

# Parallel slopes linear regression

INTERMEDIATE REGRESSION IN R



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# The previous course

This course assumes knowledge from [Introduction to Regression in R](#).

# From simple regression to multiple regression

*Multiple regression* is a regression model with more than one explanatory variable.

More explanatory variables can give **more insight** and **better predictions**.

# The course contents

## Chapter 1

- "Parallel slopes" regression

## Chapter 3

- More explanatory variables
- How linear regression works

## Chapter 2

- Interactions
- Simpson's Paradox

## Chapter 4

- Multiple logistic regression
- The logistic distribution
- How logistic regression works

# The fish dataset

mass_g	length_cm	species
242.0	23.2	Bream
5.9	7.5	Perch
200.0	30.0	Pike
40.0	12.9	Roach

- Each row represents a fish
- `mass_g` is the response variable
- 1 numeric, 1 categorical explanatory variable

# One explanatory variable at a time

```
mdl_mass_vs_length <- lm(mass_g ~ length_cm, data = fish)
```

```
Call:
lm(formula = mass_g ~ length_cm, data = fish)

Coefficients:
(Intercept)    length_cm
      -536.2         34.9
```

- 1 intercept coefficient
- 1 slope coefficient

```
mdl_mass_vs_species <- lm(mass_g ~ species + 0, data = fish)
```

```
Call:
lm(formula = mass_g ~ species + 0, data = fish)

Coefficients:
speciesBream  speciesPerch  speciesPike  speciesRoach
       617.8        382.2        718.7        152.0
```

- 1 intercept coefficient for each category

# Both variables at same time

```
mdl_mass_vs_both <- lm(mass_g ~ length_cm + species + 0, data = fish)
```

Call:

```
lm(formula = mass_g ~ length_cm + species + 0, data = fish)
```

Coefficients:

length_cm	speciesBream	speciesPerch	speciesPike	speciesRoach
42.57	-672.24	-713.29	-1089.46	-726.78

- 1 slope coefficient
- 1 intercept coefficient for each category

# Comparing coefficients

```
coefficients mdl_mass_vs_length
```

(Intercept)	length_cm
-536.2	34.9

```
coefficients mdl_mass_vs_species
```

speciesBream	speciesPerch	speciesPike	speciesRoach
617.8	382.2	718.7	152.0

```
coefficients mdl_mass_vs_both
```

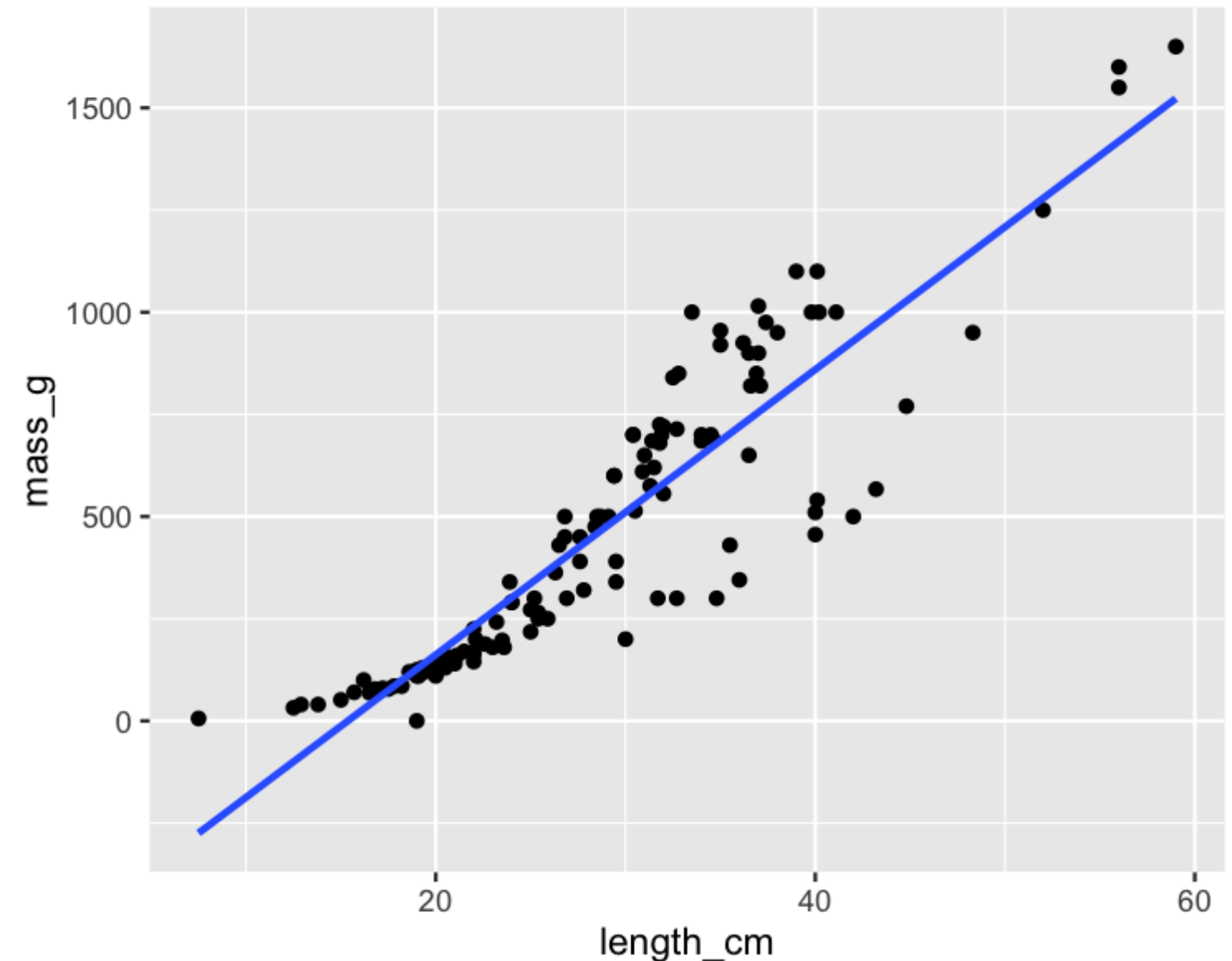
length_cm	speciesBream	speciesPerch	speciesPike	speciesRoach
42.57	-672.24	-713.29	-1089.46	-726.78



