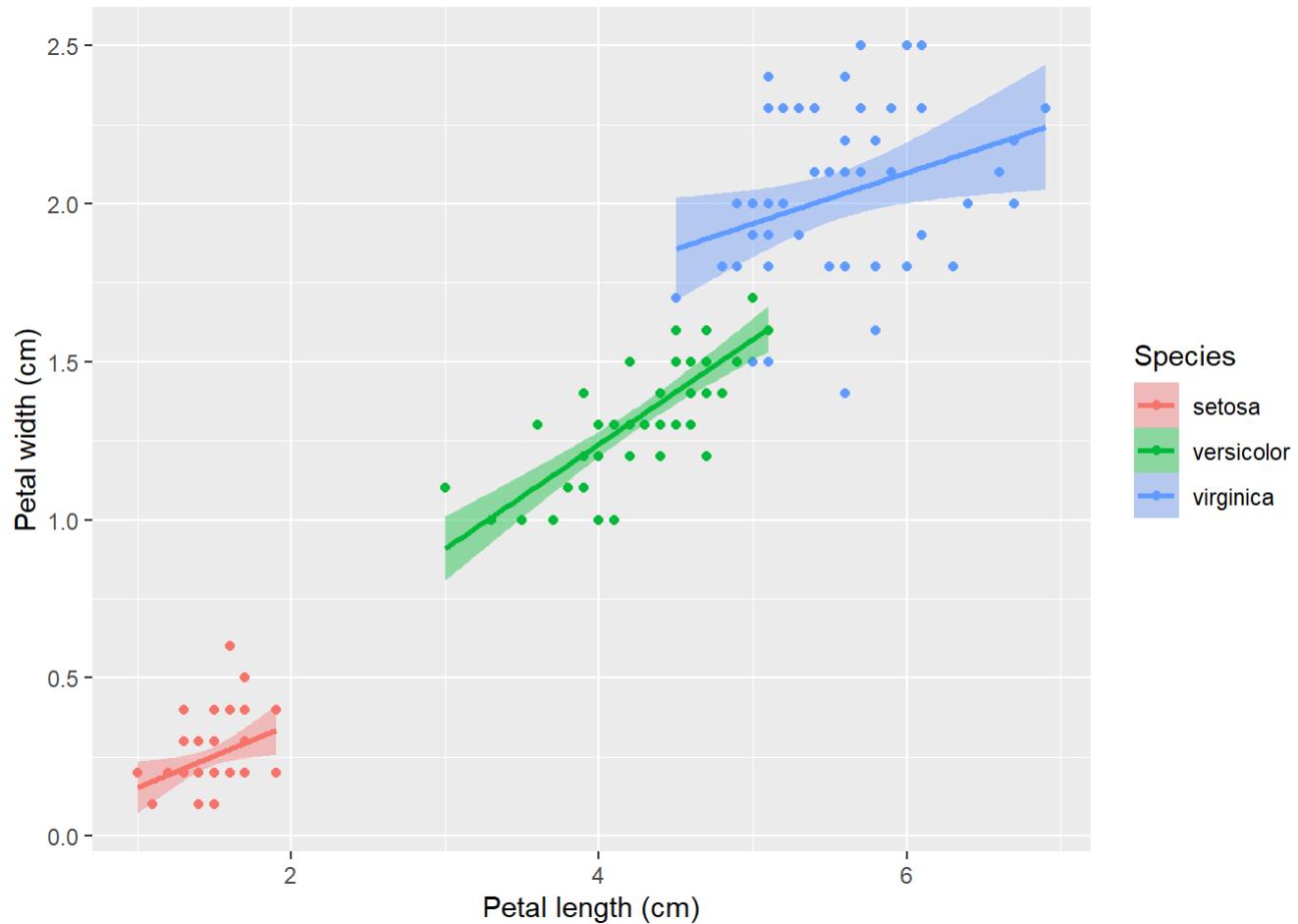
---

Now lets visualize the relationship using ggplot (notice how we only included stat`smooth to our original scatter plot).

```
p<-iris %>%
  ggplot(aes(
    x = Petal.Length,
    y = Petal.Width,
    color = Species)) + # to assign a color to each group
  geom_point() +
  stat_smooth(method = "lm", aes(fill = Species, colour = Species)) +
  labs(
    x = "Petal length (cm)",
    y = "Petal width (cm)")
```

## Linear models

`geom\_smooth()` using formula = 'y ~ x'



## Linear models

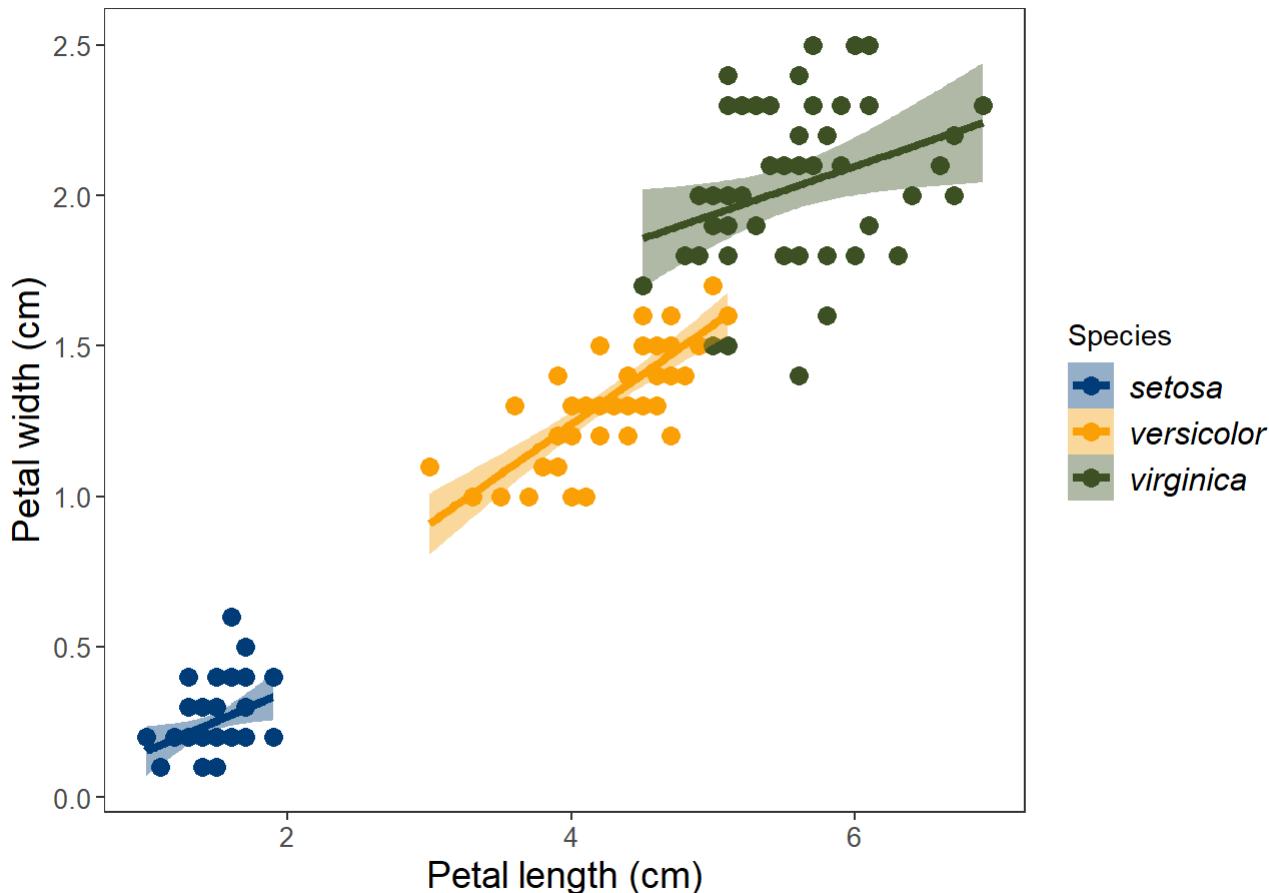
In the previous plot we just made we used the default ggplot settings. Although this is a great looking plot, we can make it even better since ggplot has a lot of power in customization, here is one example but feel free to play around with this, it can actually be quite satisfying when you get the hang of it.

```
p<-iris %>%
  ggplot(aes(
    x = Petal.Length,
    y = Petal.Width,
    color = Species # to assign a color to each group
  )) +
  geom_point(size = 3) + # to plot a scatter plot
  stat_smooth(method = "lm", aes(fill = Species, colour = Species), linewidth = 1.5) + #
  scale_color_manual(name = "Species", values = c("#023d79", "#faa307", "#3f5426")) + #
  scale_fill_manual(name = "Species", values = c("#023d79", "#faa307", "#3f5426")) + #
  labs(
    x = "Petal length (cm)", #x axis label
    y = "Petal width (cm)" #y axis label
  ) +
  theme_bw() + #theme within the ggplot2 package (different themes available, f.ex. theme_minimal())
  theme(axis.text.x = element_text(size = 10), #use the theme function to customize axis
        axis.text.y = element_text(size = 10),
        axis.title.x = element_text(size = 14, face = "plain"),
        axis.title.y = element_text(size = 14, face = "plain"),
        panel.grid.major.x = element_blank(),
        panel.grid.minor.x = element_blank(),
        panel.grid.minor.y = element_blank(),
        panel.grid.major.y = element_blank(),
        plot.margin = unit(c(0.5, 0.5, 0.5, 0.5), units = , "cm"),
        plot.title = element_text(size = 20, vjust = 1, hjust = 0.5),
        legend.text = element_text(size = 12, face = "italic"),
        legend.position = "right")
```

## Linear models

p

```
`geom_smooth()` using formula = 'y ~ x'
```



## Generalize linear models

---

Get familiar with different data distributions. Here is a brief summary of the data distributions you might encounter most often.

- Gaussian - Continuous data (normal distribution and homoscedasticity assumed)
- Poisson - Count abundance data (integer values, zero-inflated data, left-skewed data)
- Binomial - Binary variables (TRUE/FALSE, 0/1, presence/absence data)

Choosing the right statistical test for your analysis is an important step about which you should think carefully.

## Generalize linear models

---

(a non-exhaustive list of...)

