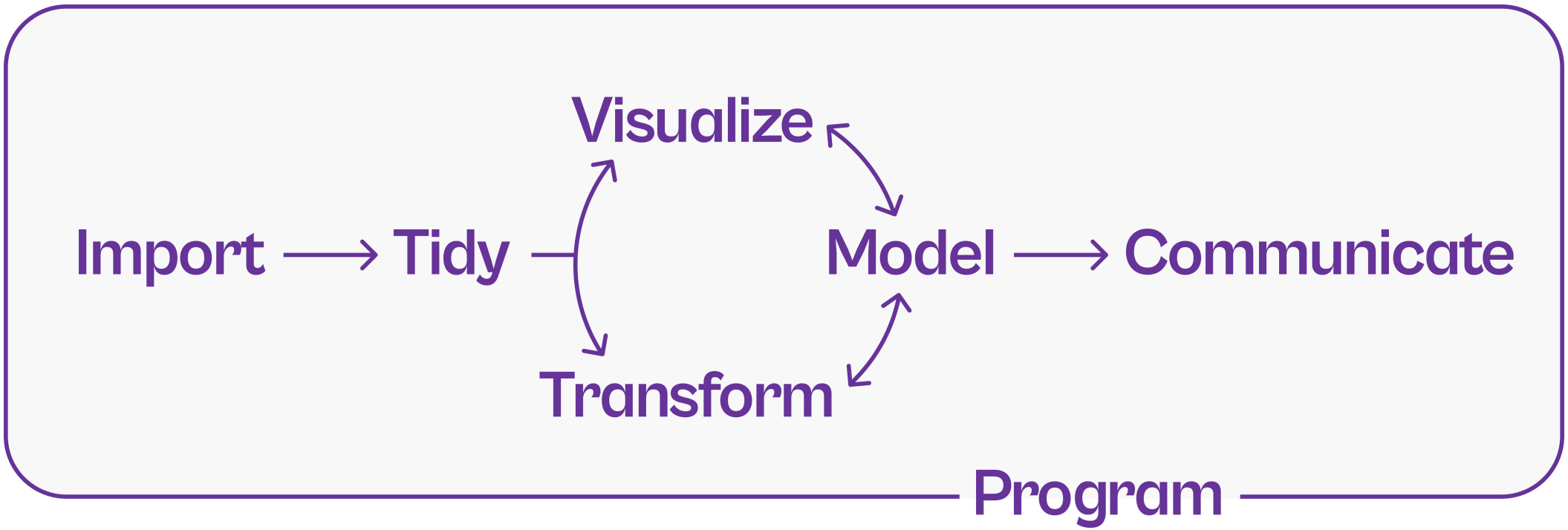
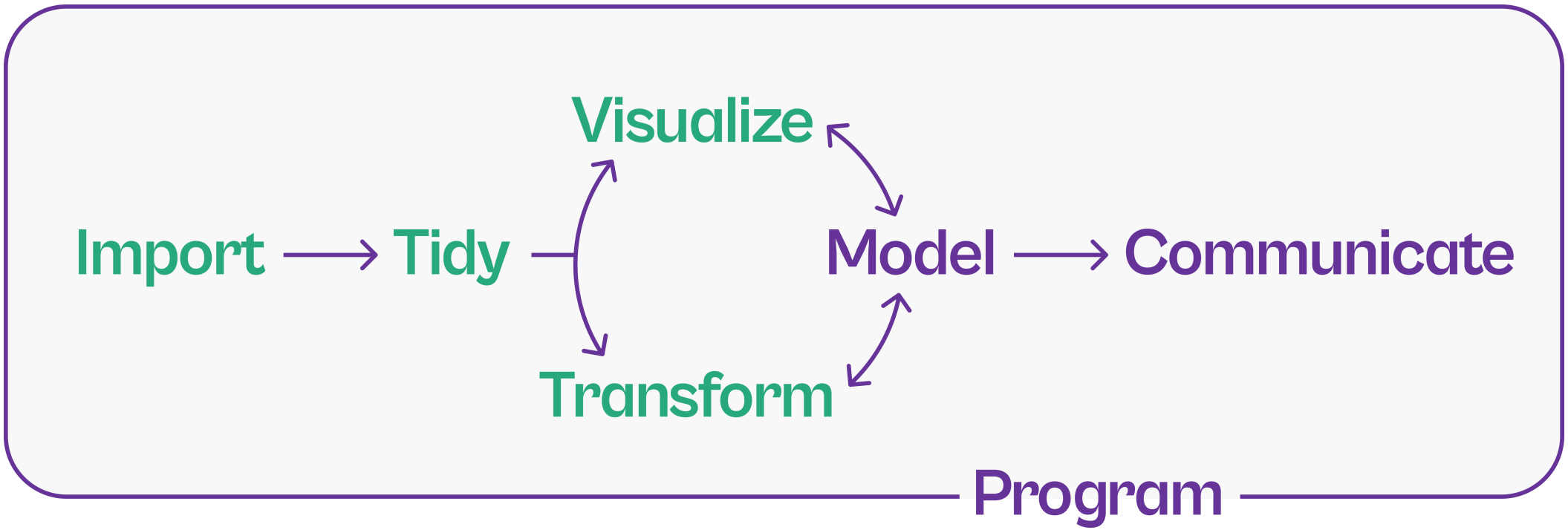
Reproducible Data Analysis with R

— Statistical Analysis & Modeling —

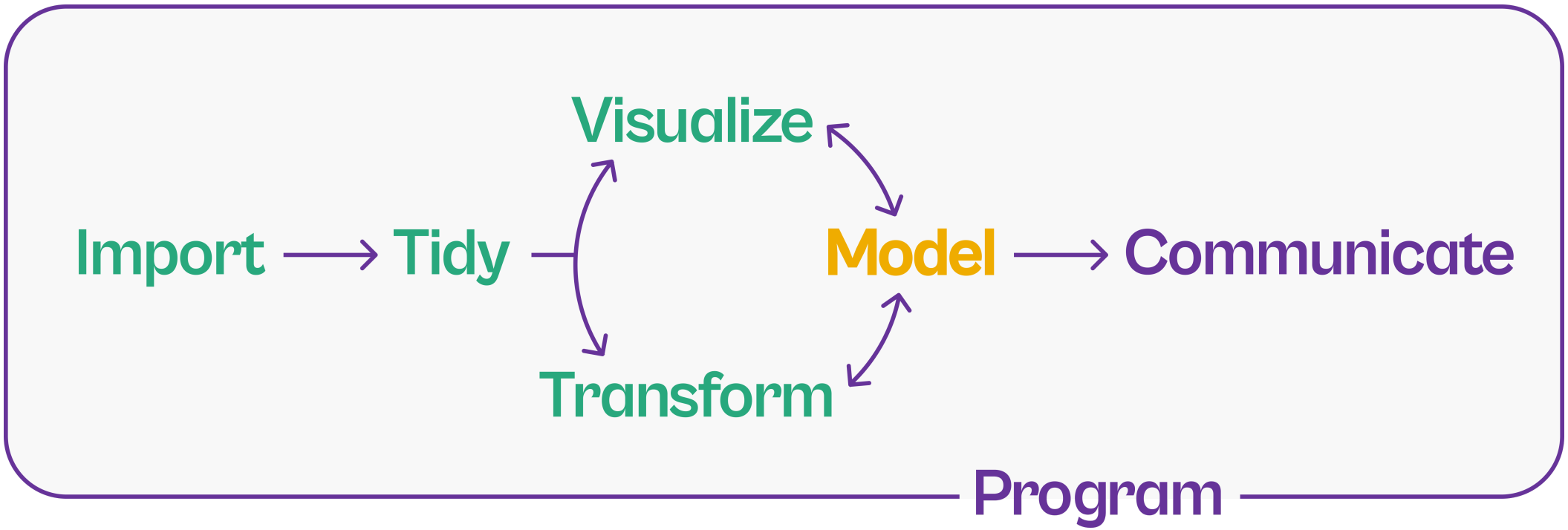
Cédric Scherer // R Course TU Dresden // Feb 27–Mar 3, 2023



The data science workflow, modified from "R for Data Science"



The data science workflow, modified from "R for Data Science"



The data science workflow, modified from "R for Data Science"

Statistical Models

A statistical model is a mathematical representation of observed data:

> *A statistical model is a class of mathematical model, which embodies a set of assumptions concerning the generation of some sample data, and similar data from a larger population.*
>
> *A statistical model represents, often in considerably idealized form, the data-generating process.*

Source: Wikipedia

Statistical Models

A statistical model is a mathematical representation of observed data:

> *A statistical model is a class of mathematical model, which embodies a set of assumptions concerning the generation of some sample data, and similar data from a larger population.*
>
> *A statistical model represents, often in considerably idealized form, the data-generating process.*

Source: Wikipedia

→ data is generated by a probabilistic process

→ each element of the population is selected with a (known) probability

→ it is *(should be)* possible to infer features of the population

Our Example Data 

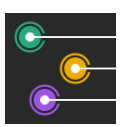
- data set on **54 bird families** recorded on a site in North America
- the following variables are reported:
  - the **species**
  - the **diet type** of the species
  - a yes/no classification if the species is a **passerine or not**
  - a yes/no classification if the species is considered **aquatic or not**
  - the **average and maximum abundance** observed at the site
  - the **average body mass** in grams
- provided as educational resource by the Quebec Centre for Biodiversity Science

Our Example Data 

```
1 birds <- readr::read_csv("./data/birds.csv")
```

```
1 birds
```

```
# A tibble: 54 × 7
   family             max_abund avg_abund   mass diet        passerine aquatic
   <chr>                  <dbl>     <dbl>  <dbl> <chr>           <dbl>   <dbl>
 1 Hawks&Eagles&Kites      2.99     0.674  716.  Vertebrate          0       0
 2 Long-tailed tits       37.8      4.04     5.3 Insect              1       0
 3 Larks                 241.      23.1     35.8 PlantInsect        1       0
 4 Kingfishers             4.4      0.595  119.  Vertebrate          0       0
 5 Auks& Puffins           4.53     2.96   315.  InsectVert          0       1
 6 Ducks& Geese           23.7      2.74  1144.  PlantInsect         0       1
 7 Anhingas               24.6      1.84  1250   Vertebrate          0       1
 8 Swifts                 44.0      3.95    27.4 Insect              0       0
 9 Limpkins                1.6      0.567 1100   Insect              0       1
10 Herons& Egrets         46.5      2.97   462.  Vertebrate          0       1
# … with 44 more rows
```

Our Example Data 

```
1 birds <- readr::read_csv("./data/birds.csv")
```

```
1 library(dplyr)
2 birds <- mutate(birds, across(c("family", "diet", "passerine", "aquatic"), factor))
```

```
1 birds
```

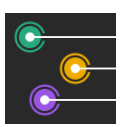
```
# A tibble: 54 × 7
   family             max_abund avg_abund   mass diet        passerine aquatic
   <fct>                  <dbl>     <dbl>  <dbl> <fct>       <fct>     <fct>
 1 Hawks&Eagles&Kites      2.99     0.674   716.  Vertebrate  0         0
 2 Long-tailed tits       37.8      4.04      5.3 Insect      1         0
 3 Larks                 241.      23.1      35.8 PlantInsect 1         0
 4 Kingfishers             4.4      0.595   119.  Vertebrate  0         0
 5 Auks& Puffins           4.53     2.96    315.  InsectVert  0         1
 6 Ducks& Geese           23.7      2.74   1144.  PlantInsect 0         1
 7 Anhingas               24.6      1.84   1250   Vertebrate  0         1
 8 Swifts                 44.0      3.95     27.4 Insect      0         0
 9 Limpkins                1.6      0.567 1100   Insect      0         1
10 Herons& Egrets         46.5      2.97    462.  Vertebrate  0         1
# … with 44 more rows
```


Our Example Data 

```
1 birds <- readr::read_csv("./data/birds.csv", col_types = "fdddfff")
```

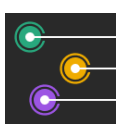
```
1 birds
```

```
# A tibble: 54 × 7
   family             max_abund avg_abund   mass diet        passerine aquatic
   <fct>                  <dbl>     <dbl>  <dbl> <fct>       <fct>     <fct>
 1 Hawks&Eagles&Kites      2.99     0.674  716.  Vertebrate  0         0
 2 Long-tailed tits       37.8      4.04     5.3 Insect      1         0
 3 Larks                 241.      23.1     35.8 PlantInsect 1         0
 4 Kingfishers             4.4      0.595  119.  Vertebrate  0         0
 5 Auks& Puffins           4.53     2.96   315.  InsectVert  0         1
 6 Ducks& Geese           23.7      2.74  1144.  PlantInsect 0         1
 7 Anhingas               24.6      1.84  1250   Vertebrate  0         1
 8 Swifts                 44.0      3.95    27.4 Insect      0         0
 9 Limpkins                1.6      0.567 1100   Insect      0         1
10 Herons& Egrets         46.5      2.97   462.  Vertebrate  0         1
# … with 44 more rows
```

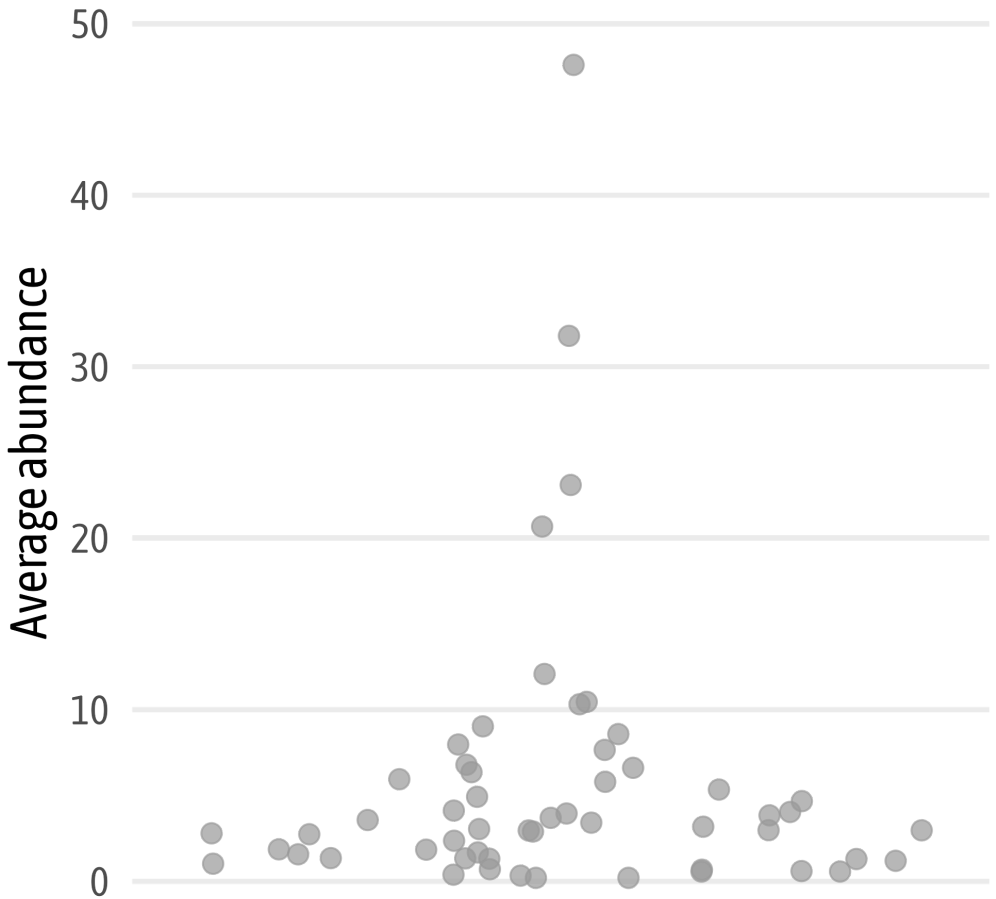
Statistical Analysis

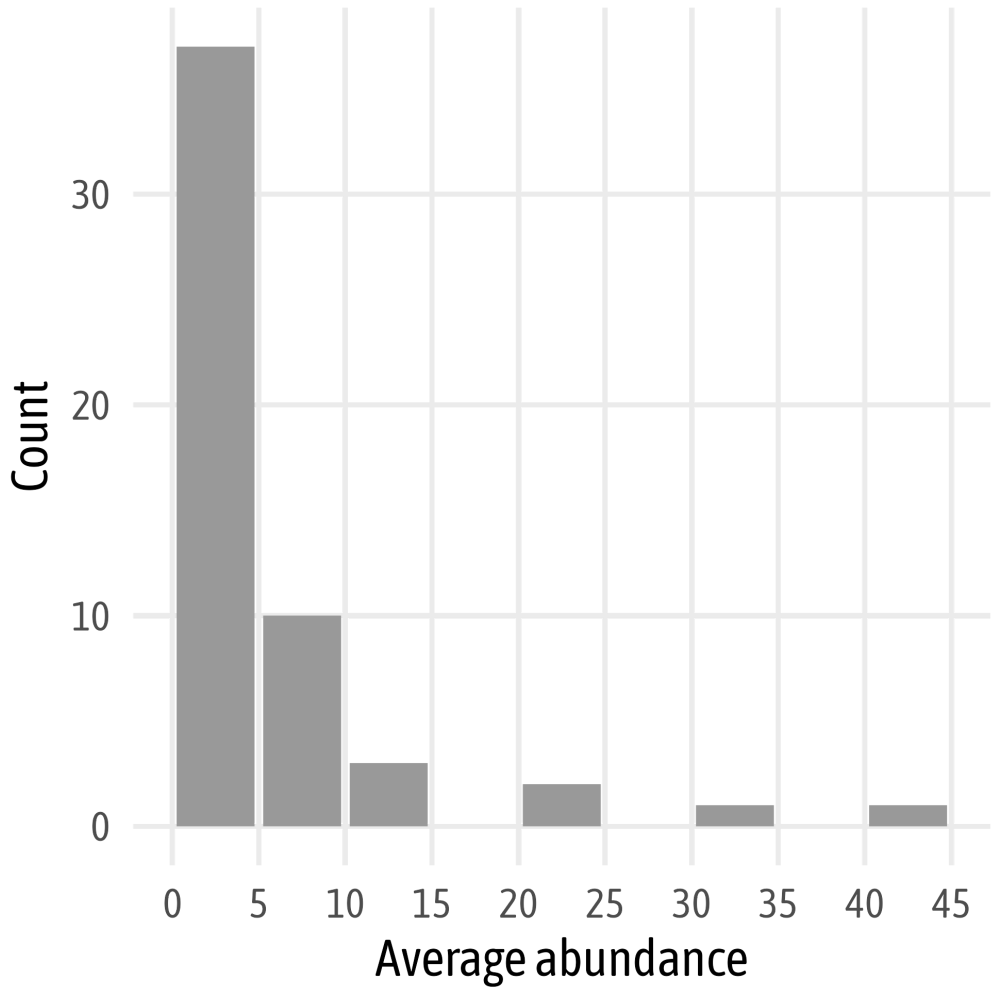
— Univariate Data —



Univariate Data

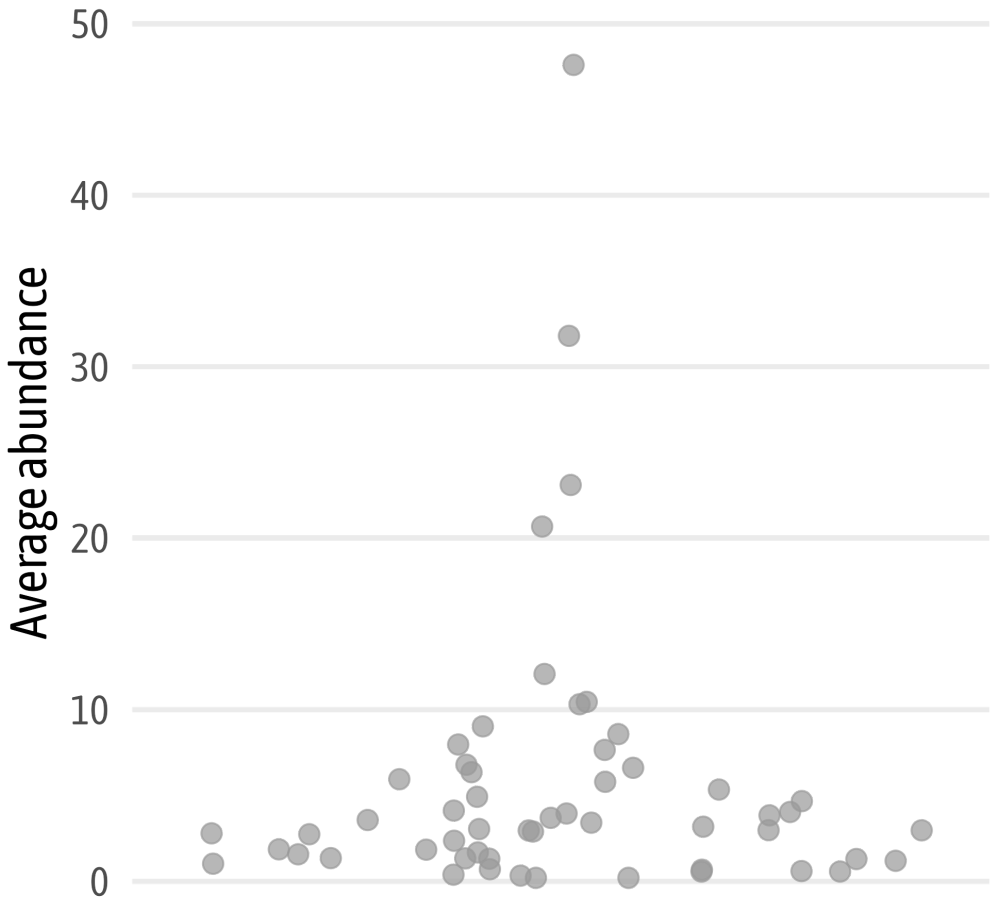
Univariate describes data that consist of **only a single characteristic**.

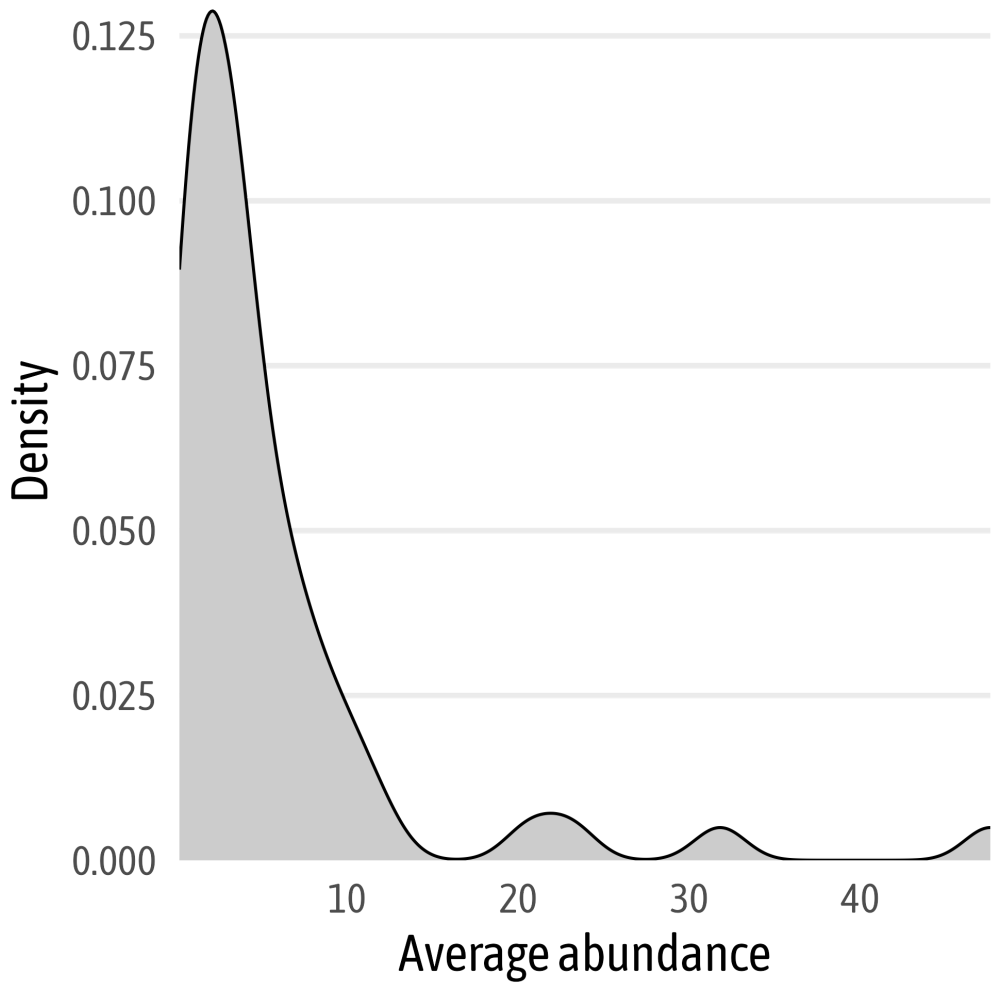




Univariate Data

Univariate describes data that consist of **only a single characteristic**.

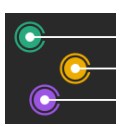




Univariate Descriptive Statistics

There are two key concepts for evaluating the distribution of a single variable:

- **localization**
- **variation**



Univariate Descriptive Statistics

Localization is a measure of **central tendency of a population**.

It can be measured with the **arithmetic mean**:

```
1 mean(birds$avg_abund)
```

```
[1] 5.686179
```

```
1 mean(birds$mass)
```

```
[1] 468.4757
```

or the **median**:

```
1 median(birds$avg_abund)
```

```
[1] 3.113586
```

```
1 median(birds$mass)
```

```
[1] 59.18297
```


Univariate Descriptive Statistics

Variation is the a measure of **dispersion (or deviation) of observations** around the mean.

It can be measured by the **variance**:

```
1 var(birds$avg_abund)
```

```
[1] 68.05705
```

```
1 var(birds$mass)
```

```
[1] 893800.9
```

Variance is the sum of the squared deviation between each value. Squaring the variance allows us to transform values into positive values without using absolute values.

Univariate Descriptive Statistics

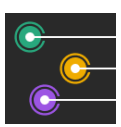
To transform the variance into appropriate units, we can calculate the **standard deviation** σ:

```
1 sd(birds$avg_abund)
```

```
[1] 8.249669
```

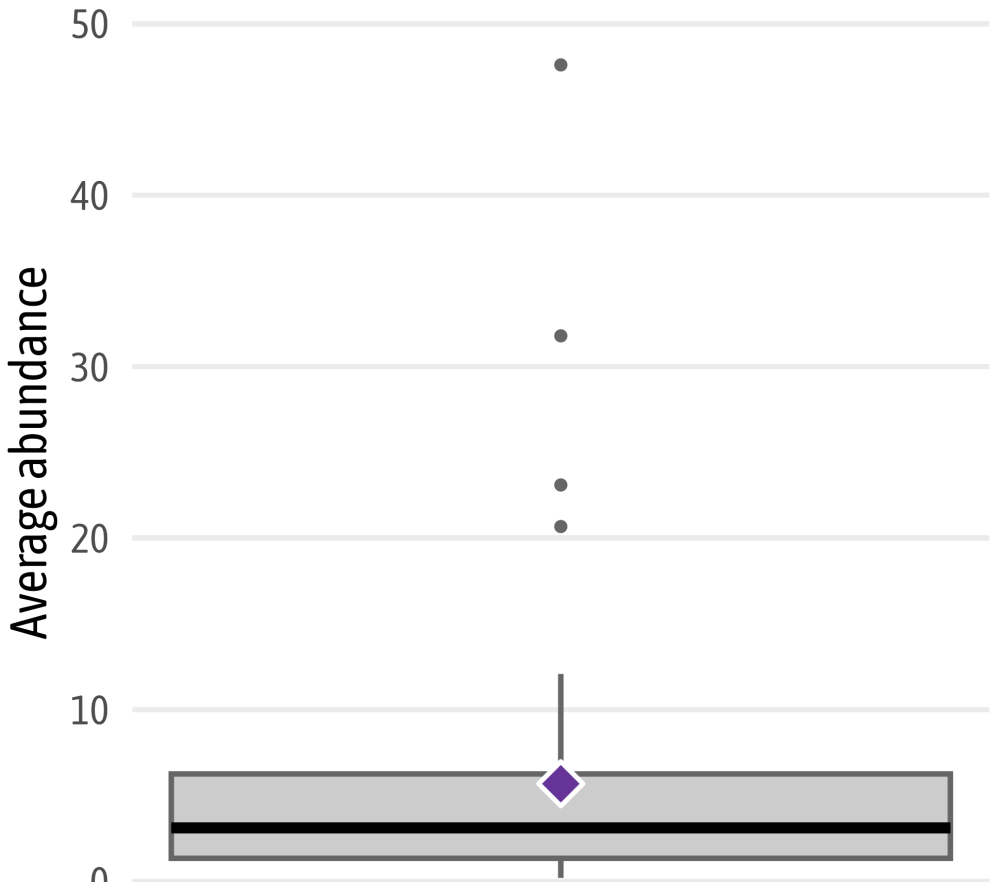
```
1 sd(birds$mass)
```

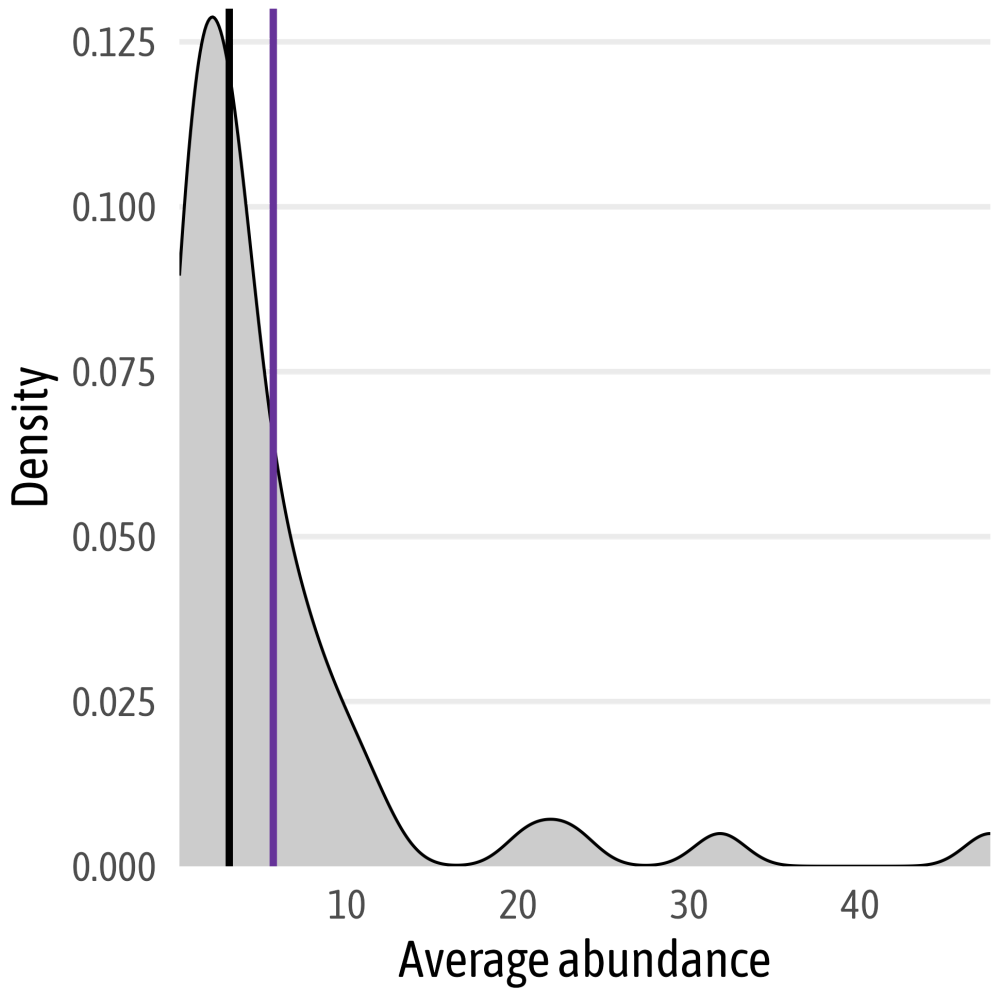
```
[1] 945.4104
```

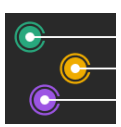
Univariate Descriptive Statistics

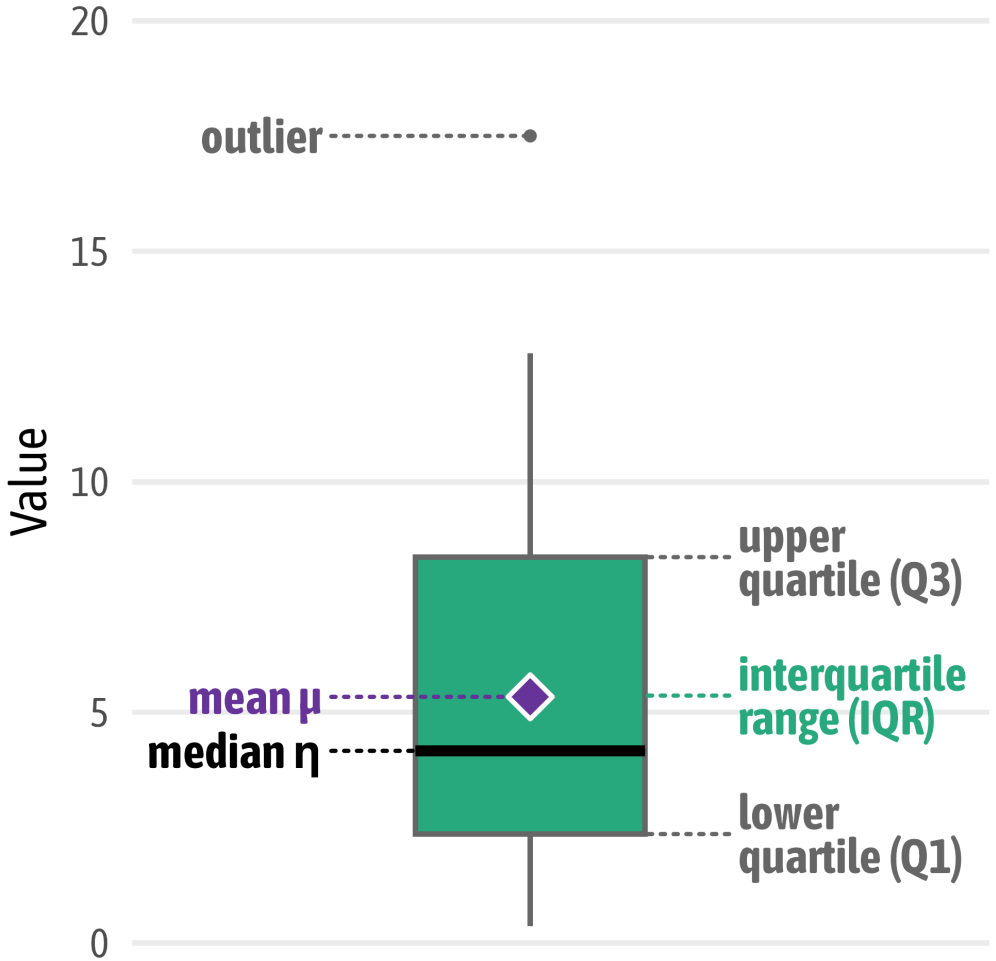
Mean and **median** differ in case the distribution is asymmetrical:

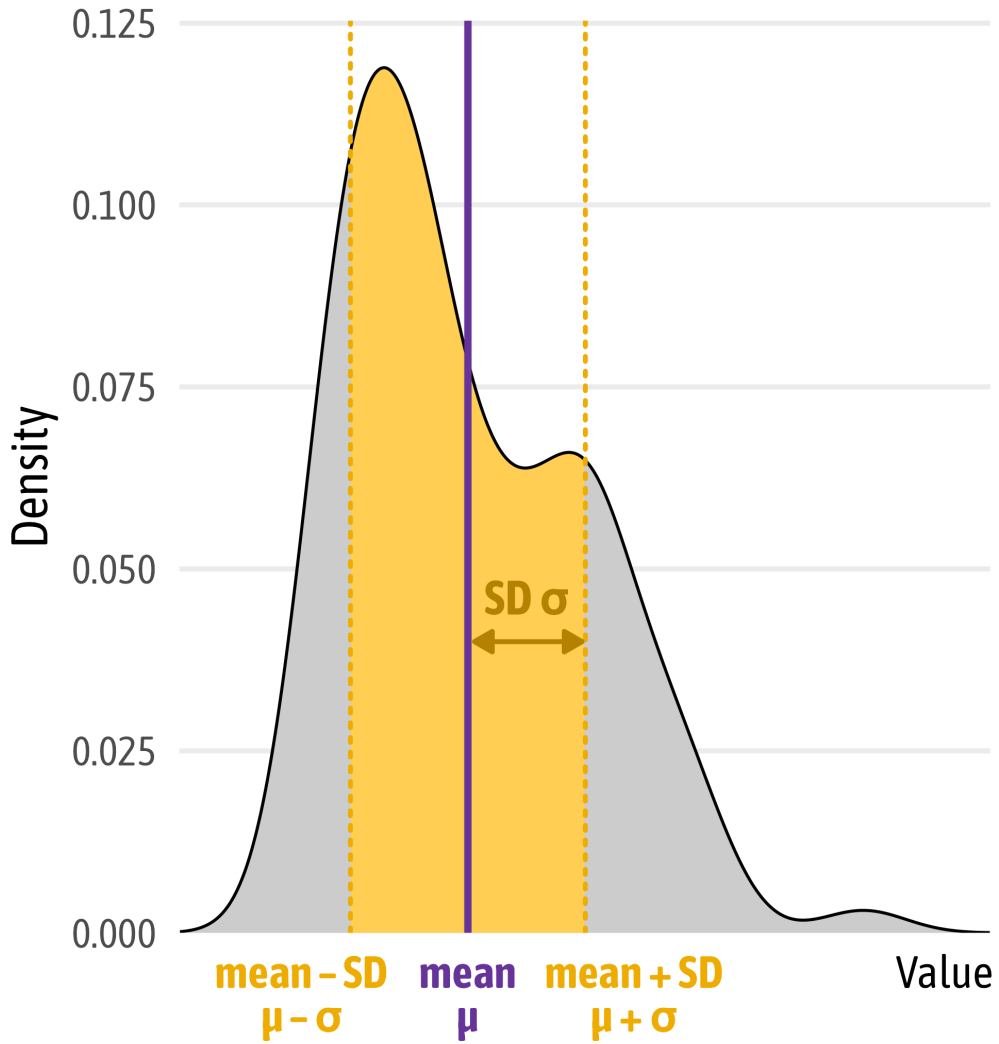




Univariate Descriptive Statistics




20
15
10
5
0
Value
outlier
mean μ
median η
upper
quartile (Q3)
interquartile
range (IQR)
lower
quartile (Q1)


0.125
0.100
0.075
0.050
0.025
0.000
Density
SD σ
mean – SD
μ – σ
mean
μ
mean + SD
μ + σ
Value

Univariate Descriptive Statistics

```
quantile(birds$avg_abund)
```

```
       0%        25%        50%        75%       100% 
 0.200000   1.339712   3.113586   6.258143 47.597600 
```

```
diff(as.numeric(quantile(birds$avg_abund, c(0.25, 0.75)))) ## also works without `as.numeric()`
```

```
[1] 4.918432
```

```
IQR(birds$avg_abund)  ## `diff(quantile(as.numeric(birds$avg_abund), c(0.25, 0.75)))`
```

```
[1] 4.918432
```

```
range(birds$avg_abund)
```

```
[1]  0.2000 47.5976
```

```
diff(range(birds$avg_abund))  ## `max(birds$avg_abund) - min(birds$avg_abund)`
```

```
[1] 47.3976
```


Compare Distributions

The **Shapiro-Wilk test** is used to compare the distribution of a variable with a reference probability probability distribution:

```
1  shapiro.test(birds$avg_abund)
```

```
    Shapiro-Wilk normality test

data:  birds$avg_abund
W = 0.59272, p-value = 5.394e-11
```

Null hypothesis: values follow a normal distribution

→ We reject H_a. The values are not distributed normally.