# Visualization: 1 numeric explanatory var

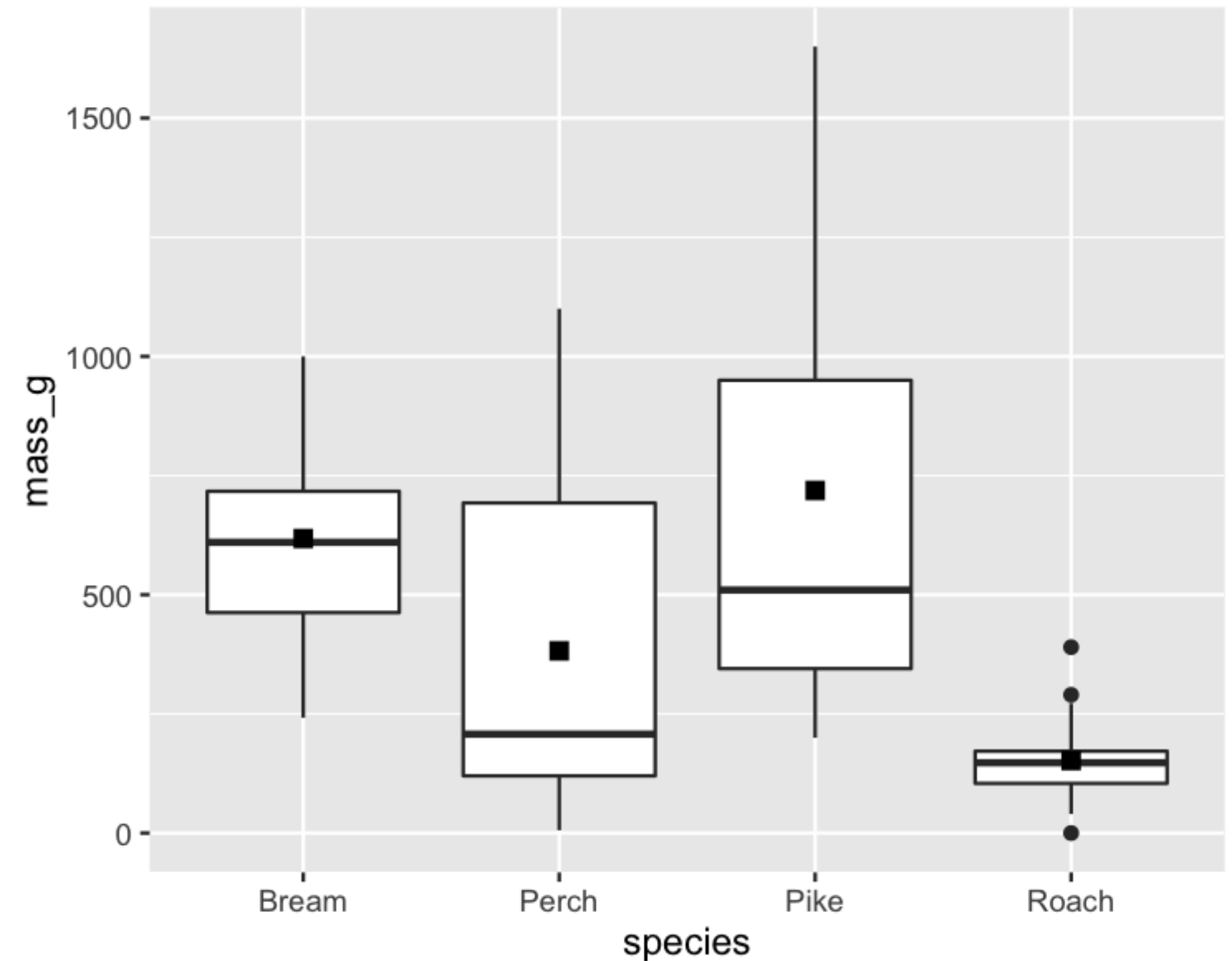
```
library(ggplot2)

ggplot(fish, aes(length_cm, mass_g)) +
  geom_point() +
  geom_smooth(method = "lm", se = FALSE)
```