## COMMON DATA TYPES IN ENVIRONMENTAL SCIENCES AND THEIR ASSOCIATED DISTRIBUTIONS & TESTS

DATA TYPE	DISTRIBUTION: TESTS	EXAMPLES
Continuous data	Gaussian (normal): lm, mixed-effects models	Traits like height, weight, nutrient content, and anything else you can measure across a range centered on a mean value
Count data (whole numbers)	Poisson: glm, glmm	Population counts, number of species in an area, of youngs in a litter, and other discrete measures
Proportion data	If 2 possible outcomes, Binomial: glm, glmm  If more outcomes: chi-squared test	Survival, seed germination trials, other events that can be described as “successes” and “failures”  Habitat selection (does a species utilise a type of habitat in greater proportion than its availability?), differences in vegetation types between sites or over time

lm which

## Generalize linear models

Syntax for a model with poisson (count) distribution

```
glm(y ~ x, family = poisson, data = df)
```

Syntax for a model with binomial distribution

```
glm(y ~ x, family = binomial, data = df)
```

## Hierarchical Linear Models

Ecological and biological data can be complex!

- Hierarchical structure in the data
- Many covariates and grouping factors
- Unbalanced study/experimental design

## What is Independence Assumption?

A linear regression model assumes that :

*Any other data point does not influence each data point in a dataset*

- We are **NOT** referring to your independent and responses variable
- *Ideally* we want them to be correlated it

We are referring withing the variable

## Diagnosis of dependence?

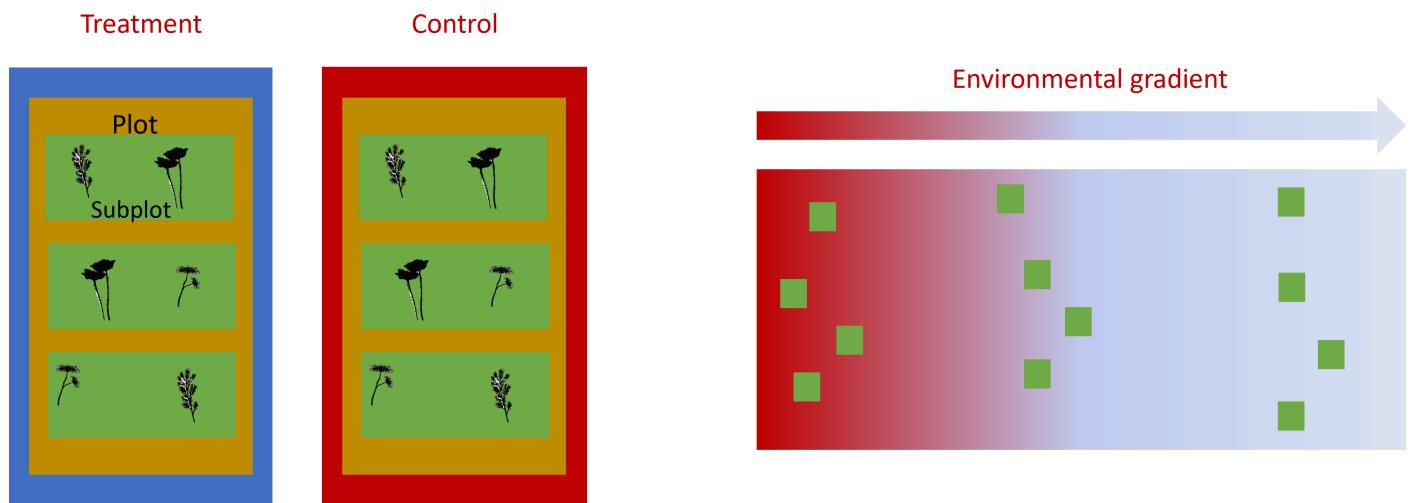
Think about how the data were collected.

### Are there clusters in my data?

For example:

Are there data from individual species clustered within sampling area?

## Hierarchical structures example



## Hierarchical structures in ecology

- Grouping factors: populations, species, sites
- Sample sizes: Species area relationship
- Time: Might take repeated measurements of the same plant in time
- Space: the closer the similar

## How could we analyze this data?

---

We need to explicitly account for the correlated nature of the data

The *random effects* structure will aid correct inference about *fixed effects*, depending on which level of the system's hierarchy is being manipulated.

- What is random effects ?
- What is fixed effects?
- When to used them ?

## When to used them ?

---

You will need to used random and fixed effects every time your data has a **Hierarchical** structure.

- It's important to note that this difference has little to do with the variables themselves, and a lot to do with your research question!
- What is just variation ("noise") that you need to control for?

## Fixed effects : deterministic processes

---

- They are like drivers, categories or groups that you think might directly influence the outcome you're studying.
- They're called "*fixed*" because you're interested in the specific levels of these categories.
- "I want to know how these different things (fixed effects) affect the outcome."
- levels of a factor (qualitative variable)
- a predictor (quantitative variable)

## Random effects : stochastic processes

---

- Name random doesn't have much to do with mathematical randomness
- They are like grouping factors for which we are trying to control
- You're not interested in the specific effect of these factors themselves
- but we know that they might be influencing the patterns we see

- "I want to know how these factors (random effects) contribute to the overall variation in the outcome."
- They are always categorical

## Data for this part of the session

---



### Coding Club Mixed models

## Explore the data

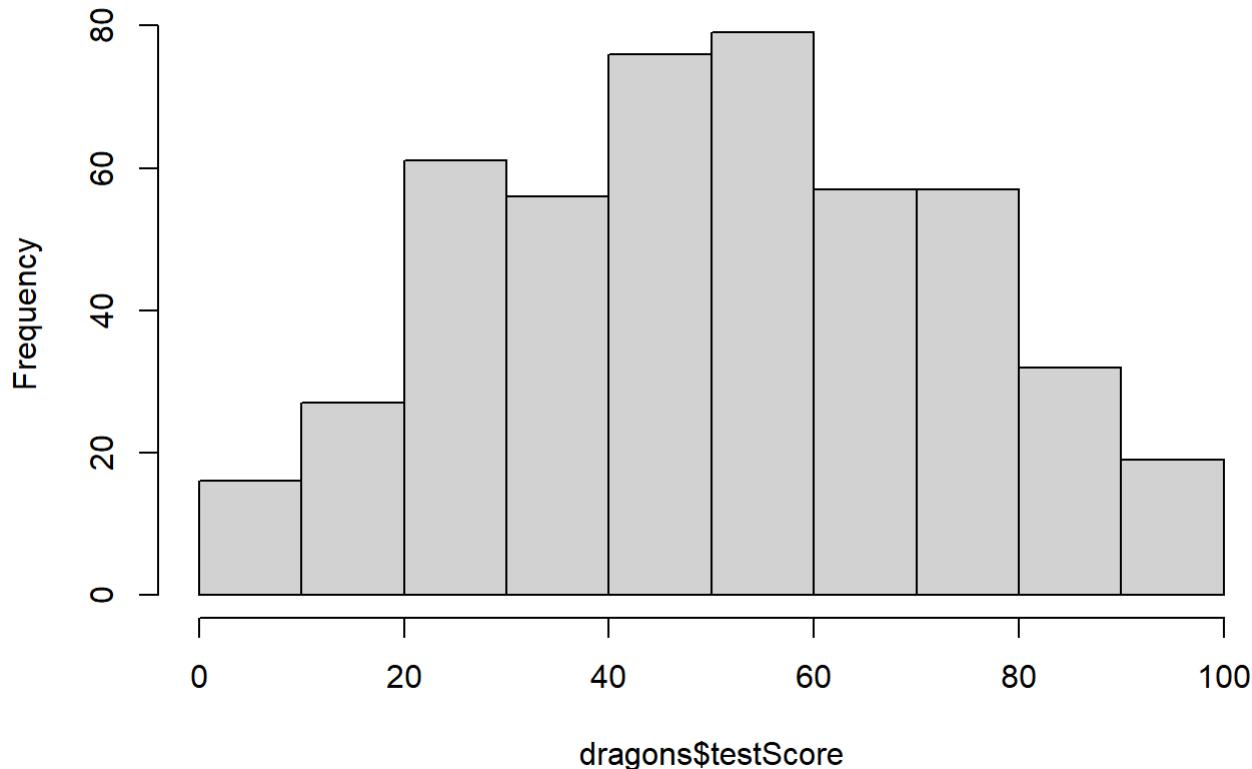
---

```
library(tidyverse)
load("CC-Linear-mixed-models/dragons.RData")
head(dragons)
```

	testScore	bodyLength	mountainRange	site
1	16.147309	165.5485	Bavarian	a
2	33.886183	167.5593	Bavarian	a
3	6.038333	165.8830	Bavarian	a
4	18.838821	167.6855	Bavarian	a
5	33.862328	169.9597	Bavarian	a
6	47.043246	168.6887	Bavarian	a

```
hist(dragons$testScore)
```

### Histogram of dragons\$testScore



## Scaling the data

It is good practice to standardize your explanatory variables before proceeding so that they have a mean of zero ("centering") and standard deviation of one ("scaling").

If two variables in the same model have very different scales, the mixed model will likely return a `convergence error` when trying to compute the parameters.

```
dragons<- dragons |>  
mutate(bodyLength2=scale(bodyLength,center = TRUE, scale = TRUE))
```

## Research question

Is the test score affected by body length?