Compare Distributions

An alternative is the **Kolmogorov-Smirnov test** to test for normality:

```
1  ks.test(birds$avg_abund, "pnorm")
```

```
    Asymptotic one-sample Kolmogorov-Smirnov test

data:  birds$avg_abund
D = 0.69907, p-value < 2.2e-16
alternative hypothesis: two-sided
```

Null hypothesis: values follow a normal distribution

→ We reject H_0. The values are not distributed normally.

Compare Distributions

The **Chi-square goodness-of-fit test** is much more flexible and can also be used for other distributions:

```
1  chisq.test(birds$avg_abund, p = rep(1 / nrow(birds), nrow(birds))) ## uniform distribution
```

```
    Chi-squared test for given probabilities

data:  birds$avg_abund
X-squared = 634.35, df = 53, p-value < 2.2e-16
```

Null hypothesis: values do not follow a uniform distribution

→ We reject H_a. The values are not distributed uniformly.

```
1  rep(1 / nrow(birds), nrow(birds))
```

```
 [1] 0.01851852 0.01851852 0.01851852 0.01851852 0.01851852 0.01851852 0.01851852 0.01851852 0.01851852
[10] 0.01851852 0.01851852 0.01851852 0.01851852 0.01851852 0.01851852 0.01851852 0.01851852 0.01851852
[19] 0.01851852 0.01851852 0.01851852 0.01851852 0.01851852 0.01851852 0.01851852 0.01851852 0.01851852
[28] 0.01851852 0.01851852 0.01851852 0.01851852 0.01851852 0.01851852 0.01851852 0.01851852 0.01851852
[37] 0.01851852 0.01851852 0.01851852 0.01851852 0.01851852 0.01851852 0.01851852 0.01851852 0.01851852
[46] 0.01851852 0.01851852 0.01851852 0.01851852 0.01851852 0.01851852 0.01851852 0.01851852 0.01851852
```


Univariate Statistics

There are multiple tests to compare the mean of a single, continuous explanatory variable to a theoretical or hypothetical mean:

$$H_0: \bar{x} = \mu_0$$

The three possible alternative hypotheses are:

- two-tailed $\longrightarrow$ H_a: $\bar{x} = \mu_0$ (`two.sided`)
- right-tailed $\longrightarrow$ H_a: $\bar{x} > \mu_0$ (`greater`)
- left-tailed $\longrightarrow$ H_a: $\bar{x} < \mu_0$ (`less`)

One-Sample Student's t-Test

A formal statistical test to compare the mean of a continuous variable to a theoretical or hypothetical mean is the **one-sample student's t-test**.

```
1  t.test(birds$avg_abund, mu = 0, alternative = "two.sided")
```

```
    One Sample t-test

data:  birds$avg_abund
t = 5.065, df = 53, p-value = 5.28e-06
alternative hypothesis: true mean is not equal to 0
95 percent confidence interval:
 3.434453 7.937905
sample estimates:
mean of x
 5.686179
```

→ We accept H_a. The mean is not equal to 0.

One-Sample Student's t-Test

A formal statistical test to compare the mean of a continuous variable to a theoretical or hypothetical mean is the **one-sample student's t-test**.

```
1  t.test(birds$avg_abund, mu = 5, alternative = "two.sided")  ## true mean: 5.7
```

```
    One Sample t-test

data:  birds$avg_abund
t = 0.61122, df = 53, p-value = 0.5437
alternative hypothesis: true mean is not equal to 5
95 percent confidence interval:
 3.434453 7.937905
sample estimates:
mean of x
 5.686179
```

→ We reject H_a. The mean is equal to 5.

One-Sample Student's t-Test

A formal statistical test to compare the mean of a continuous variable to a theoretical or hypothetical mean is the **one-sample student's t-test**.

```
1  t.test(birds$avg_abund, mu = 0, alternative = "two.sided")  ## true mean: 5.7
```

```
    One Sample t-test

data:  birds$avg_abund
t = 5.065, df = 53, p-value = 5.28e-06
alternative hypothesis: true mean is not equal to 0
95 percent confidence interval:
 3.434453 7.937905
sample estimates:
mean of x
 5.686179
```

→ We accept H_a. The mean is not equal to 0.

One-Sample Student's t-Test

A formal statistical test to compare the mean of a continuous variable to a theoretical or hypothetical mean is the **one-sample student's t-test**.

```
1  t.test(birds$avg_abund, mu = 0, alternative = "greater")  ## true mean: 5.7
```

```
    One Sample t-test

data:  birds$avg_abund
t = 5.065, df = 53, p-value = 2.64e-06
alternative hypothesis: true mean is greater than 0
95 percent confidence interval:
 3.806753      Inf
sample estimates:
mean of x
 5.686179
```

→ We accept H_a. The mean is greater than 0.

One-Sample Student's t-Test

A formal statistical test to compare the mean of a continuous variable to a theoretical or hypothetical mean is the **one-sample student's t-test**.

Assumption that needs to be fulfilled:

- a random sample of continuous measurements
- normality of the data (non-skewed distribution)
- no knowledge of the true population variance

Check Normality of the Data

```
1  shapiro.test(birds$avg_abund)
```

```
    Shapiro-Wilk normality test

data:  birds$avg_abund
W = 0.59272, p-value = 5.394e-11
```

Null hypothesis: values follow a normal distribution

→ We accept H_a. The values are not distributed normally.

```
1  shapiro.test(log10(birds$avg_abund))
```

```
    Shapiro-Wilk normality test

data:  log10(birds$avg_abund)
W = 0.9846, p-value = 0.7124
```

Null hypothesis: values follow a normal distribution

→ We reject H_a. The (log-transformed) values are distributed normally.

One-Sample Student's t-Test

A formal statistical test to compare the mean of a continuous variable to a theoretical or hypothetical mean is the **one-sample student's t-test**.

```
1  t.test(log10(birds$avg_abund), mu = 0, alternative = "two.sided")  ## true mean: .5
```

```
    One Sample t-test

data:  log10(birds$avg_abund)
t = 6.5546, df = 53, p-value = 2.347e-08
alternative hypothesis: true mean is not equal to 0
95 percent confidence interval:
 0.3227987 0.6074655
sample estimates:
mean of x
0.4651321
```

→ We accept H_a. The mean is not equal to 0.

One-Sample Student's t-Test

A formal statistical test to compare the mean of a continuous variable to a theoretical or hypothetical mean is the **one-sample student's t-test**.

```
1  t.test(log10(birds$avg_abund), mu = .5, alternative = "two.sided")  ## true mean: .5
```

```
    One Sample t-test

data:  log10(birds$avg_abund)
t = -0.49135, df = 53, p-value = 0.6252
alternative hypothesis: true mean is not equal to 0.5
95 percent confidence interval:
 0.3227987 0.6074655
sample estimates:
mean of x
0.4651321
```

→ We reject H_a. The mean is equal to 0.5.

One-Sample z-Test

Another approach to test for differences of the population average is the *z-test*.

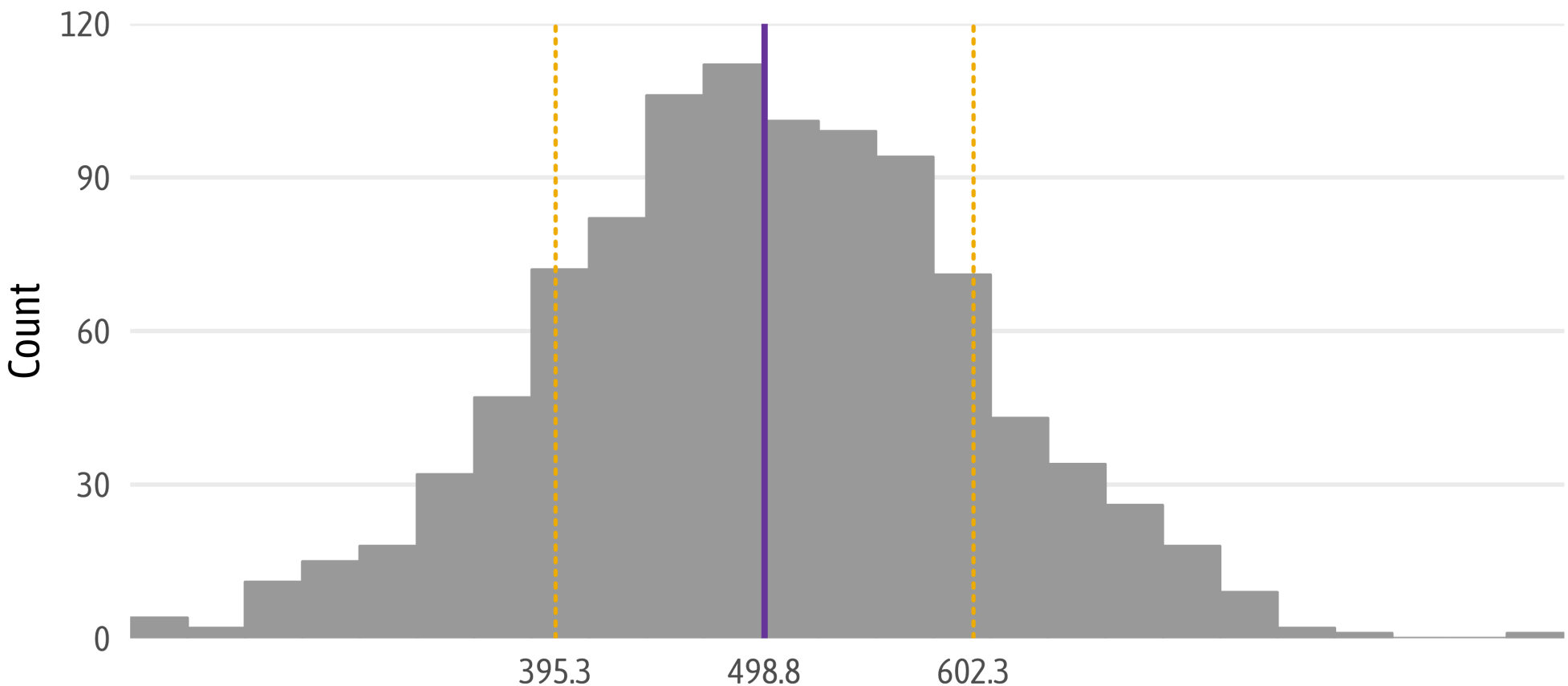
Why and When?

- If the variation in the population is known **and**
- if the sample size is ≥ 30

One-Sample z-Test

Let's create some large sample with a known mean and variation:

```
1 set.seed(1)
2 dist <- rnorm(n = 1000, mean = 500, sd = 100)
```



One-Sample z-Test

Let's create some large sample with a known mean and variation:

```r
set.seed(1)
dist <- rnorm(n = 1000, mean = 500, sd = 100)
```

```r
# install.packages("BSDA")
BSDA::z.test(dist, mu = 500, sigma.x = 100)
```

```
    One-sample z-Test

data:  dist
z = -0.36835, p-value = 0.7126
alternative hypothesis: true mean is not equal to 500
95 percent confidence interval:
 492.6372 505.0331
sample estimates:
mean of x
 498.8352
```

→ We reject H_a. The mean is equal to 500.

One-Sample z-Test

Let's create some large sample with a known mean and variation:

```r
set.seed(1)
dist <- rnorm(n = 1000, mean = 500, sd = 100)
```

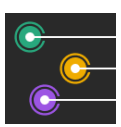
```r
# install.packages("BSDA")
BSDA::z.test(dist, mu = 500, sigma.x = 10) ## note that mu fits but sigma.x doesn't!
```

```
    One-sample z-Test

data:  dist
z = -3.6835, p-value = 0.0002301
alternative hypothesis: true mean is not equal to 500
95 percent confidence interval:
 498.2154 499.4550
sample estimates:
mean of x
 498.8352
```

→ We accept H_a. The mean is not equal to 500.

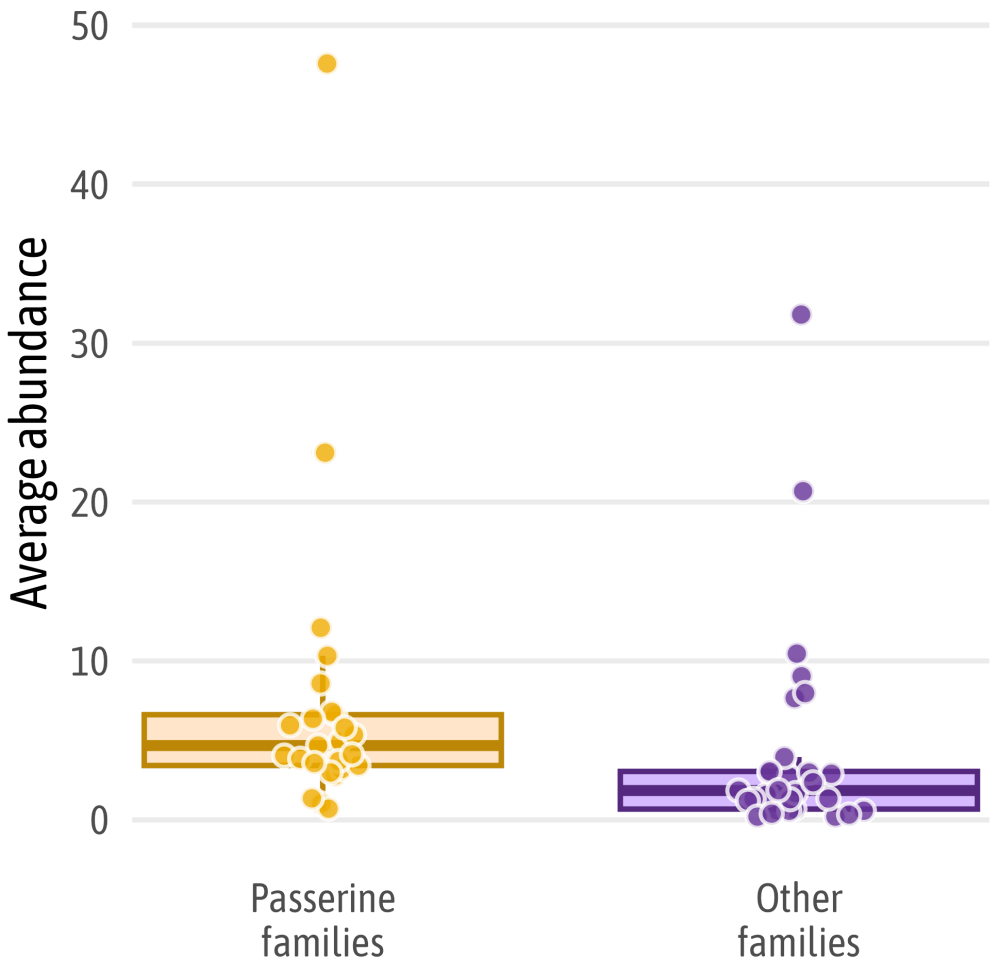
Statistical Analysis

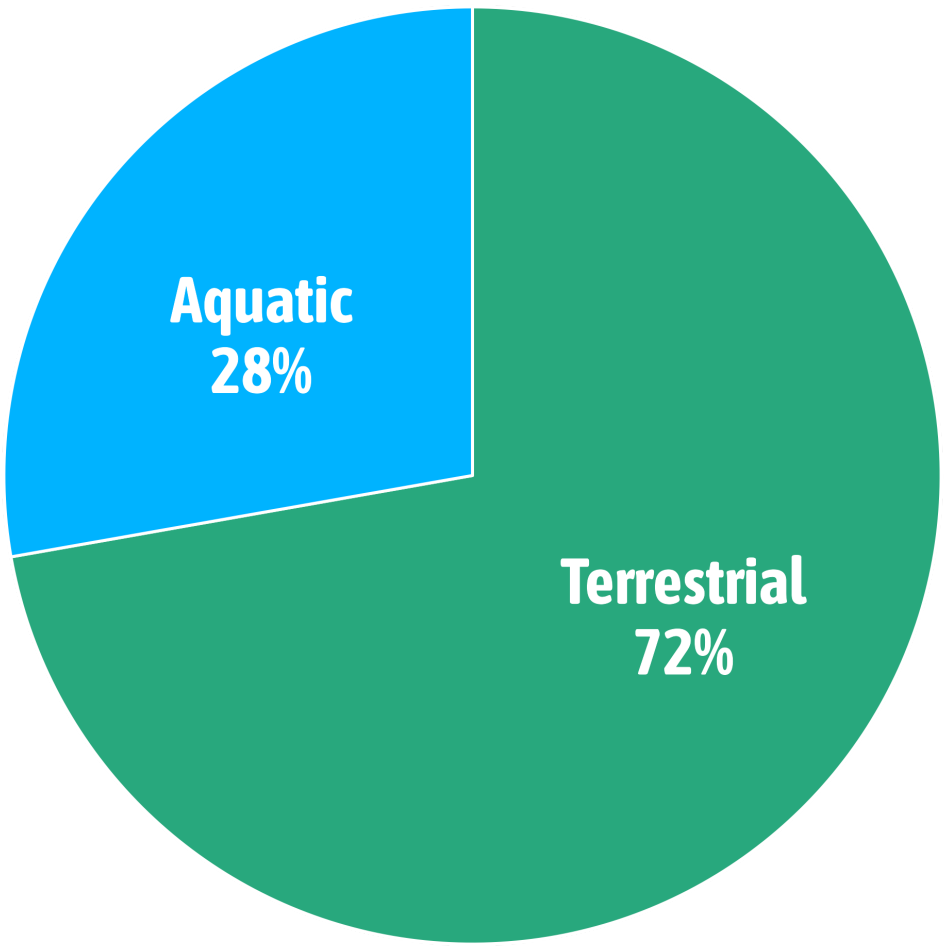
— Bivariate Data —



Bivariate Data

Bivariate describes data that consist of **two characteristics**.

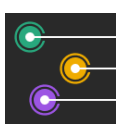




Responses and Predictors

A bivariate statistical model describes the relationship between **a response variable** and **one or more predictor variables**.

- **response variable:**
  variable we want to explain, also known as the **dependent variable**
- **explanatory variable(s):**
  variable(s) that can (potentially) explain the response variable



Our Research Question

Hypothesis

> *The **habitat preferences of different bird species affect the average abundance** due to different availability of habitat.*

Prediction

> *The average abundance differs between aquatic and terrestrial bird families.*

Two-Sample Student's t-Test

A formal statistical test to test for difference a single, categorical explanatory variable with two levels is the **two-sample student's t-test**.

Assumptions that needs to be fulfilled:

- Normality of the data (non-skewed distribution)
- Homoscedasticity (similar variance of both levels)

The robustness of the t-test increases with sample size and is higher when groups have equal sizes.

Verify Assumptions for t-Test

Check sample sizes:

```
1 count(birds, aquatic)
```

```
# A tibble: 2 × 2
  aquatic     n
  <fct>   <int>
1 0          39
2 1          15
```

Check equality of variances:

```
1 var.test(avg_abund ~ aquatic, data = birds)
```

```
    F test to compare two variances

data:  avg_abund by aquatic
F = 0.84667, num df = 38, denom df = 14, p-value = 0.6559
alternative hypothesis: true ratio of variances is not equal to 1
95 percent confidence interval:
 0.3155069 1.8900778
sample estimates:
ratio of variances
         0.8466711
```

→ We reject H_a. The ratio is equal to 1, i.e. variances are equal.

Two-Sample Student's t-Test

A formal statistical test to test for difference a single, categorical explanatory variable with two levels is the **two-sample student's t-test**:

```
1  t.test(avg_abund ~ aquatic, data = birds, alternative = "two.sided", var.equal = TRUE)
```

```
    Two Sample t-test

data:  avg_abund by aquatic
t = -0.14964, df = 52, p-value = 0.8816
alternative hypothesis: true difference in means between group 0 and group 1 is not equal to 0
95 percent confidence interval:
 -5.455121  4.697991
sample estimates:
mean in group 0 mean in group 1
       5.581022        5.959587
```

→ We reject H_a. The abundance does not differ between groups.

Our Research Question

Hypothesis

> *The* ***habitat preferences of different bird species affect the average abundance*** *due to different availability of habitat.*

Prediction

> *The average* ***abundance of aquatic families is lower*** *than the average abundance of terrestrial families.*

Unilateral Two-Sample Student's t-Test

One can also test whether one mean is higher than the other one:

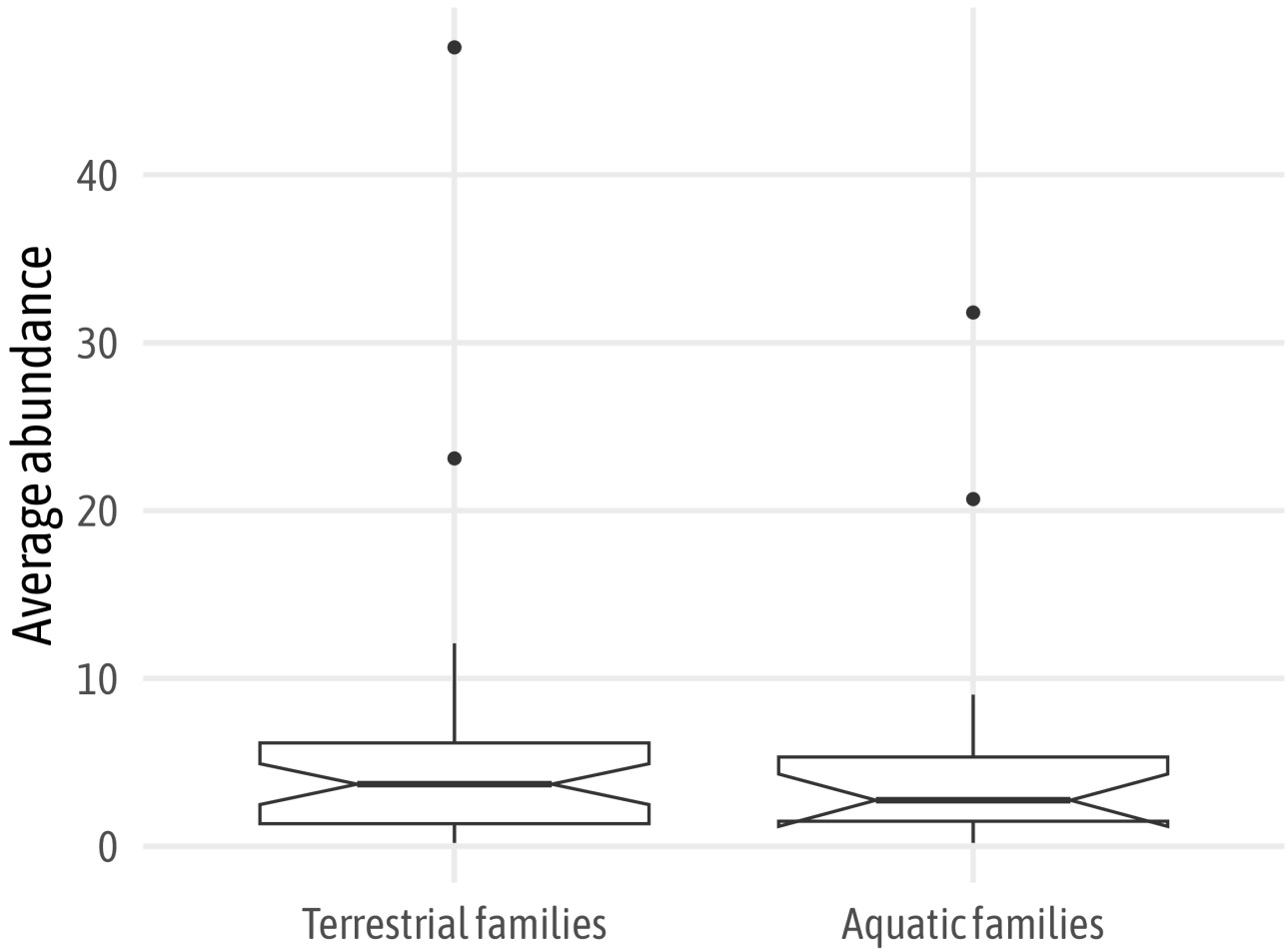
```r
## mean of level 1 is "greater" than that of level 2
t.test(avg_abund ~ aquatic, data = birds, alternative = "greater", var.equal = TRUE)
```

```
    Two Sample t-test

data:  avg_abund by aquatic
t = -0.14964, df = 52, p-value = 0.5592
alternative hypothesis: true difference in means between group 0 and group 1 is greater than 0
95 percent confidence interval:
 -4.615312       Inf
sample estimates:
mean in group 0 mean in group 1
       5.581022        5.959587
```

→ We reject H_a. The means do not differ between groups.

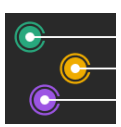
Visualize the Populations

```
1 ggplot(birds, aes(x = aquatic, y = avg_abund)) +
2   geom_boxplot(notch = TRUE) +
3   scale_x_discrete(labels = c("Terrestrial families", "Aquatic families")) +
4   labs(x = NULL, y = "Average abundance")
```



Theme Settings

```
1 theme_set(theme_minimal(
2   base_size = 18,
3   base_family = "Asap Condensed"
4 ))
5
6 theme_update(panel.grid.minor = element_blank())
```

Your Turn: t-Test

- Test for difference of mass in passerine versus other bird families.
  - Check the assumptions for a t-test.
  - If needed, account for potential problems.
- Test if the mass of passerine families is significantly lower than that of non-passerine bird families.
- Visualize the relationship.

Prediction

> *In bird families belonging to the passerine order we observe lower body masses compared to the non-passerine families.*

Verify Assumptions for t-Test

Check sample sizes:

```
1 count(birds, passerine)
```

```
# A tibble: 2 × 2
  passerine     n
  <fct>     <int>
1 0            29
2 1            25
```

Check equality of variances:

```
1 var.test(mass ~ passerine, data = birds)
```

```
    F test to compare two variances

data:  mass by passerine
F = 2212.2, num df = 28, denom df = 24, p-value < 2.2e-16
alternative hypothesis: true ratio of variances is not equal to 1
95 percent confidence interval:
  993.6119 4808.3462
sample estimates:
ratio of variances
          2212.237
```

→ We accept H_a. The ratio is not equal to 1, i.e. variances are not equal.

Verify Assumptions for t-Test

Check sample sizes:

```
1 count(birds, passerine)
```

```
# A tibble: 2 × 2
  passerine     n
  <fct>     <int>
1 0            29
2 1            25
```

Check equality of variances:

```
1 var.test(log10(mass) ~ passerine, data = birds)
```

```
    F test to compare two variances

data:  log10(mass) by passerine
F = 4.1318, num df = 28, denom df = 24, p-value = 0.0007421
alternative hypothesis: true ratio of variances is not equal to 1
95 percent confidence interval:
 1.855784 8.980621
sample estimates:
ratio of variances
          4.131828
```

→ We accept H_a. The ratio is not equal to 1, i.e. variances are not equal.

Welch t-Test

In case the equality in variance assumption is violated, one can run a Welch Two-Sample test:

```
1  t.test(log10(mass) ~ passerine, data = birds, alternative = "two.sided", var.equal = FALSE)
```

```
    Welch Two Sample t-test

data:  log10(mass) by passerine
t = 8.16, df = 42.061, p-value = 3.313e-10
alternative hypothesis: true difference in means between group 0 and group 1 is not equal to 0
95 percent confidence interval:
 0.8969327 1.4863194
sample estimates:
mean in group 0 mean in group 1
       2.503130        1.311504
```

→ We accept H_a. The means differ between groups.

→ Masses differ significantly between passserine and other families.

Welch t-Test

In case the equality in variance assumption is violated, one can run a Welch Two-Sample test:

```r
## log10(mass) is greater in 0 compared to 1 => passerine less
t.test(log10(mass) ~ passerine, data = birds, alternative = "greater", var.equal = FALSE)
```

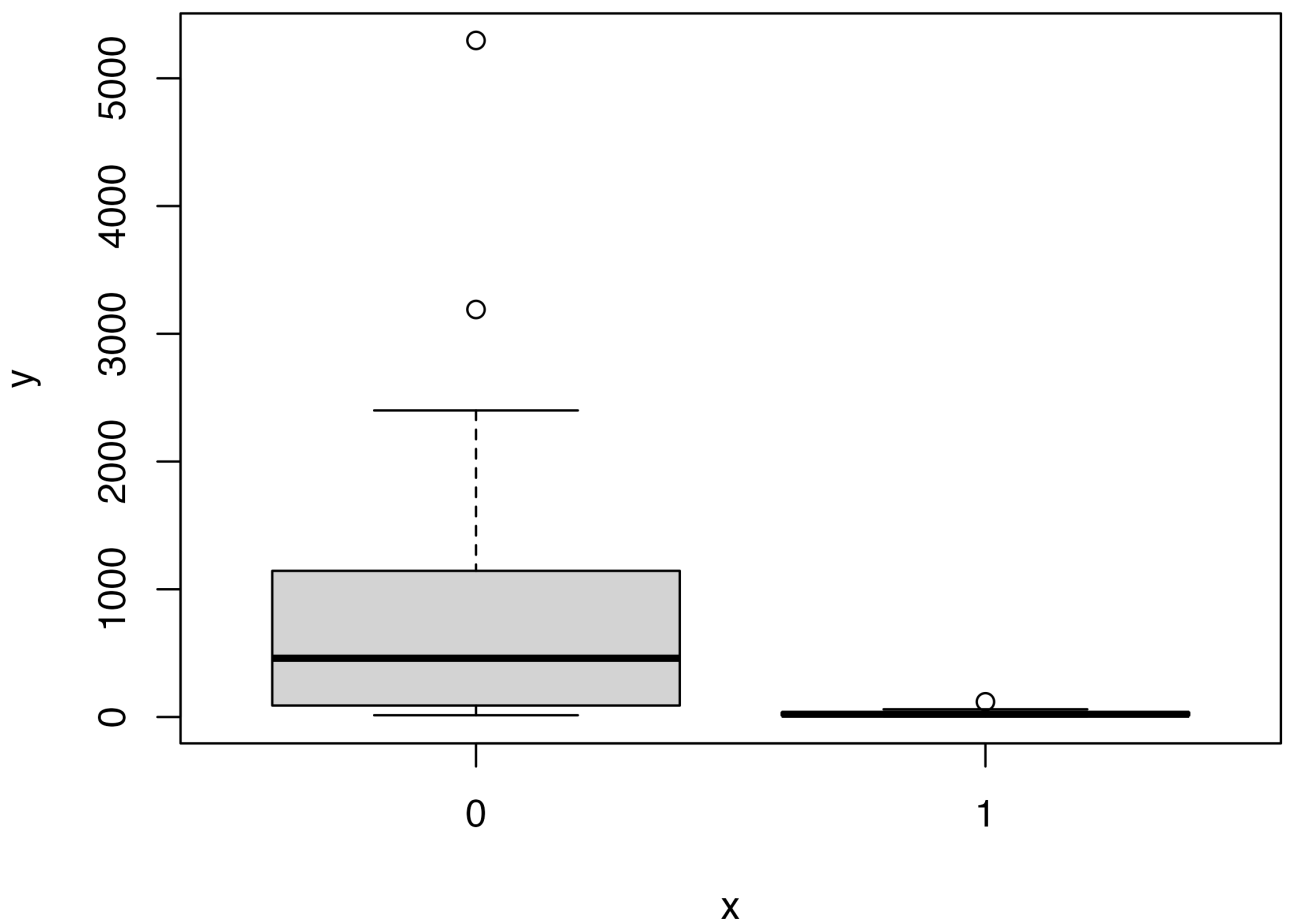
```
    Welch Two Sample t-test

data:  log10(mass) by passerine
t = 8.16, df = 42.061, p-value = 1.657e-10
alternative hypothesis: true difference in means between group 0 and group 1 is greater than 0
95 percent confidence interval:
 0.946014      Inf
sample estimates:
mean in group 0 mean in group 1
       2.503130        1.311504
```

→ We accept H_a. The mean of 0 is greater than that of 1.

→ Passserines are significantly lighter than other families.

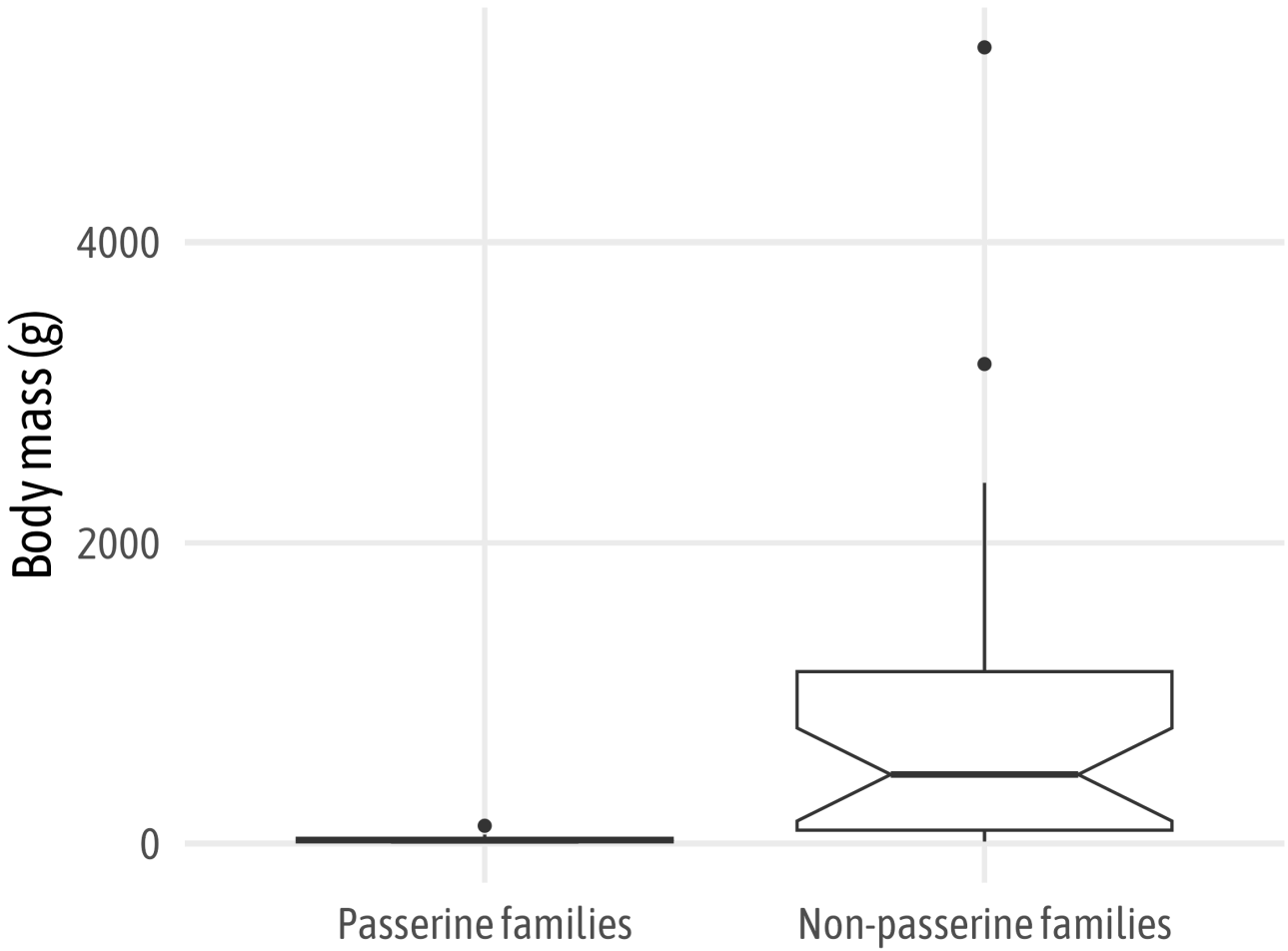
Visualize the Populations

```
1 plot(birds$passerine, birds$mass)
```



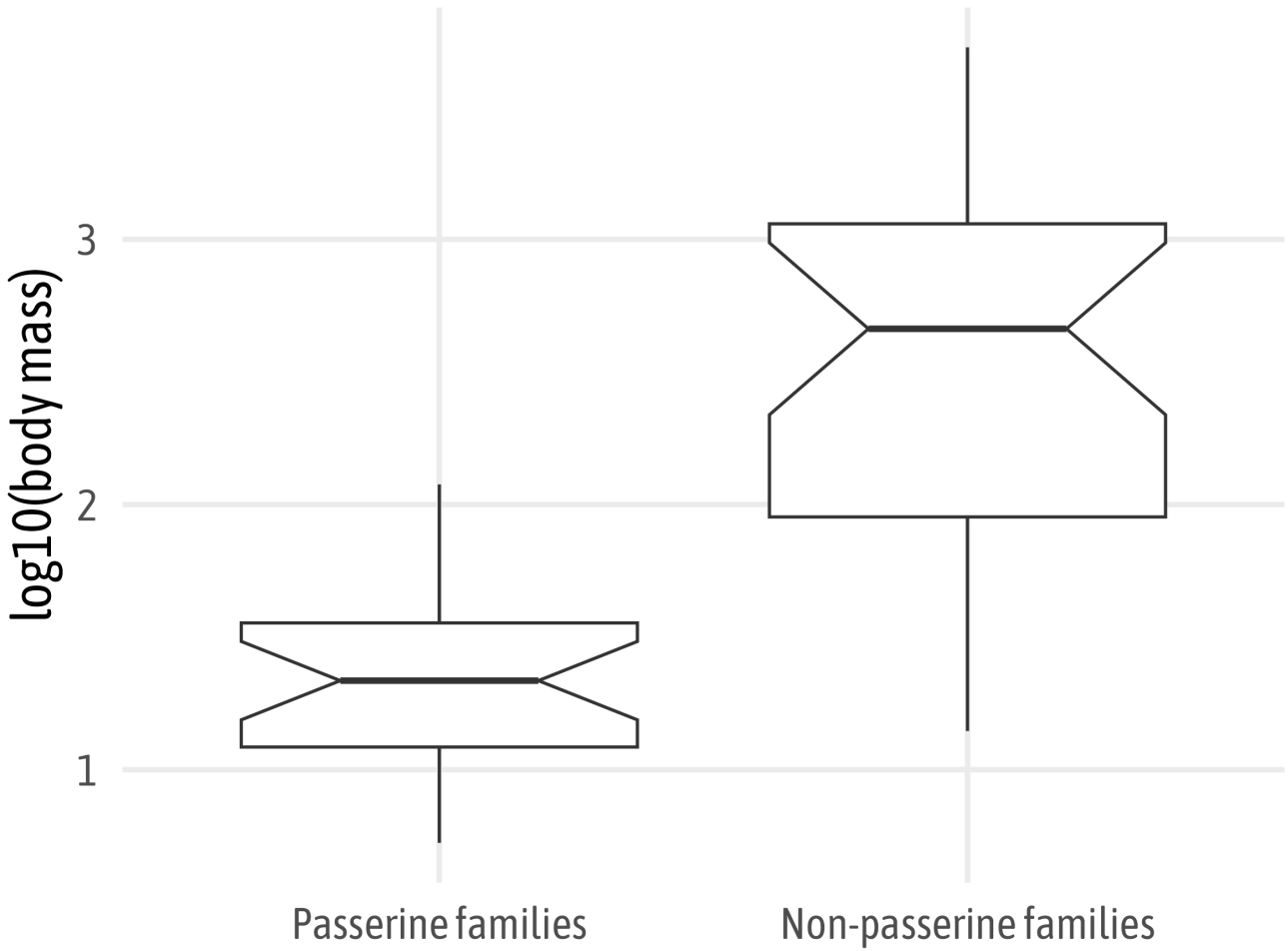
Visualize the Populations

```
1 ggplot(birds, aes(x = forcats::fct_rev(passerine), y = mass)) +
2   geom_boxplot(notch = TRUE) +
3   scale_x_discrete(labels = c("Passerine families", "Non-passerine families")) +
4   labs(x = NULL, y = "Body mass (g)")
```



Visualize the Populations

```
1 ggplot(birds, aes(x = forcats::fct_rev(passerine), y = log10(mass))) +
2   geom_boxplot(notch = TRUE) +
3   scale_x_discrete(labels = c("Passerine families", "Non-passerine families")) +
4   labs(x = NULL, y = "log10(body mass)")
```



Mann-Whitney U Test

The **Mann-Whitney U test** (or **Wilcoxon rank-sum test**) is the nonparametric equivalent of the two sample t-test which is more flexible to compare distributions of two populations.