# Visualization: 1 categorical explanatory var

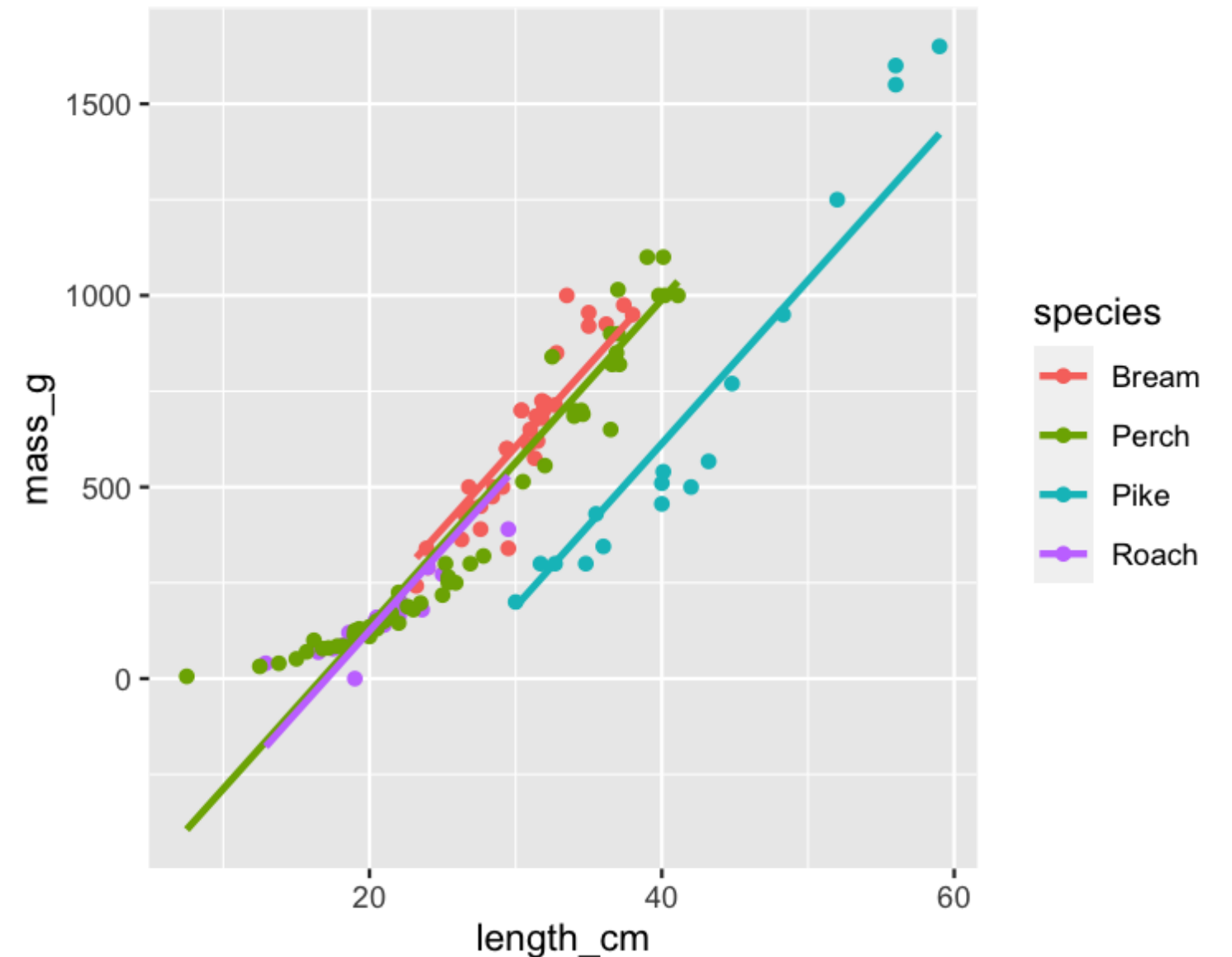
```
ggplot(fish, aes(species, mass_g)) +  
  geom_boxplot() +  
  stat_summary(fun.y = mean, shape = 15)
```