## Linear model

```
basic.lm <- lm(testScore ~ bodyLength2, data = dragons)
summary(basic.lm)
```

Call:

```
lm(formula = testScore ~ bodyLength2, data = dragons)
```

Residuals:

Min	1Q	Median	3Q	Max
-56.962	-16.411	-0.783	15.193	55.200

Coefficients:

	Estimate	Std. Error	t value	Pr(> t )							
(Intercept)	50.3860	0.9676	52.072	<2e-16 ***							
bodyLength2	8.9956	0.9686	9.287	<2e-16 ***							
---											
Signif. codes:	0	'***'	0.001	'**'	0.01	'*'	0.05	'. '	0.1	' '	1

Residual standard error: 21.2 on 478 degrees of freedom

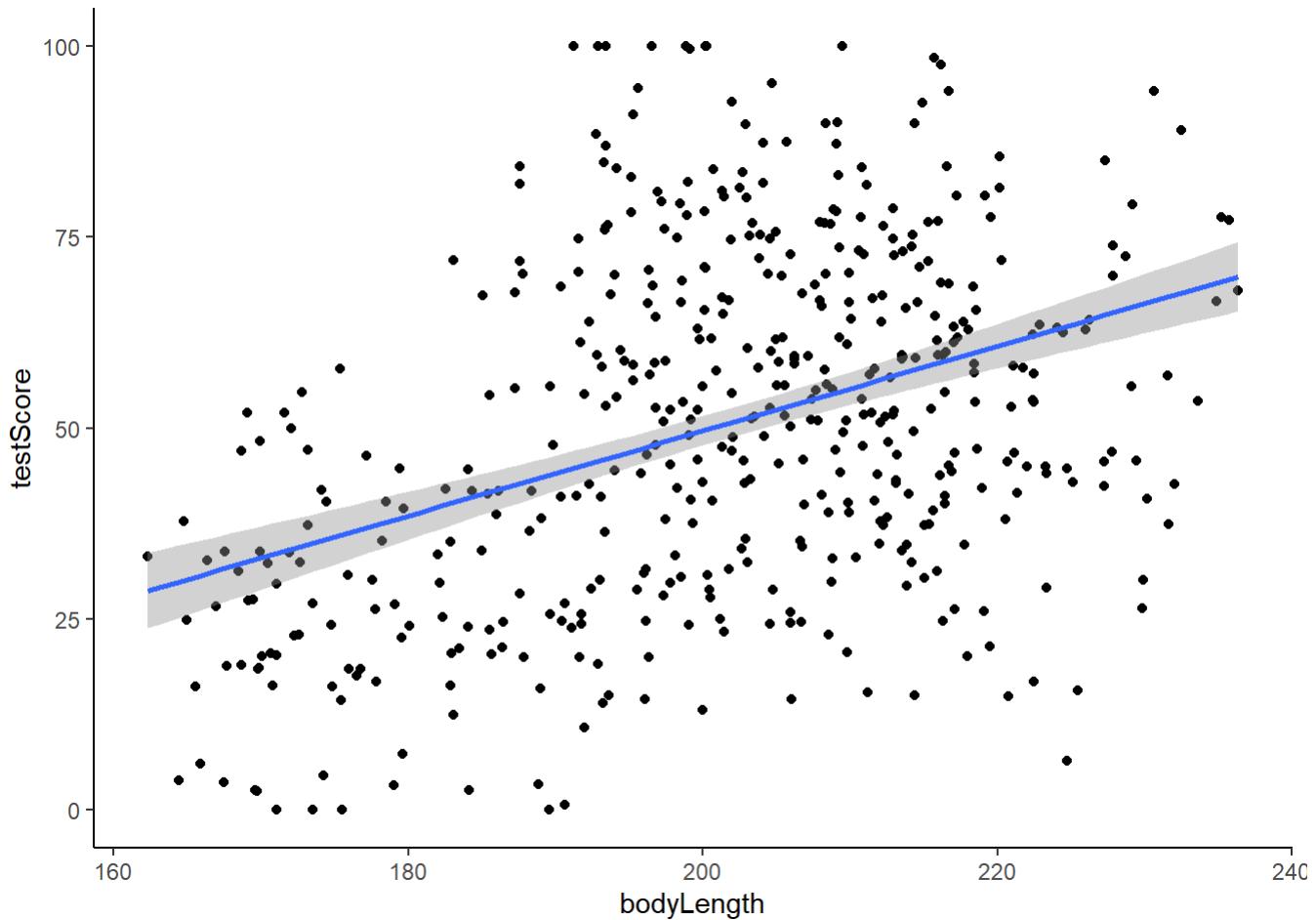
Multiple R-squared: 0.1529, Adjusted R-squared: 0.1511

F-statistic: 86.25 on 1 and 478 DF, p-value: < 2.2e-16

## Linear model

```
(prelim_plot <- ggplot(dragons, aes(x = bodyLength, y = testScore)) +
  geom_point() +
  geom_smooth(method = "lm")+
  theme_classic())
```

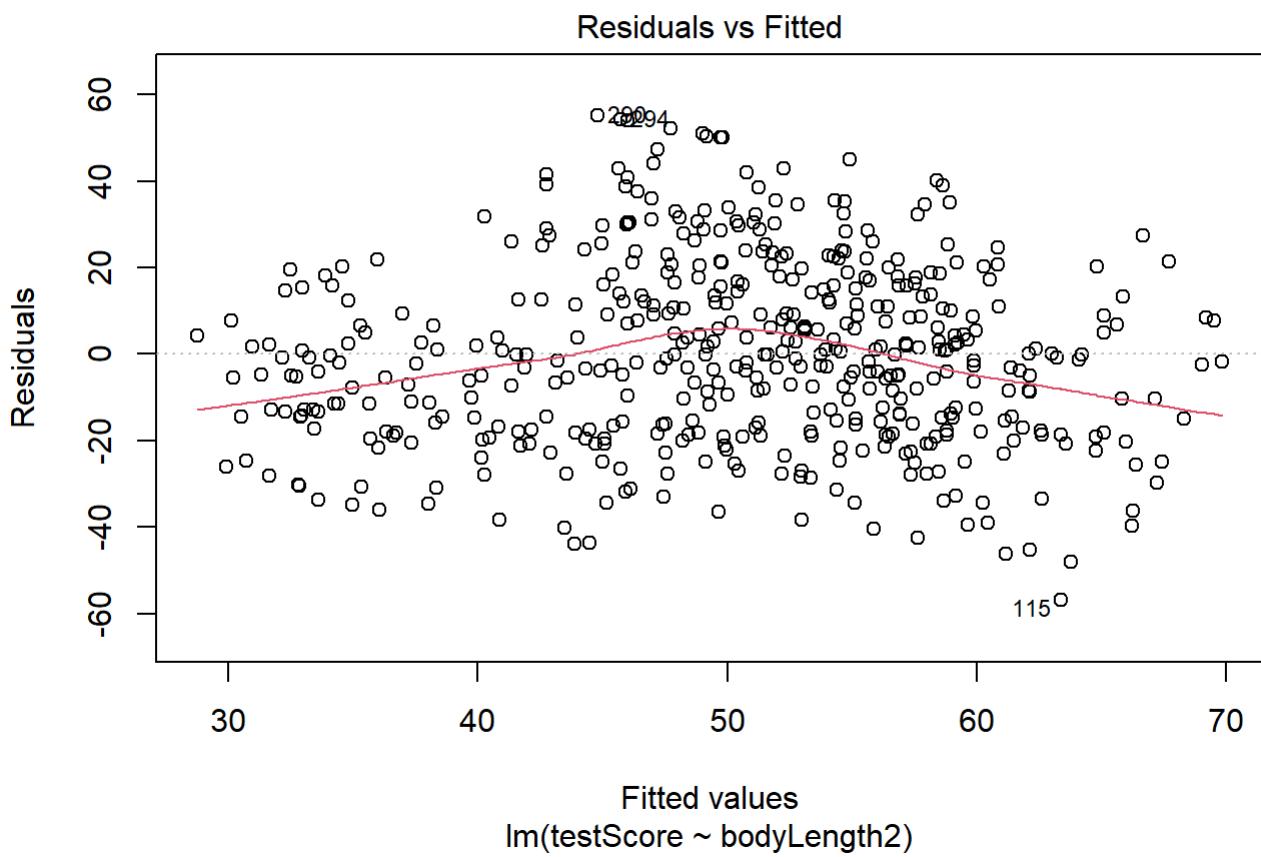
```
`geom_smooth()` using formula = 'y ~ x'
```