Why and When?

- If the distribution of the data is not symmetric* **and**
- if your sample size is rather low (n < 100)

* We have ignored that fact so far

Mann-Whitney U Test

```
1  wilcox.test(birds$mass[birds$aquatic == 0], birds$mass[birds$aquatic == 1])
```

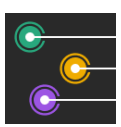
```
    Wilcoxon rank sum exact test

data:  birds$mass[birds$aquatic == 0] and birds$mass[birds$aquatic == 1]
W = 31, p-value = 7.63e-09
alternative hypothesis: true location shift is not equal to 0
```

→ We accept H_a. The abundance differ between groups.

Note that before, using the t-test (which assumes normality!) we have rejected H_a!

Statistical Analysis

— Linear Model —



Our Research Question

Hypothesis

> *For different bird species, the* ***average mass of an individual affects the maximum abundance of the species****, due to ecological constraints (e.g. due to the amount of food sources needed and habitat availability).*

What would be a suitable prediction to test our hypothesis?

Our Research Question

Hypothesis

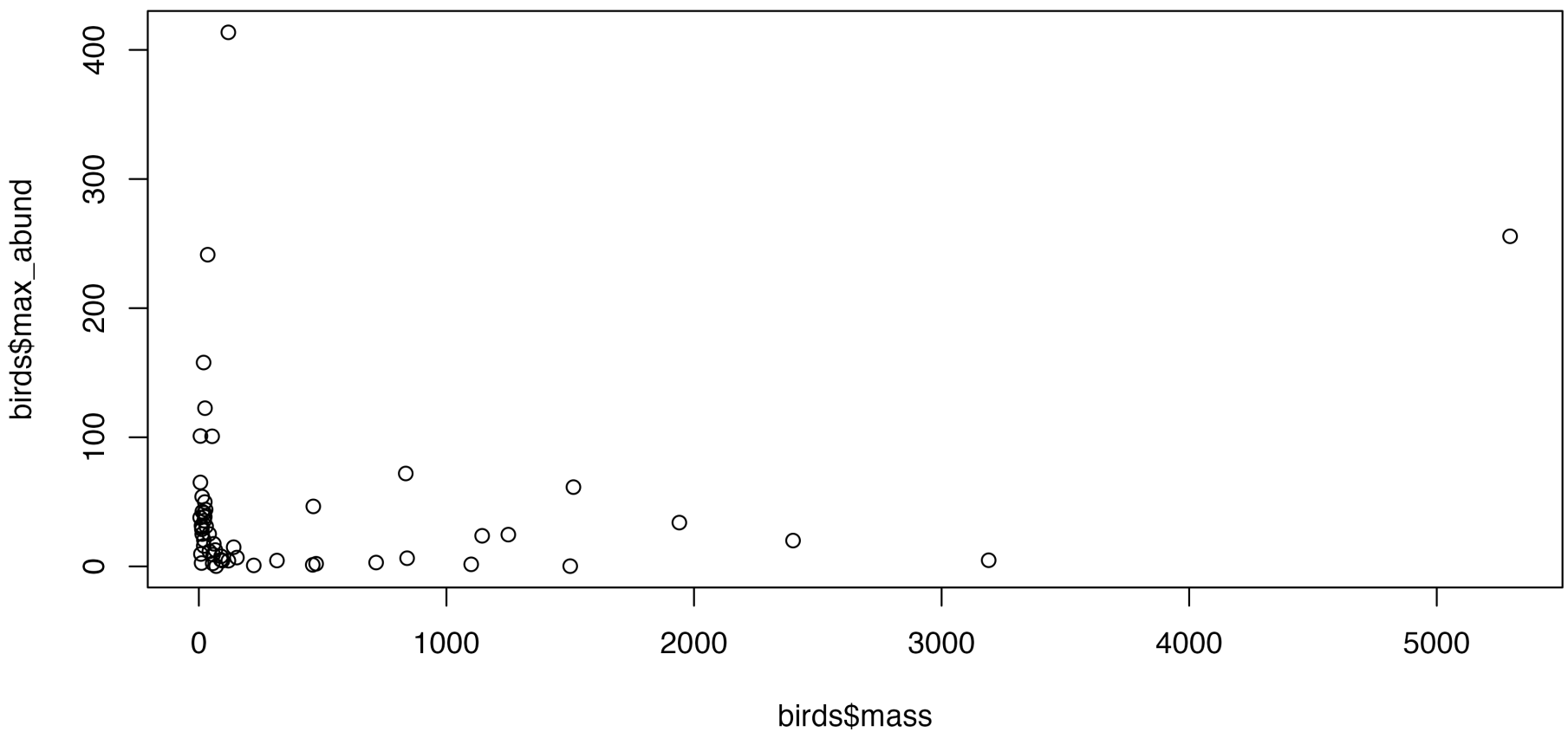
> *For different bird species, the* ***average mass of an individual affects the maximum abundance of the species****, due to ecological constraints (e.g. due to the amount of food sources needed and habitat availability).*

Prediction

> *Species characterized by larger individuals have lower maximum abundance.*

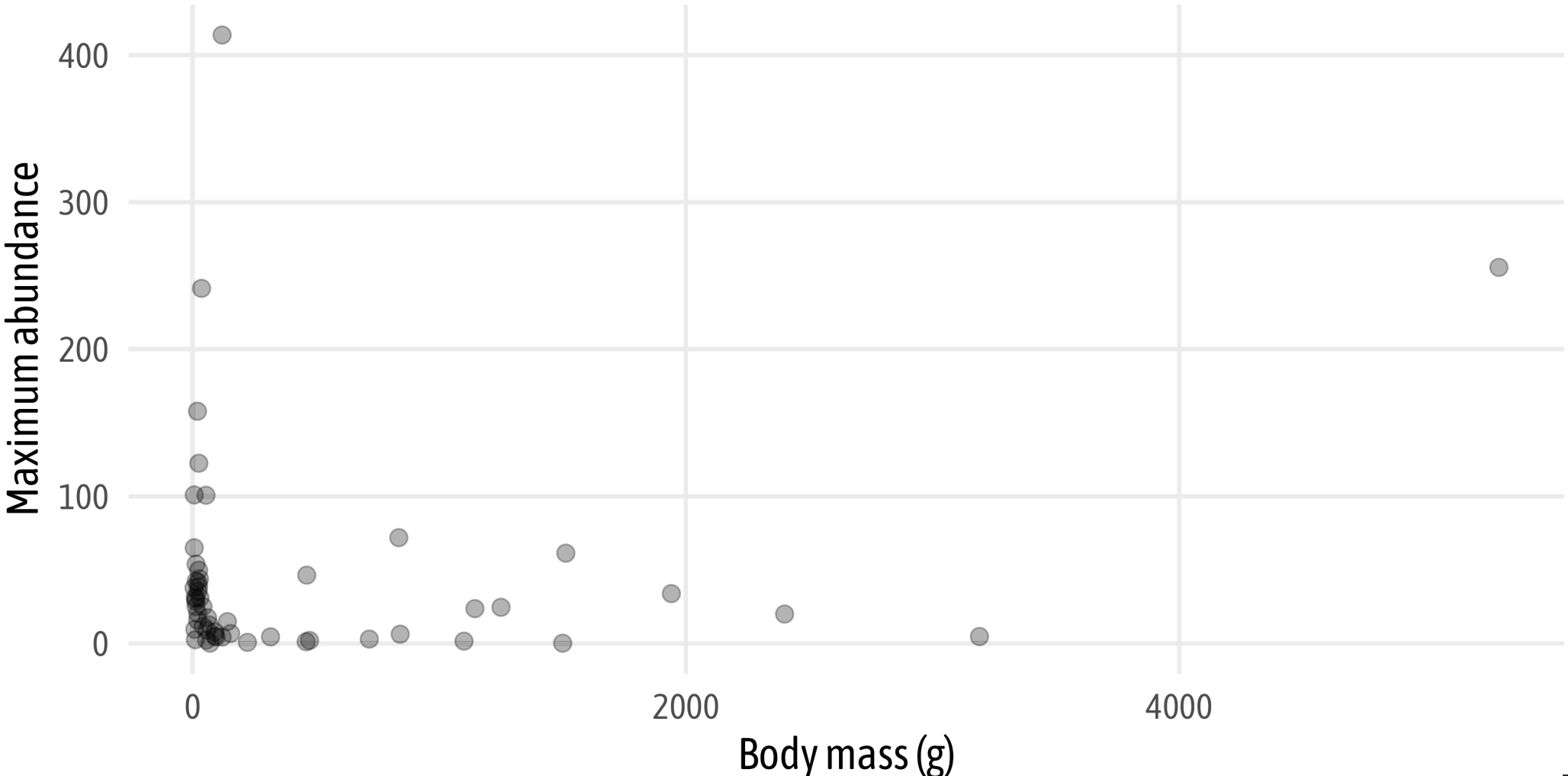
Visual Exploration

```
1 plot(birds$mass, birds$max_abund)
```



Visual Exploration

```
1 (g <- ggplot(birds, aes(x = mass, y = max_abund)) +
2       geom_point(size = 3, alpha = .3) + labs(x = "Body mass (g)", y = "Maximum abundance"))
```



Linear Model (LM)

Linear Models describe a continuous response variable as a function of one or more predictor variables and are also called **linear regression** models.

There are multiple types of LMs (and different names), including:

- **simple LM**: one predictor and one response variable
- **multiple LM**: one predictor and several response variables
- **multivariate LM**: multiple predictors and one or several response variables

Formulation of the Linear Model

In a simple linear model, we define an observation of

- the **response variable `y`** as y_1
  - here: `max_abund` of bird family `i`
- the **predictor `x`** as x_1
  - here: `mass` of bird family `i`

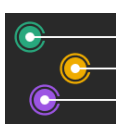
Formulation of the Linear Model

$$y_i = \beta_0 + \beta_1 \times x_i + \varepsilon_i$$

- y_i is the **response variable**
- x_i is the **predictor**
- β_0 is the **intercept**
- β_1 is the **effect of x on y**
- ε_i is the **unexplained variation** (called residual)
- the **predicted value** of y_i is defined as $\hat{y} = \beta_0 + \beta_1 \times x_i$

Formulation of the Linear Model

$$max\_abund_i = \beta_0 + \beta_1 \times mass_i + \varepsilon_i$$



The Residuals

The residuals ε_i must follow a normal distribution.

$$\varepsilon_i \sim \mathcal{N}(0, \sigma^2)$$

- with a mean of $\mathbf{0}$
  - the majority of the residuals have a value close to 0
  - i.e. the error is very small
- with a variance of $\boldsymbol{\sigma^2}$
  - their distribution is symmetrical
  - i.e. the response variable is underestimated as well as overestimated)

The Residuals

Thus, each observation y_i follows a normal distribution.

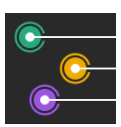
$$y_i \sim \mathcal{N}(\hat{y}, \sigma^2)$$

- with a mean of $\hat{y} = \beta_0 + \beta_1 \times x_i$
- with a variance of σ^2

The Residuals

The residuals must be homoscedastic.

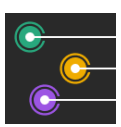
- the error does not change much for different values of the explanatory variables
  - all residuals $\boldsymbol{\varepsilon}$ follow the same distribution
  - the variance $\boldsymbol{\sigma}^2$ remains constant



The Residuals

The residuals must be independent.

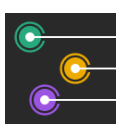
- no missing structure in the model
  - e.g. no presence of temporal or spatial autocorrelation



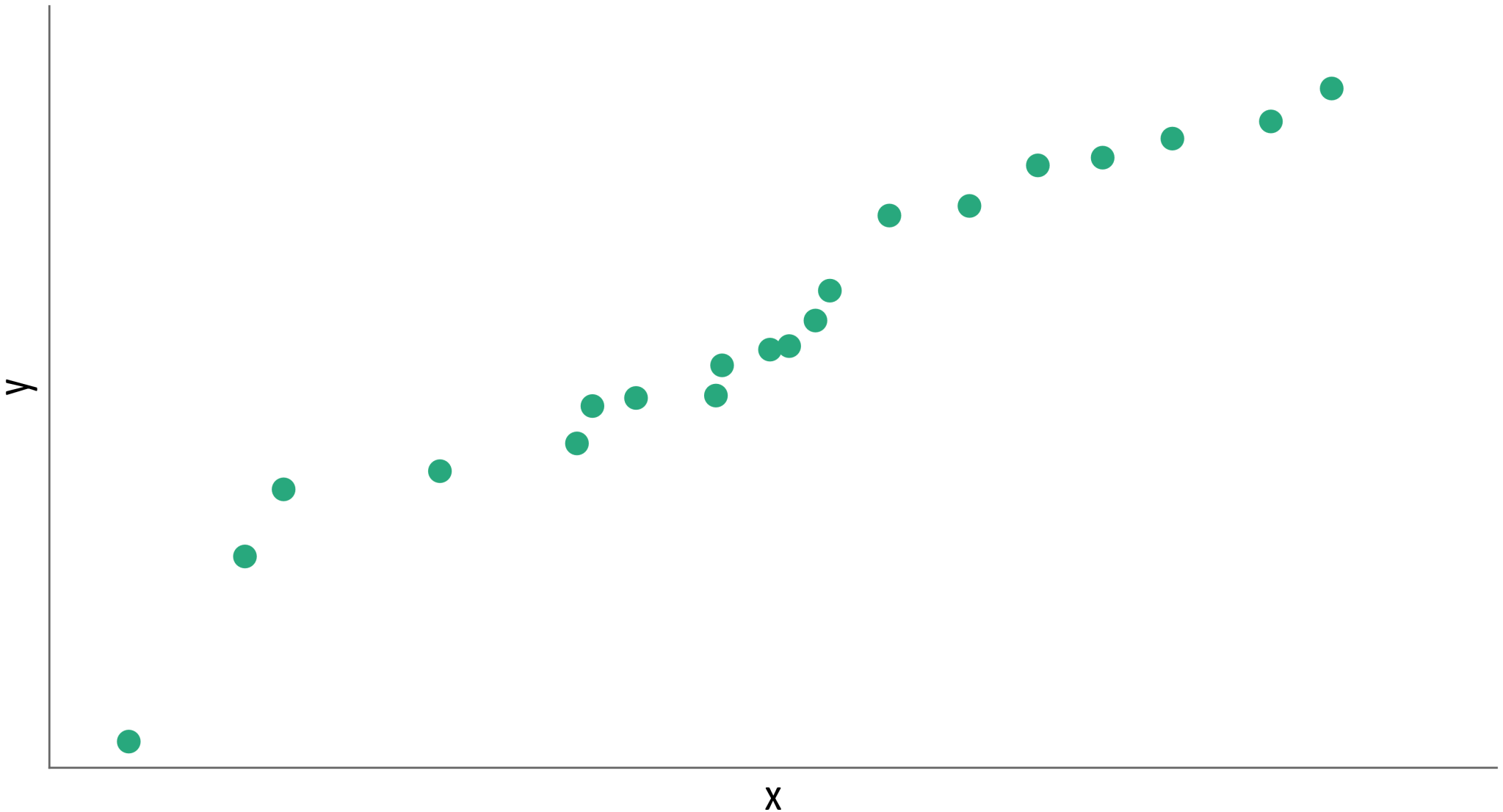
Model Estimation

→ find the "best" estimates of the parameters of the parameters b_0 and b_1.

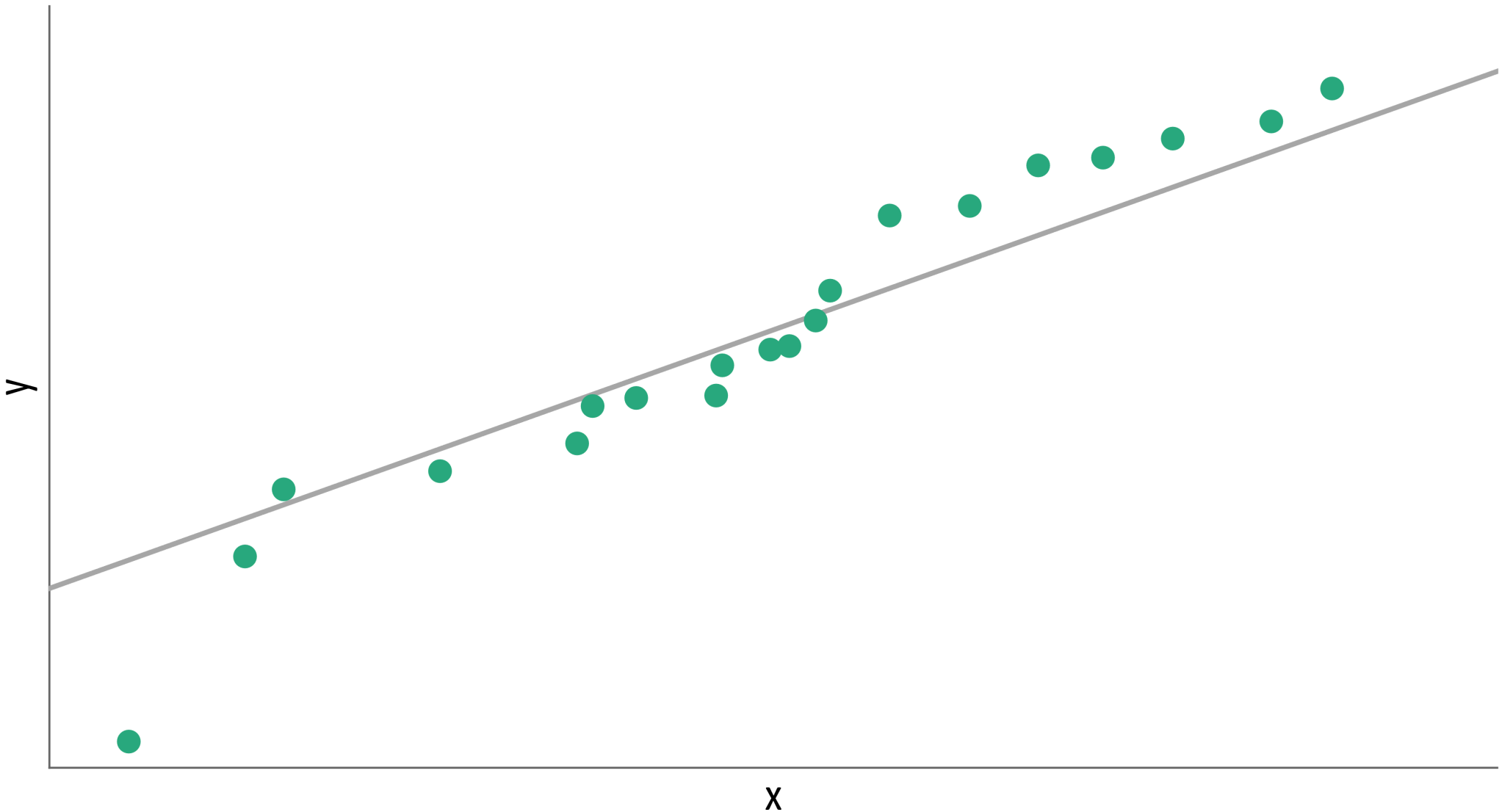
- "best" parameters are those that minimize the variation in the response variable
- the most common method is called **ordinary least squares (OLS)**



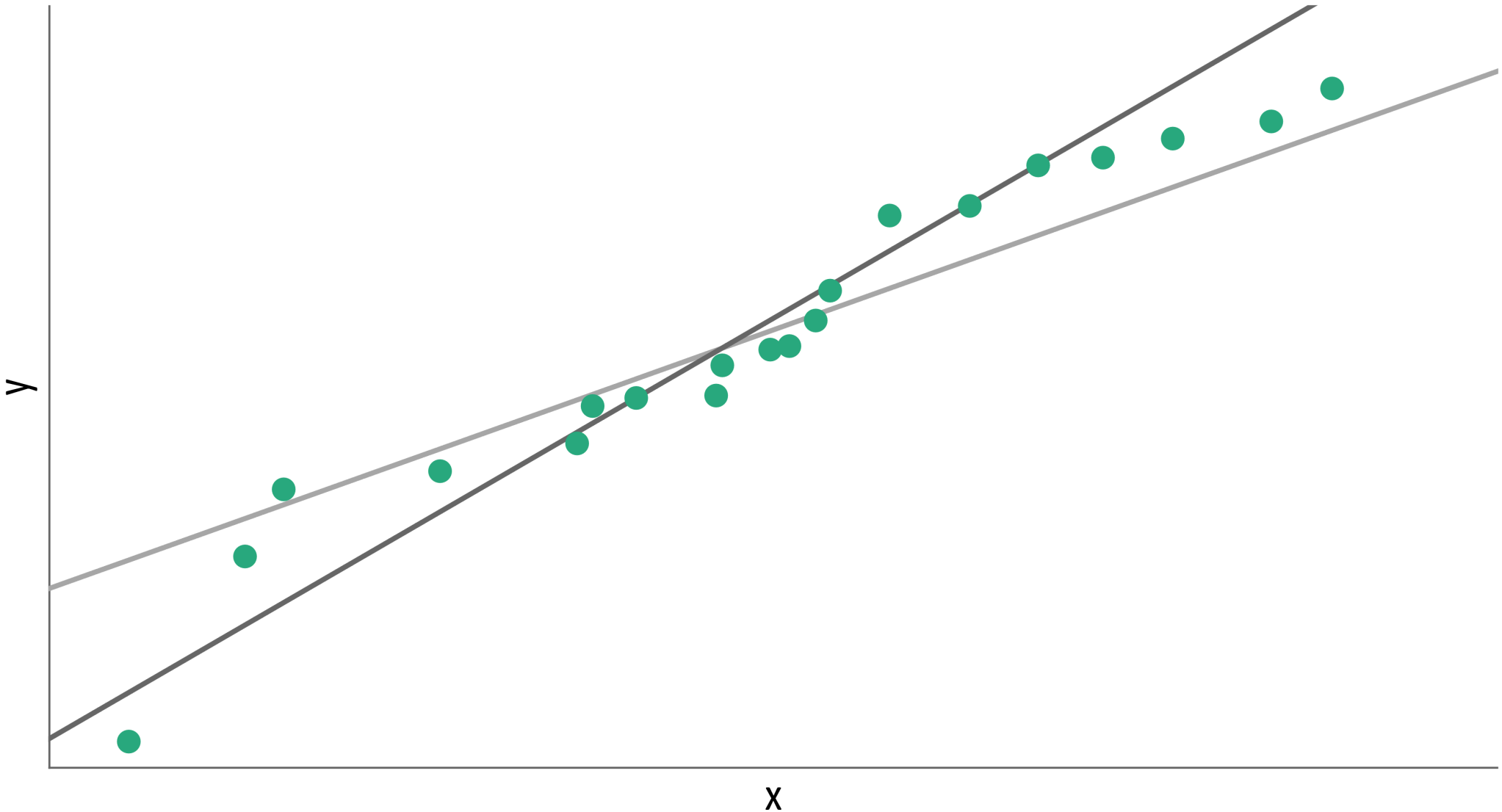
Finding the Best Fit: OLS



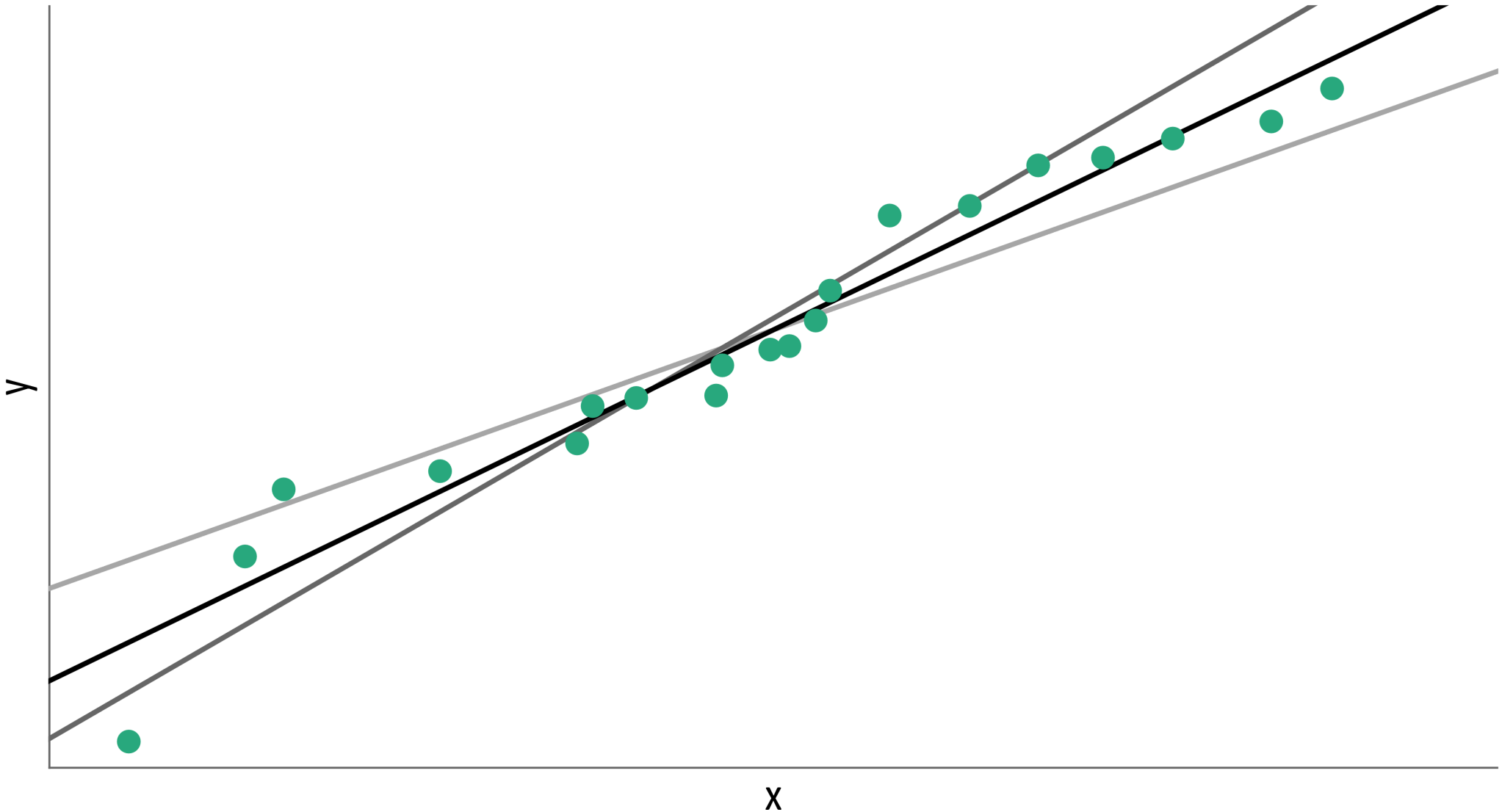
Finding the Best Fit: OLS



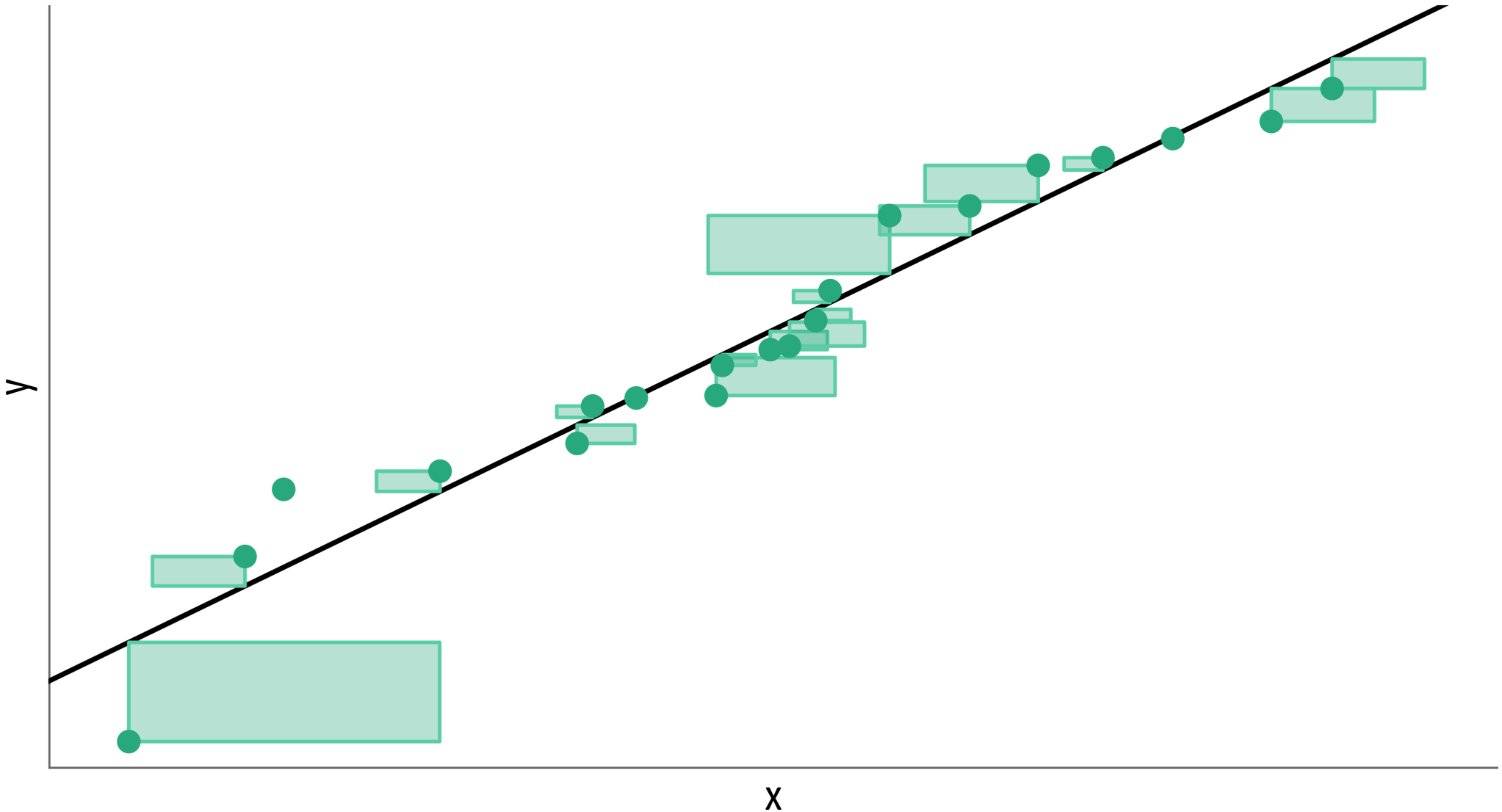
Finding the Best Fit: OLS



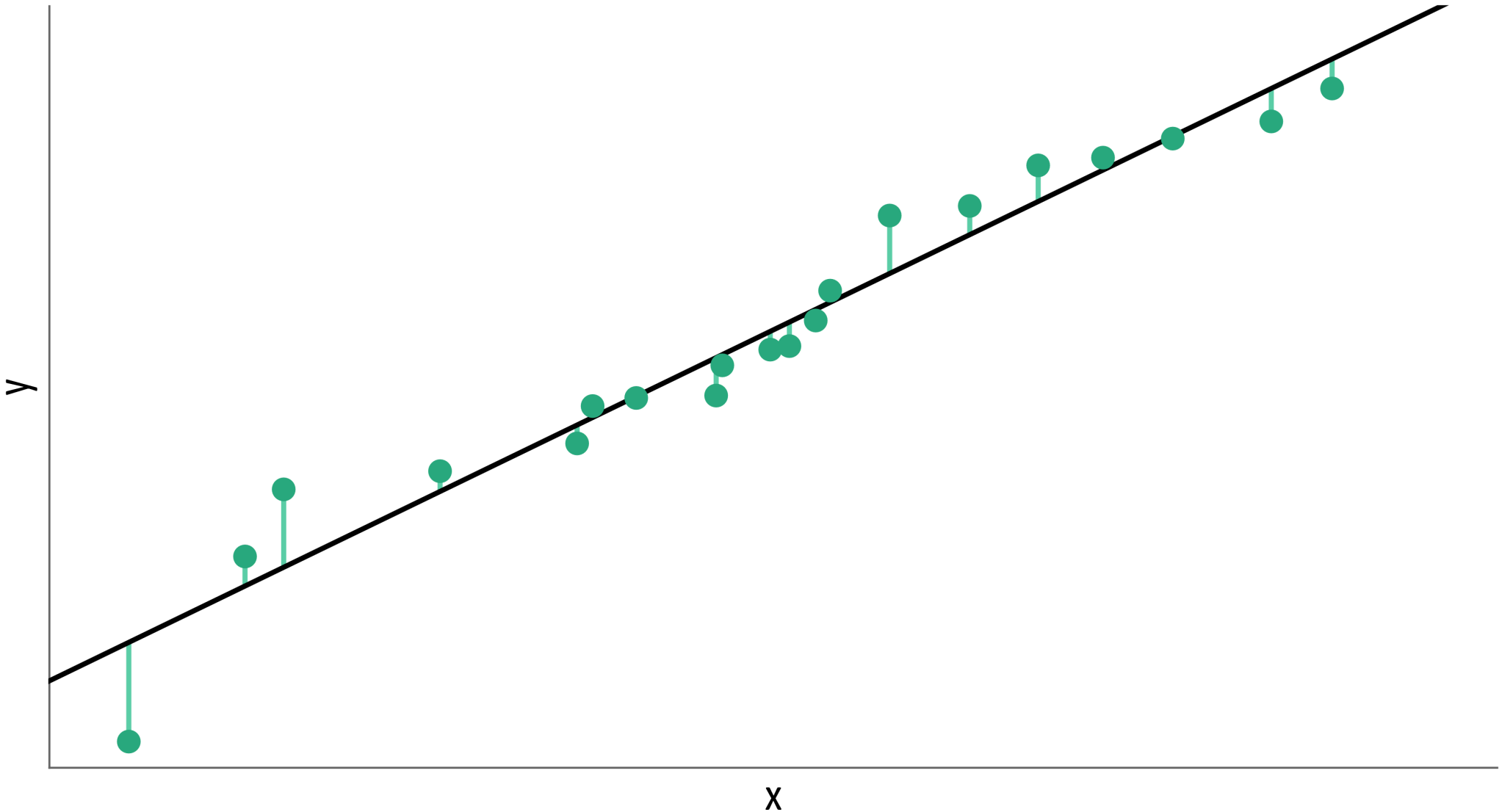
Finding the Best Fit: OLS



Finding the Best Fit: OLS

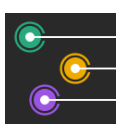


Finding the Best Fit: OLS



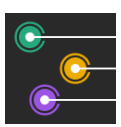
Formulation of the Linear Model

$$y_i = \beta_0 + \beta_1 \times x_i + \varepsilon_i$$
$$with \;\; \varepsilon_i \sim \mathcal{N}(0, \sigma^2)$$



Formulation of the Linear Model

$$max\_abund_i = \beta_0 + \beta_1 \times mass_i + \varepsilon_i$$
$$with \;\; \varepsilon_i \sim \mathcal{N}(0, \sigma^2)$$

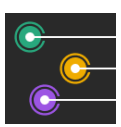


Formulation of the Linear Model

In R, the model formula is way less complex—it's simply

```
max_abund ~ mass
```

with the response variable on the left and the predictor variable(s) on the right



Formulate and Run the Model

The `lm()` command is used to fit a linear model:

```
1  lm_birds <- lm(max_abund ~ mass, data = birds)
```

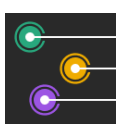
where the first argument is the model formula and the second is the input data.