# Visualization: both explanatory vars

```
library(moderndive)

ggplot(fish, aes(length_cm, mass_g, color = species)) +
  geom_point() +
  geom_parallel_slopes(se = FALSE)
```



# Let's practice!

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# Predicting parallel slopes

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# The prediction workflow 1

```
library(dplyr)

explanatory_data <- tibble(
  length_cm = seq(5, 60, 5)
)
```

```
glimpse(explanatory_data)
```

```
Rows: 12
Columns: 1
$ length_cm <dbl> 5, 10, 15, 20, 25, 30, 35, 40...
```

```
library(dplyr)
library(tidyr)
explanatory_data <- expand_grid(
  length_cm = seq(5, 60, 5),
  species = unique(fish$species)
)
```

```
glimpse(explanatory_data)
```

```
Rows: 48
Columns: 2
$ length_cm <dbl> 5, 5, 5, 5, 10, 10, 10, 10, 1...
$ species    <chr> "Bream", "Roach", "Perch", "P..."
```

# The prediction workflow 2

```
library(dplyr)

explanatory_data <- tibble(
  length_cm = seq(5, 60, 5)
)
```

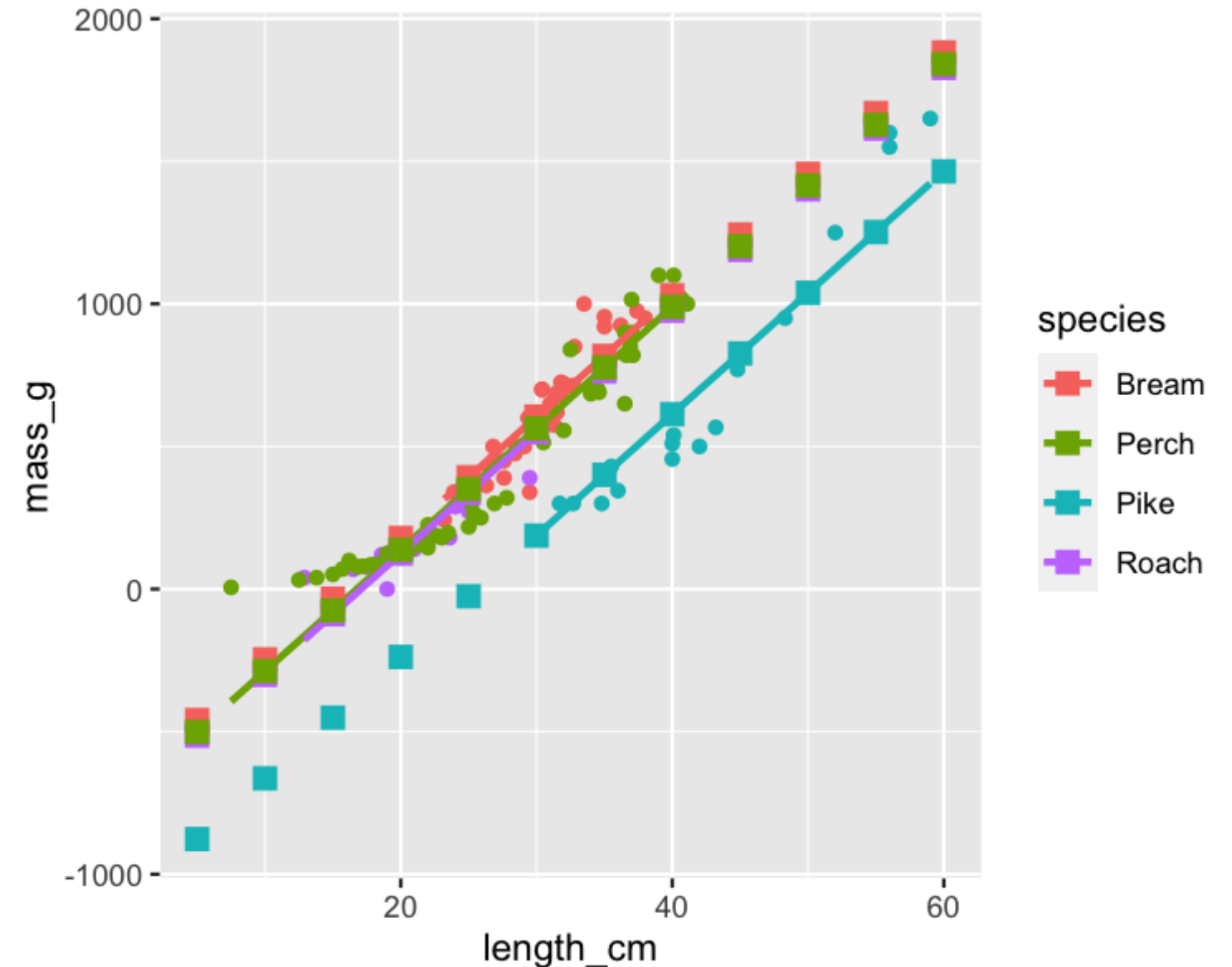
```
prediction_data <- explanatory_data %>%
  mutate(
    mass_g = predict(
      mdl_mass_vs_length, explanatory_data
    )
  )
```

```
library(dplyr)
library(tidyr)
explanatory_data <- expand_grid(
  length_cm = seq(5, 60, 5),
  species = unique(fish$species)
)
```

```
prediction_data <- explanatory_data %>%
  mutate(
    mass_g = predict(
      mdl_mass_vs_both, explanatory_data
    )
  )
```

# Visualizing the predictions

```
library(ggplot2)
library(moderndiver)