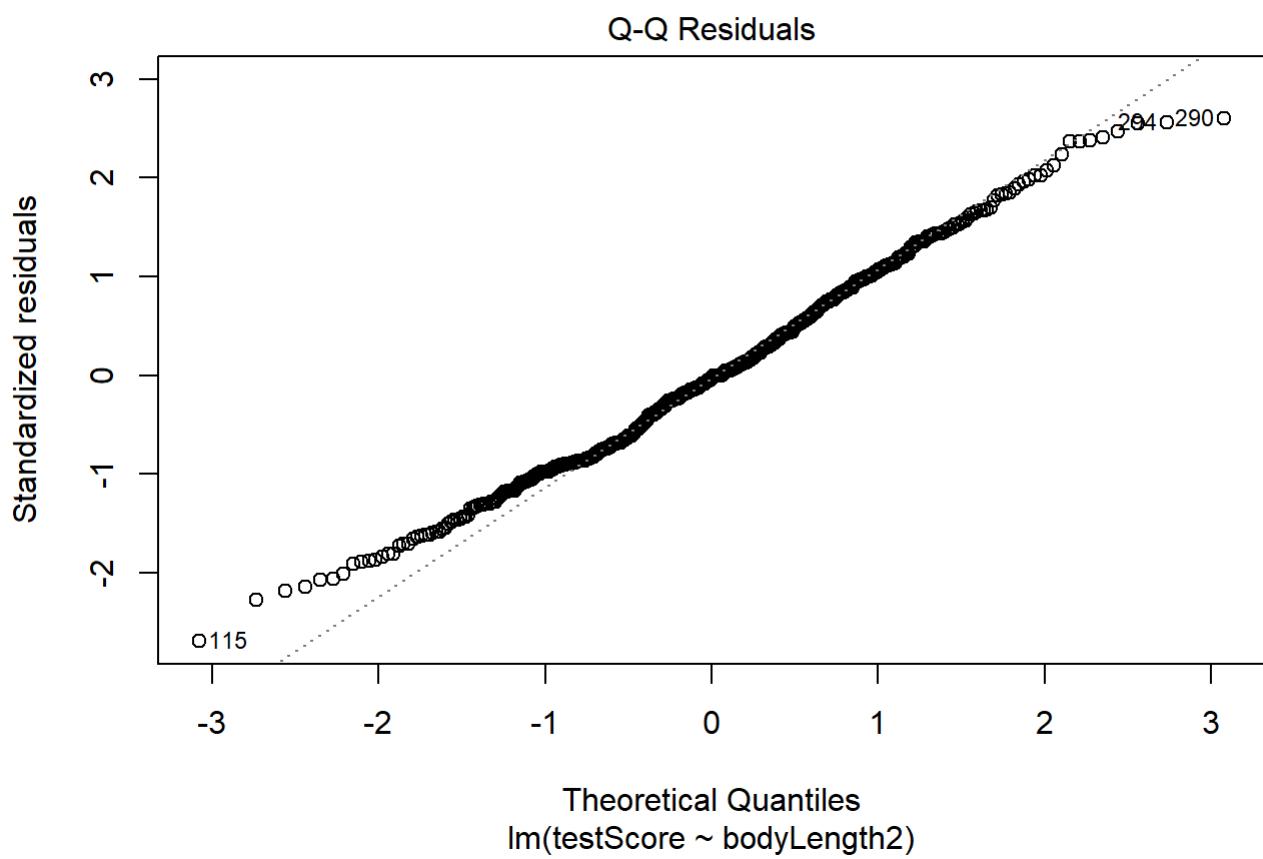


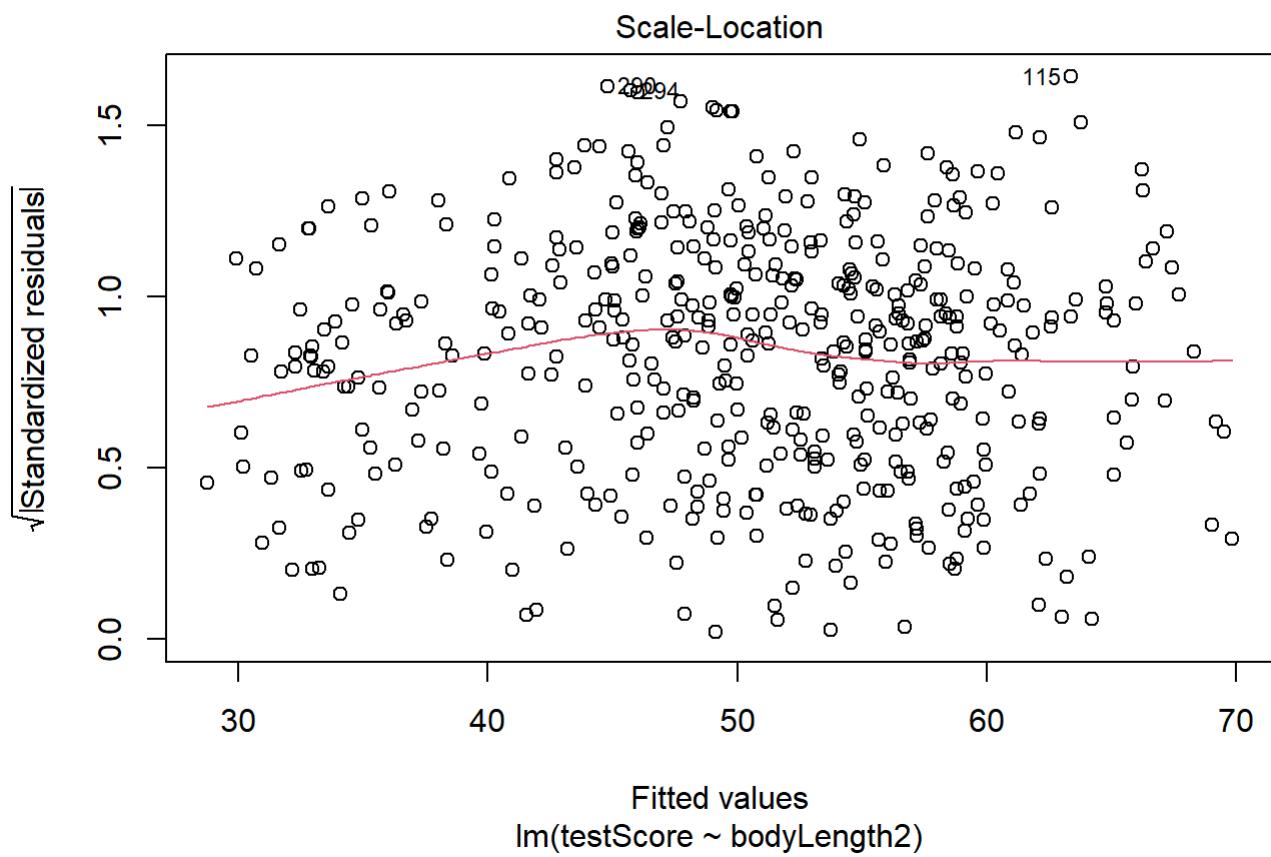
- it seems like bigger dragons do better in our intelligence test. That seems a bit odd: size shouldn't really affect the test scores.

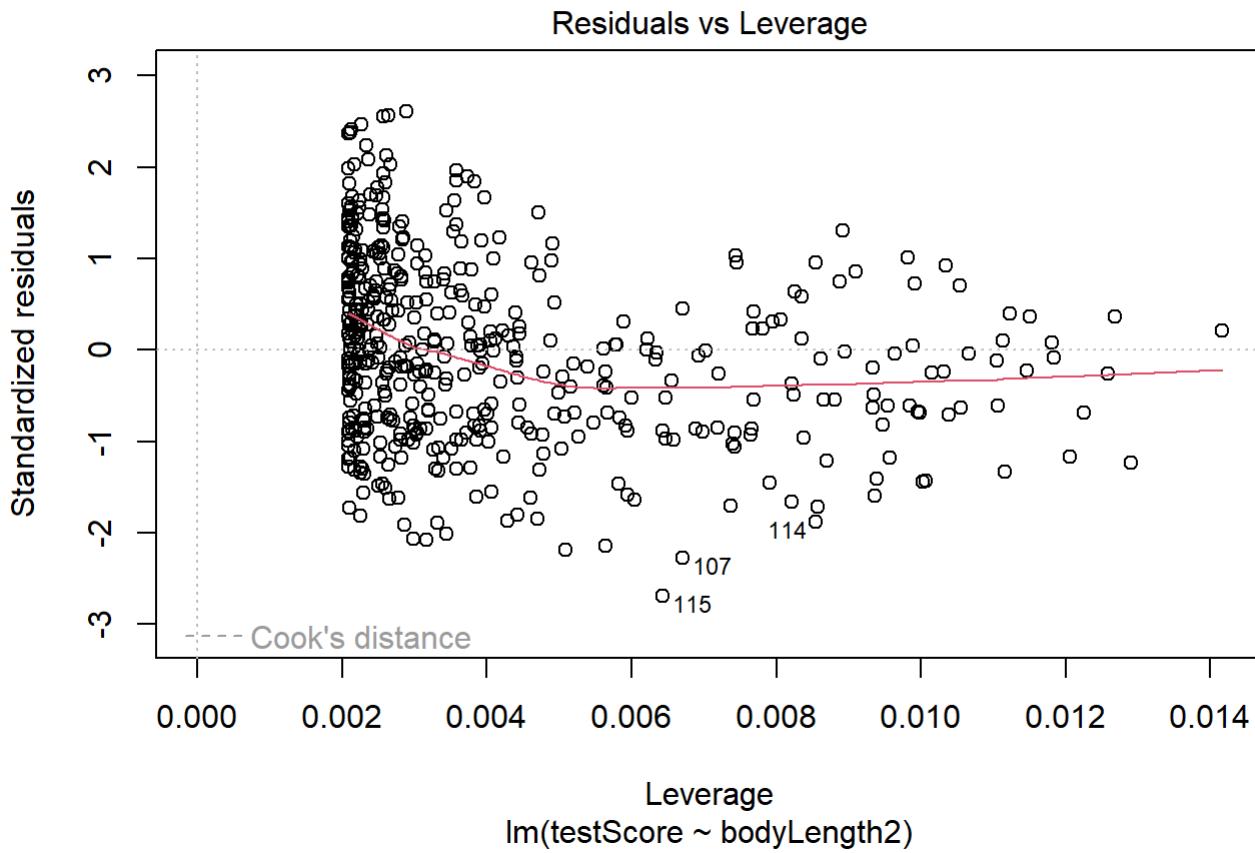
## Assumptions check

```
plot(basic.lm)
```









## Assumptions check

Are our data independent?

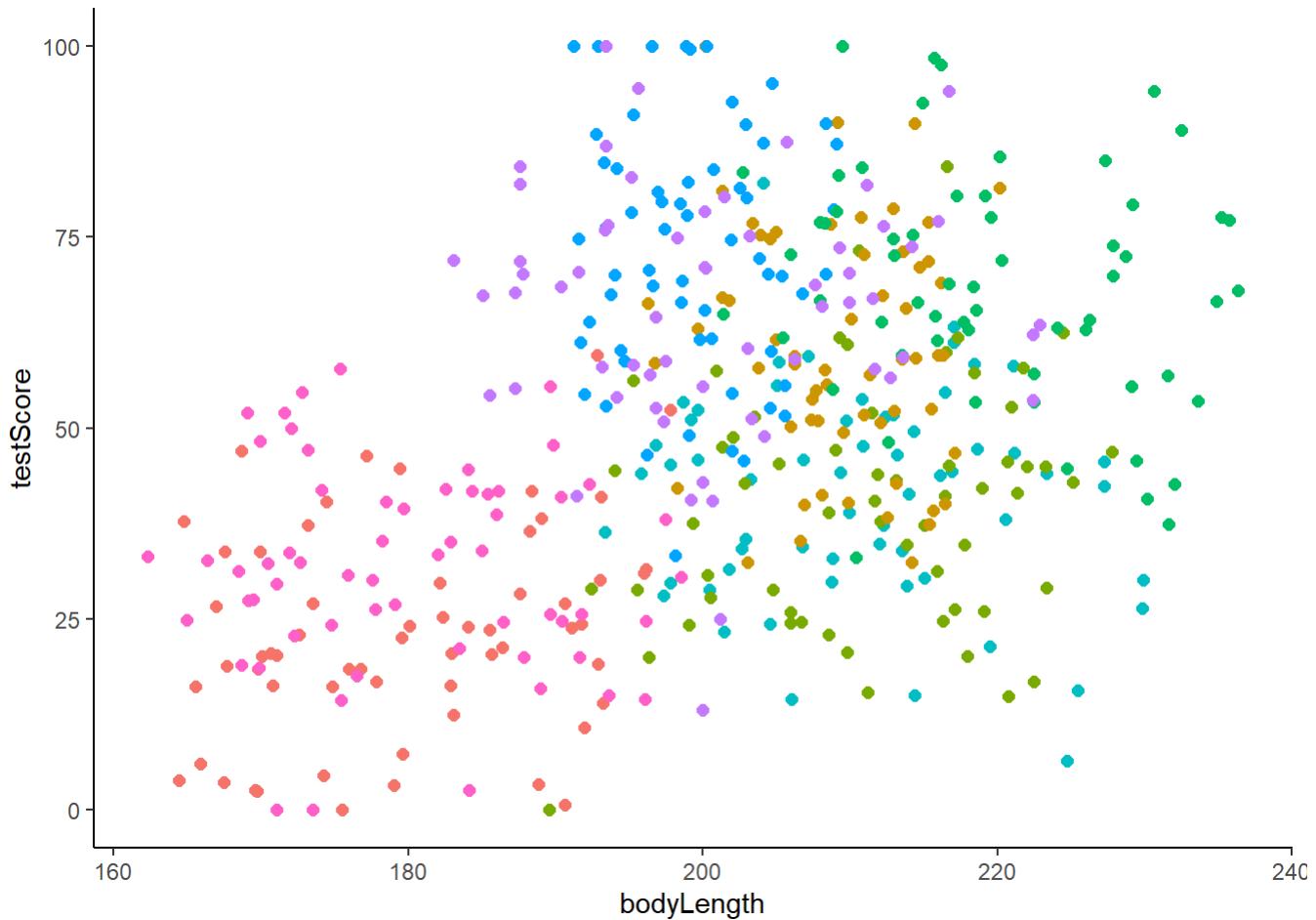
## Assumptions check

**Data description:** The data were collected from multiple samples from eight mountain ranges.

- It's perfectly plausible that the data from within each mountain range are more similar to each other than the data from different mountain ranges
- they are Hierarchical!