Examine the Model Output

By printing the `lm_birds` object, we can inspect the parameter estimates:

```
1  lm_birds
```

```
Call:
lm(formula = max_abund ~ mass, data = birds)

Coefficients:
(Intercept)         mass
   38.16646      0.01439
```

Examine the Model Output

We can retrieve a more informative output of the model with `summary()`:

```
1  summary(lm_birds)
```

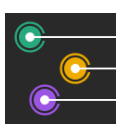
```
Call:
lm(formula = max_abund ~ mass, data = birds)

Residuals:
   Min     1Q Median     3Q    Max
-79.30 -35.39 -22.06   2.62 373.72

Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept) 38.16646   11.09065   3.441  0.00115 **
mass         0.01439    0.01059   1.358  0.18021
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 72.89 on 52 degrees of freedom
Multiple R-squared:  0.03427,   Adjusted R-squared:  0.0157
F-statistic: 1.845 on 1 and 52 DF,  p-value: 0.1802
```


Examine the Model Output

We can also retrieve the **"Analysis of Variance"** table with `anova()`:

```
1 anova(lm_birds)
```

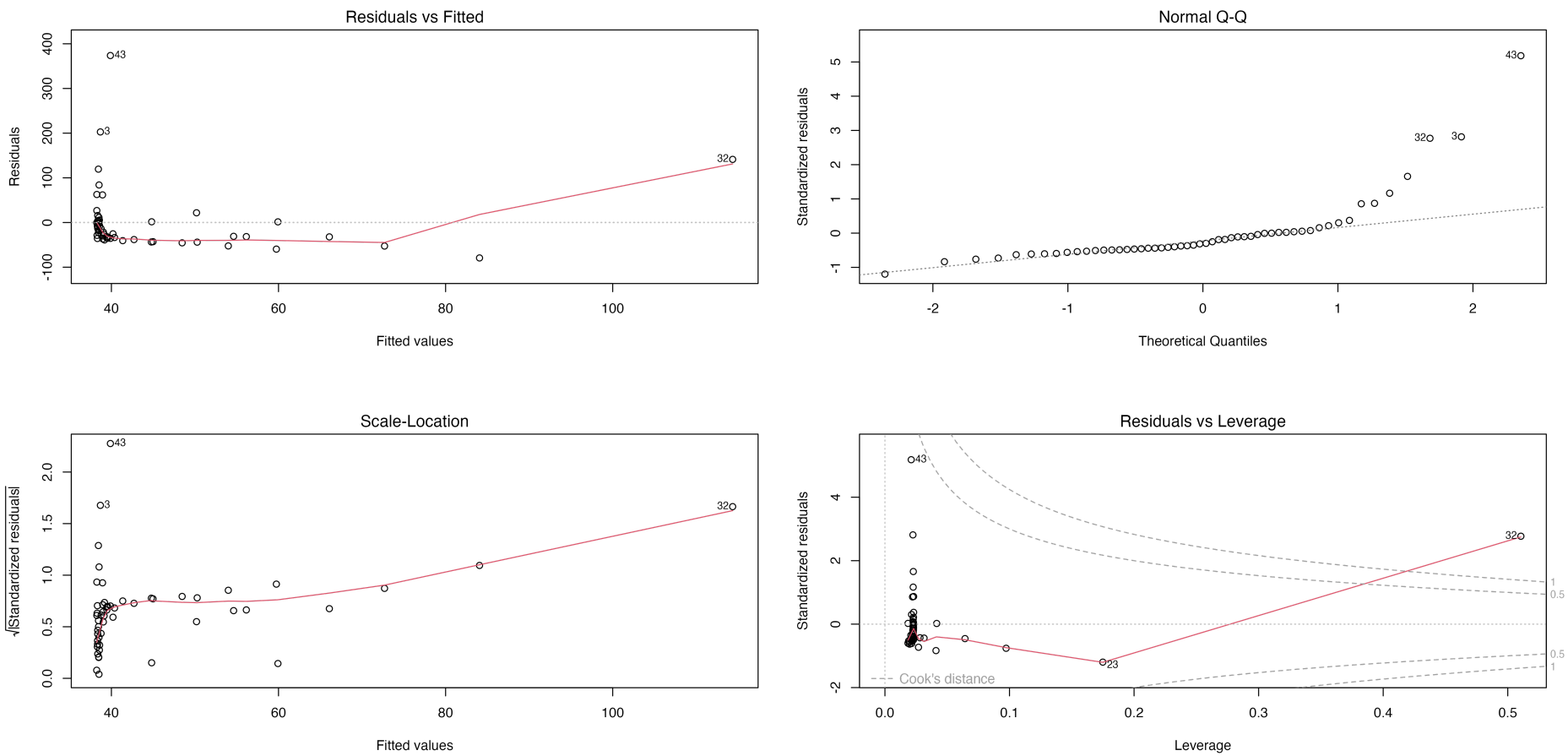
```
Analysis of Variance Table

Response: max_abund
          Df Sum Sq Mean Sq F value Pr(>F)
mass       1   9803  9803.3  1.8452 0.1802
Residuals 52 276273  5313.0
```

Verify Assumptions for LM

To check if the residuals do not violate the four basic assumptions, we can retrieve diagnostic plots via `plot(lm_birds)`:

```
1  plot(lm_birds)
```



Diagnostic Plot 1: Residuals vs Fitted

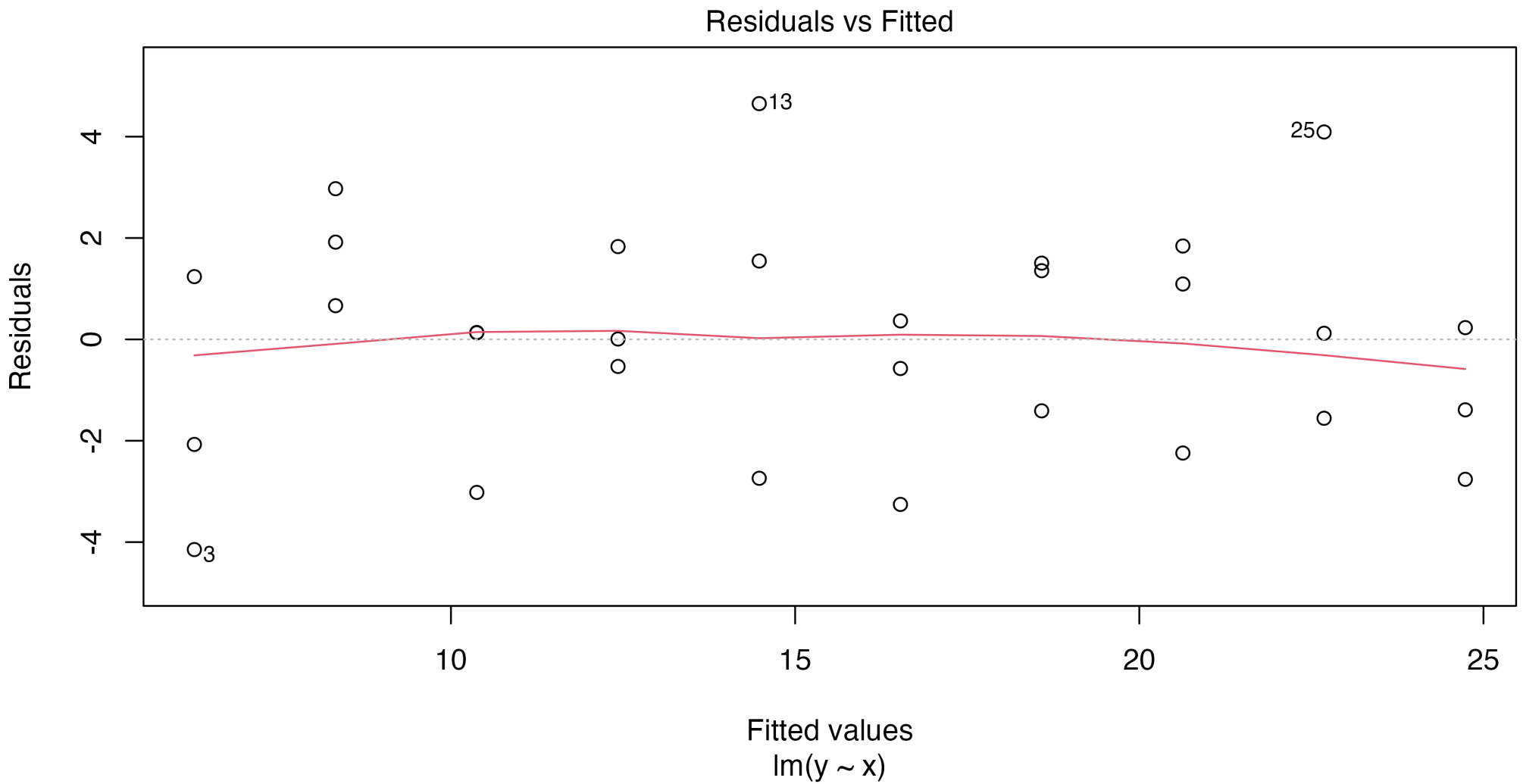
What the plot shows:

- **distribution of the residuals versus predicted values**
  - point show the distance between the response variable and the model prediction
  - allows to check the **independence of the residuals and their distribution**

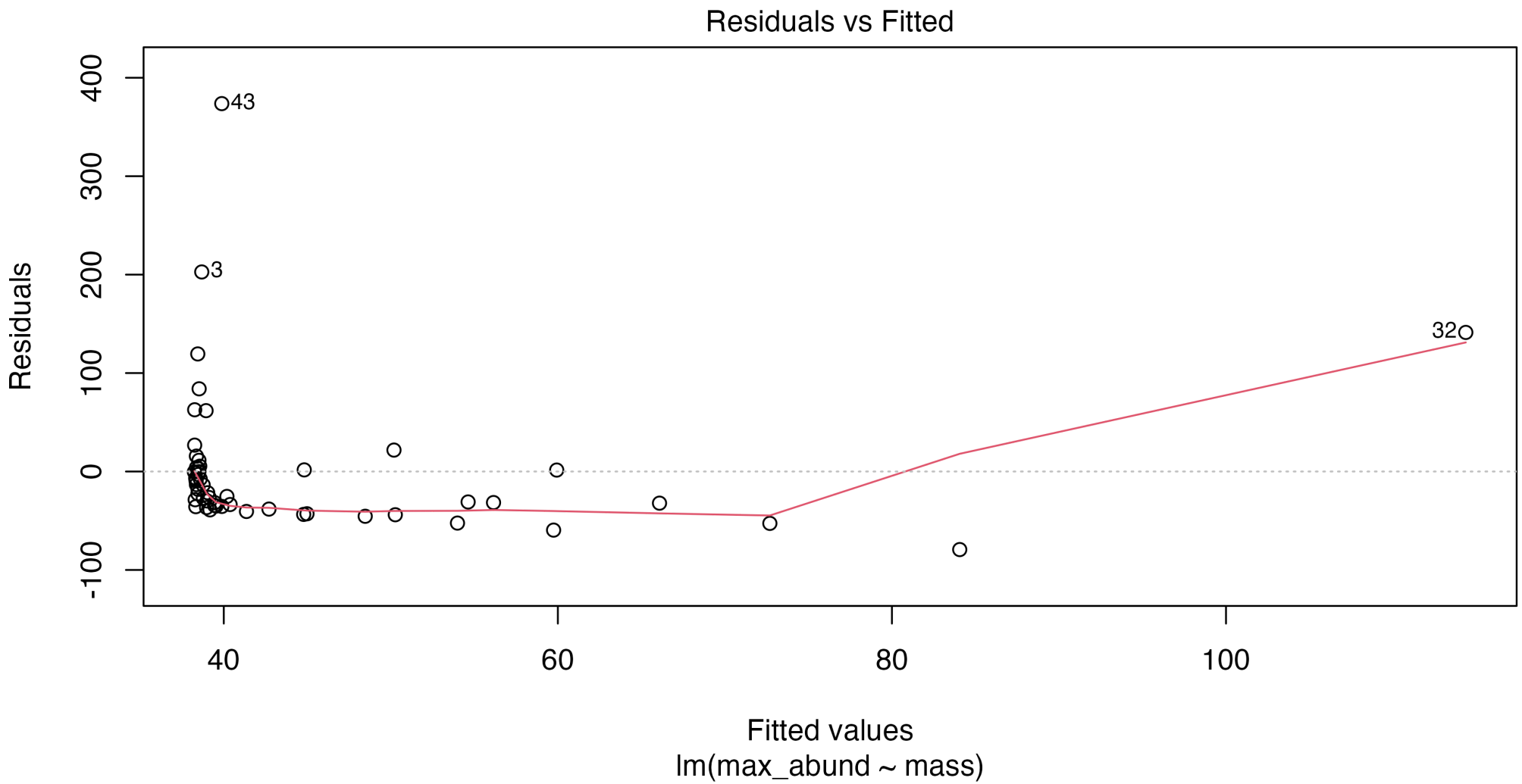
What we want to see:

- **no dispersion of the points → homoscedasticity**
  - randomly scattered points across fitted values
  - a horizontal red line around a value of 0

Diagnostic Plot 1: Residuals vs Fitted

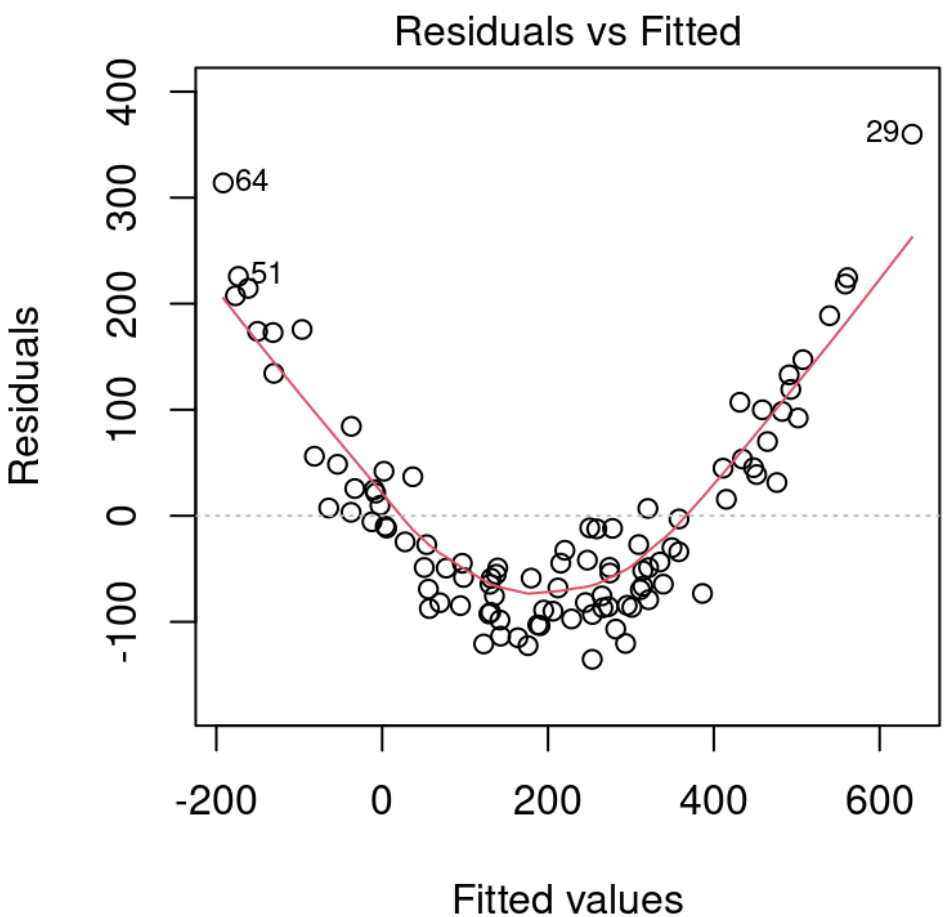


Diagnostic Plot 1: Residuals vs Fitted

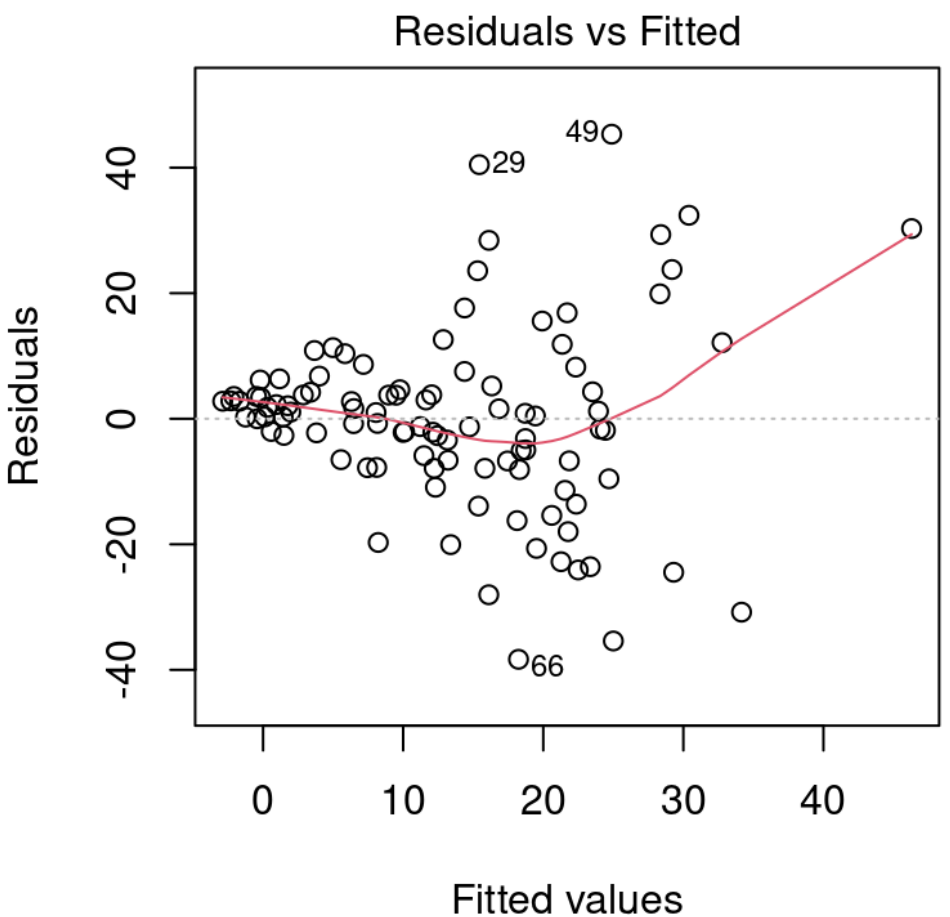


Diagnostic Plot 1: Residuals vs Fitted

Nonlinear



Heteroscedastic



Source: Quebec Centre for Biodiversity Science

Diagnostic Plot 2: Normal Q-Q

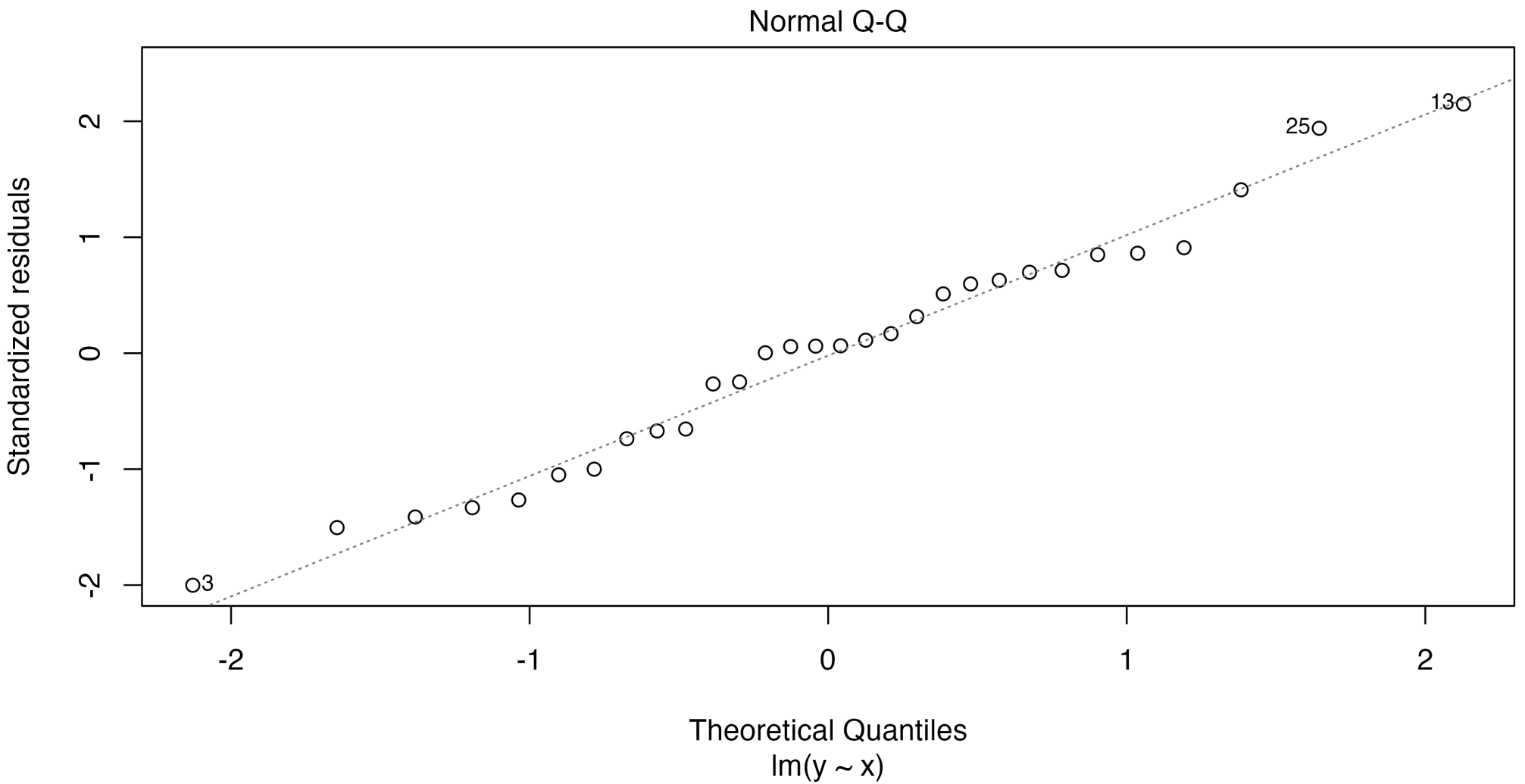
What the plot shows:

- **distribution of the residuals versus quantiles of a Normal distribution**
  - points show the distance between normally distributed values and the model prediction
  - allows to check the **if the distribution of residuals can be considered normaly distributed**

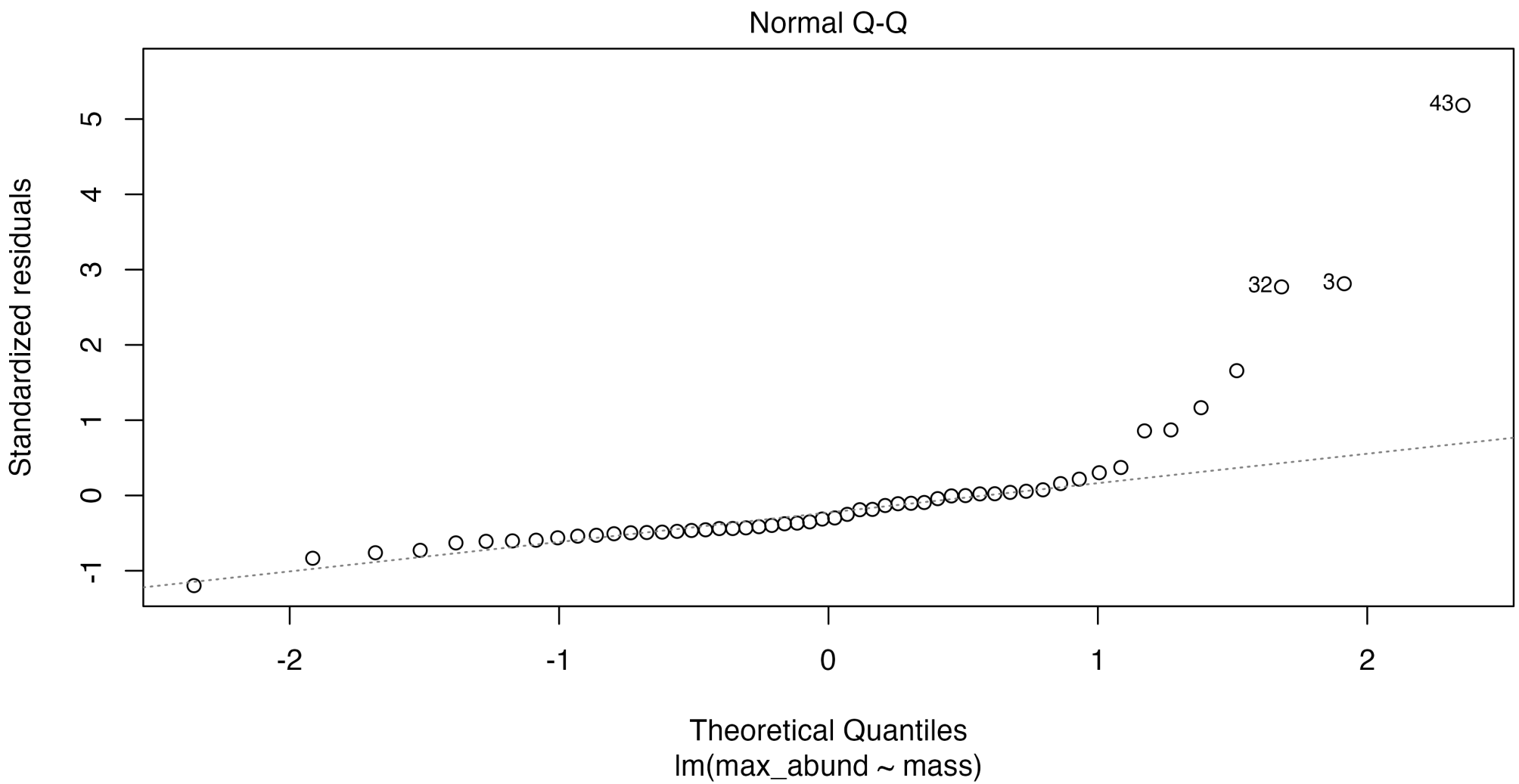
What we want to see:

- **a 1:1 relationship → normal distribution**
  - the points fall on or close to the grey line

Diagnostic Plot 2: Normal Q-Q



Diagnostic Plot 2: Normal Q-Q



Test for Normality

A formal statistical test to check the assumption of normally distributed residuals is the **Shapiro-Wilk test**.

```
1  shapiro.test(residuals(lm_birds))
```

```
    Shapiro-Wilk normality test

data:  residuals(lm_birds)
W = 0.64158, p-value = 3.172e-10
```

Null hypothesis: values follow a normal distribution

→ We accept H_a. The residuals are not distributed normally.

Diagnostic Plot 3: Scale Location

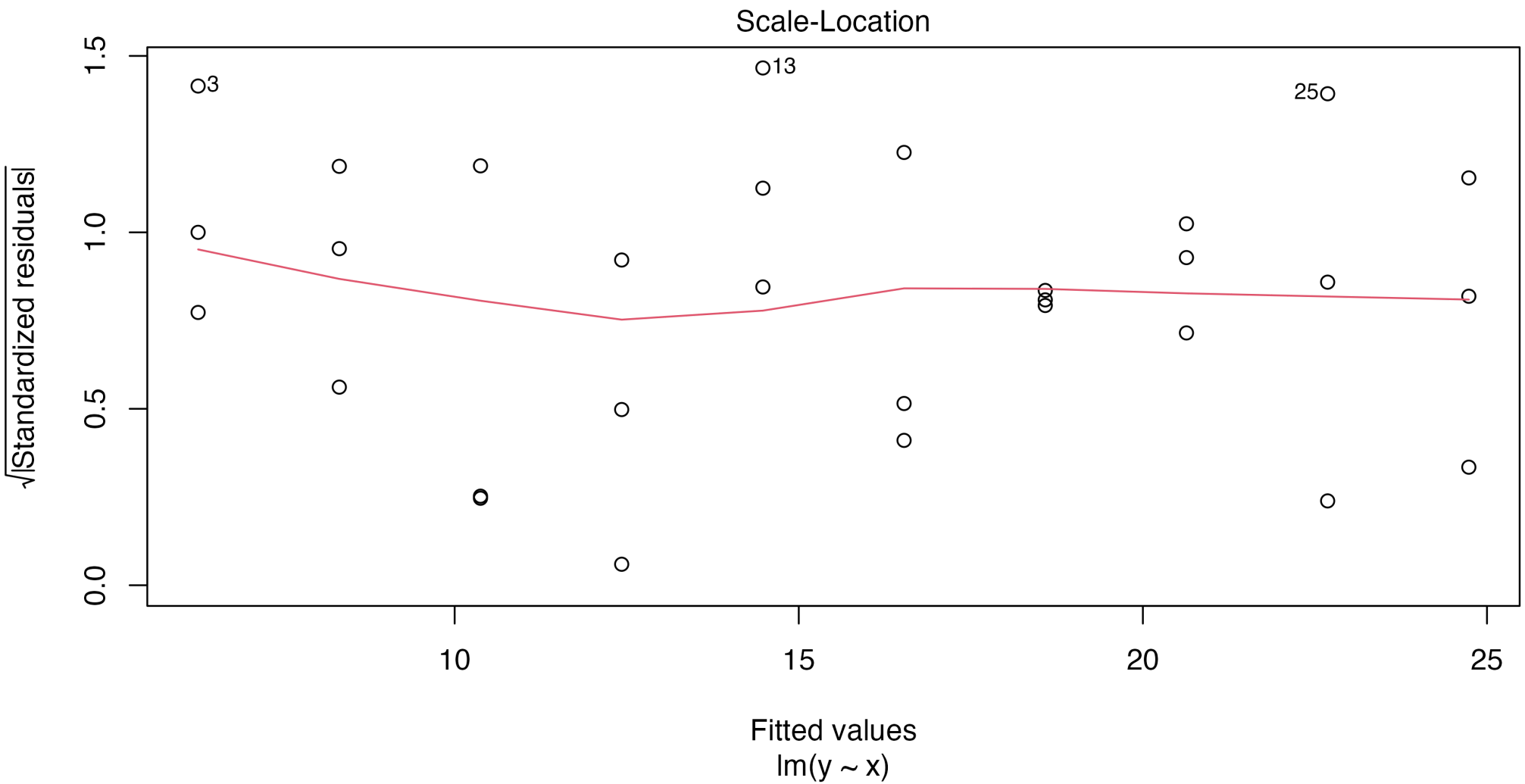
What the plot shows:

- **distribution of the square-rooted residuals versus predicted values**
  - points show the distance between the response variable and the model prediction
  - allows to check the **dispersion of the residuals**

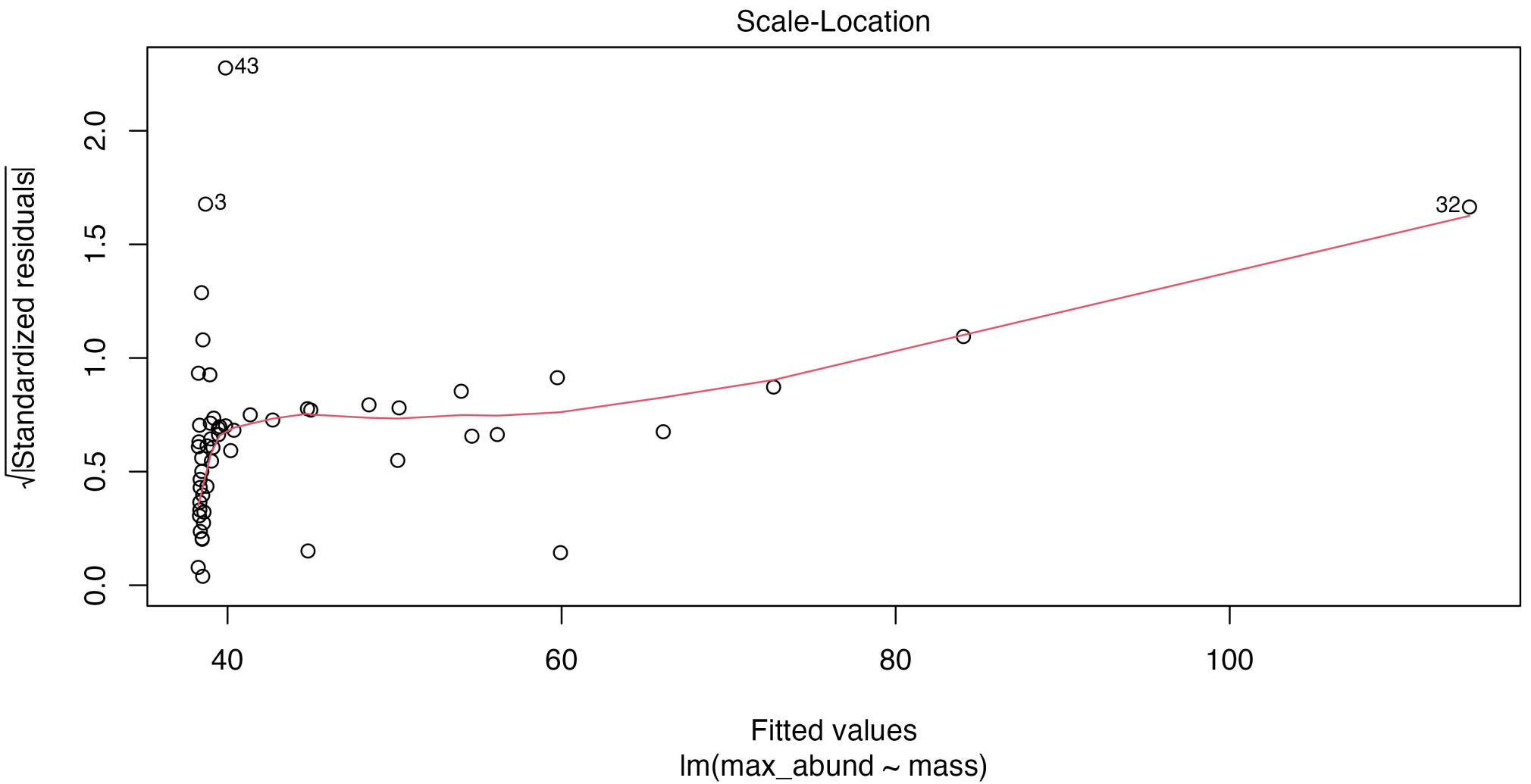
What we want to see:

- **no trends → evenly distributed predictor**
  - randomly scattered points across fitted values
  - a flat red line

Diagnostic Plot 3: Scale Location



Diagnostic Plot 3: Scale Location



Test for Homoscedasticity

A formal statistical test to check the assumption of homoscedasticity is the **Breusch-Pagan test**.

```
1 # install.packages("lmtest")
2 lmtest::bptest(lm_birds)
```

```
    studentized Breusch-Pagan test

data:  lm_birds
BP = 0.096381, df = 1, p-value = 0.7562
```

Null hypothesis: homoscedasticity

→ Our model does not meet the assumption of homoscedasticity.