ggplot(fish, aes(length_cm, mass_g, color = species)) +
  geom_point() +
  geom_parallel_slopes(se = FALSE) +
  geom_point(
    data = prediction_data,
    size = 3, shape = 15
  )
)
```





# Manually calculating predictions

```
coeffs <- coefficients mdl_price_vs_length
```

```
(Intercept)  length_cm  
    -536.2         34.9
```

```
intercept <- coeffs[1]  
slope <- coeffs[2]
```

```
explanatory_data %>%  
  mutate(  
    mass_g = intercept + slope * length_cm  
  )
```

length_cm	mass_g
5	-361.73
10	-187.23
15	-12.74
20	161.76
25	336.26
30	510.75

# Coefficients for parallel slopes

```
coefficients mdl_mass_vs_both)
```

```
length_cm speciesBream speciesPerch speciesPike speciesRoach  
42.57      -672.24      -713.29      -1089.46      -726.78
```

```
slope <- coeffs[1]  
intercept_bream <- coeffs[2]  
intercept_perch <- coeffs[3]  
intercept_pike <- coeffs[4]  
intercept_roach <- coeffs[5]
```

# Choosing an intercept with ifelse()

```
explanatory_data %>%  
  mutate(  
    intercept = ifelse(  
      species == "Bream",  
      intercept_bream,  
      ifelse(  
        species == "Perch",  
        intercept_perch,  
        ifelse(  
          species == "Pike",  
          intercept_pike,  
          intercept_roach  
        )  
      )  
    )  
  )  
)
```

# case\_when()

```
dataframe %>%  
  mutate(  
    case_when(  
      condition_1 ~ value_1,  
      condition_2 ~ value_2,  
      # ...  
      condition_n ~ value_n  
    )  
  )
```