## Assumptions check

```
(colour_plot <- ggplot(dragons, aes(x = bodyLength, y = testScore, colour = mountainRange)
  geom_point(size = 2) +
  theme_classic() +
  theme(legend.position = "none"))
```



## How to implement mixed models in R?

- Step 1: Model building
- Step 2: Model validation
- Step 3: Model interpretation
- Step 4: Model visualization

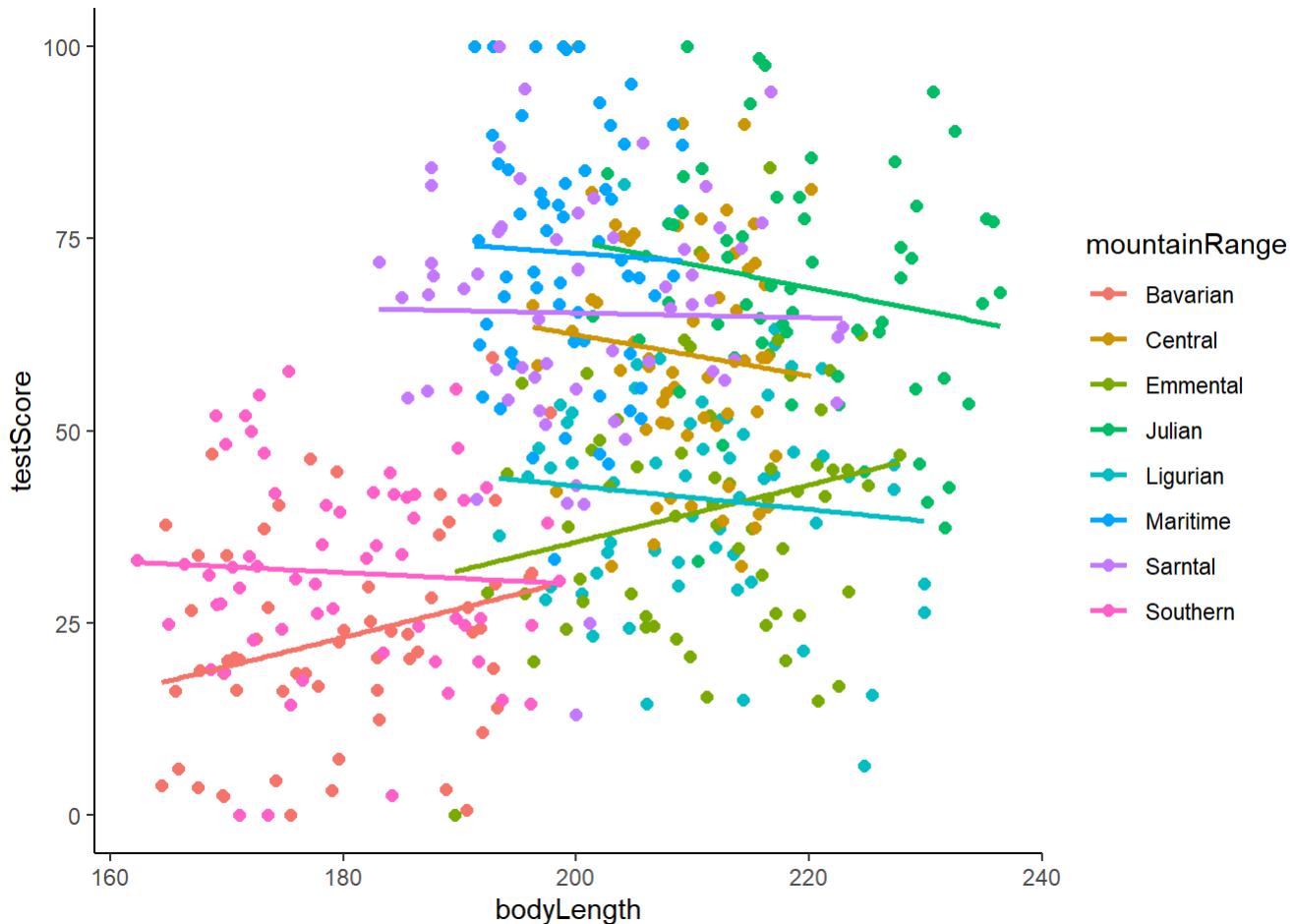
### Step 1: Model building

Hierarchical linear models do is they essentially fit a separate regression line for each and every cluster.

### Step 1: Model building Dragons

```
(colour_plot <- ggplot(dragons, aes(x = bodyLength, y = testScore, colour = mountainRange)
  geom_point(size = 2) +
  geom_smooth(method = "lm", se=FALSE) +
  theme_classic() )
```

`geom\_smooth()` using formula = 'y ~ x'



## Step 1: Model building

Hierarchical linear models do is they essentially fit a separate regression line for each and every cluster. And then estimates what we call the *Fixed slope*. Average slope between x and y across my clusters.

Mathematically speaking it is more complicated than that.

## Step 1: Model building Dragons

```
1 library(lme4) # "linear mixed model" function from lme4 package
```

Loading required package: Matrix

Attaching package: 'Matrix'

The following objects are masked from 'package:tidyverse':

expand, pack, unpack

```

1 mixed.lmer <- lmer(testScore ~ bodyLength2 +
2                               (1|mountainRange), #random effect
3                               data = dragons,
4                               REML = TRUE #estimation method other method ML but it has a bias
5                               )
6 summary(mixed.lmer)

```

Linear mixed model fit by REML ['lmerMod']  
 Formula: testScore ~ bodyLength2 + (1 | mountainRange)  
 Data: dragons

REML criterion at convergence: 3985.6

Scaled residuals:

Min	1Q	Median	3Q	Max
-3.4815	-0.6513	0.0066	0.6685	2.9583

Random effects:

Groups	Name	Variance	Std.Dev.
mountainRange	(Intercept)	339.7	18.43
Residual		223.8	14.96

Number of obs: 480, groups: mountainRange, 8

Fixed effects:

	Estimate	Std. Error	t value
(Intercept)	50.3860	6.5517	7.690
bodyLength2	0.5377	1.2750	0.422

Correlation of Fixed Effects:

(Intr)
bodyLength2 0.000

## Step 1: Model building Dragons

Mountain ranges are clearly important: they explain a lot of variation:

Factor	Variance
Mountain range	339.7
Residuals	223.8
Body length	?