Diagnostic Plot 4: Residuals vs Leverage

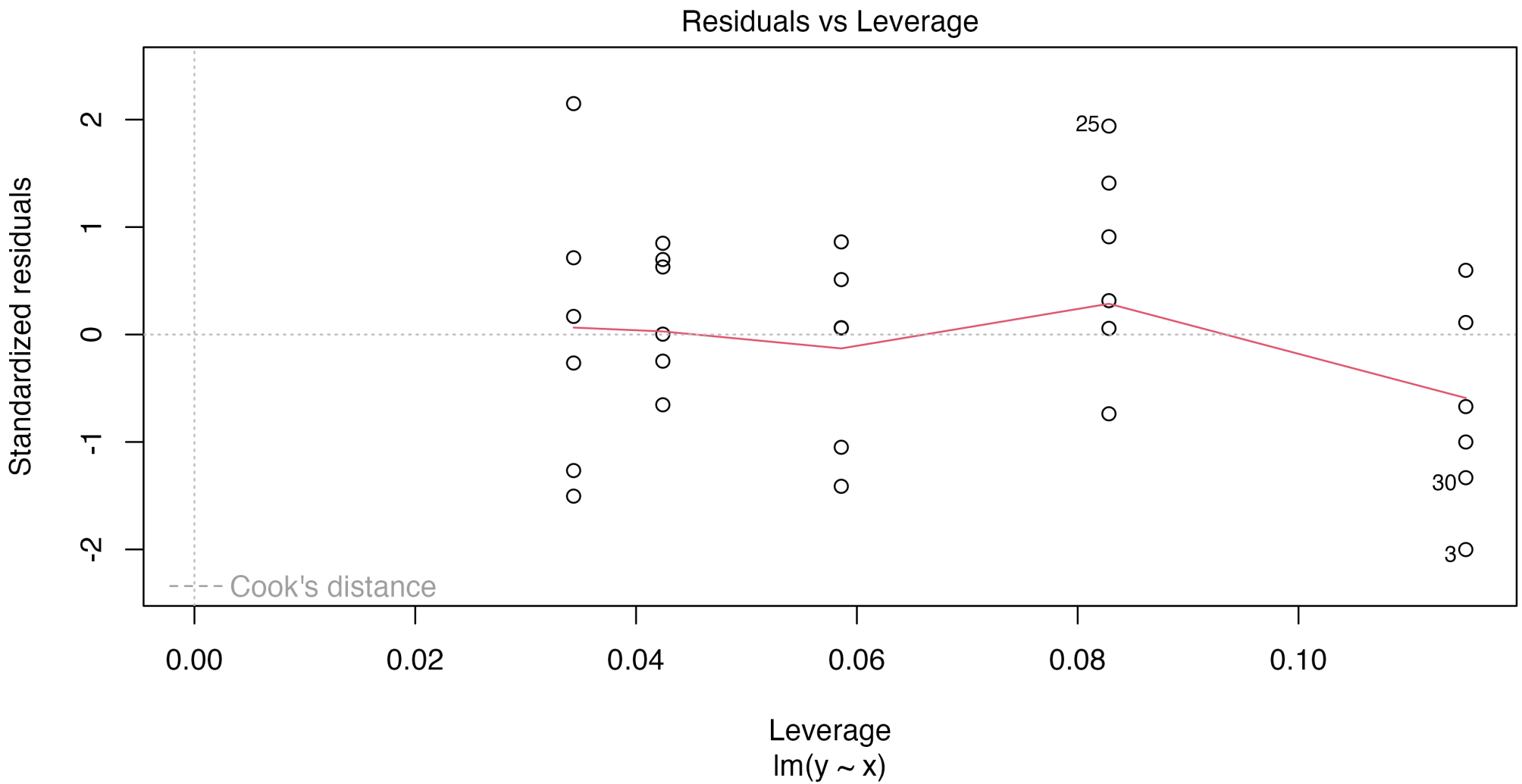
What the plot shows:

- **distribution of the residuals versus leverage**
  - leverage refers to the extent to which the coefficients would change if a particular observation was removed
  - allows to check **if certain values have a strong(er) influence**

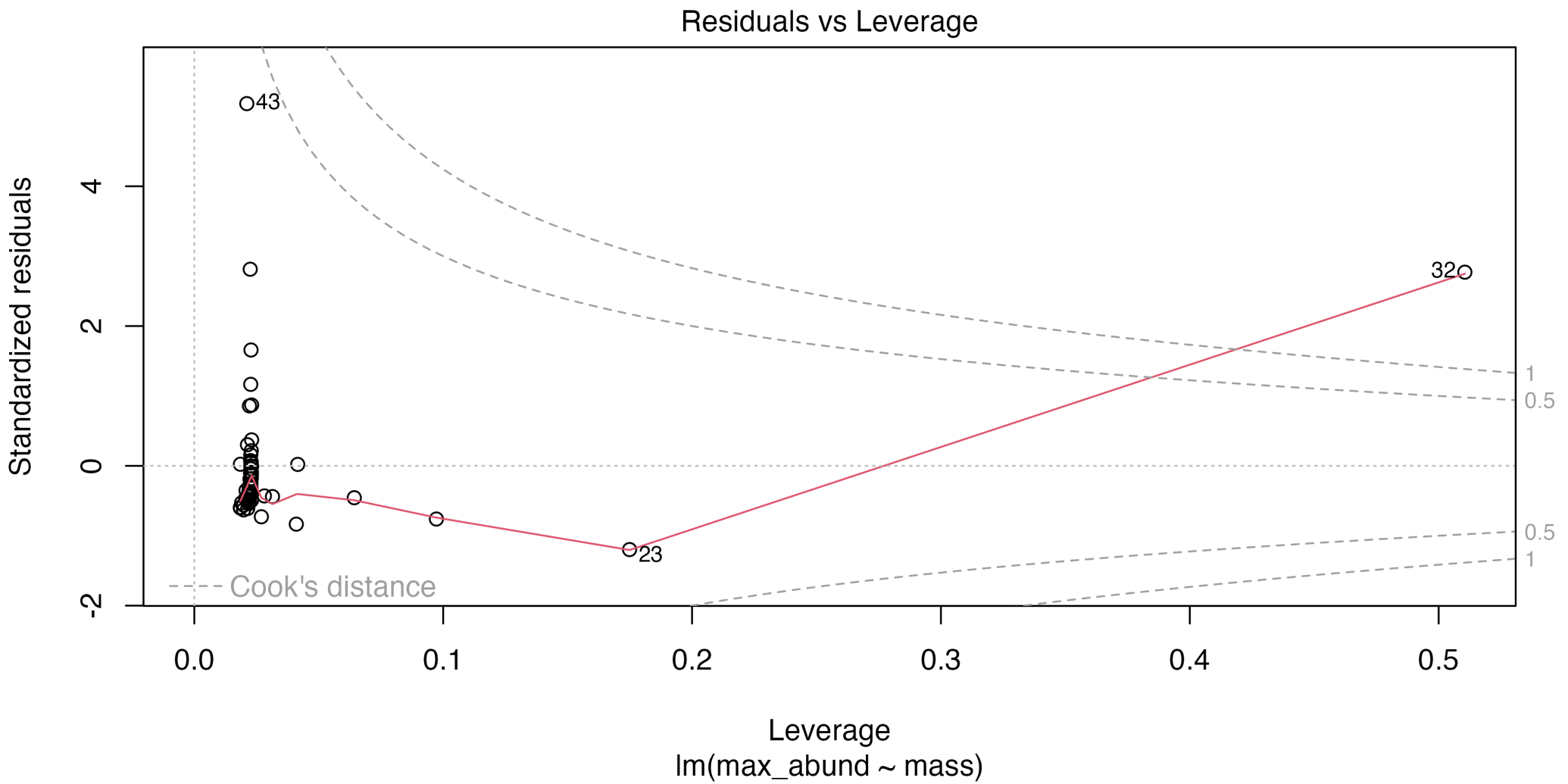
What we want to see:

- **no influential obervations → homoscedastic residuals**
  - points inside of *Cook's distance*
  - especially no outliers for high values of leverage

Diagnostic Plot 4: Residuals vs Leverage

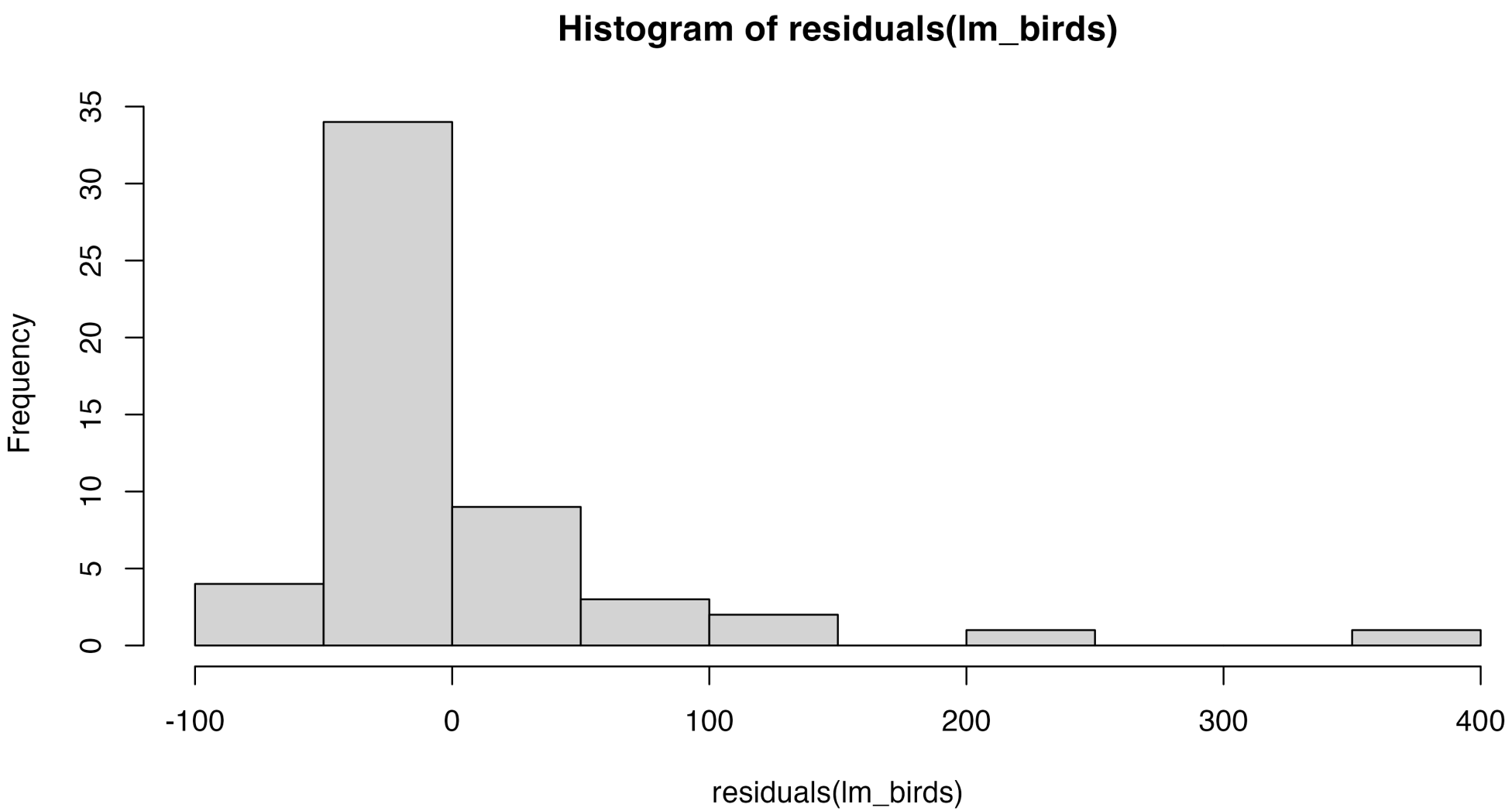


Diagnostic Plot 4: Residuals vs Leverage



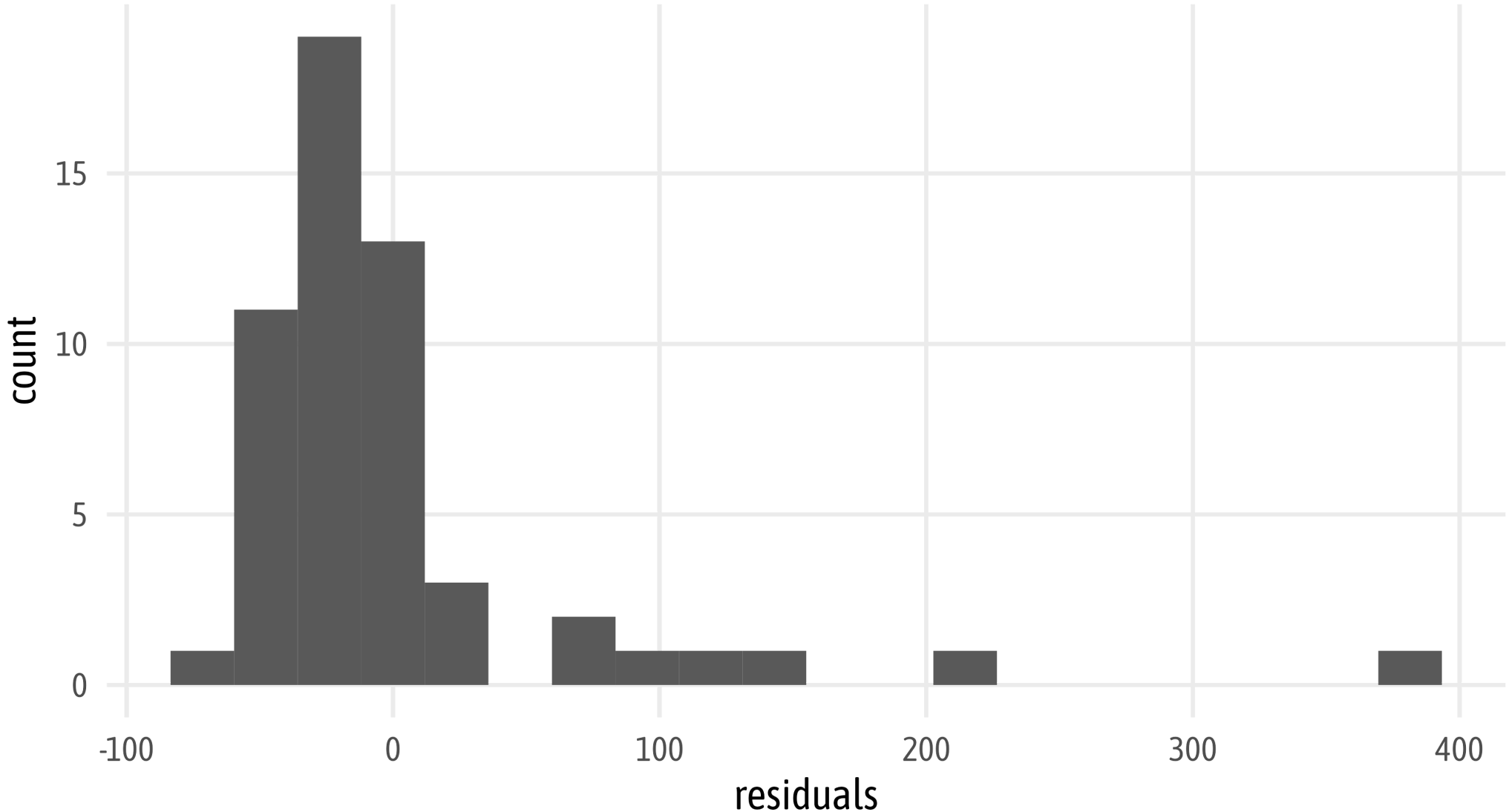
Assumptions Not Met—What's Wrong?

```
1 hist(residuals(lm_birds))
```



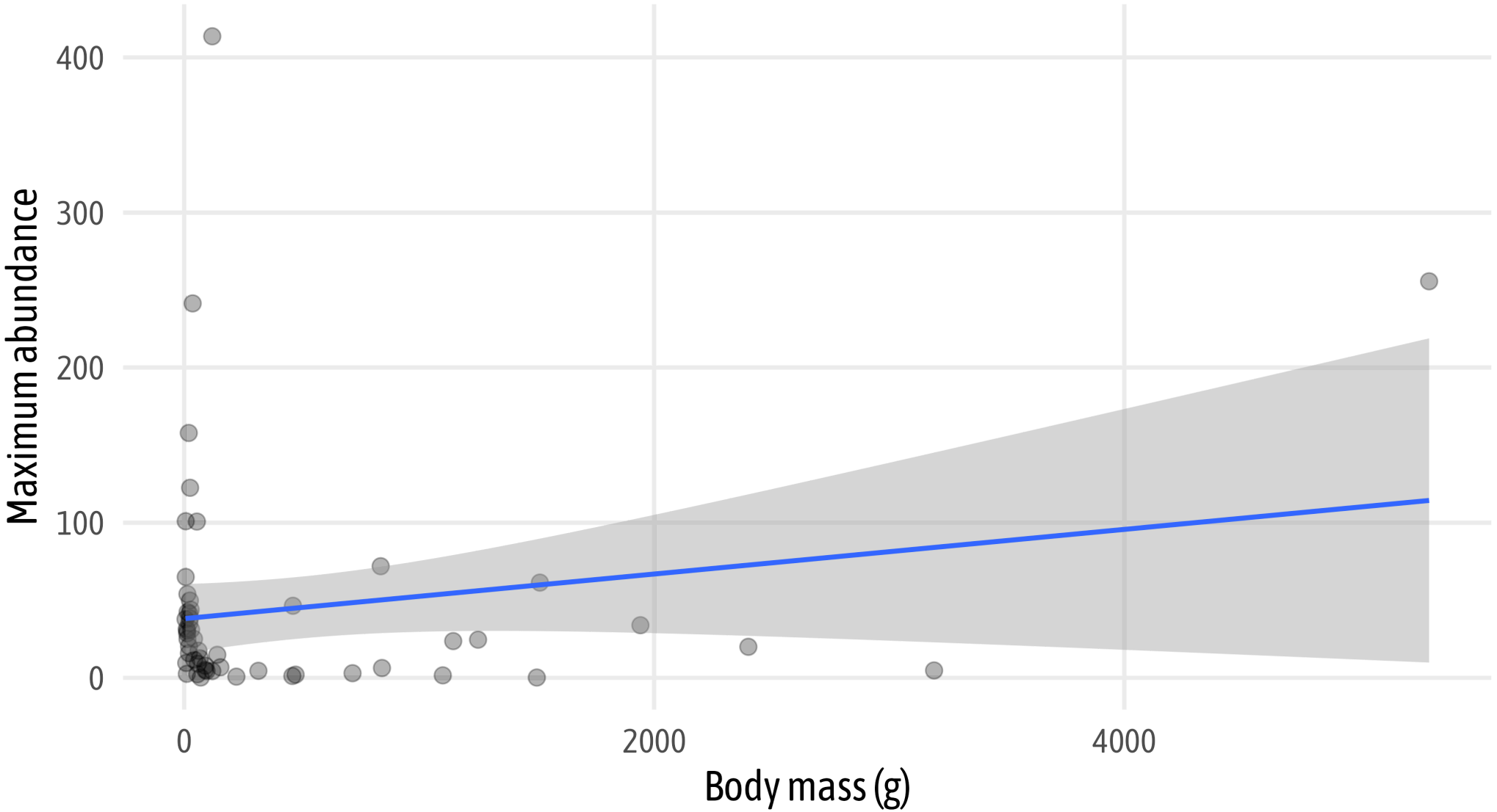
Assumptions Not Met—What's Wrong?

```
1  ggplot(tibble(residuals = residuals(lm_birds)), aes(x = residuals)) + geom_histogram(bins = 20)
```



Assumptions Not Met—What's Wrong?

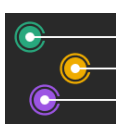
```
1  g + stat_smooth(method = "lm")
```



Assumptions Not Met—What Now?

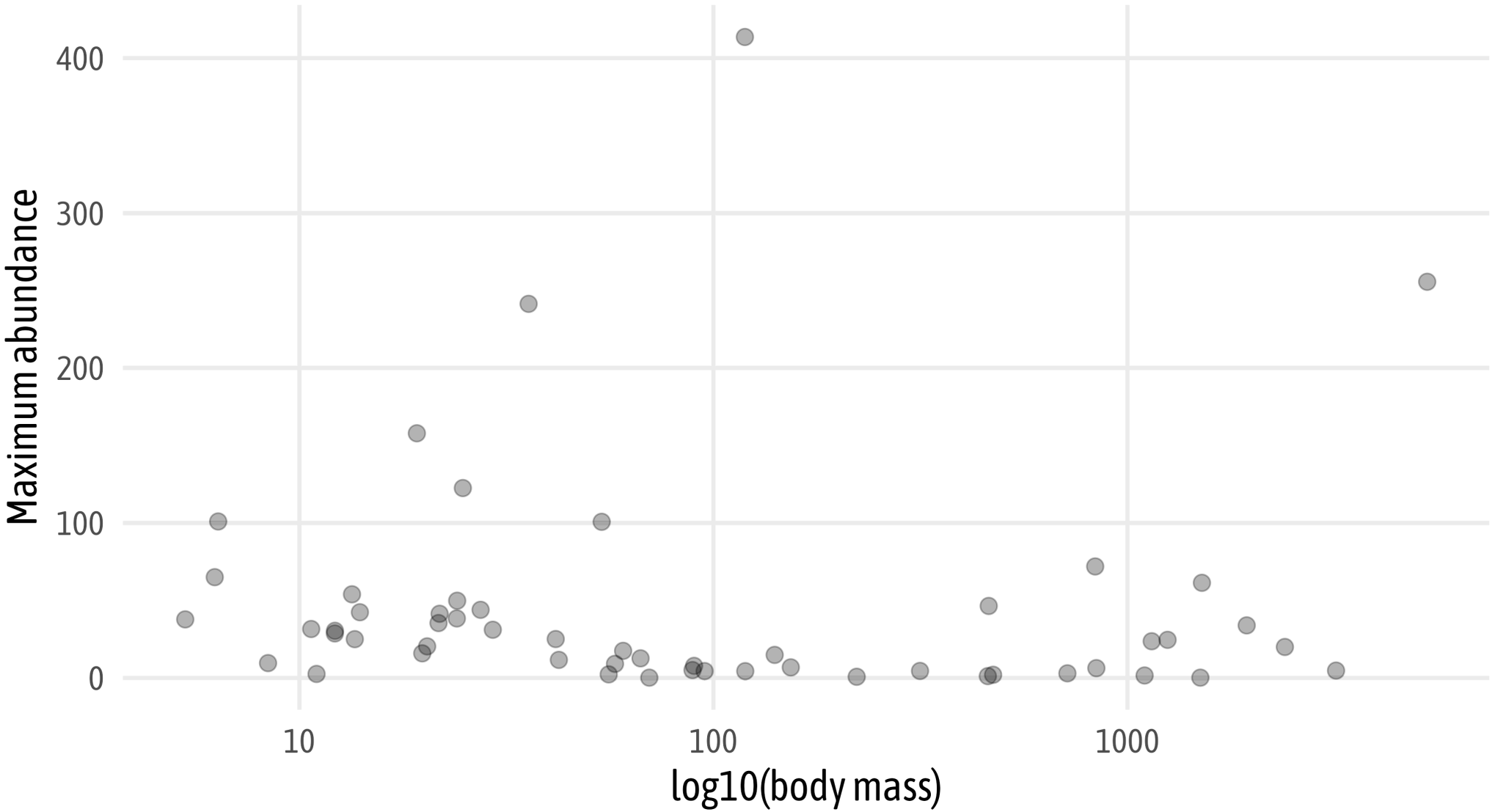
Potential Solutions:

- use a different model approach, e.g. a generalized linear model (GLM)
- transformation of the response and/or predictor variable(s)
  - transforming variables and interpreting the results is often tricky in practice



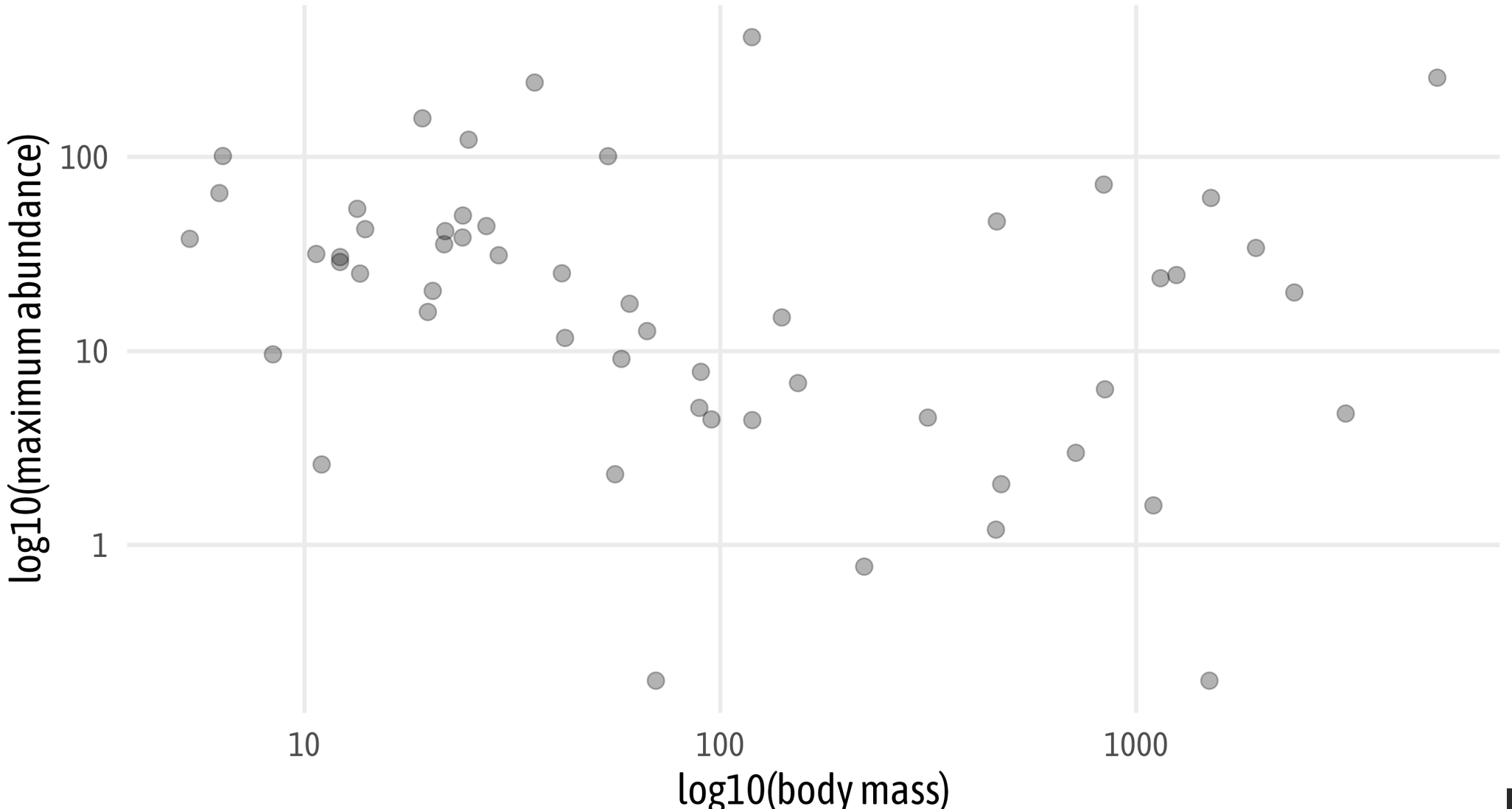
Transform the Variables (Visually)

```
1  g + scale_x_log10(name = "log10(body mass)")
```



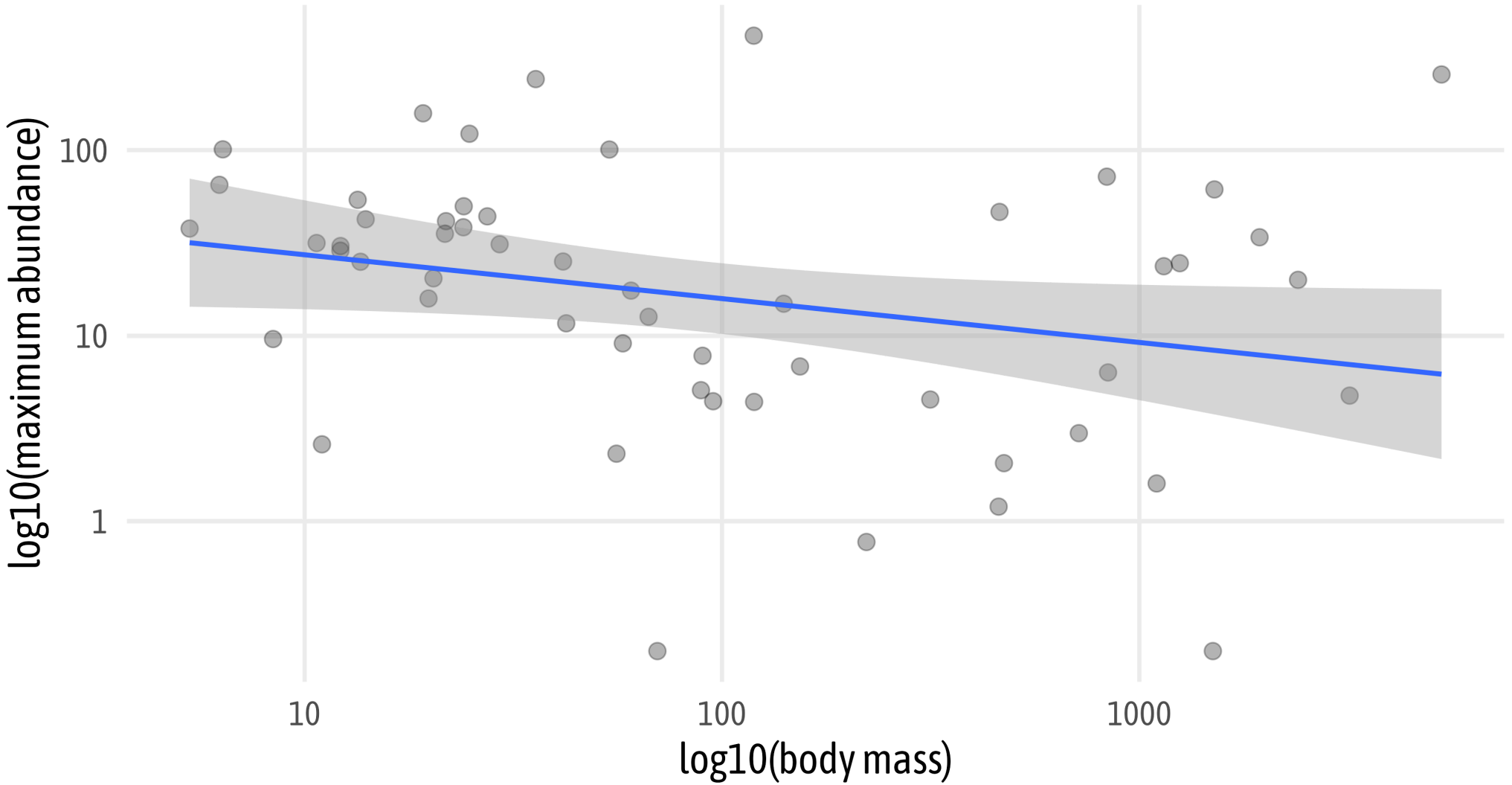
Transform the Variables (Visually)

```
1  g + scale_x_log10(name = "log10(body mass)") + scale_y_log10(name = "log10(maximum abundance)")
```



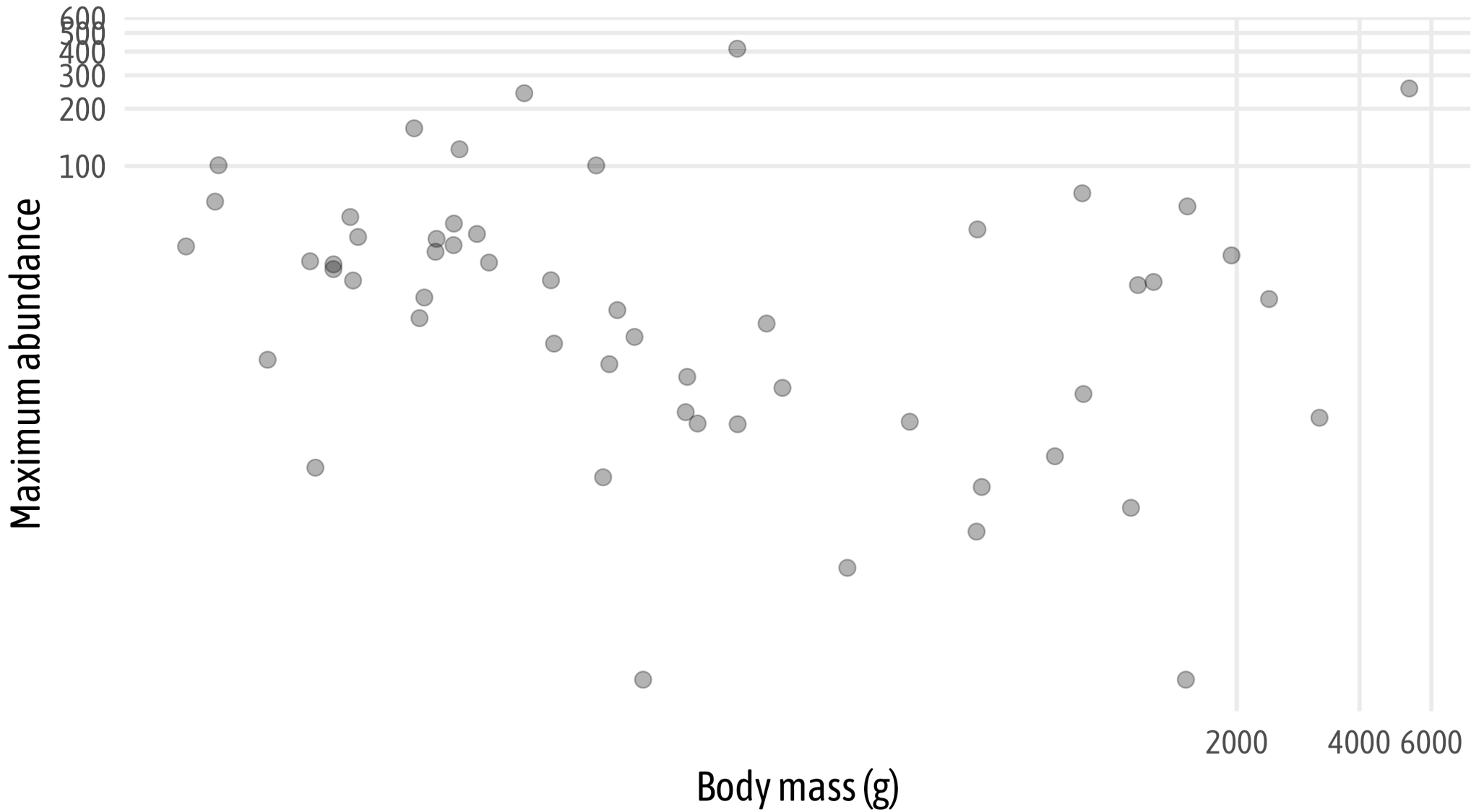
Transform the Variables (Visually)

```
1  g + scale_x_log10(name = "log10(body mass)") + scale_y_log10(name = "log10(maximum abundance)") +
2    stat_smooth(method = "lm")
```



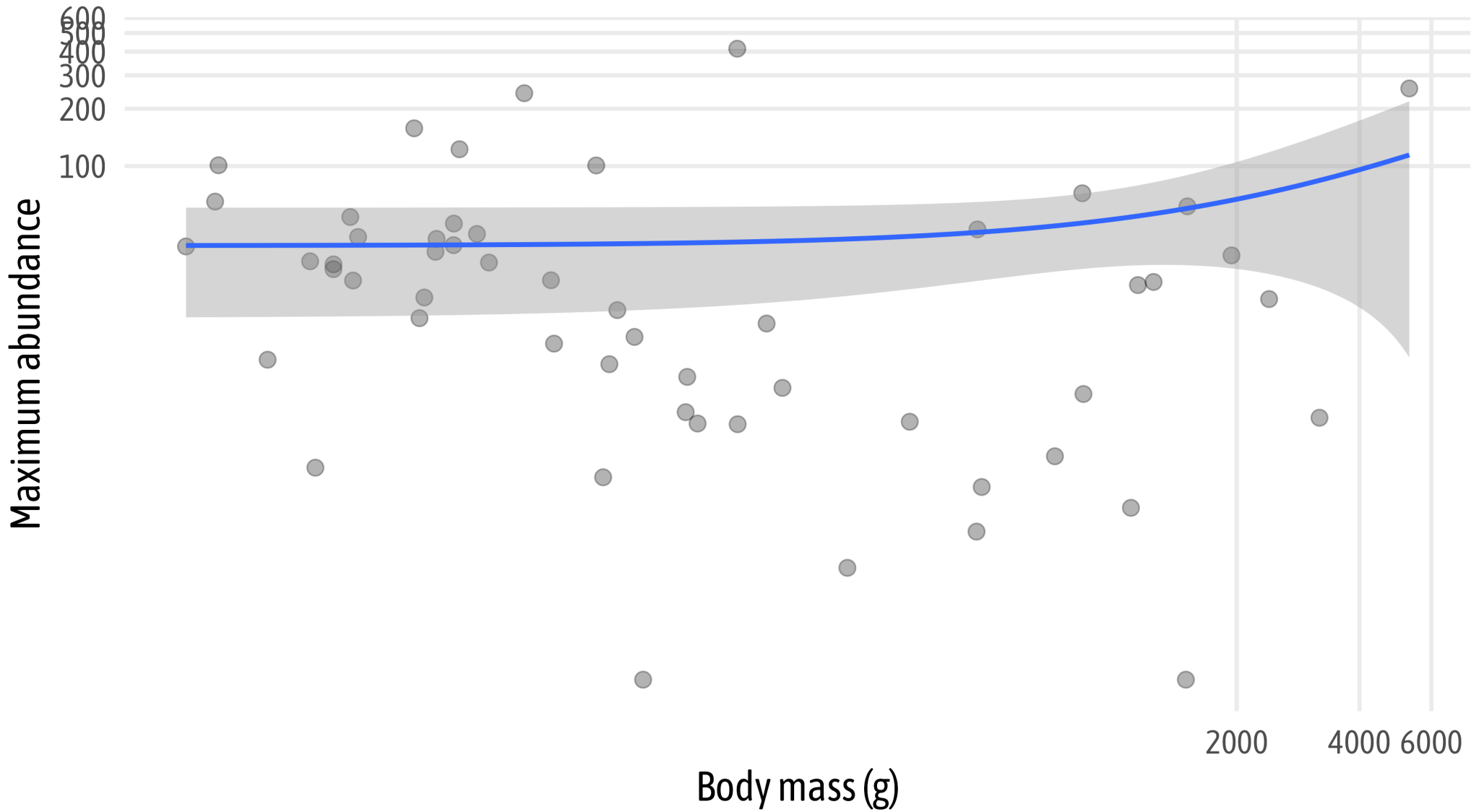
Transform the Variables (Visually)

```
1 g + coord_trans(x = "log10", y = "log10")
```



Transform the Variables (Visually)

```
1 g + coord_trans(x = "log10", y = "log10") + stat_smooth(method = "lm")
```



Your Turn: Linear Models

- Add columns to our `birds` data frame that hold the transformed values for both, the response and the predictor variable.
- Run the linear model using the transformed values as inputs.
- Inspect the diagnostic plots to check if all assumptions are met.
- Interpret the model outcomes.
- Visualize the model trend and the distribution of residuals.
- **Bonus:** Fit and explore a model for terrestrial birds only.