# Choosing an intercept with case\_when()

```
explanatory_data %>%  
  mutate(  
    intercept = case_when(  
      species == "Bream" ~ intercept_bream,  
      species == "Perch" ~ intercept_perch,  
      species == "Pike" ~ intercept_pike,  
      species == "Roach" ~ intercept_roach  
    )  
  )
```

# The final prediction step

```
explanatory_data %>%
  mutate(
    intercept = case_when(
      species == "Bream" ~ intercept_bream,
      species == "Perch" ~ intercept_perch,
      species == "Pike" ~ intercept_pike,
      species == "Roach" ~ intercept_roach
    ),
    mass_g = intercept + slope * length_cm
  )
```

```
# A tibble: 48 x 4
  length_cm species intercept mass_g
    <dbl> <chr>      <dbl>   <dbl>
1         5 Bream    -672.  -459.
2         5 Roach    -727.  -514.
3         5 Perch    -713.  -500.
4         5 Pike    -1089.  -877.
5        10 Bream    -672.  -247.
6        10 Roach    -727.  -301.
7        10 Perch    -713.  -288.
8        10 Pike    -1089.  -664.
9        15 Bream    -672.   -33.7
10       15 Roach    -727.   -88.2
# ... with 38 more rows
```

# Compare to predict()

```
predict(mdl_mass_vs_both, explanatory_data)
```

```
      1      2      3      4
-459.39910 -513.93503 -500.45009 -876.61328
      5      6      7      8
-246.55633 -301.09226 -287.60732 -663.77051
# ...
```

```
# A tibble: 48 x 4
  length_cm species intercept mass_g
  <dbl> <chr>      <dbl>   <dbl>
1         5 Bream    -672.  -459.
2         5 Roach    -727.  -514.
3         5 Perch    -713.  -500.
4         5 Pike   -1089.  -877.
5        10 Bream    -672.  -247.
6        10 Roach    -727.  -301.
7        10 Perch    -713.  -288.
8        10 Pike   -1089.  -664.
9        15 Bream    -672.   -33.7
10       15 Roach    -727.  -88.2
# ... with 38 more rows
```

# Let's practice!

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# Assessing model performance

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# Model performance metrics

- *Coefficient of determination (R-squared)*: how well the linear regression line fits the observed values.
  - Larger is better.
- *Residual standard error (RSE)*: the typical size of the residuals.
  - Smaller is better.

# Getting the coefficient of determination

```
library(dplyr)
library(broom)
```

```
mdl_mass_vs_length %>%
  glance() %>%
  pull(r.squared)
```

0.8226

```
mdl_mass_vs_species %>%
  glance() %>%
  pull(r.squared)
```

0.7163

```
mdl_mass_vs_both %>%
  glance() %>%
  pull(r.squared)
```

0.9694

# Adjusted coefficient of determination

- More explanatory variables increases  $R^2$ .
- Too many explanatory variables causes overfitting.
- *Adjusted coefficient of determination* penalizes more explanatory variables.
- $\bar{R}^2 = 1 - (1 - R^2) \frac{n_{obs} - 1}{n_{obs} - n_{var} - 1}$
- Penalty is noticeable when  $R^2$  is small, or  $n_{var}$  is large fraction of  $n_{obs}$ .
- In `glance()`, it's the `adj.r.squared` element.

# Getting the adjusted coefficient of determination

```
library(dplyr)
library(broom)
```

```
mdl_mass_vs_length %>%
  glance() %>%
  select(r.squared, adj.r.squared)
```

	r.squared	adj.r.squared
	<dbl>	<dbl>
1	0.8226	0.8212

```
mdl_mass_vs_species %>%
  glance() %>%
  select(r.squared, adj.r.squared)
```

	r.squared	adj.r.squared
	<dbl>	<dbl>
1	0.7163	0.7072

```
mdl_mass_vs_both %>%
  glance() %>%
  select(r.squared, adj.r.squared)
```

	r.squared	adj.r.squared
	<dbl>	<dbl>
1	0.9694	0.9682

# Getting the residual standard error

```
library(dplyr)
library(broom)
```

```
mdl_mass_vs_length %>%
  glance() %>%
  pull(sigma)
```

152.1

```
mdl_mass_vs_species %>%
  glance() %>%
  pull(sigma)
```

313.6

```
mdl_mass_vs_both %>%
  glance() %>%
  pull(sigma)
```

103.4

# Let's practice!

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