$$(339.7 / (339.7 + 223.8)) * 100$$

[1] 60.28394

Variance Body length

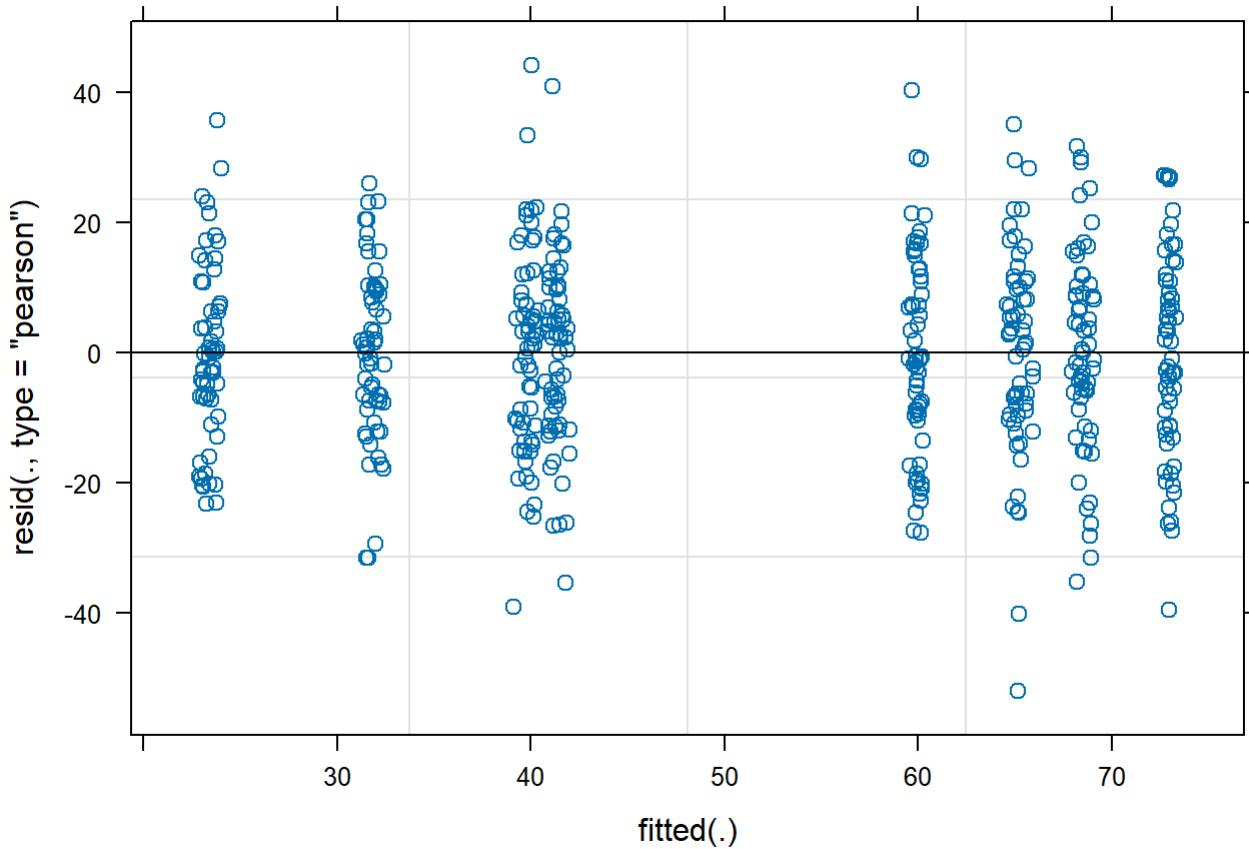
100-60.28

[1] 39.72

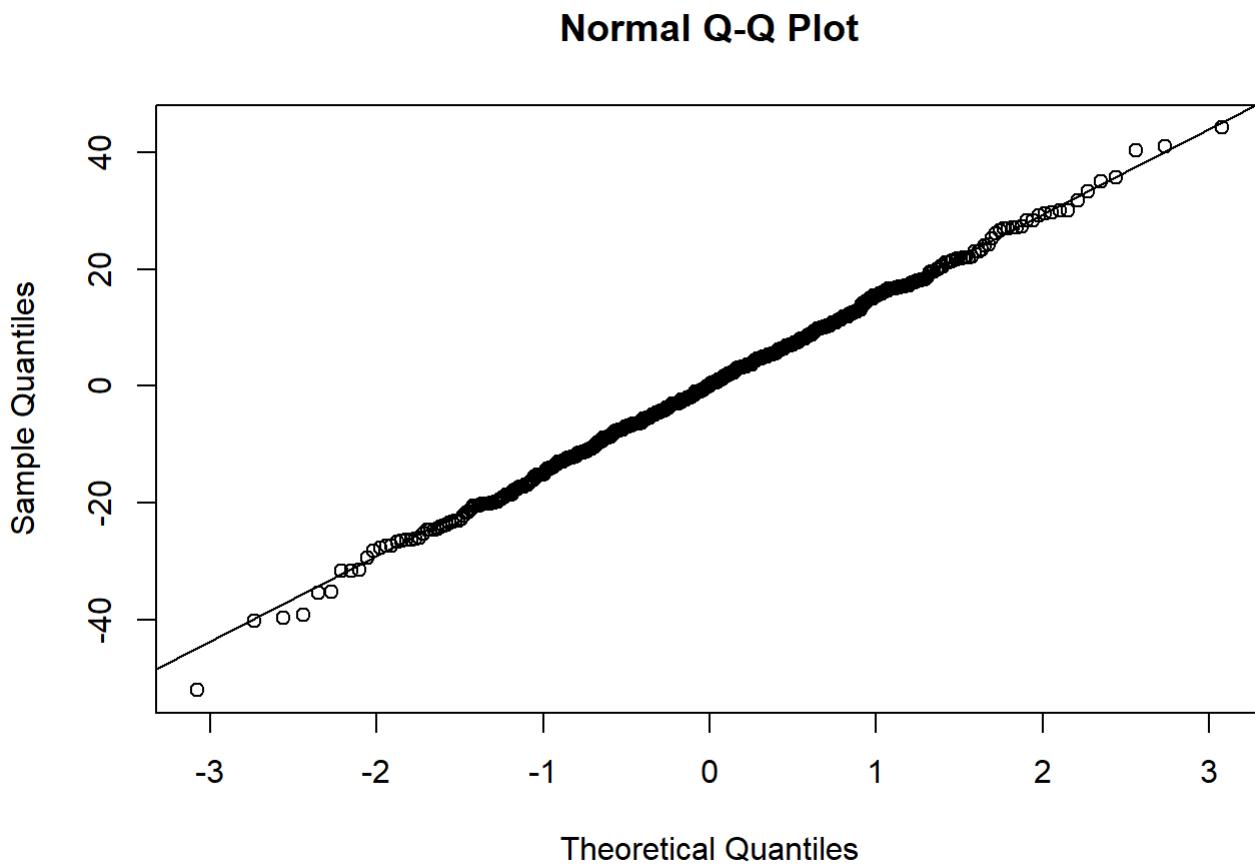
## Step 2: Model validation Dragons

Assumptions check

plot(mixed.lmer)



qqnorm(resid(mixed.lmer))  
qqline(resid(mixed.lmer))



## Step 1: Model building Nesting

---

Example:

10 control | 10 experimental

- 3 years
- Each season
- 20 beds
- 50 seedlings
- 5 leaves
- $5 \text{ leaves} \times 50 \text{ seedlings} \times 20 \text{ beds} \times 4 \text{ seasons} \times 3 \text{ years} = 60\,000 \text{ measurements per treatment}$

## Step 1: Model building Nesting

---

Effect of treatment in leaf length

```
leafLength ~ treatment
```

- *Pseudoreplication*
- Massively increasing sampling size

Better model

```
leafLength ~ treatment + (1|Bed/Plant/Leaf)
```

What about the crossed effects ?

- Crossed (or partially crossed) random factors that do not represent levels in a hierarchy.
- This account for the fact that all plants in the experiment, regardless of the fixed (treatment) effect, may have experienced a very hot summer in the second year.

```
leafLength ~ treatment + (1|Bed/Plant/Leaf) + (1|Season)
```

## Step 1: Model building Dragons Nesting

```
1 mixed.lmer2 <- lmer(testScore ~ bodyLength2+
2                               (1|mountainRange/site),
3                               data = dragons)
4 summary(mixed.lmer2)
```

```
Linear mixed model fit by REML ['lmerMod']
Formula: testScore ~ bodyLength2 + (1 | mountainRange/site)
Data: dragons
```

REML criterion at convergence: 3970.4

Scaled residuals:

Min	1Q	Median	3Q	Max
-3.2425	-0.6752	-0.0117	0.6974	2.8812

Random effects:

Groups	Name	Variance	Std.Dev.
site:mountainRange	(Intercept)	23.09	4.805
mountainRange	(Intercept)	327.56	18.099
Residual		208.58	14.442

Number of obs: 480, groups: site:mountainRange, 24; mountainRange, 8

Fixed effects:

	Estimate	Std. Error	t value
(Intercept)	50.386	6.507	7.743
bodyLength2	0.831	1.681	0.494

Correlation of Fixed Effects:

```
(Intr)
bodyLength2 0.000
```

```
1 mixed.lmer3 <- lmer(testScore ~ bodyLength2
2                               +(1|mountainRange) + (1|mountainRange:site),
3                               data = dragons)
4 summary(mixed.lmer3)
```

Linear mixed model fit by REML ['lmerMod']

Formula:

testScore ~ bodyLength2 + (1 | mountainRange) + (1 | mountainRange:site)

Data: dragons

REML criterion at convergence: 3970.4

Scaled residuals:

Min	1Q	Median	3Q	Max
-3.2425	-0.6752	-0.0117	0.6974	2.8812

Random effects:

Groups	Name	Variance	Std.Dev.
mountainRange:site	(Intercept)	23.09	4.805
mountainRange	(Intercept)	327.56	18.099
Residual		208.58	14.442

Number of obs: 480, groups: mountainRange:site, 24; mountainRange, 8

Fixed effects:

	Estimate	Std. Error	t value
(Intercept)	50.386	6.507	7.743
bodyLength2	0.831	1.681	0.494

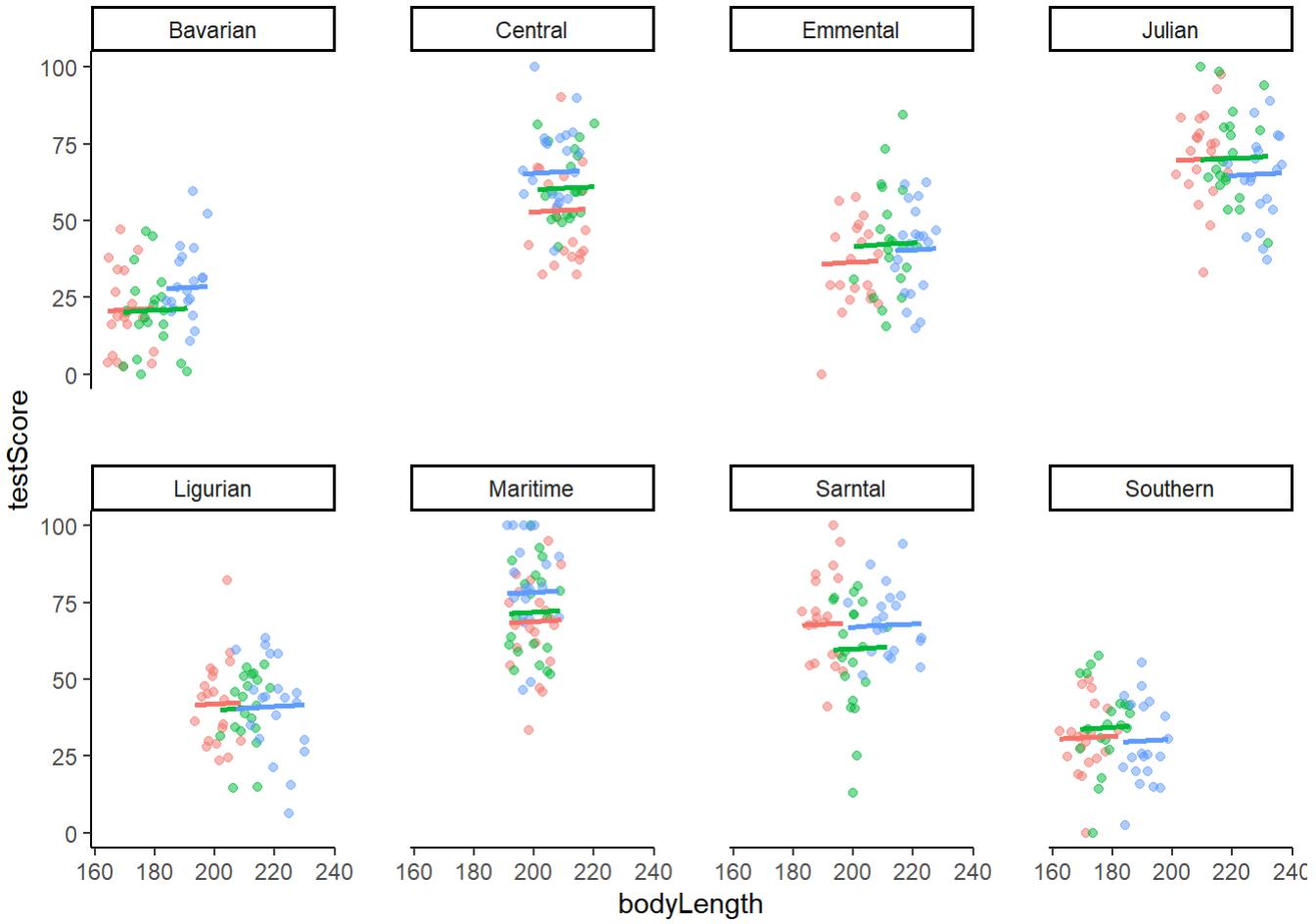
Correlation of Fixed Effects:

```
(Intr)
bodyLength2 0.000
```

## Step 1: Model building Dragons Nesting

Warning: Using `size` aesthetic for lines was deprecated in ggplot2 3.4.0.

i Please use `linewidth` instead.