Transform the Variables

```
birds <- birds %>%
  mutate(across(c(max_abund, mass), log10, .names = "{col}_log"))
```

```
birds
```

```
# A tibble: 54 × 9
   family             max_abund avg_abund   mass diet        passerine aquatic max_abund_log mass_log
   <fct>                  <dbl>     <dbl>  <dbl> <fct>       <fct>     <fct>           <dbl>    <dbl>
 1 Hawks&Eagles&Kites      2.99     0.674   716.  Vertebrate  0         0               0.475    2.85
 2 Long-tailed tits       37.8      4.04      5.3 Insect      1         0               1.58     0.724
 3 Larks                 241.      23.1      35.8 PlantInsect 1         0               2.38     1.55
 4 Kingfishers             4.4      0.595   119.  Vertebrate  0         0               0.643    2.08
 5 Auks& Puffins           4.53     2.96    315.  InsectVert  0         1               0.656    2.50
 6 Ducks& Geese           23.7      2.74   1144.  PlantInsect 0         1               1.37     3.06
 7 Anhingas               24.6      1.84   1250   Vertebrate  0         1               1.39     3.10
 8 Swifts                 44.0      3.95     27.4 Insect      0         0               1.64     1.44
 9 Limpkins                1.6      0.567 1100   Insect      0         1               0.204    3.04
10 Herons& Egrets         46.5      2.97    462.  Vertebrate  0         1               1.67     2.66
# … with 44 more rows
```

Alternatively:

```
birds <- birds %>%
  mutate(log_max_abund = log10(max_abund), log_mass = log10(mass))
```


Transform the Variables

```
birds <- birds %>%
  mutate(across(c(max_abund, mass), log10, .names = "{col}_log"))
```

```
birds
```

```
# A tibble: 54 × 9
   family             max_abund avg_abund   mass diet        passerine aquatic max_abund_log mass_log
   <fct>                  <dbl>     <dbl>  <dbl> <fct>       <fct>     <fct>           <dbl>    <dbl>
 1 Hawks&Eagles&Kites      2.99     0.674   716.  Vertebrate  0         0               0.475    2.85
 2 Long-tailed tits       37.8      4.04      5.3 Insect      1         0               1.58     0.724
 3 Larks                 241.      23.1      35.8 PlantInsect 1         0               2.38     1.55
 4 Kingfishers             4.4      0.595   119.  Vertebrate  0         0               0.643    2.08
 5 Auks& Puffins           4.53     2.96    315.  InsectVert  0         1               0.656    2.50
 6 Ducks& Geese           23.7      2.74   1144.  PlantInsect 0         1               1.37     3.06
 7 Anhingas               24.6      1.84   1250   Vertebrate  0         1               1.39     3.10
 8 Swifts                 44.0      3.95     27.4 Insect      0         0               1.64     1.44
 9 Limpkins                1.6      0.567 1100   Insect      0         1               0.204    3.04
10 Herons& Egrets         46.5      2.97    462.  Vertebrate  0         1               1.67     2.66
# … with 44 more rows
```

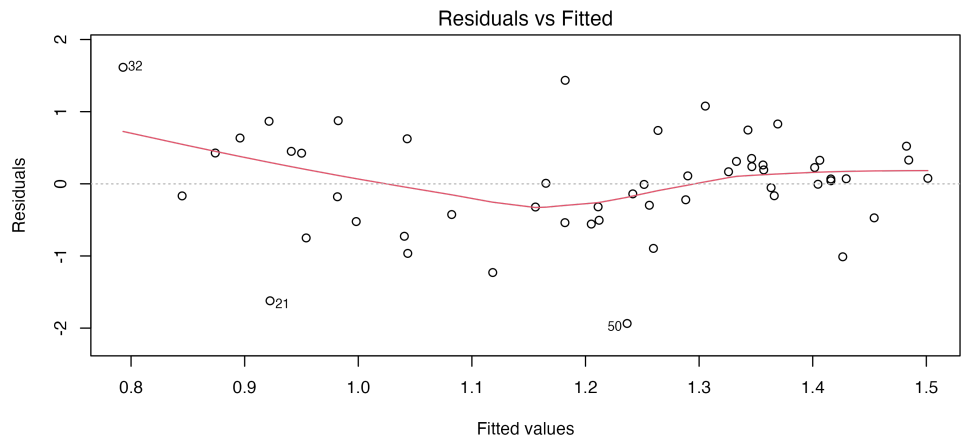
Equivalent code in base R:

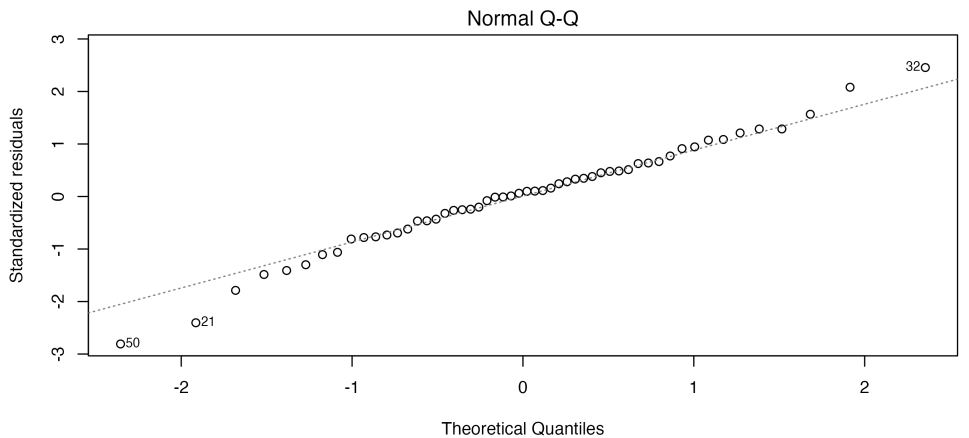
```
birds$log_max_abund <- log10(birds$max_abund)
birds$log_mass      <- log10(birds$mass)
```

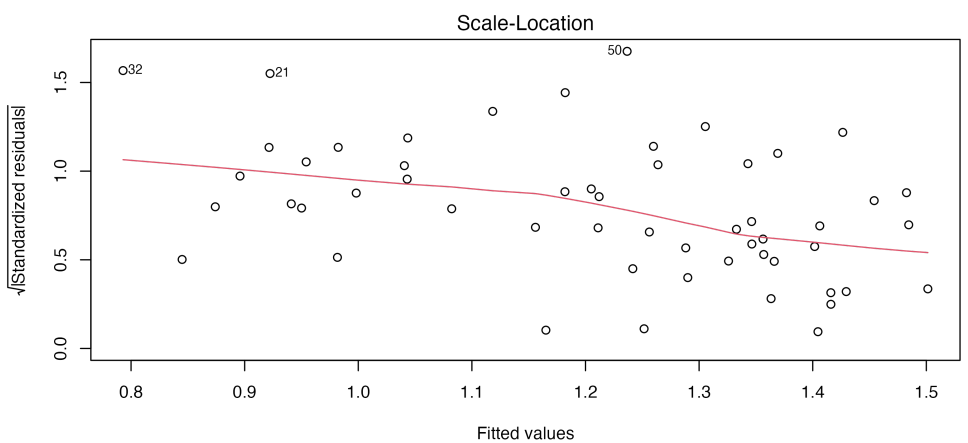

Run the Model and Inspect Outcomes

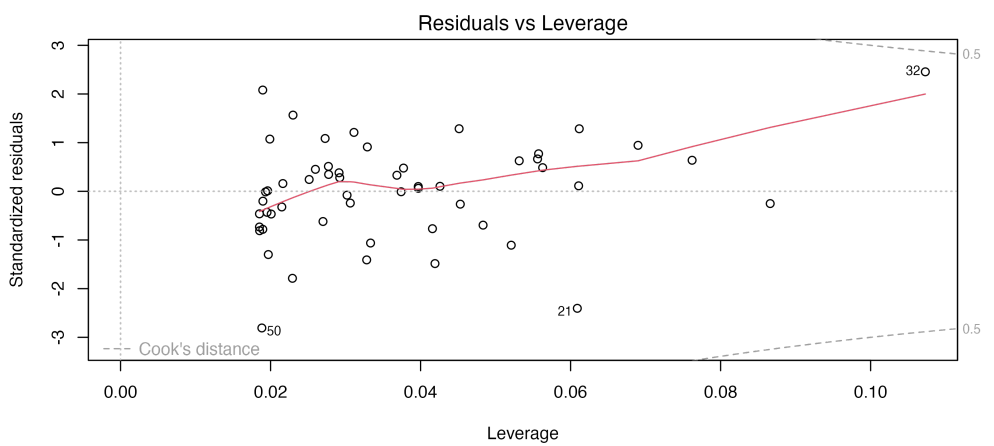
```
1 lm_log <- lm(max_abund_log ~ mass_log, data = birds)
```

```
1 plot(lm_log)
```



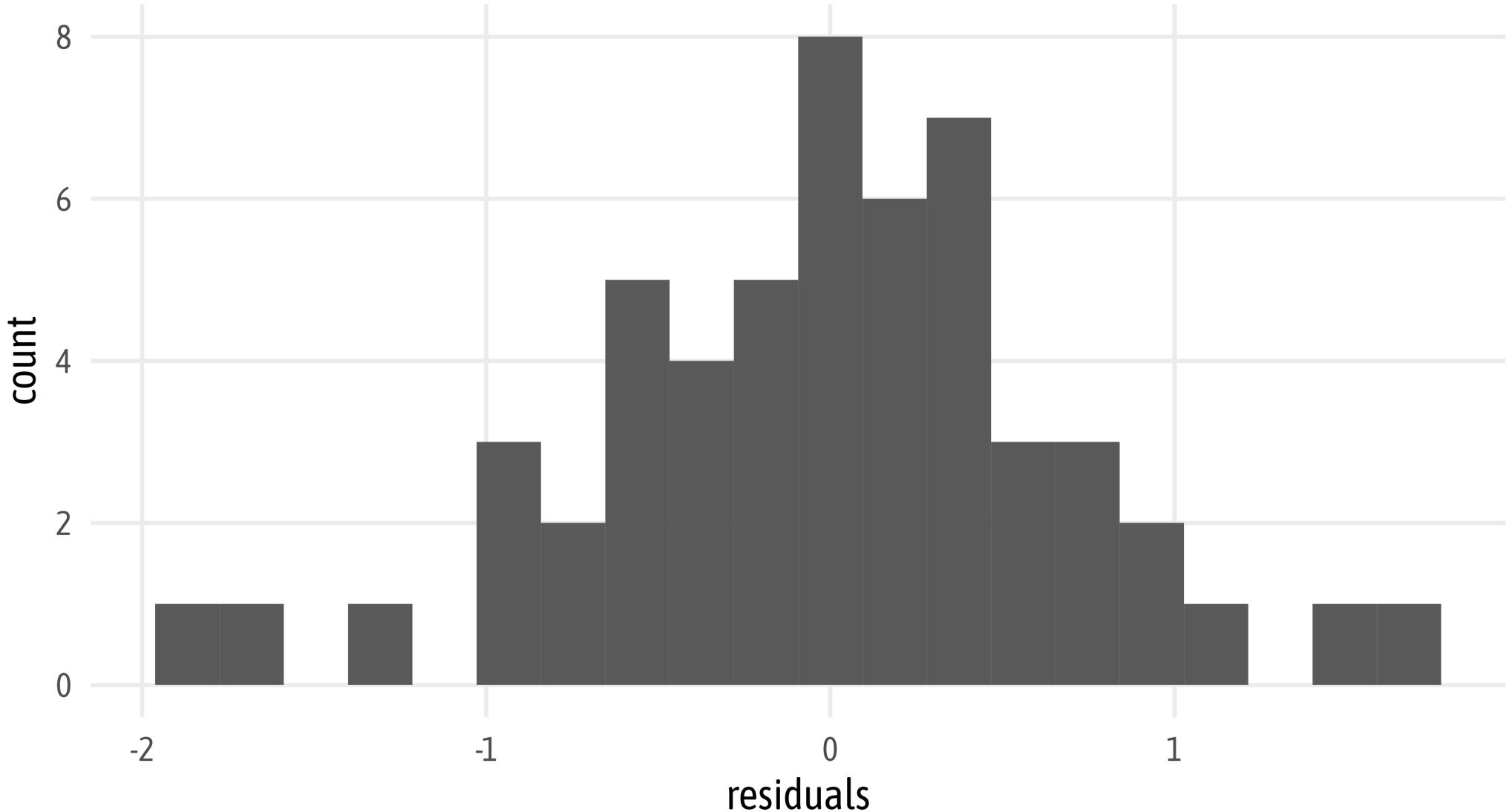






Visualize the Residuals

```
1 ggplot(tibble(residuals = residuals(lm_log)), aes(x = residuals)) + geom_histogram(bins = 20)
```



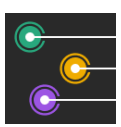
Test for Normality

```
1  shapiro.test(residuals(lm_log))
```

```
    Shapiro-Wilk normality test

data:  residuals(lm_log)
W = 0.98557, p-value = 0.7582
```

Null hypothesis: values follow a normal distribution

→ We reject H_a. The residuals are distributed normally.

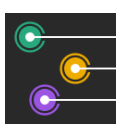


Model Interpretation

> *For different bird species, the* ***average mass of an individual affects the maximum abundance of the species****, due to ecological constraints.*

```
1 summary(lm_log)
```

```
Call:
lm(formula = max_abund_log ~ mass_log, data = birds)

Residuals:
     Min       1Q   Median       3Q      Max
-1.93562 -0.39982  0.05487  0.40625  1.61469

Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept)   1.6724     0.2472   6.767 1.17e-08 ***
mass_log     -0.2361     0.1170  -2.019   0.0487 *
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 0.6959 on 52 degrees of freedom
Multiple R-squared:  0.07267,   Adjusted R-squared:  0.05484
F-statistic: 4.075 on 1 and 52 DF,  p-value: 0.04869
```

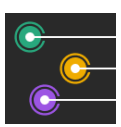



Model Interpretation

> *For different bird species, the* ***average mass of an individual affects the maximum abundance of the species****, due to ecological constraints.*

```
1 anova(lm_log)
```

```
Analysis of Variance Table

Response: max_abund_log
          Df  Sum Sq Mean Sq F value  Pr(>F)
mass_log   1  1.9736 1.97357   4.075 0.04869 *
Residuals 52 25.1844 0.48431
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Model Interpretation

> *For different bird species, the* ***average mass of an individual affects the maximum abundance of the species****, due to ecological constraints.*

```
1 summary(lm_log)$coefficients
```

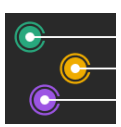
```
              Estimate Std. Error   t value     Pr(>|t|)
(Intercept)  1.6723673  0.2471519  6.766557 1.166186e-08
mass_log    -0.2361498  0.1169836 -2.018658 4.869342e-02
```

```
log10(abundance) = 1.672 - 0.236(log10(mass))
```

```
1 summary(lm_log)$adj.r.squared
```

```
[1] 0.05483696
```

The model using transformed response and predictor variables has very little evidence to support the hypothesis.

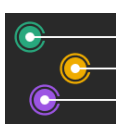


Create a Subset

```
1 birds_terrestrial <- filter(birds, aquatic == "0")
```

```
1 birds_terrestrial
```

```
# A tibble: 39 × 9
   family                          max_abund avg_abund  mass diet        passerine aquatic max_abund…¹ mass_…²
   <fct>                               <dbl>     <dbl> <dbl> <fct>       <fct>     <fct>          <dbl>   <dbl>
 1 Hawks&Eagles&Kites                   2.99     0.674 716.  Vertebrate  0         0              0.475   2.85
 2 Long-tailed tits                    37.8      4.04    5.3 Insect      1         0              1.58    0.724
 3 Larks                              241.      23.1    35.8 PlantInsect 1         0              2.38    1.55
 4 Kingfishers                          4.4      0.595 119.  Vertebrate  0         0              0.643   2.08
 5 Swifts                              44.0      3.95   27.4 Insect      0         0              1.64    1.44
 6 Waxwings                            11.7      2.80   42.3 PlantInsect 1         0              1.07    1.63
 7 Nightjars                            9.10     1.57   57.8 Insect      0         0              0.959   1.76
 8 Cardinals& Buntings& Grosbreaks     49.8      6.62   24.0 PlantInsect 1         0              1.70    1.38
 9 Creepers                             9.6      1.03    8.4 Insect      1         0              0.982   0.924
10 Pigeons & Doves                     14.9      3.04  141.  Plant       0         0              1.17    2.15
# … with 29 more rows, and abbreviated variable names ¹max_abund_log, ²mass_log
```

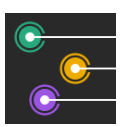



Run the Model

```
1  lm_terr <- lm(max_abund_log ~ mass_log, data = birds_terrestrial)
```

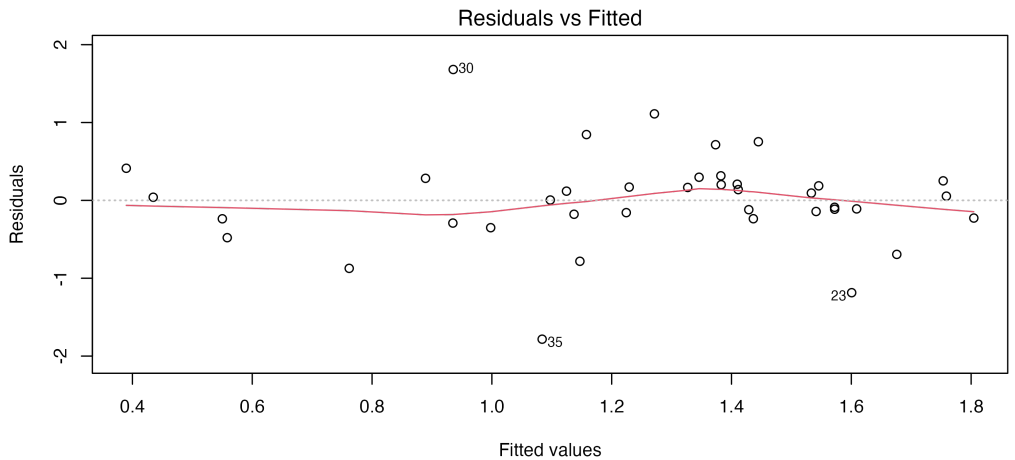
Alternatively, you can also specify the subset in the `lm()` call:

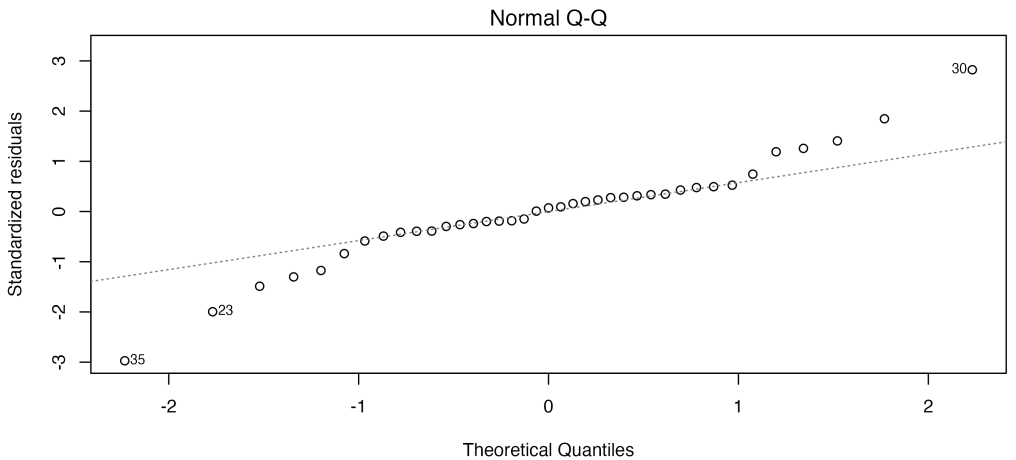
```
1  lm_terr <- lm(max_abund_log ~ mass_log, data = birds, subset = birds$aquatic == "0")
```

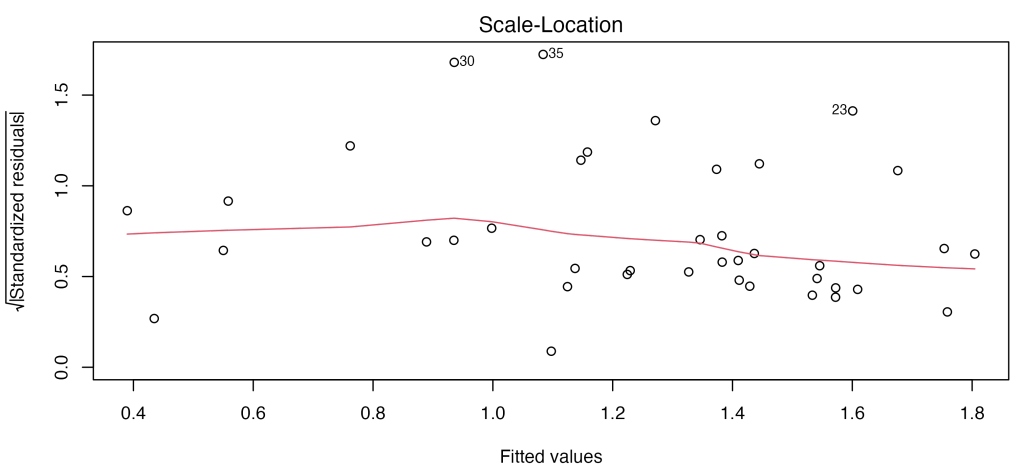



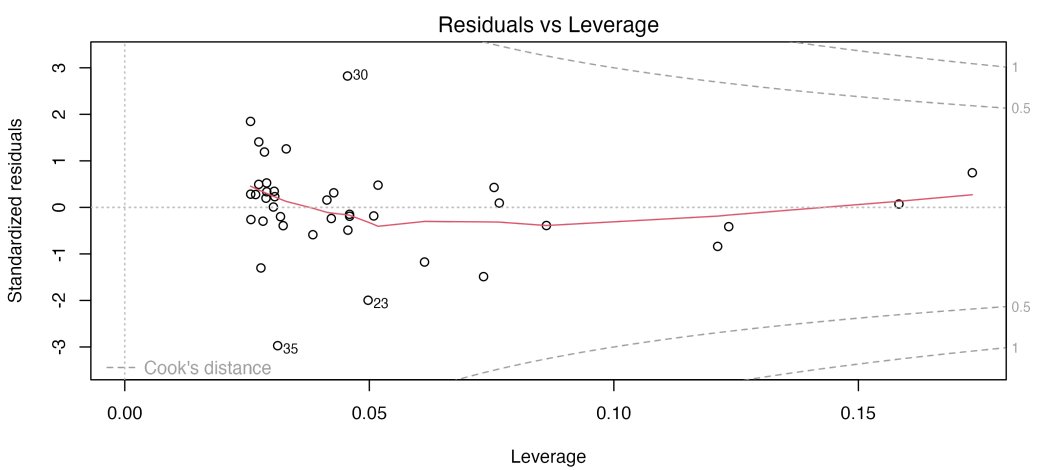
Verify Assumptions for LM

```
1 plot(lm_terr)
```



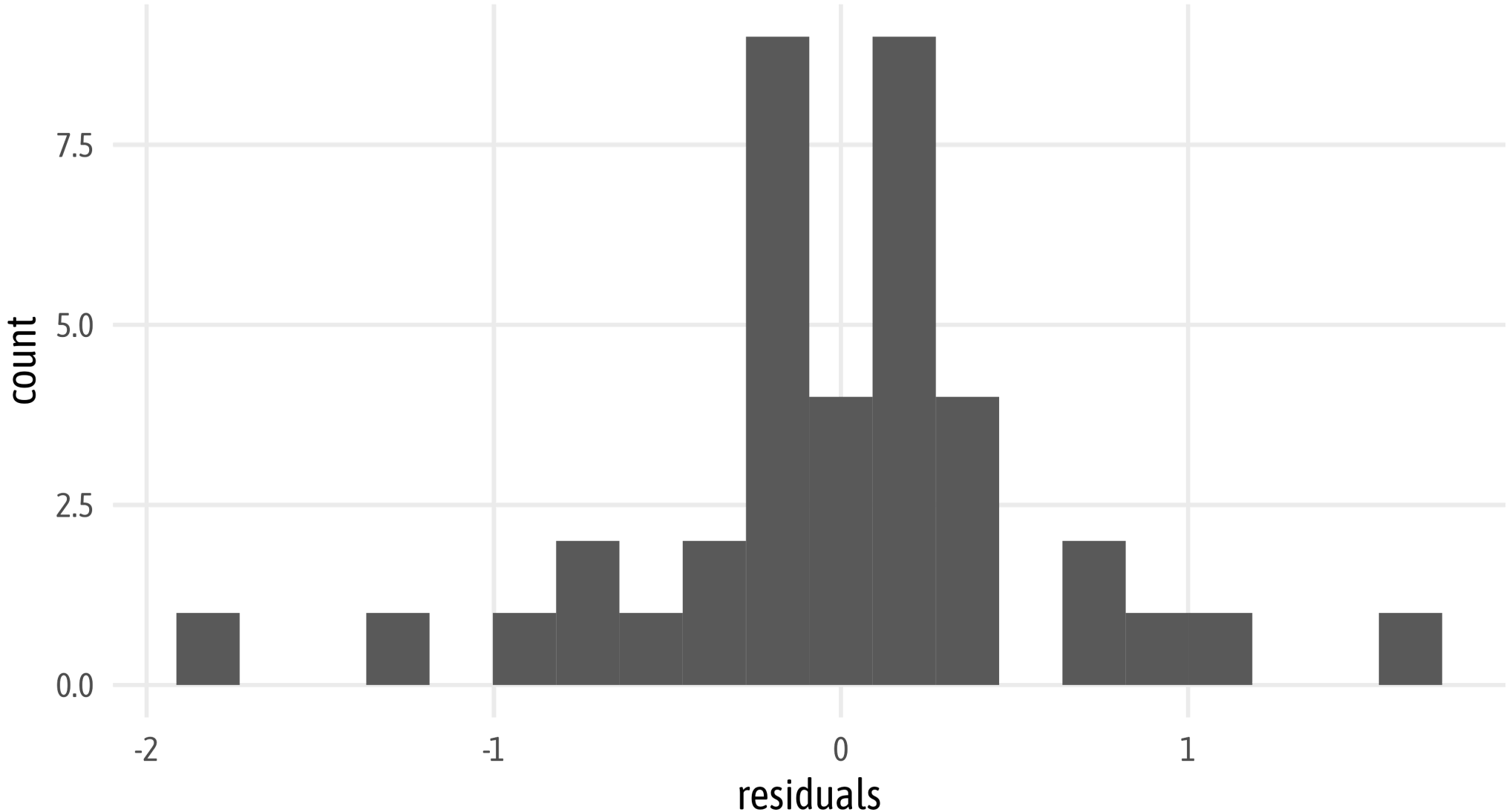






Visualize the Residuals

```
1  ggplot(tibble(residuals = residuals(lm_terr)), aes(x = residuals)) + geom_histogram(bins = 20)
```



Test for Normality

```
1  shapiro.test(residuals(lm_terr))
```

```
    Shapiro-Wilk normality test

data:  residuals(lm_terr)
W = 0.94367, p-value = 0.05041
```

Null hypothesis: values follow a normal distribution

→ We reject H_a. The resdiuals are distributed normally (but only barely).

Model Interpretation

> For *different* ***terrestial bird species***, *the* ***average mass of an individual affects the maximum abundance of the species***, *due to ecological constraints.*

```
1 summary(lm_terr)
```

```
Call:
lm(formula = max_abund_log ~ mass_log, data = birds_terrestrial)

Residuals:
     Min       1Q   Median       3Q      Max
-1.78289 -0.23135  0.04031  0.22932  1.68109

Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept)   2.2701     0.2931   7.744 2.96e-09 ***
mass_log     -0.6429     0.1746  -3.683 0.000733 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 0.6094 on 37 degrees of freedom
Multiple R-squared:  0.2682,    Adjusted R-squared:  0.2485
F-statistic: 13.56 on 1 and 37 DF,  p-value: 0.000733
```


Model Interpretation

> For *different* ***terrestial bird species***, *the* ***average mass of an individual affects the maximum abundance of the species***, *due to ecological constraints.*

```
1 anova(lm_terr)
```

```
Analysis of Variance Table

Response: max_abund_log
          Df  Sum Sq Mean Sq F value   Pr(>F)
mass_log   1  5.0374  5.0374  13.562 0.000733 ***
Residuals 37 13.7426  0.3714
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```


Model Interpretation

> For *different* ***terrestial bird species***, *the* ***average mass of an individual affects the maximum abundance of the species***, *due to ecological constraints.*

```
summary(lm_terr)$coefficients
```

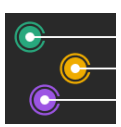
```
             Estimate Std. Error   t value     Pr(>|t|)
(Intercept)  2.2701276  0.2931420  7.744122 2.961050e-09
mass_log    -0.6428946  0.1745703 -3.682726 7.329516e-04
```

$$log10(abundance) = 2.27 - 0.643(log10(mass))$$

```
summary(lm_terr)$adj.r.squared
```

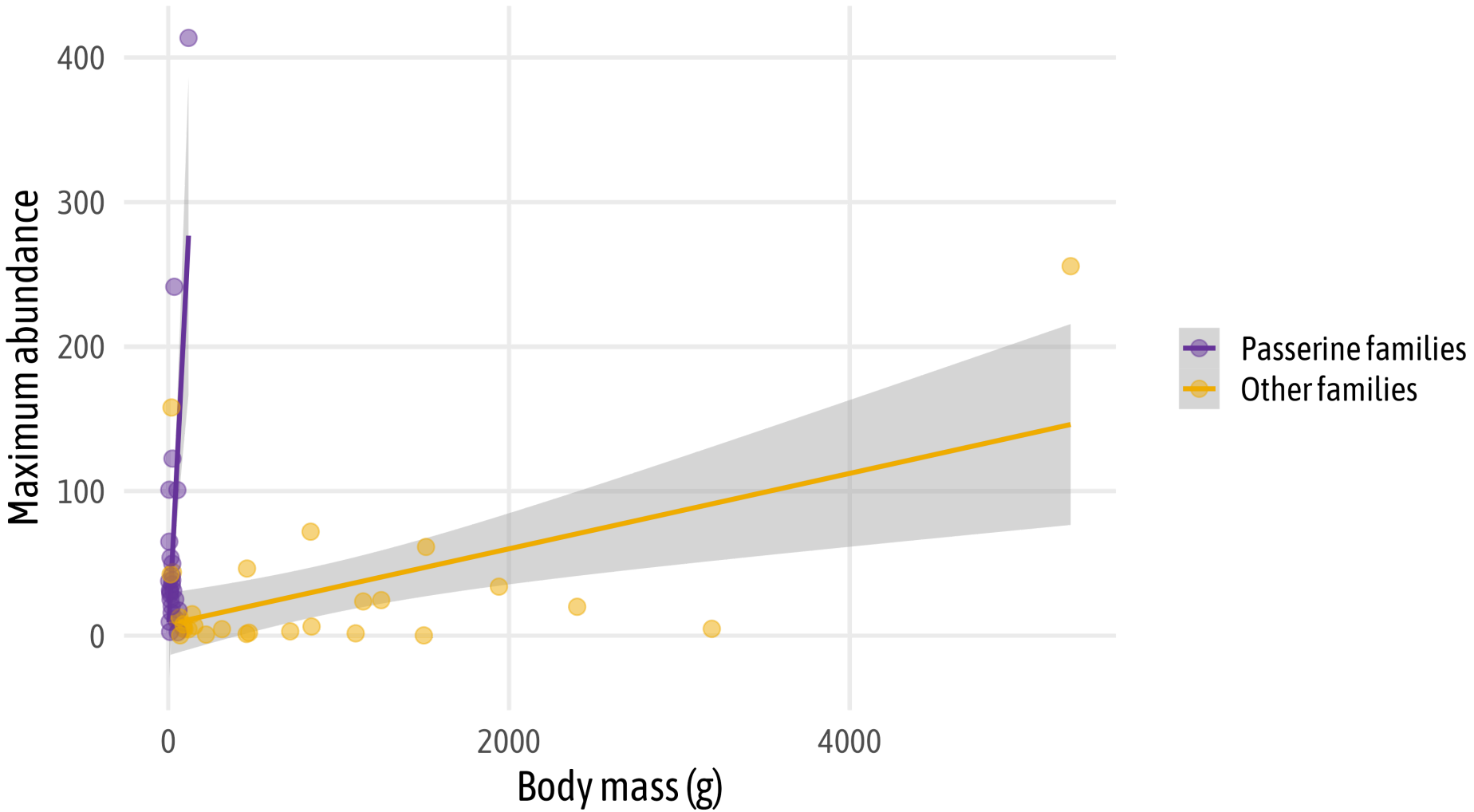
```
[1] 0.2484544
```

The model provides evidence to support the hypothesis.



Including More Predictor Variables

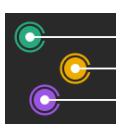
We can also use more than a single predictor. Let's explore the relationship but including the information on passerine families and habitat preference:



Including More Predictor Variables

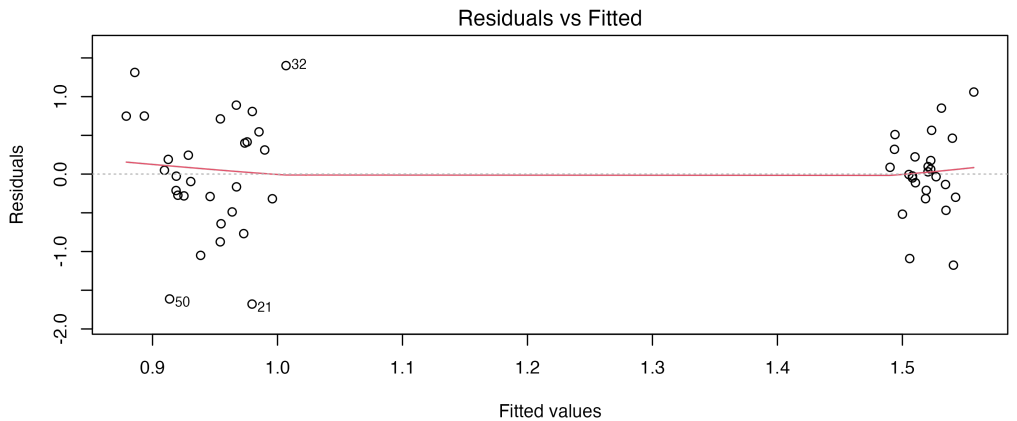
We can also use more than a single predictor. Let's explore the relationship but including the information on passerine families:

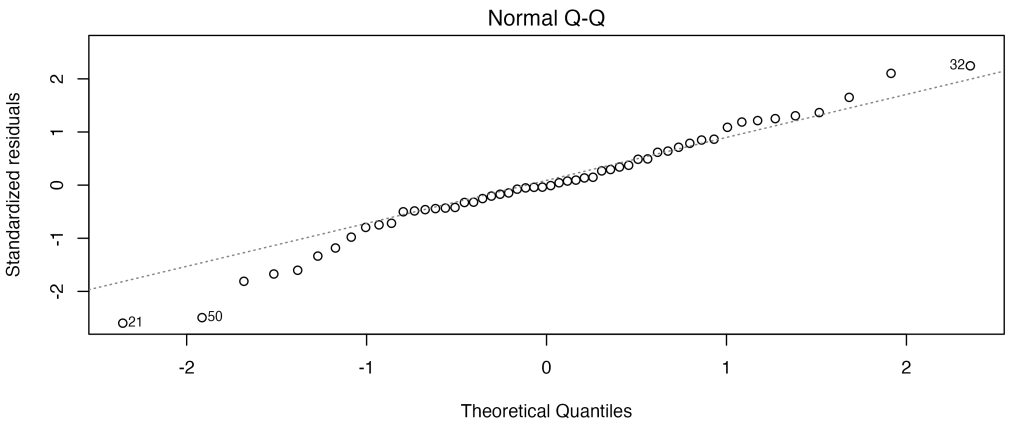
```
1  lm_mult <- lm(max_abund_log ~ mass_log + passerine, data = birds)
```

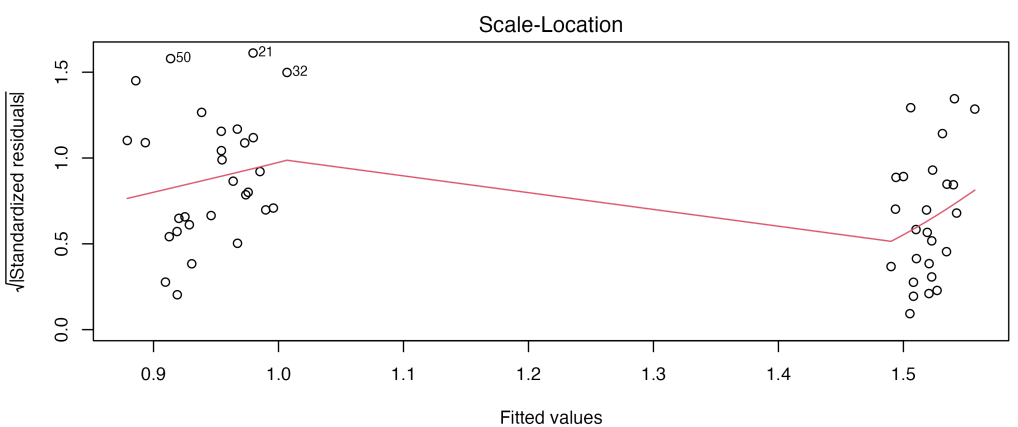



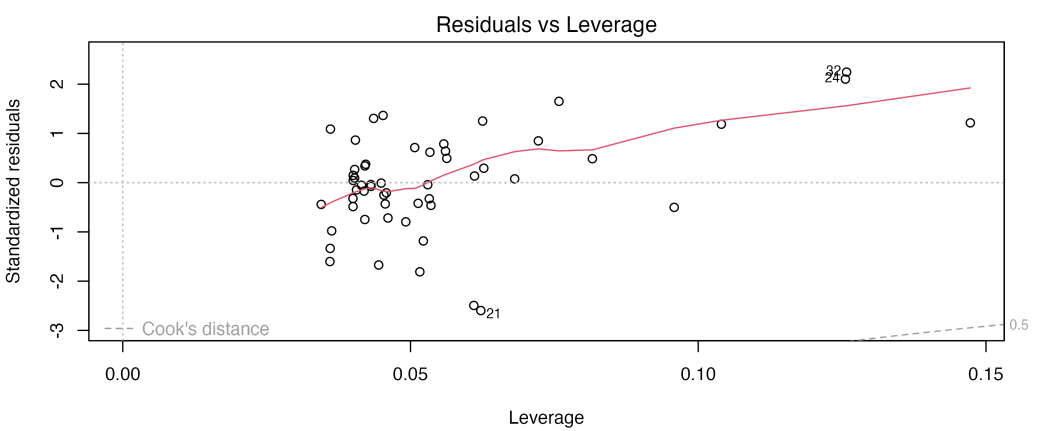
Including More Predictor Variables

```
1 plot(lm_mult)
```









Model Interpretation

```
1 summary(lm_mult)
```

```
Call:
lm(formula = max_abund_log ~ mass_log + passerine, data = birds)

Residuals:
     Min       1Q   Median       3Q      Max
-1.67861 -0.29704 -0.01518  0.41162  1.40084

Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept)  0.82215    0.43158   1.905   0.0624 .
mass_log     0.04958    0.16516   0.300   0.7652
passerine1   0.63206    0.26814   2.357   0.0223 *
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 0.6673 on 51 degrees of freedom
Multiple R-squared:  0.1638,    Adjusted R-squared:  0.131
F-statistic: 4.994 on 2 and 51 DF,  p-value: 0.01045
```

$$\log10(\text{abundance}) = 0.882 + 0.049(\log10(\text{mass})) + 0.632(\text{passerine})$$

The model provides evidence to support the hypothesis.

Back to t-Tests

Note that a t-test is equal to a **linear model for a factor with two levels**:

```
1 lm_ttest <- lm(mass_log ~ aquatic, data = birds)
```

```
1 ttest_lm <- t.test(mass_log ~ aquatic, data = birds, var.equal = TRUE)
```

When variances are equal we can see that t^2 == F:

```
1 anova(lm_ttest)
```

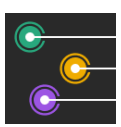
```
Analysis of Variance Table

Response: mass_log
          Df Sum Sq Mean Sq F value    Pr(>F)
aquatic    1 19.015 19.0150  60.385 2.936e-10 ***
Residuals 52 16.375  0.3149
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
1 ttest_lm$statistic^2
```

```
      t
60.3845
```


Statistical Analysis

— Analysis of Variance —



Analysis of Variance (ANOVA)

An **analysis of Variance (ANOVA)** is used to **compare variances across the means** of different groups (factors).

Why and When?

An ANOVA tells you if the dependent variable changes according to the level of the independent variable.

- If you collected data about one categorical independent variable and one quantitative dependent variable.
- If the categorical independent variable has three or more levels.