## Random slopes and Random intercept

A *random-intercept* model recognizes that each cluster might have its own starting point (intercept), but keeps the slope constant among them. So in our example we acknowledge that some populations may be smarter or dumber to begin with.

Lets say we expect that dragons in all mountain ranges do not exhibit the same relationship between body length and intelligence (rando, slope)

## Random slopes and Random intercept

We only need to make one change to our model to allow for random slopes as well as intercept, and that's adding the fixed variable into the random effect brackets:

```

1 mixed.ranslope <- lmer(testScore ~ bodyLength2 +
2                               (1 + bodyLength2 | mountainRange/site),
3                               data = dragons)

```

boundary (singular) fit: see help('isSingular')

```
1 summary(mixed.ranslope)
```

Linear mixed model fit by REML ['lmerMod']  
Formula: testScore ~ bodyLength2 + (1 + bodyLength2 | mountainRange/site)  
Data: dragons

REML criterion at convergence: 3968.4

Scaled residuals:

Min	1Q	Median	3Q	Max
-3.2654	-0.6737	-0.0200	0.6931	2.8432

Random effects:

Groups	Name	Variance	Std.Dev.	Corr
site:mountainRange	(Intercept)	19.8156	4.4515	
	bodyLength2	0.7178	0.8472	1.00
mountainRange	(Intercept)	310.9691	17.6343	
	bodyLength2	6.1119	2.4722	-1.00
Residual		208.5025	14.4396	

Number of obs: 480, groups: site:mountainRange, 24; mountainRange, 8

Fixed effects:

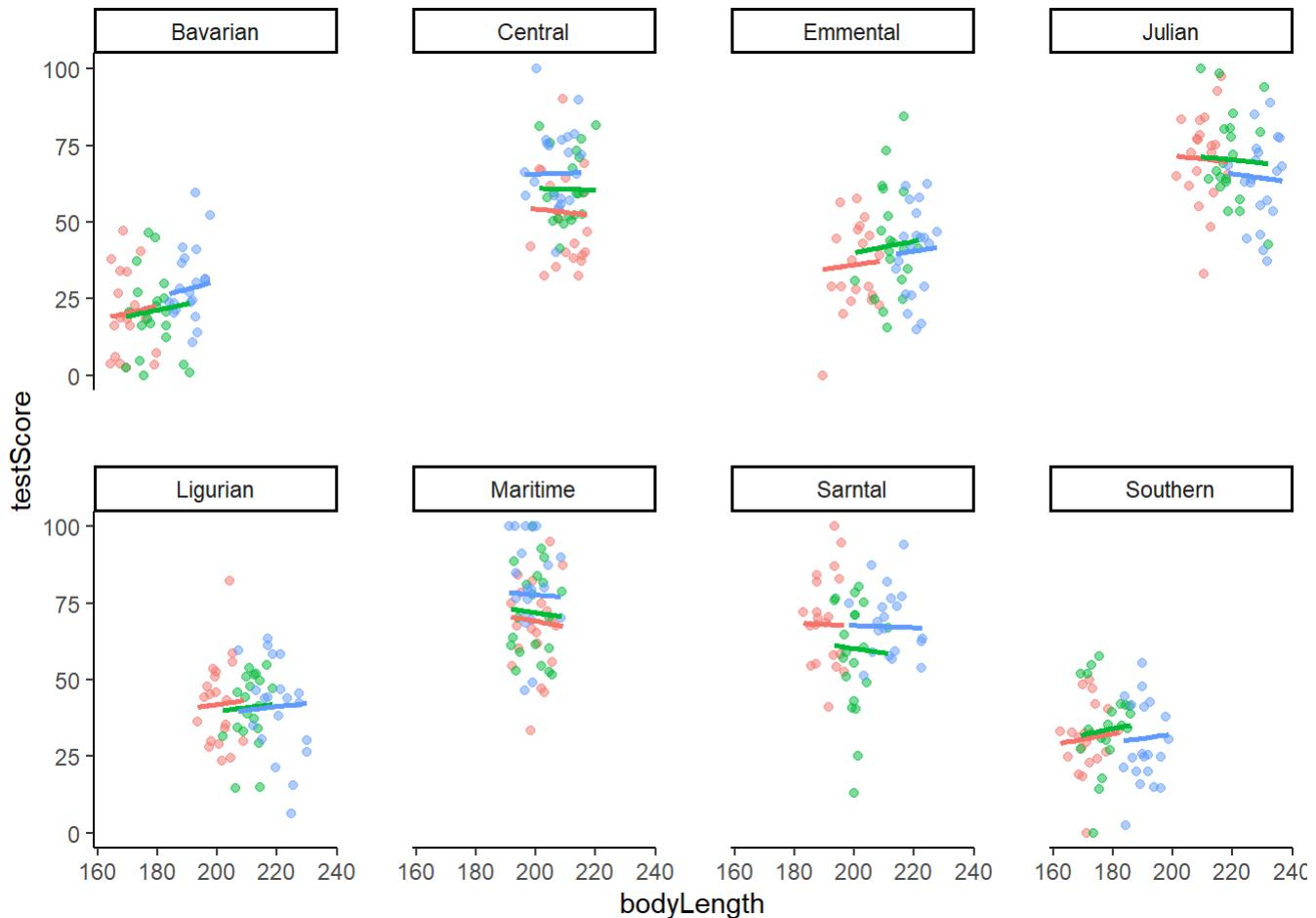
	Estimate	Std. Error	t value
(Intercept)	51.4263	6.3408	8.110
bodyLength2	0.6691	1.8729	0.357

Correlation of Fixed Effects:

	(Intr)
bodyLength2	-0.461
optimizer (nloptwrap) convergence code: 0 (OK)	
boundary (singular) fit: see help('isSingular')	

## Random slopes and Random intercept

---



## Step 3: Model interpretation

```
library(stargazer)
```

Please cite as:

Hlavac, Marek (2022). stargazer: Well-Formatted Regression and Summary Statistics Tables.

R package version 5.2.3. <https://CRAN.R-project.org/package=stargazer>

```
stargazer(mixed.lmer2,
          digits = 3,
          type="text",
          star.cutoffs = c(0.05, 0.01, 0.001),
          digit.separator = "")
```

```
=====
Dependent variable:
-----
```

```

testScore
-----
bodyLength2           0.831
                      (1.681)

Constant             50.386*** 
                      (6.507)

-----
Observations          480
Log Likelihood       -1985.195
Akaike Inf. Crit.    3980.389
Bayesian Inf. Crit.  4001.258
=====
Note:               *p<0.05; **p<0.01; ***p<0.001

```

## Step 4. Visualization

---

```

1 library(ggeffects)
2
3 # Extract the prediction data frame
4 pred.mm <- ggpredict(mixed.lmer2, terms = c("bodyLength2")) # this gives overall p
5 head(pred.mm)

```

# Predicted values of testScore

bodyLength2	Predicted	95% CI
-3	47.89	31.72, 64.07
-2	48.72	34.33, 63.12
-1	49.56	36.35, 62.76
0	50.39	37.60, 63.17
1	51.22	38.01, 64.42
2	52.05	37.66, 66.44

Adjusted for:

- \* site = 0 (population-level)
- \* mountainRange = 0 (population-level)

## Step 4. Visualization

---

```

1 # Plot the predictions
2 p<-ggplot(pred.mm) +
3   # slope
4   geom_line(aes(x = x, y = predicted)) +
5   # error band
6   geom_ribbon(

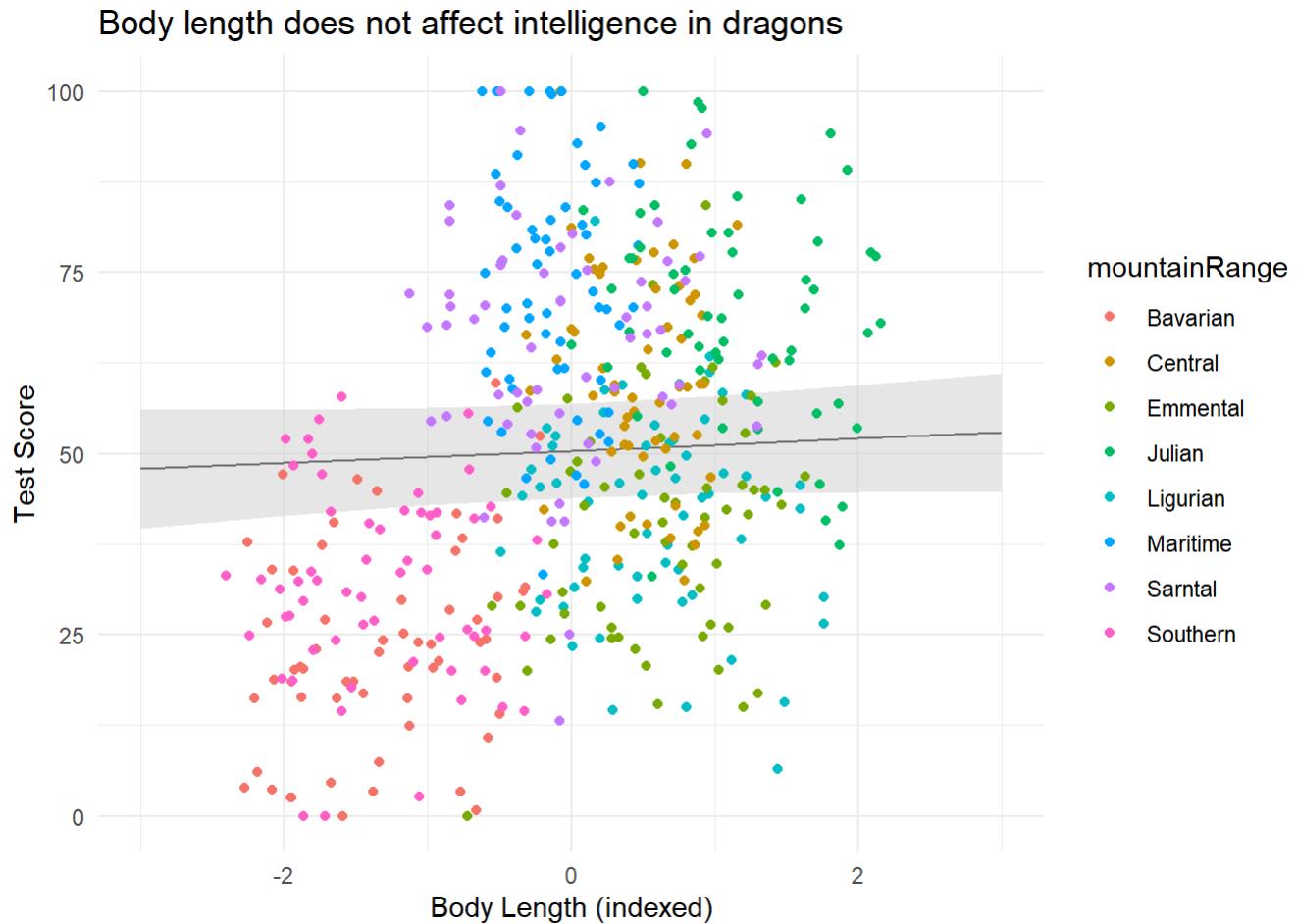
```

```

7   aes(
8     x = x,
9     ymin = predicted - std.error,
10    ymax = predicted + std.error
11  ),
12  fill = "lightgrey",
13  alpha = 0.5
14 ) +
15 # adding the raw data (scaled values)
16 geom_point(data = dragons,
17             aes(x = bodyLength2, y = testScore, colour = mountainRange)) +
18 labs(x = "Body Length (indexed)",
19       y = "Test Score",
20       title = "Body length does not affect intelligence in dragons") +
21 theme_minimal()

```

## Step 4. Visualization



## Step 4. Visualization

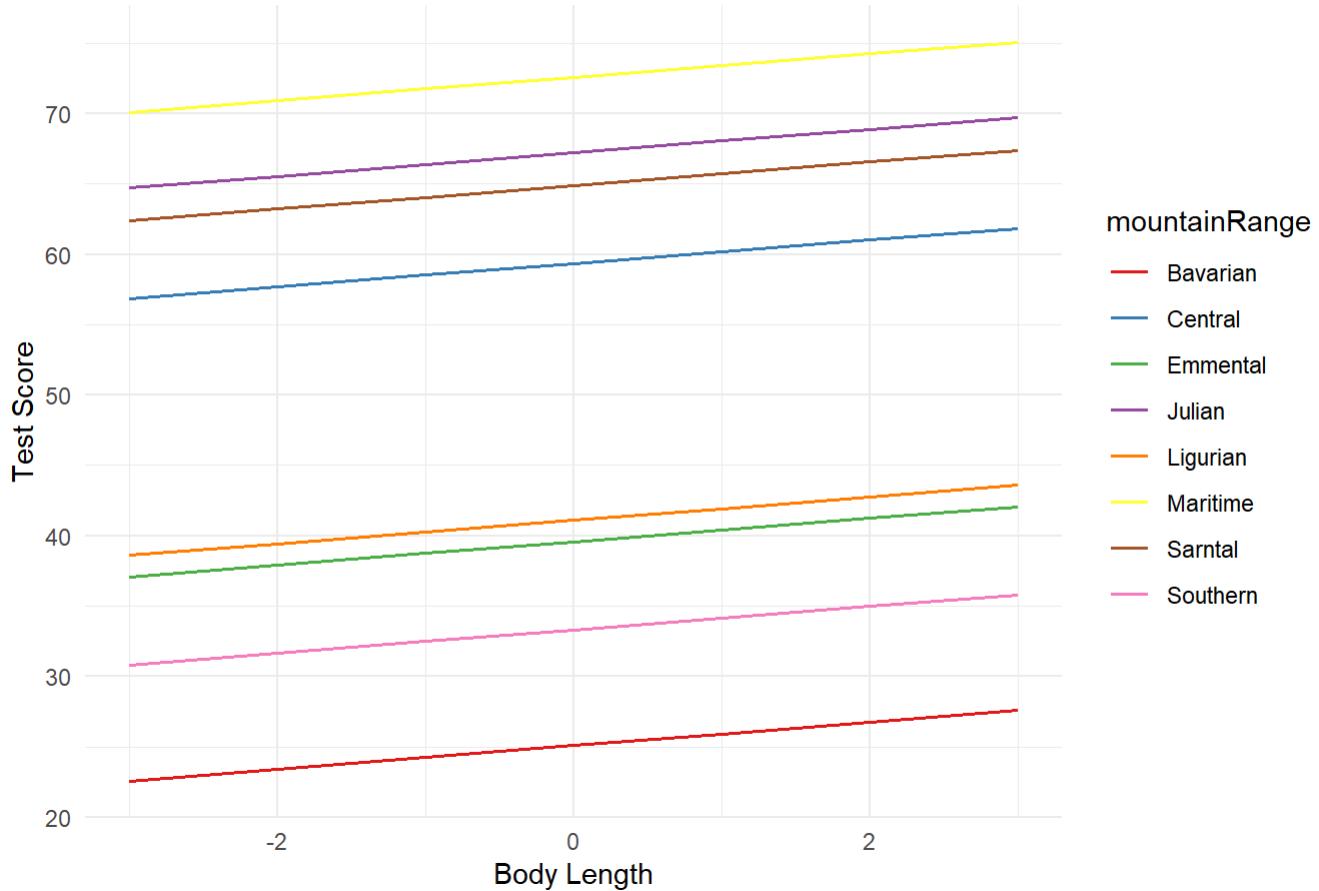
```

1 p<-
2   ggpredict(mixed.lmer2, terms = c("bodyLength2", "mountainRange"),
3             type = "random") %>%
4   plot(show_ci = FALSE) +
5   labs(x = "Body Length", y = "Test Score",
6        title = "Effect of body size on intelligence in dragons") +
7   theme_minimal()

```

## Step 4. Visualization

Effect of body size on intelligence in dragons



## Additional resources

Popular libraries for (G)LMMs:

- Frequentist : `nlme`, `lme4`, `glmmTMB`
- Bayesian : `brms`, `rstan`, `rstanarm`, `MCMCglmm`
- Nice visualization : [link](#)
- Most of the material comes from : [Coding Club](#)

## BREAK

---



## Exercise

---

Now let's practice ...

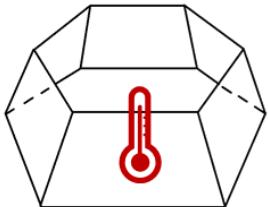


## ITEX

---

We will be using a dataset from the ITEX network.

- ITEX is a long-term warming experiment that uses standardized protocols to examine impacts of warming on Arctic ecosystems.
- Established in the 1990s - vegetation monitoring over three decades.
- Uses a simple method that is easy to establish in the field - open top chambers



## ITEX

---



---

**Let's look at the data**

```
itex <- read_csv("Data/ITEX_diversity_data.csv")
```

New names:

Rows: 1303 Columns: 11

— Column specification

Delimiter: "," chr

(4): SITE, SUBSITE, PLOT, TRTMT dbl (7): ...1, YEAR, Latitude, WarmQuarterTemp, SppRich, row\_number(), PlotTemp

i Use `spec()` to retrieve the full column specification for this data. i

Specify the column types or set `show\_col\_types = FALSE` to quiet this message.

• `` -> `...1`

```
head(itex)
```

# A tibble: 6 × 11

	...1 SITE	SUBSITE	PLOT	YEAR	TRTMT	Latitude	WarmQuarterTemp	SppRich
	<dbl>	<chr>	<chr>	<dbl>	<chr>	<dbl>	<dbl>	<dbl>
1	1 ALEXFIORD	ALEXFIORD:...	Cas...	2007	CTL	78.9	25.6	9
2	2 ALEXFIORD	ALEXFIORD:...	Cas...	2007	CTL	78.9	25.6	9
3	3 ALEXFIORD	ALEXFIORD:...	Cas...	2007	CTL	78.9	25.6	7
4	4 ALEXFIORD	ALEXFIORD:...	Cas...	2007	CTL	78.9	25.6	8
5	5 ALEXFIORD	ALEXFIORD:...	Cas...	2007	CTL	78.9	25.6	6
6	6 ALEXFIORD	ALEXFIORD:...	Cas...	2007	CTL	78.9	25.6	10

# i 2 more variables: `row\_number()` <dbl>, PlotTemp <dbl>

```
length(unique(itex$SITE)) #this code tells you how many different samples we have within
```

[1] 24

```
unique(itex$SITE) #you can also do this and then it gives you the name of all samples wi
```

```
[1] "ALEXFIORD"      "ANWR"          "ATQASUK"        "AUDKULUHEIDI"   "BARROW"
[6] "BROOKS"         "BYLOT"         "DOVRE"          "ENDALEN"        "FAROE"
[11] "GAVIA"          "KLUANE"        "KYTALYK"        "LATNJA"         "NIWOT"
[16] "QHI"            "SADVENT"       "STEPSTONES"    "TAISETSU"       "THINGVELLIR"
[21] "TIBET"          "TOOLIK"        "TORNGATS"      "VALBERCLA"
```

## Exercises

Ex. 1 - Using the ITEX diversity dataset, what is the relationship between diversity and temperature across sites?

- Think about what will be the response variable, what to include as fixed effects and what to include as a random effect.
- Does the summary output correspond to the structure of the data? Think about how the data was sampled and how you structured your model.

Ex. 2 - What is the relationship between diversity and temperature WITHIN sites?

- Think about how to restructure your model based on the new question.