Analysis of Variance (ANOVA)

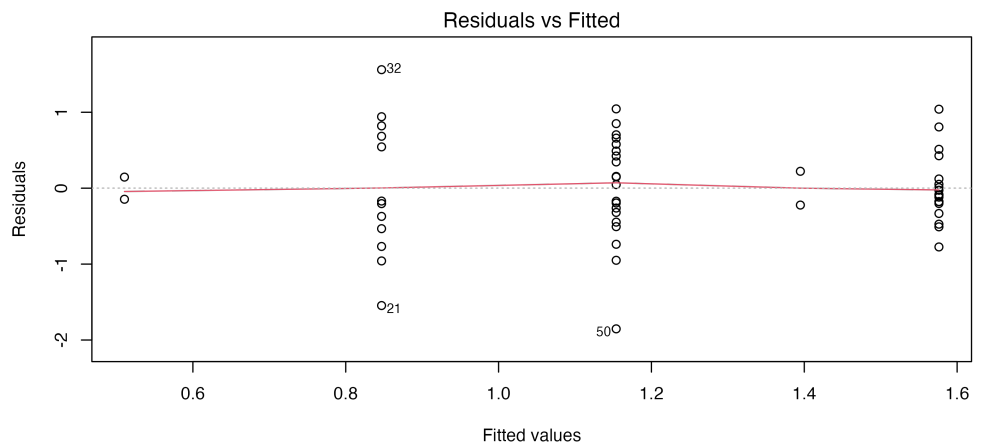
```
1  aov_diet <- aov(max_abund_log ~ diet, data = birds)
```

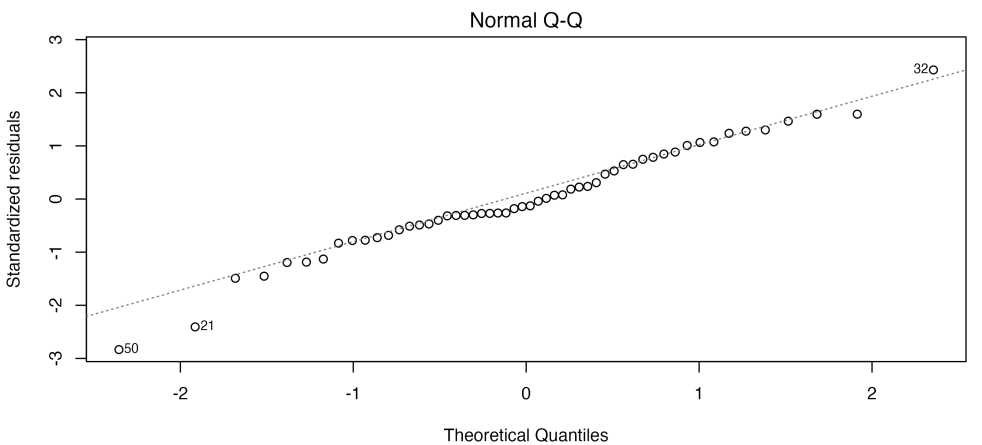
Note that a simple ANOVA is equal to a **linear model for a factor with more than two levels**.

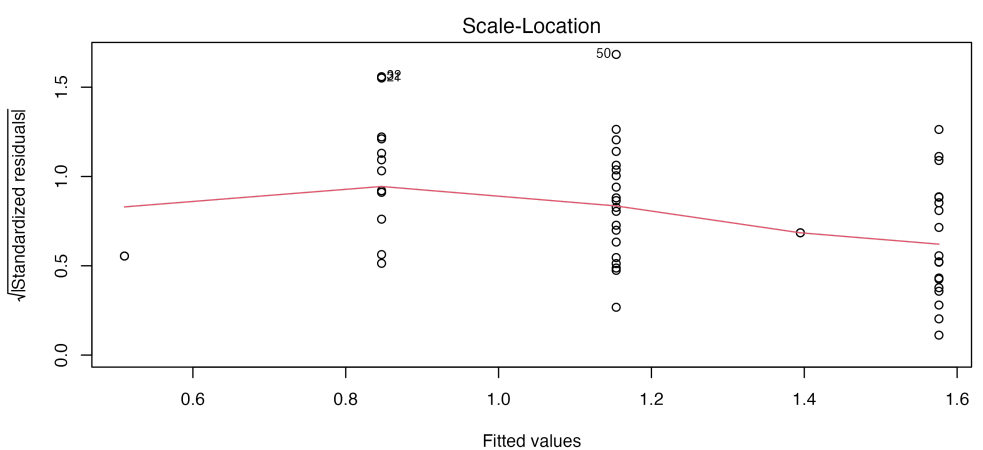
Verify Assumptions for ANOVA

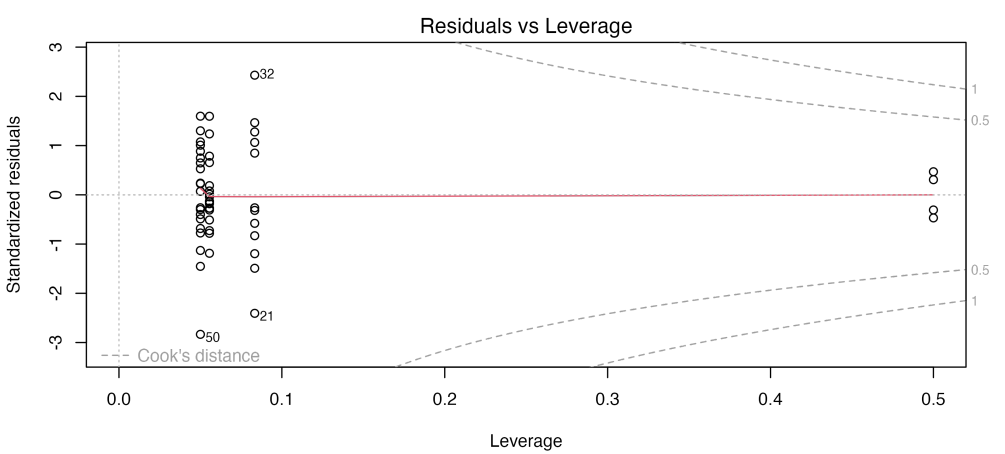
An ANOVA must meet the same four residual assumptions as linear models:

```
1  plot(aov_diet)
```









Verify Assumptions for ANOVA

Test for normality with the **Shapiro-Wilk test**:

```
1  shapiro.test(resid(aov_diet))
```

```
    Shapiro-Wilk normality test

data:  resid(aov_diet)
W = 0.97995, p-value = 0.4982
```

Null hypothesis: values follow a normal distribution

→ We reject H_a. The residuals are distributed normally.

Verify Assumptions for ANOVA

Assess the homogeneity of residuals variance with a **Bartlett test**:

```
1  bartlett.test(max_abund_log ~ diet, data = birds)
```

```
    Bartlett test of homogeneity of variances

data:  max_abund_log by diet
Bartlett's K-squared = 7.4728, df = 4, p-value = 0.1129
```

Null hypothesis: the variances are equal

→ We reject H_a. The residuals are equal (homoscedastic).

Model Output

```
1 summary(aov_diet)
```

```
            Df Sum Sq Mean Sq F value Pr(>F)
diet         4  5.106   1.276   2.836 0.0341 *
Residuals   49 22.052   0.450
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

... which is the same as the outcome of the simple LM:

```
1 anova(lm(max_abund_log ~ diet, data = birds))
```

```
Analysis of Variance Table

Response: max_abund_log
          Df  Sum Sq Mean Sq F value Pr(>F)
diet       4  5.1059 1.27647  2.8363 0.0341 *
Residuals 49 22.0521 0.45004
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```


Complementary Tests

An ANOVA (or LM) only detects if a difference is present;
it cannot identify which levels are different from the others.

Complementary **post-hoc tests** are used compare the levels of the explanatory variables (i.e. the treatments) two by two, e.g.

- Fischer's least significant difference
- Duncan's new multiple range test
- Newman-Keuls method
- Dunnett's test
- Tukey honest significant differences

Tukey Post-Hoc Test

```r
TukeyHSD(aov_diet, ordered = TRUE)
```

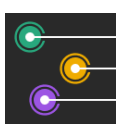
```
  Tukey multiple comparisons of means
    95% family-wise confidence level
    factor levels have been ordered

Fit: aov(formula = max_abund_log ~ diet, data = birds)

$diet
                             diff          lwr      upr     p adj
Vertebrate-InsectVert  0.3364295 -1.11457613 1.787435 0.9645742
Insect-InsectVert      0.6434334 -0.76550517 2.052372 0.6965047
Plant-InsectVert       0.8844338 -1.01537856 2.784246 0.6812494
PlantInsect-InsectVert 1.0657336 -0.35030287 2.481770 0.2235587
Insect-Vertebrate      0.3070039 -0.38670951 1.000717 0.7204249
Plant-Vertebrate       0.5480043 -0.90300137 1.999010 0.8211024
PlantInsect-Vertebrate 0.7293041  0.02128588 1.437322 0.0405485
Plant-Insect           0.2410004 -1.16793813 1.649939 0.9884504
PlantInsect-Insect     0.4223003 -0.19493574 1.039536 0.3117612
PlantInsect-Plant      0.1812999 -1.23473664 1.597336 0.9961844
```

The only significant difference in abundance occurs between the diet types `PlantInsect` and `Vertebrate`.

```
                             diff        lwr      upr      p adj
PlantInsect-Vertebrate 0.7293041 0.02128588 1.437322 0.04054849
```


Statistical Analysis

— Mixed Effect Model —



Linear Mixed Model (LMM)

Linear mixed models (LMMs) (also known as **mixed effect models**) are an extension of simple linear models that **allow both fixed and random effects**.

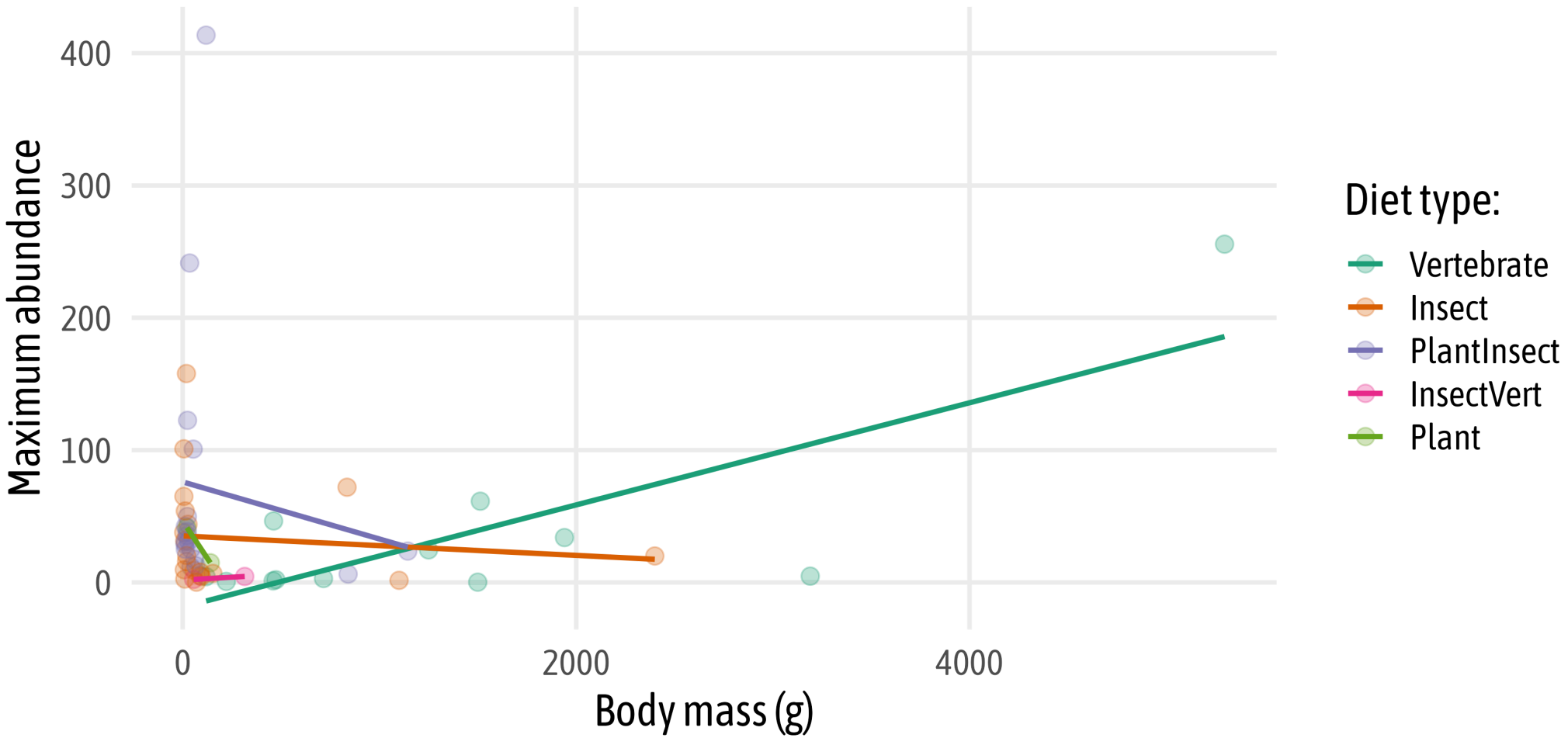
Why and when?

A **random effect** specifies grouping factors for which we want to control for but their specific effect on the response variable is not necessarily of interest.

- If there is an inherent structure to data (i.e. single observations are not strictly independent), relationships between variables of interest might differ depending on grouping factors.
- If sample sizes are low, it is difficult to fit models that require many parameters to be estimated.

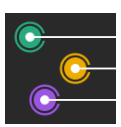
Linear Mixed Model (LMM)

```
1 ggplot(birds, aes(x = mass, y = max_abund, color = diet)) +
2   geom_point(size = 3, alpha = .3) + stat_smooth(method = "lm", se = FALSE) +
3   scale_color_brewer(palette = "Dark2") +
4   labs(x = "Body mass (g)", y = "Maximum abundance", color = "Diet type:")
```



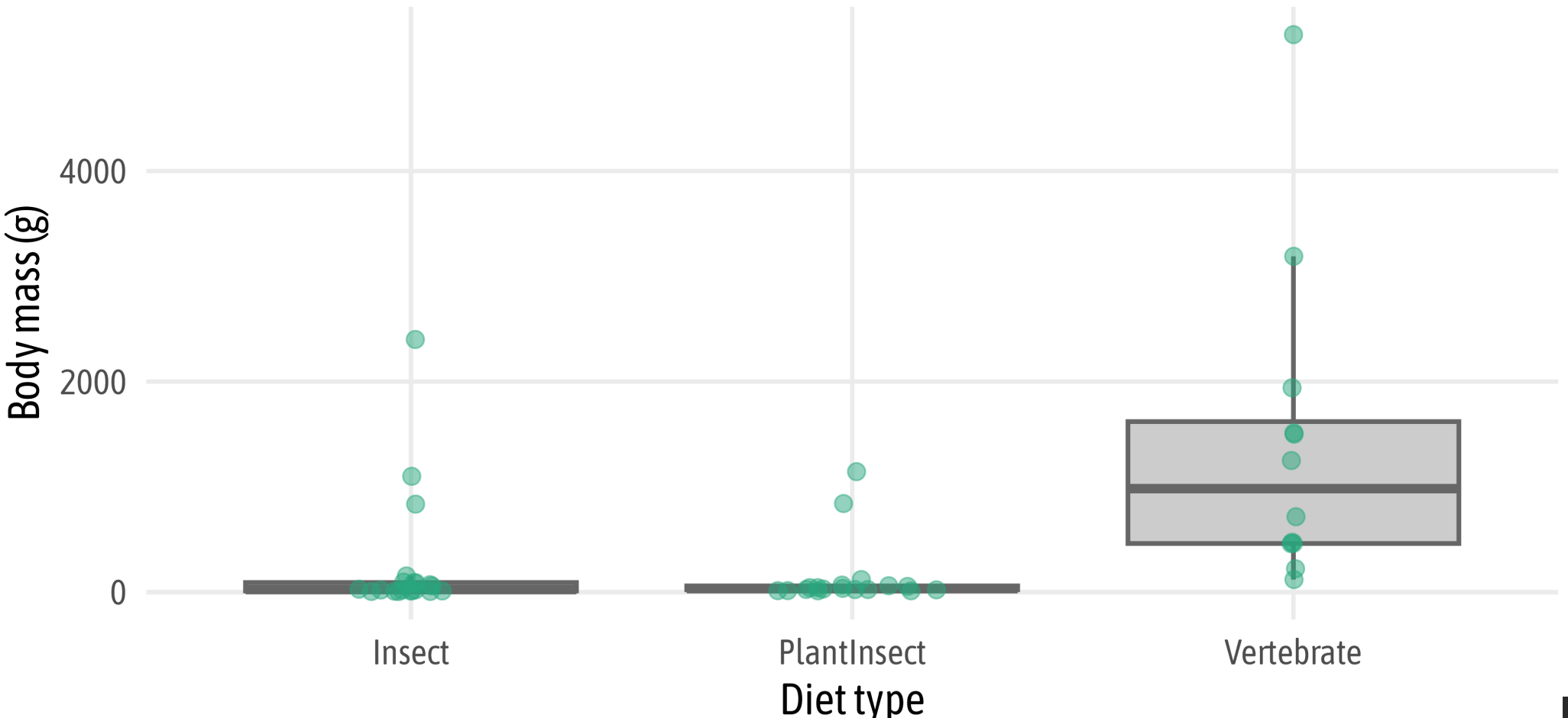
Prepare Data

```
1 birds_diet <-
2   birds %>%
3   add_count(diet) %>%
4   filter(n > 5) %>%
5   mutate(diet = factor(as.character(diet)))
```

Prepare Data

```
1 ggplot(birds_diet, aes(x = diet, y = mass)) +
2   geom_boxplot(color = "grey40", fill = "grey80", lwd = .9, outlier.shape = NA) +
3   ggforce::geom_sina(maxwidth = .5, alpha = .5, size = 3, color = "#28A87D") +
4   labs(x = "Diet type", y = "Body mass (g)")
```



Linear Mixed Model (LMM)

> *One point of particular relevance to 'modern' mixed model estimation (rather than 'classical' method-of-moments estimation) is that, for practical purposes, there must be a reasonable number of random-effects levels — more than 5 or 6 at a minimum.*

Ben Bolker

> *It may be acceptable to use fewer than five levels of random effects if one is not interested in making inferences about the random effects terms.*

Gomes 2022 PeerJ

Linear Mixed Model: Random Intercepts

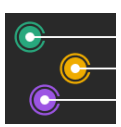
```
# install.packages("lme4")
lm_mixed1 <- lme4::lmer(max_abund_log ~ mass_log + (1 | diet), data = birds_diet)
```

As with regular linear models, we define our response variable as the column name to the left of the ~ and define our fixed effects to the right.

The random effect is defined as **random intercept for each diet type**.
The connotation in R is `(1 | diet)`.

```
coef(lm_mixed1)$diet
```

```
            (Intercept)   mass_log
Insect         1.473102 -0.1723018
PlantInsect    1.761541 -0.1723018
Vertebrate     1.438901 -0.1723018
```

Linear Mixed Model: Random Slopes

```
# install.packages("lme4")
lm_mixed2 <- lme4::lmer(max_abund_log ~ mass_log + (0 + mass_log | diet), data = birds_diet)
```

As with regular linear models, we define our response variable as the column name to the left of the ~ and define our fixed effects to the right.

The random effect is defined as **random slopes for each diet type**.
The connotation in R is `(0 + mass_log | diet)`.

```
coef(lm_mixed2)$diet
```

```
            (Intercept)   mass_log
Insect          1.61115 -0.2385155
PlantInsect     1.61115 -0.1158075
Vertebrate      1.61115 -0.2183231
```


Linear Mixed Model: Intercepts + Slopes

```
1  # install.packages("lme4")
2  lm_mixed3 <- lme4::lmer(max_abund_log ~ mass_log + (1 + mass_log | diet), data = birds_diet)
```

As with regular linear models, we define our response variable as the column name to the left of the ~ and define our fixed effects to the right.

The random effect is defined as **random intercepts and slopes for each diet type**. The connotation in R is `(1 + mass_log | diet)`.

```
1  coef(lm_mixed3)$diet
```

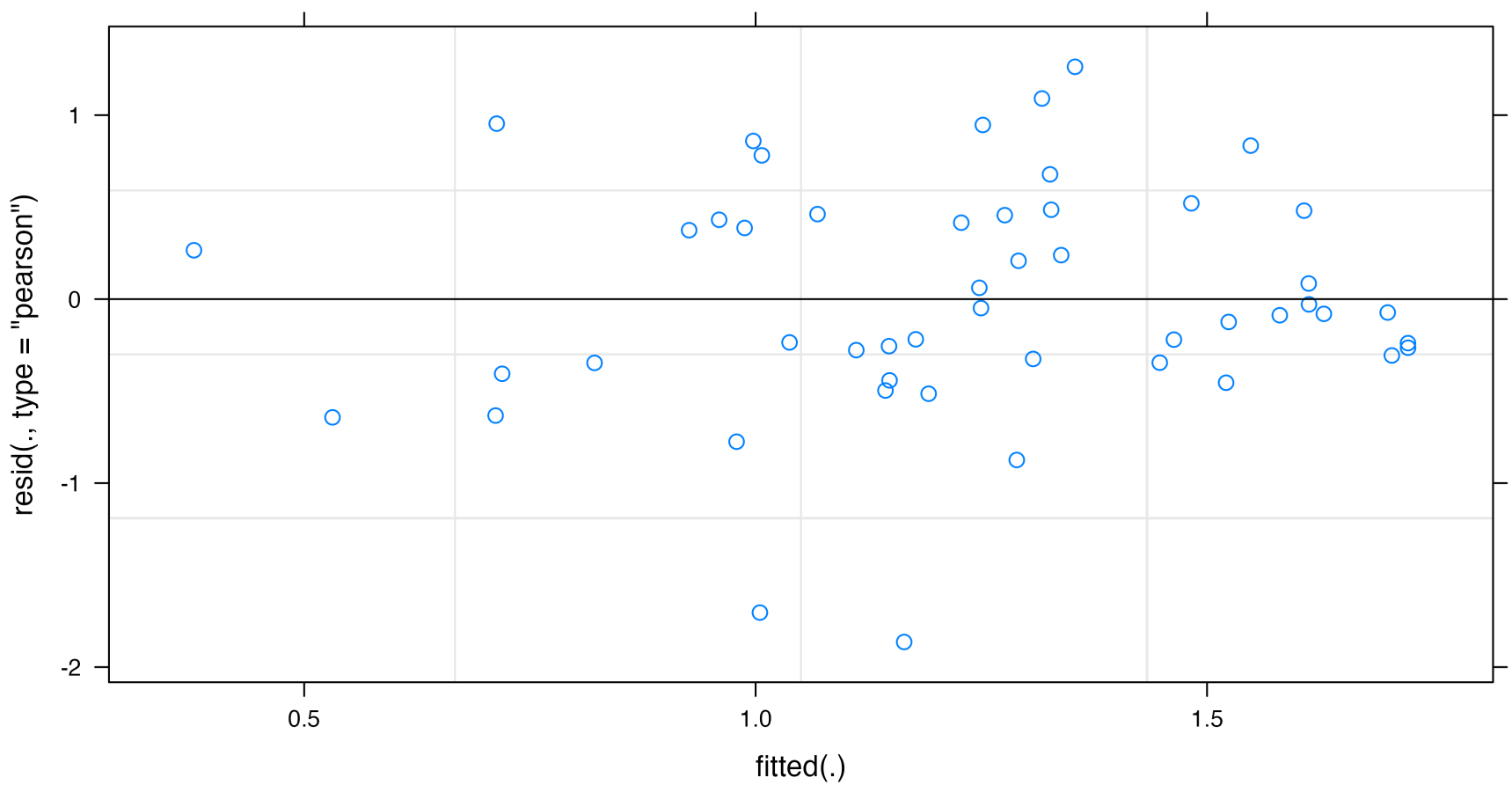
```
            (Intercept)   mass_log
Insect        1.4508274 -0.1551592
PlantInsect   2.1270137 -0.3724646
Vertebrate   -0.8065533  0.5702934
```

```
log10(abundance) = 1.451 - 0.155(log10(mass))
log10(abundance) = 2.127 - 0.372(log10(mass))
log10(abundance) = -0.807 + 0.57(log10(mass))
```


Linear Mixed Model: Intercepts + Slopes

```
1  # install.packages("lme4")
2  lm_mixed3 <- lme4::lmer(max_abund_log ~ mass_log + (1 + mass_log | diet), data = birds_diet)
```

```
1  plot(lm_mixed3)
```



Linear Mixed Model: Intercepts + Slopes

```r
# install.packages("lme4")
lm_mixed3 <- lme4::lmer(max_abund_log ~ mass_log + (1 + mass_log | diet), data = birds_diet)
```

```r
summary(lm_mixed3)
```

```
Linear mixed model fit by REML ['lmerMod']
Formula: max_abund_log ~ mass_log + (1 + mass_log | diet)
   Data: birds_diet

REML criterion at convergence: 107.3

Scaled residuals:
    Min      1Q  Median      3Q     Max
-2.8628 -0.5229 -0.1174  0.6914  1.9400

Random effects:
 Groups   Name        Variance Std.Dev. Corr
 diet     (Intercept) 2.7626   1.6621
          mass_log    0.2853   0.5342   -1.00
 Residual             0.4237   0.6509
Number of obs: 50, groups:  diet, 3

Fixed effects:
            Estimate Std. Error t value
```

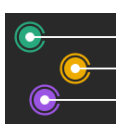

Linear Mixed Model: Intercepts + Slopes

```
# install.packages("lme4")
lm_mixed3 <- lme4::lmer(max_abund_log ~ mass_log + (1 + mass_log | diet), data = birds_diet)
```

```
anova(lm_mixed3)
```

```
Analysis of Variance Table
         npar     Sum Sq    Mean Sq F value
mass_log    1 0.00072047 0.00072047  0.0017
```

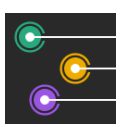
The model provides evidence to support the hypothesis that bird families with a higher body mass are more abundant (but it differs per diet typ).



Statistical Analysis

— Model Comparison —

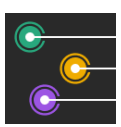
Cédric Scherer // R Course TU Dresden // Statistical Analysis & Modeling



Model Comparison

An important part of model evaluation is not only their performance in terms of explanation but also their **parsimony**.

A **parsimonious model** is a model that accomplishes the desired level of **explanation or prediction with as few predictor variables as possible**.



Model Comparison

To compare the fits of two models, you can use the `anova()` function with the regression objects as two separate arguments.

```
1  anova(lm_log, lm_mult)
```

```
Analysis of Variance Table

Model 1: max_abund_log ~ mass_log
Model 2: max_abund_log ~ mass_log + passerine
  Res.Df    RSS Df Sum of Sq      F  Pr(>F)
1     52 25.184
2     51 22.710  1    2.4742 5.5564 0.02229 *
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

If the p-value is sufficiently low, we conclude that the more complex model is significantly better than the simpler model.

→ We accept H_a. The complex model is more parsimonious.

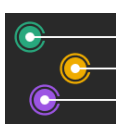
Model Comparison

To compare the fits of two models, you can use the `anova()` function with the regression objects as two separate arguments.

```
1  anova(lm_mixed1, lm_mixed3)
```

```
Data: birds_diet
Models:
lm_mixed1: max_abund_log ~ mass_log + (1 | diet)
lm_mixed3: max_abund_log ~ mass_log + (1 + mass_log | diet)
           npar    AIC    BIC  logLik deviance  Chisq Df Pr(>Chisq)
lm_mixed1     4 113.08 120.72 -52.538   105.08
lm_mixed3     6 116.71 128.18 -52.355   104.71 0.3665  2     0.8326
```

→ We reject H_a. The complex model is not more parsimonious.



Your Turn 

- Import the dragons data set which reports hypothetical outcomes for a fictional study system.
- Inspect the data and visualize the distributions of the variables.
- Explore the relationship of `test_score` and `body_length`.
  - Create a scatter plot showing the relationship of the two variables.
  - Run a **linear model** to test how `body_length` is affecting `test_score`.
  - Check if the assumptions for the LM are met or not. If they are met, interpret the model outcomes.
  - Inspect the relationship of the two vasriables for different mountain ranges.
  - Afterwards, run a **linear mixed model** which accounts for `mountain_range` as random effect.
  - Check if the asumptions for the LMM are met or not. If they are met, interpret the model outcomes and compre the two LMMs for parsimony.

Data

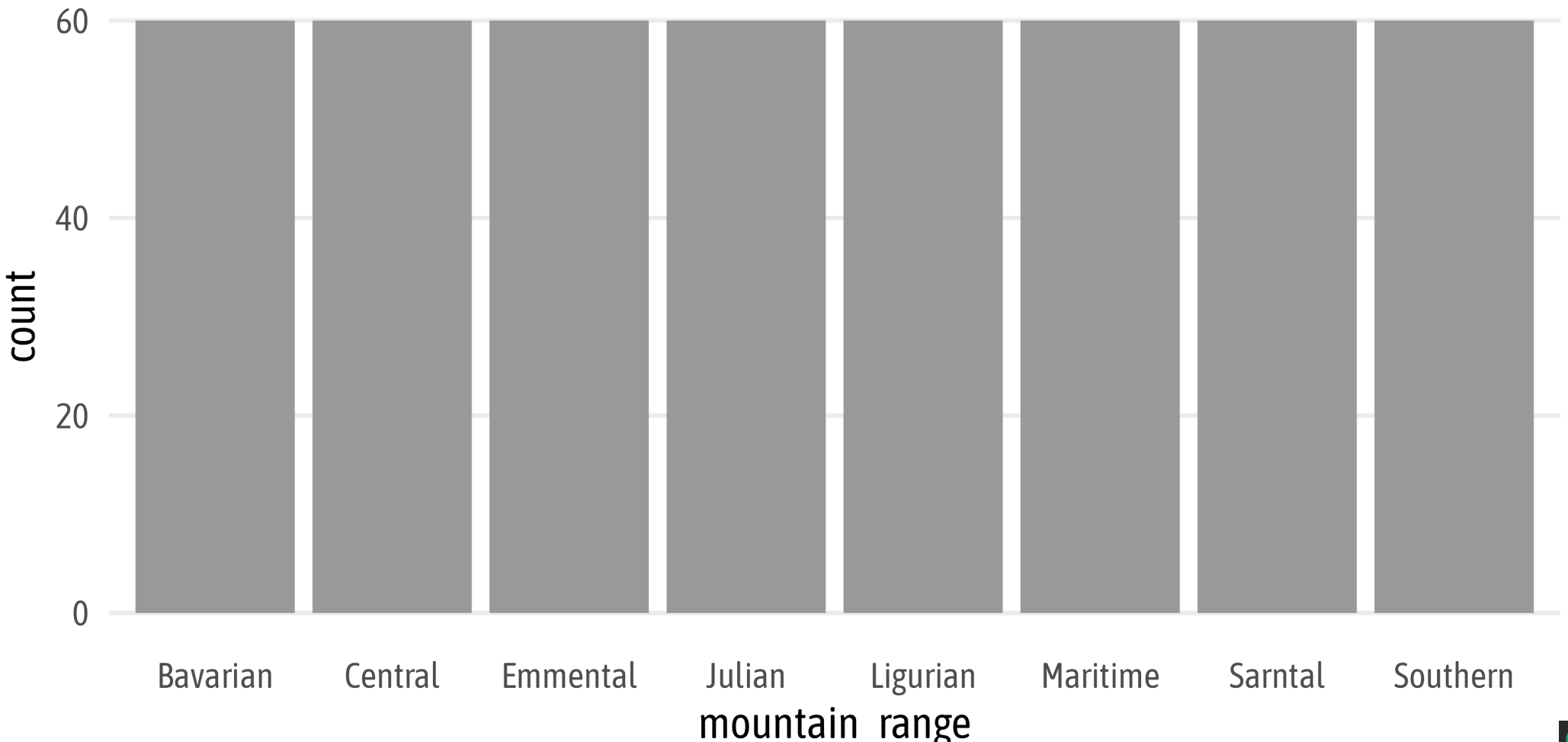
```
1 dragons <- readr::read_csv("./data/dragons.csv")
```

```
1 glimpse(dragons)
```

```
Rows: 480
Columns: 4
$ test_score     <dbl> 16.1473095, 33.8861835, 6.0383329, 18.8388213, 33.8623279, 47.0432459, 2.5578905, 3.8…
$ body_length    <dbl> 165.5485, 167.5593, 165.8830, 167.6855, 169.9597, 168.6887, 169.6194, 164.4163, 167.5…
$ mountain_range <chr> "Bavarian", "Bavarian", "Bavarian", "Bavarian", "Bavarian", "Bavarian", "Bavarian", "…
$ site           <chr> "a", "a", "a", "a", "a", "a", "a", "a", "a", "a", "a", "a", "a", "a", "a", "a", "a", …
```

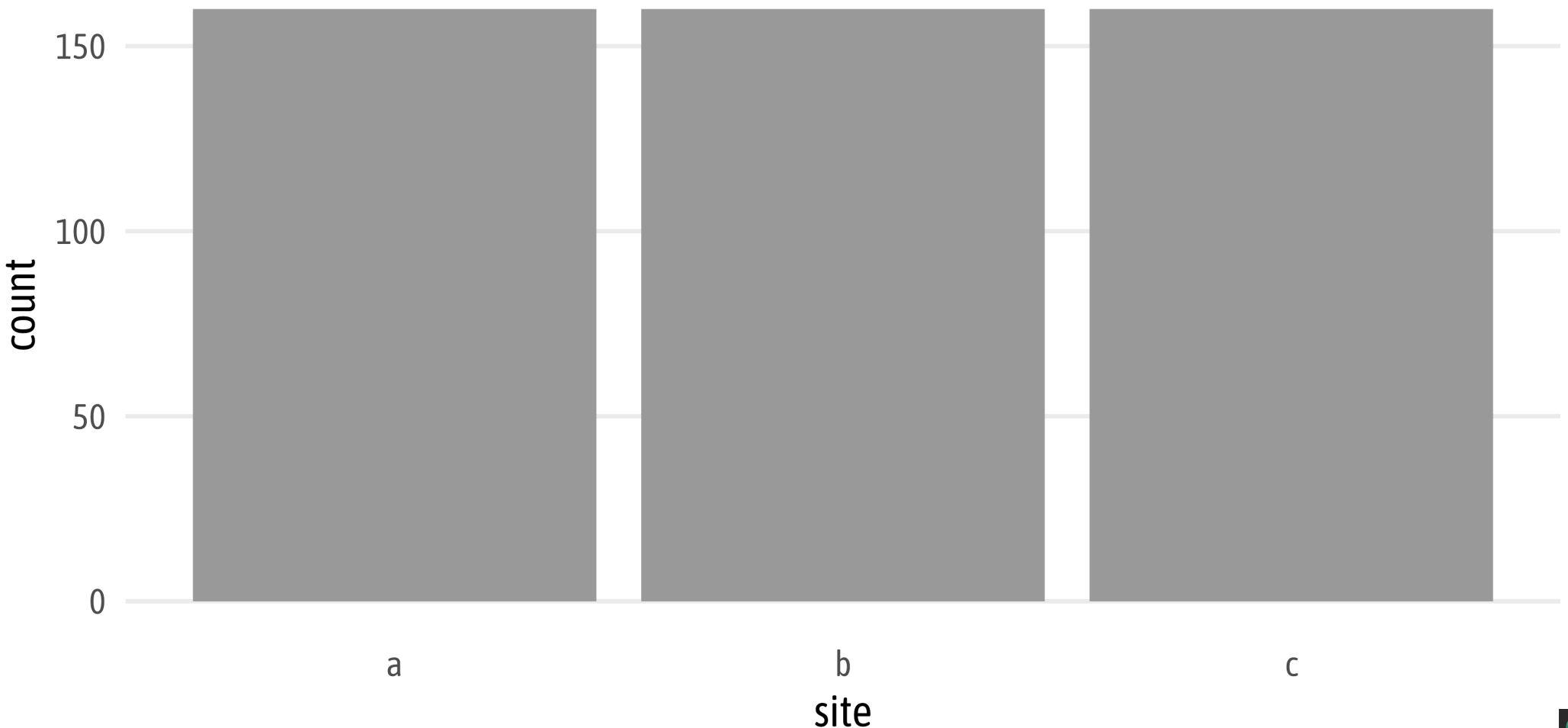

Visualize Distributions

```
1 ggplot(dragons, aes(x = mountain_range)) +
2   geom_bar(fill = "grey60") +
3   theme(panel.grid.major.x = element_blank())
```



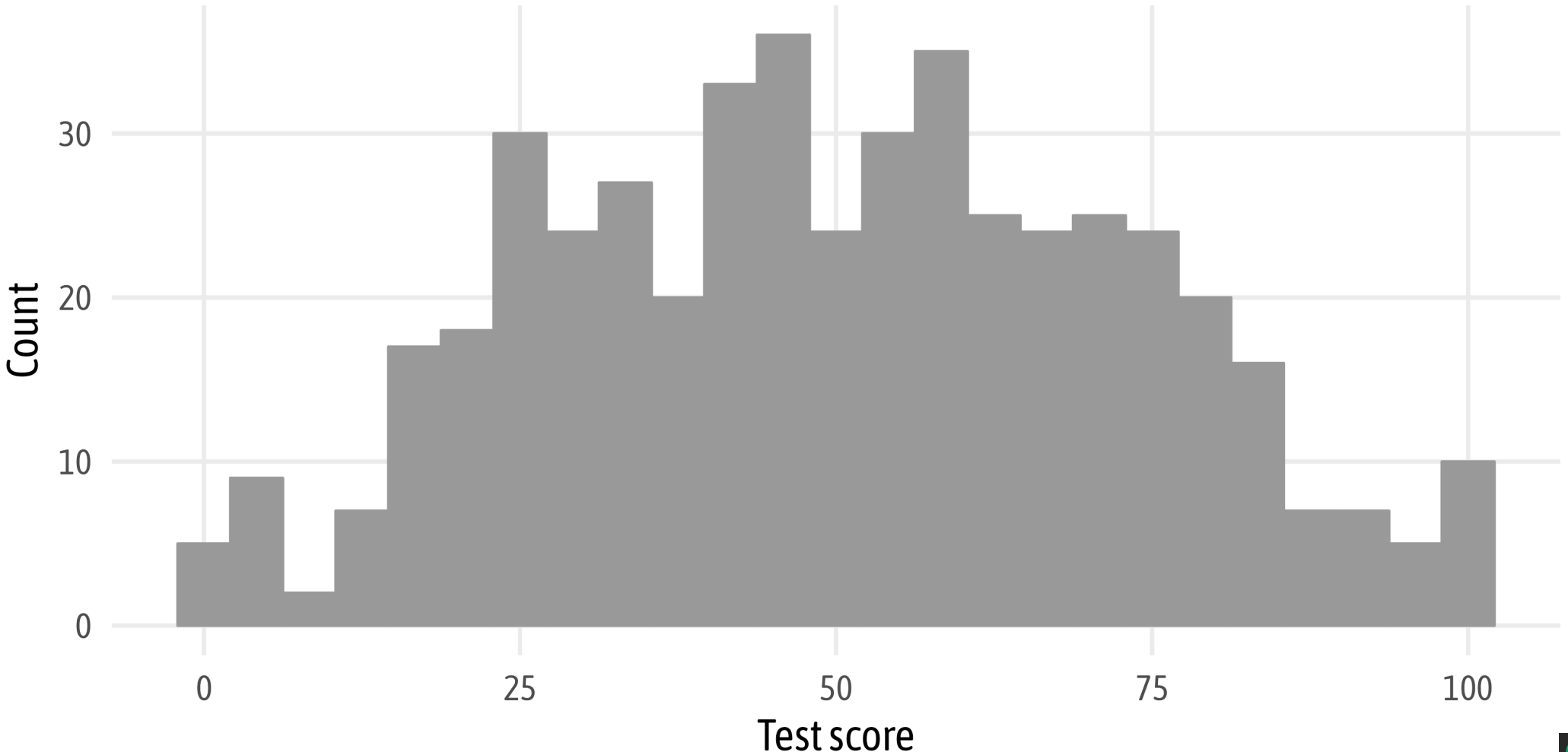
Visualize Distributions

```
1 ggplot(dragons, aes(x = site)) +
2   geom_bar(fill = "grey60") +
3   theme(panel.grid.major.x = element_blank())
```



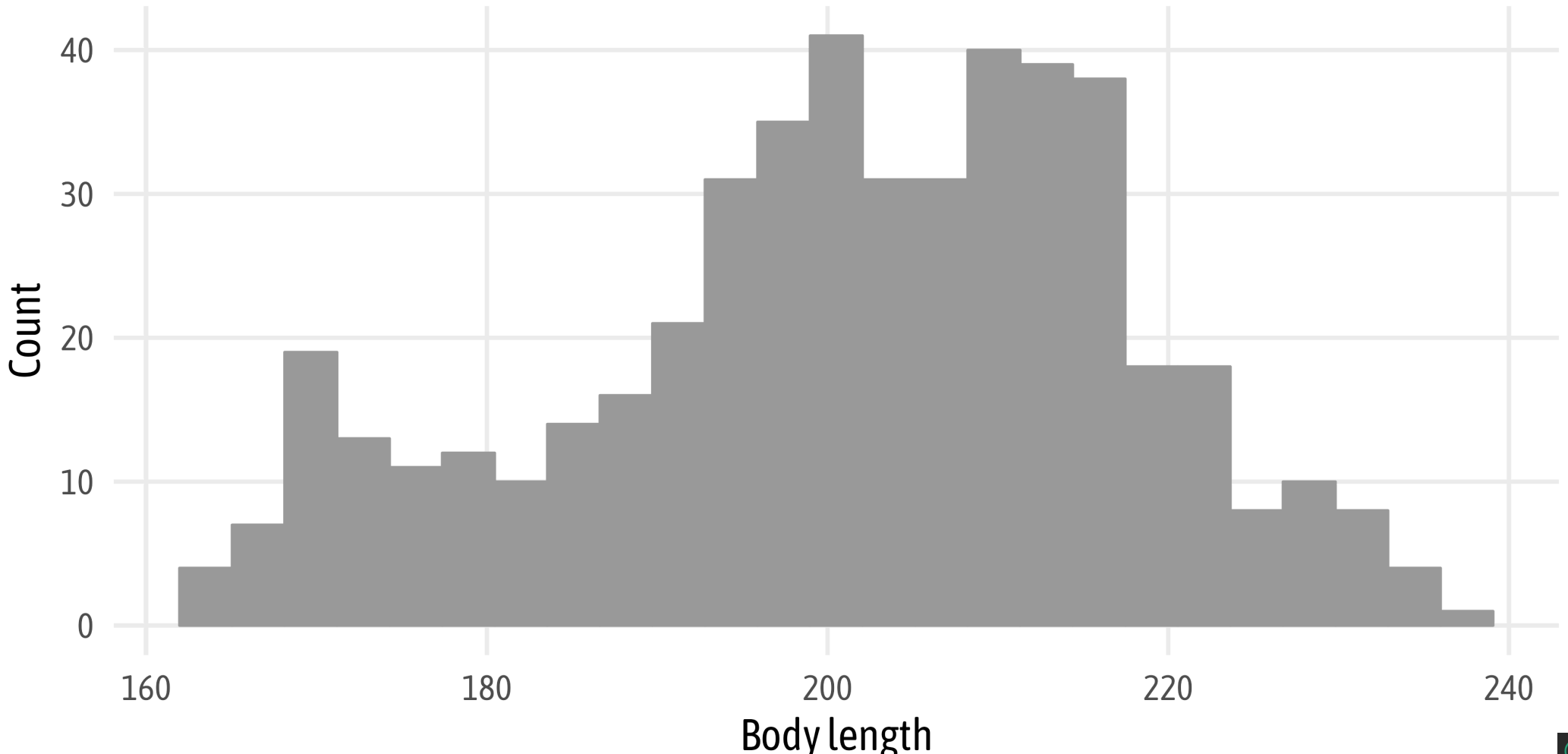
Visualize Distributions

```
1 ggplot(dragons, aes(x = test_score)) +
2   geom_histogram(bins = 25, color = "grey60", fill = "grey60") +
3   labs(x = "Test score", y = "Count")
```



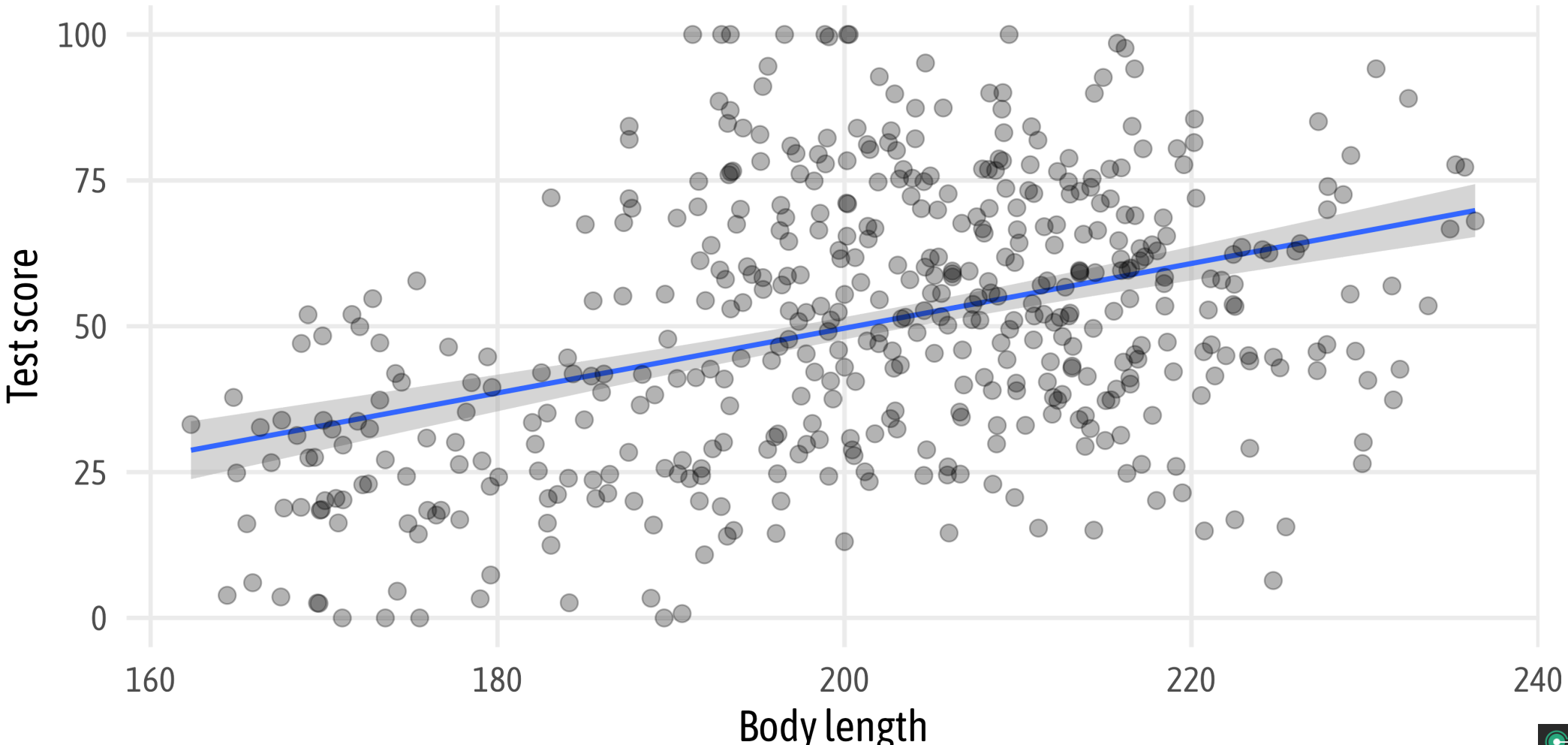
Visualize Distributions

```
1 ggplot(dragons, aes(x = body_length)) +
2   geom_histogram(bins = 25, color = "grey60", fill = "grey60") +
3   labs(x = "Body length", y = "Count")
```



Visualize Relationship

```
1 ggplot(dragons, aes(x = body_length, y = test_score)) +
2   stat_smooth(method = "lm") + geom_point(size = 3, alpha = .3) +
3   labs(x = "Body length", y = "Test score")
```



Run Linear Model

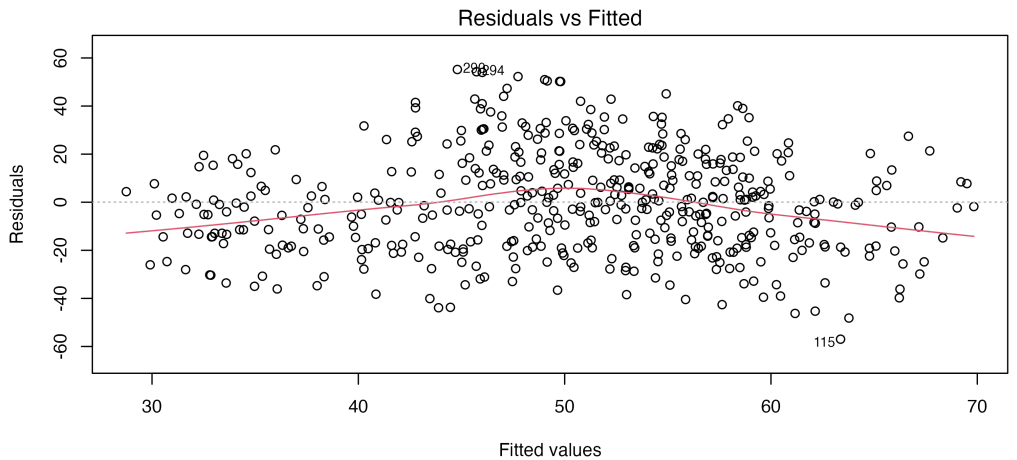
```
1  lm_dragons <- lm(test_score ~ body_length, data = dragons)
```

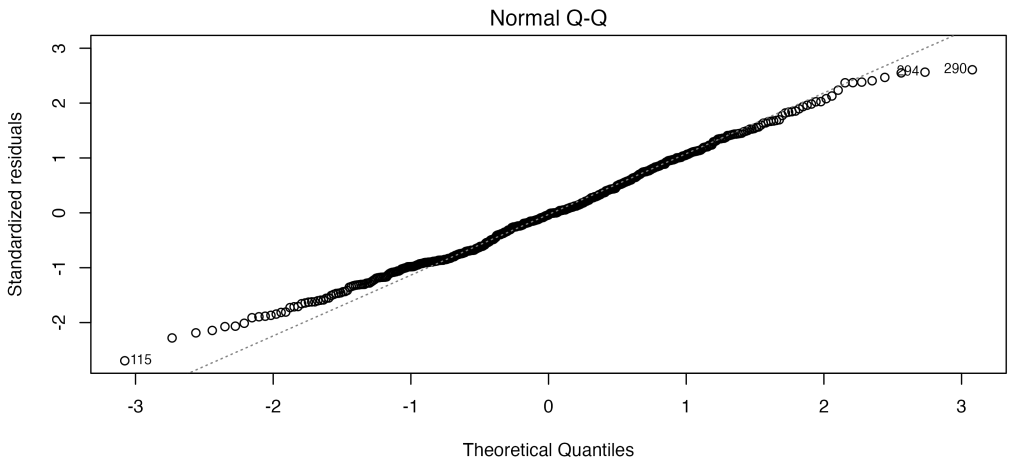
```
1  summary(lm_dragons)
```

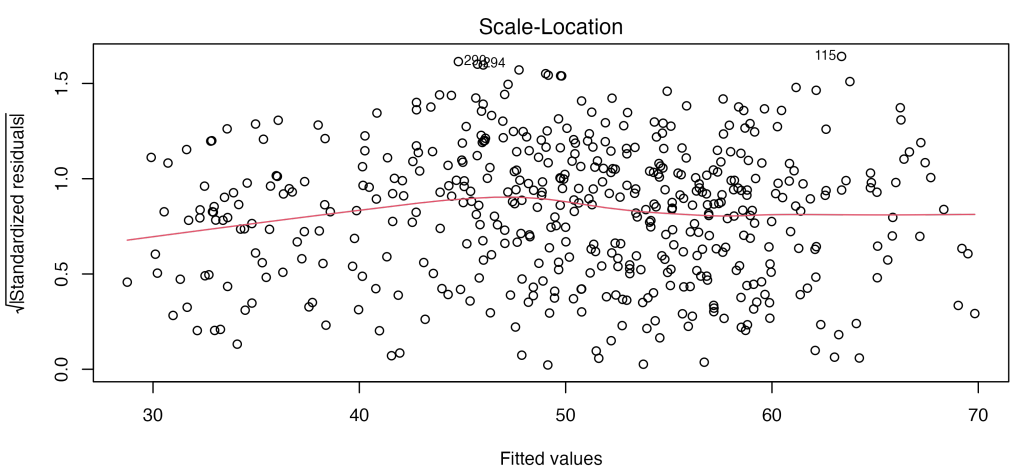
```
Call:
lm(formula = test_score ~ body_length, data = dragons)

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) -61.31783   12.06694  -5.081 5.38e-07 ***
body_length   0.55487    0.05975   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
```

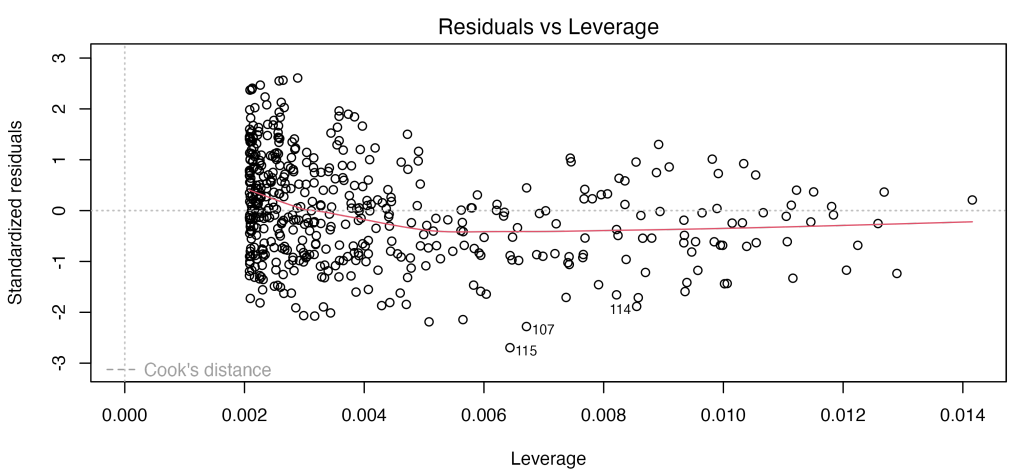

Verify Assumptions for LM

```
1 plot(lm_dragons)
```









Test for Normality

```
1  shapiro.test(residuals(lm_dragons))
```

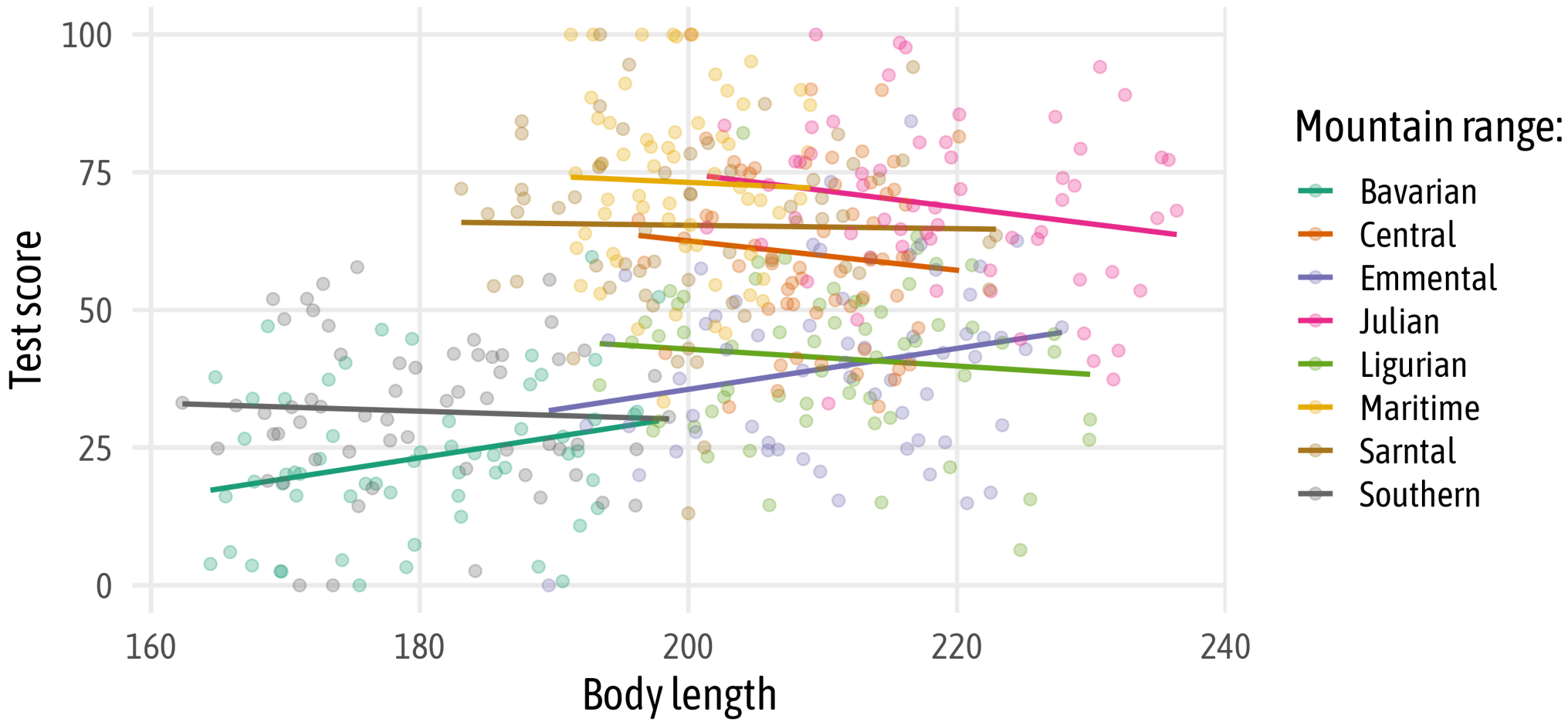
```
    Shapiro-Wilk normality test

data:  residuals(lm_dragons)
W = 0.99277, p-value = 0.02053
```

Null hypothesis: values follow a normal distribution

→ We accept H_a. The residuals are not distributed normally.

Visualize Relationship incl. Groups

```
1 ggplot(dragons, aes(x = body_length, y = test_score, color = mountain_range)) +
2   stat_smooth(method = "lm", se = FALSE) + geom_point(size = 2, alpha = .3) +
3   labs(x = "Body length", y = "Test score") +
4   scale_color_brewer(palette = "Dark2", name = "Mountain range:")
```



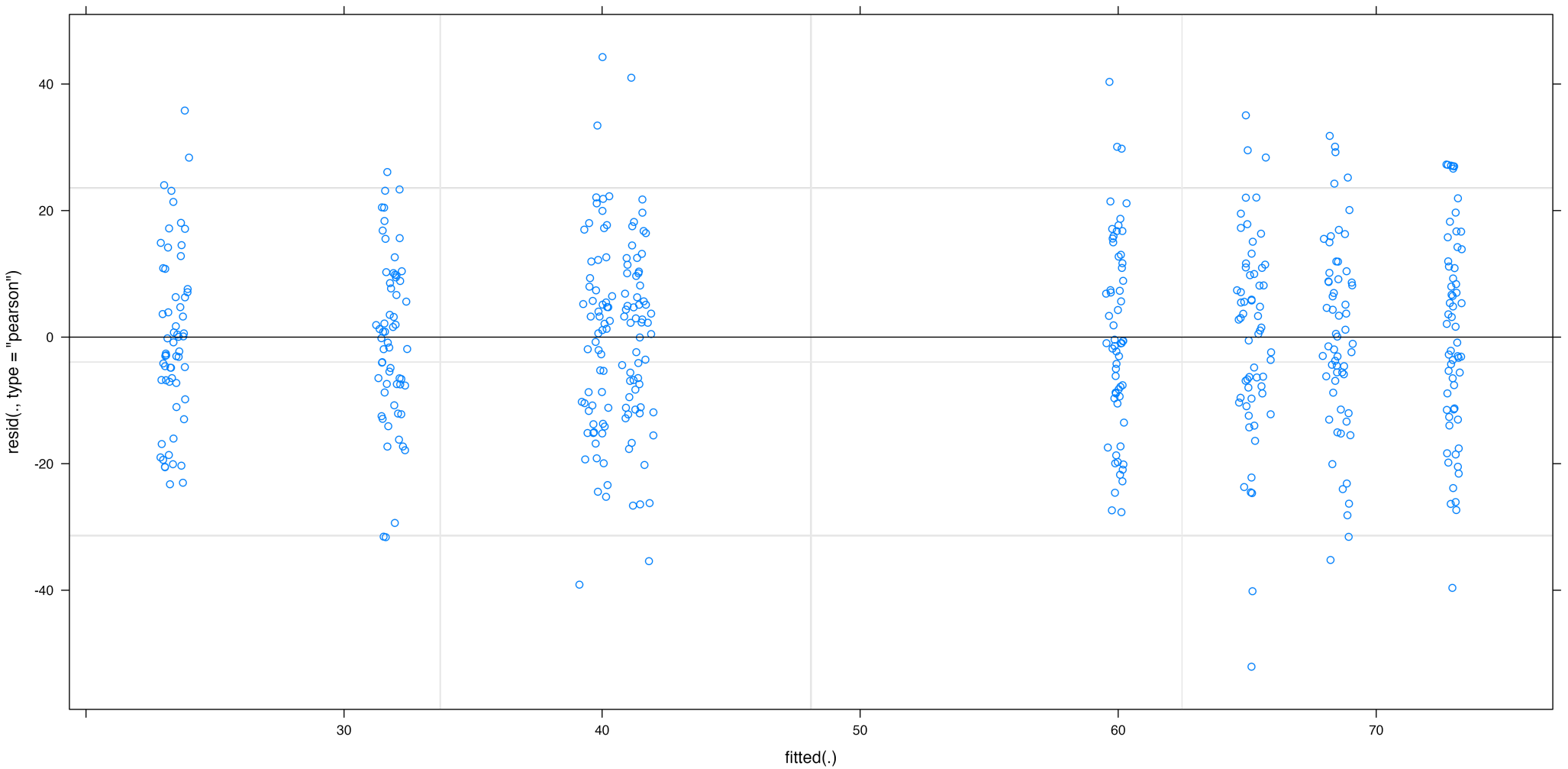
Run Linear Mixed Model

We run a model with random intercept only:

```
1  lmm_dragons1 <- lme4::lmer(test_score ~ body_length + (1 | mountain_range), data = dragons)
```


Verify Assumptions for LMM

```
1  plot(lmm_dragons1)
```



Test for Normality

```
1  shapiro.test(residuals(lmm_dragons1))
```

```
    Shapiro-Wilk normality test

data:  residuals(lmm_dragons1)
W = 0.99883, p-value = 0.9899
```

Null hypothesis: values follow a normal distribution

→ We reject H_a. The residuals are distributed normally.

Inspect Model Outcomes

```
summary(lmm_dragons1)
```

```
Linear mixed model fit by REML ['lmerMod']
Formula: test_score ~ body_length + (1 | mountain_range)
   Data: dragons

REML criterion at convergence: 3991.2

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

Random effects:
 Groups         Name        Variance Std.Dev.
 mountain_range (Intercept) 339.7    18.43
 Residual                   223.8    14.96
Number of obs: 480, groups:  mountain_range, 8

Fixed effects:
            Estimate Std. Error t value
(Intercept) 43.70938   17.13489   2.551
```

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

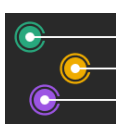
```
[1] 60.28394
```

→ Differences between mountain ranges explain ~60% of the variance.

Inspect Model Outcomes

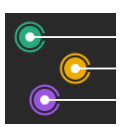
```
1  anova(lmm_dragons1)
```

```
Analysis of Variance Table
            npar Sum Sq Mean Sq F value
body_length    1   39.8    39.8  0.1778
```

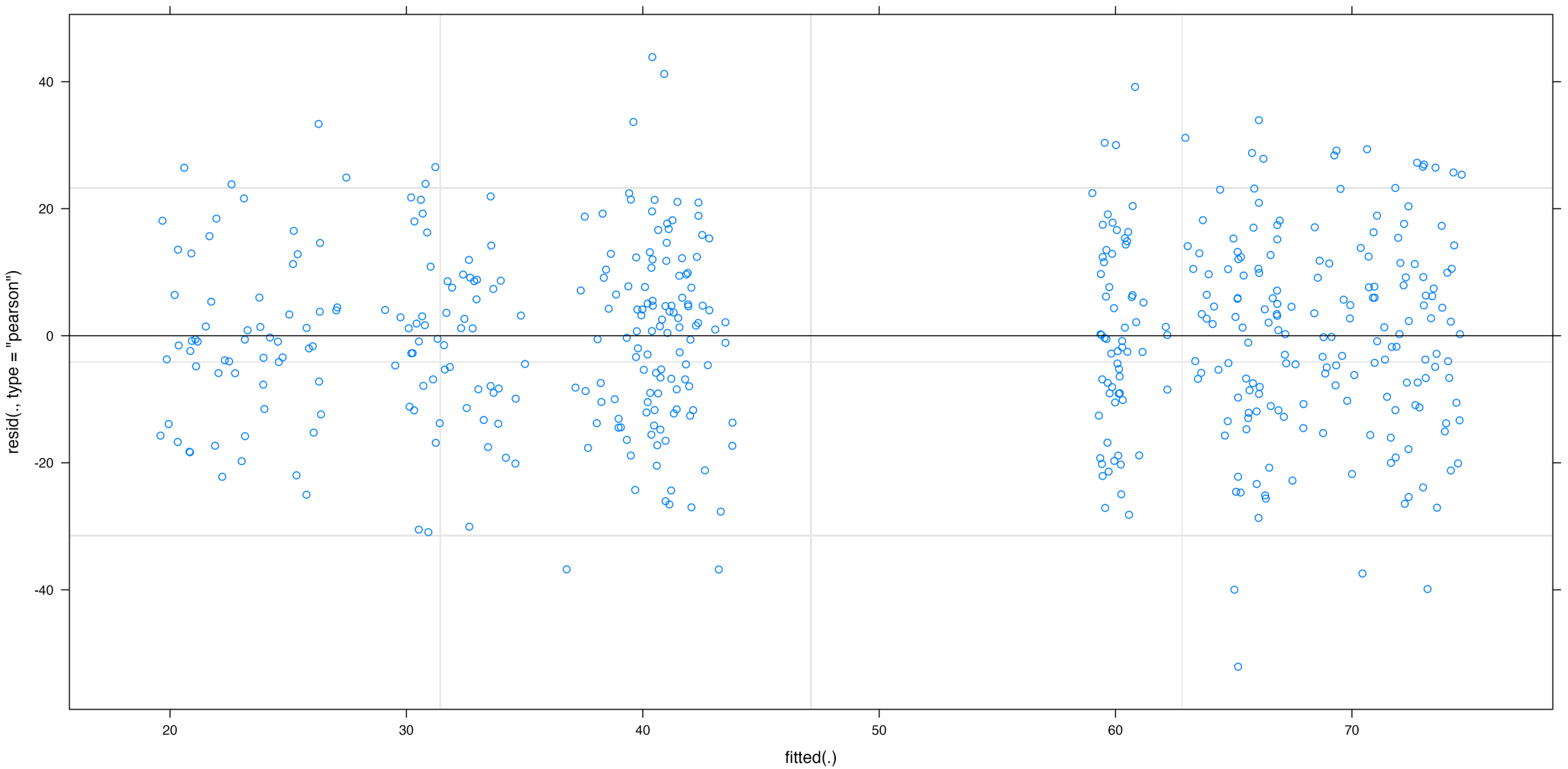
Add Random Slope

```
1  lmm_dragons2 <- lme4::lmer(test_score ~ body_length + (1 + body_length | mountain_range), data = dr
```

Verify Assumptions for 2nd LMM

```
1  plot(lmm_dragons2)
```



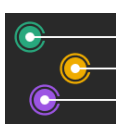
Test for Normality

```
1  shapiro.test(residuals(lmm_dragons2))
```

```
    Shapiro-Wilk normality test

data:  residuals(lmm_dragons2)
W = 0.9988, p-value = 0.9885
```

Null hypothesis: values follow a normal distribution

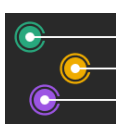
→ We reject H_a. The residuals are distributed normally.



Model Outcomes

```
1 summary(lmm_dragons2)
```

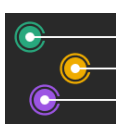
```
Linear mixed model fit by REML ['lmerMod']
Formula: test_score ~ body_length + (1 + body_length | mountain_range)
   Data: dragons

REML criterion at convergence: 3986.1

Scaled residuals:
    Min      1Q  Median      3Q     Max
-3.4983 -0.6666  0.0170  0.6636  2.9454

Random effects:
 Groups         Name        Variance  Std.Dev. Corr
 mountain_range (Intercept) 2.757e+03 52.5027
                body_length 3.047e-02  0.1745  -1.00
 Residual                   2.218e+02 14.8940
Number of obs: 480, groups:  mountain_range, 8

Fixed effects:
             Estimate Std. Error t value
```

Model Outcomes

```
1 anova(lmm_dragons2)
```

```
Analysis of Variance Table
            npar    Sum Sq   Mean Sq F value
body_length    1 0.0071647 0.0071647       0
```

Compare Models

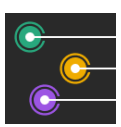
```
1 anova(lmm_dragons1, lmm_dragons2)
```

```
Data: dragons
Models:
lmm_dragons1: test_score ~ body_length + (1 | mountain_range)
lmm_dragons2: test_score ~ body_length + (1 + body_length | mountain_range)
             npar    AIC    BIC  logLik deviance  Chisq Df Pr(>Chisq)
lmm_dragons1    4 4001.5 4018.2 -1996.7   3993.5
lmm_dragons2    6 4000.3 4025.3 -1994.1   3988.3 5.2019  2     0.0742 .
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

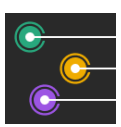
→ We reject H_a. The complex model is not more parsimonious.

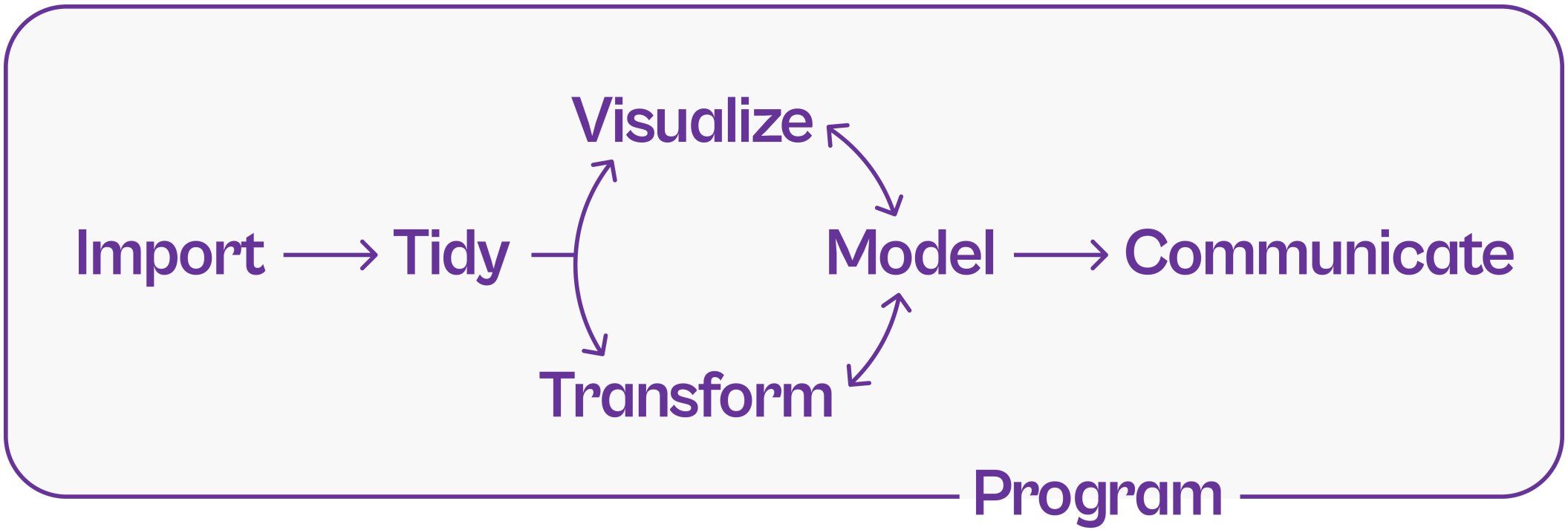
Resources

- "YaRrr! The Pirate's Guide to R" (Ch. 13-15)
- "Introduction to Linear Mixed Models" 🐲
- "R for Psych" (Ch. 6-9)
- "R Cookbook" (Ch. 9+11)
- tiymodels Get-Started Tutorial
- {dharma} Package (diagnostics for hiercharchical models)

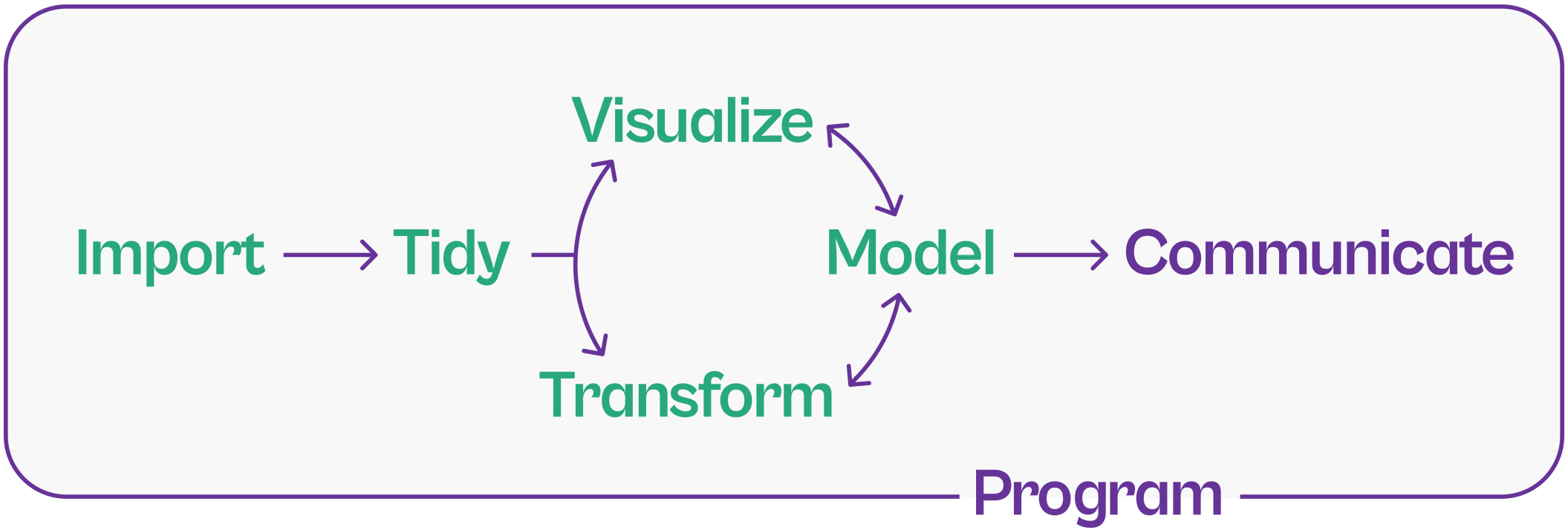


What's Next?

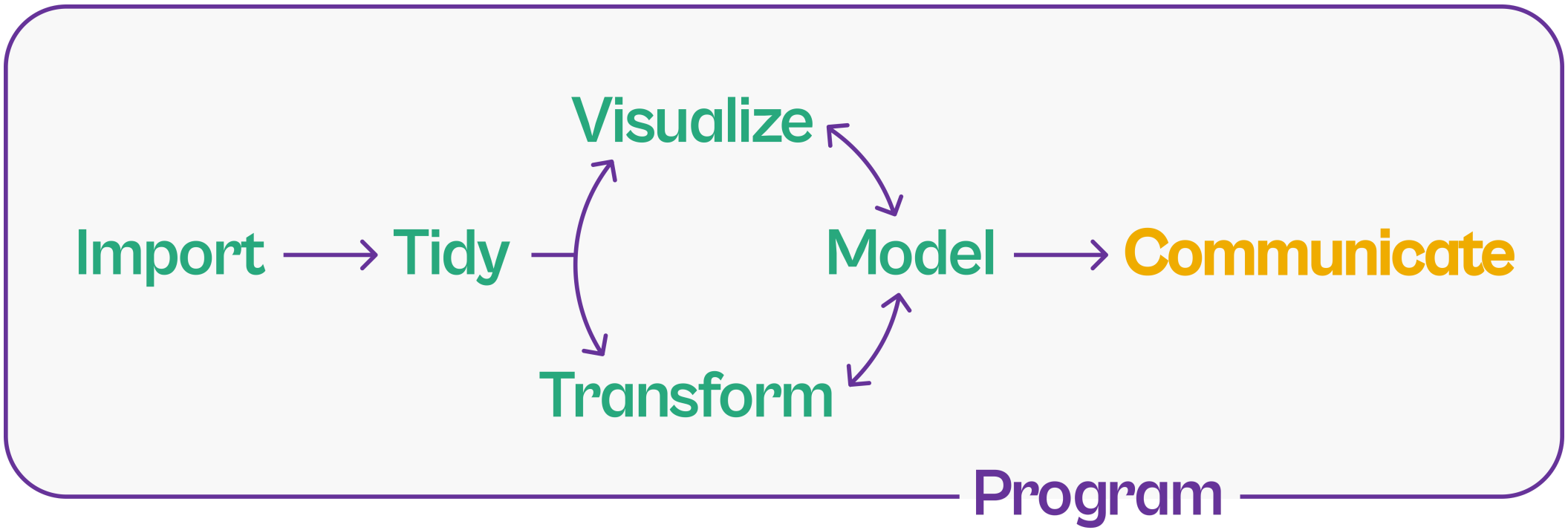




The data science workflow, modified from "R for Data Science"



The data science workflow, modified from "R for Data Science"



The data science workflow, modified from "R for Data Science"

That's it Folks...

— Thank you! —