University of Antwerp

ico

ICO Workshop R & RStudio

Part 5

Statistical analyses in R

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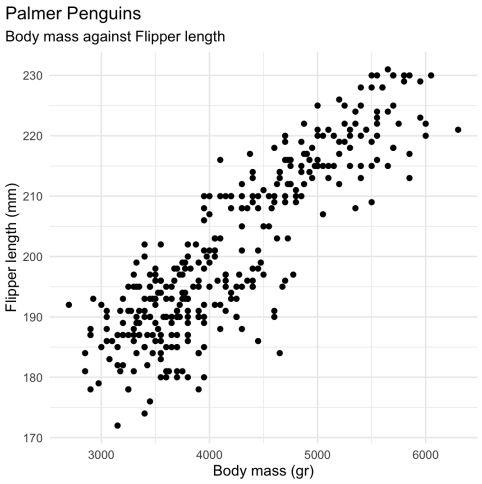
Overview

- Correlation --- (Click here)
- t-test --- (Click here)
- Linear regression --- (Click here)
- Other analyses --- (Click here)

1. Correlation

The `cor( )` function



Watch out for NA's!!

```
library(palmerpenguins)
data("penguins")

cor(penguins$flipper_length_mm,
    penguins$body_mass_g)
```

```
## [1] NA
```

```
cor(penguins$flipper_length_mm,
    penguins$body_mass_g,
   use = "complete.obs")
```

```
## [1] 0.8712018
```

Statistical tests with `cor.test( )`

```
cor.test(penguins$flipper_length_mm,
         penguins$body_mass_g)
```

```
##
##     Pearson's product-moment correlation
##
## data:  penguins$flipper_length_mm and penguins$body_mass_g
## t = 32.722, df = 340, p-value < 2.2e-16
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
##  0.843041 0.894599
## sample estimates:
##       cor
## 0.8712018
```


The `broom` package

- Package in `tidyverse`
- Creates **tibbles** based on results from a statistical analysis!

`tidy()`: output from an analysis as a tibble

```
library(broom)
C <- cor.test(penguins$flipper_length_mm,
         penguins$body_mass_g)

tidy(C)
```

```
## # A tibble: 1 × 8
##   estimate statistic   p.value parameter conf.low conf.high method       alter…¹
##      <dbl>     <dbl>     <dbl>     <int>    <dbl>     <dbl> <chr>        <chr>
## 1    0.871      32.7 4.37e-107       340    0.843     0.895 Pearson's p… two.si…
## # … with abbreviated variable name ¹alternative
```

Correlation between multiple variabeles

```
penguins %>%
  select(
    bill_depth_mm,
    bill_length_mm,
    flipper_length_mm,
    body_mass_g
  ) %>%
  cor(use = "pairwise.complete.obs")
```

```
##                   bill_depth_mm bill_length_mm flipper_length_mm body_mass_g
## bill_depth_mm         1.0000000     -0.2350529        -0.5838512  -0.4719156
## bill_length_mm       -0.2350529      1.0000000         0.6561813   0.5951098
## flipper_length_mm    -0.5838512      0.6561813         1.0000000   0.8712018
## body_mass_g          -0.4719156      0.5951098         0.8712018   1.0000000
```

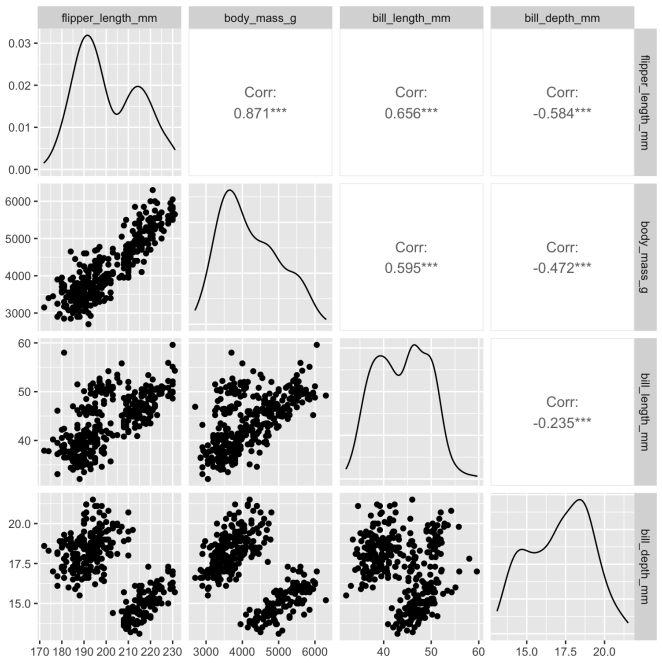

Correlations between multiple variabeles visualized

Package: `GGally`

Function: `ggpairs()`

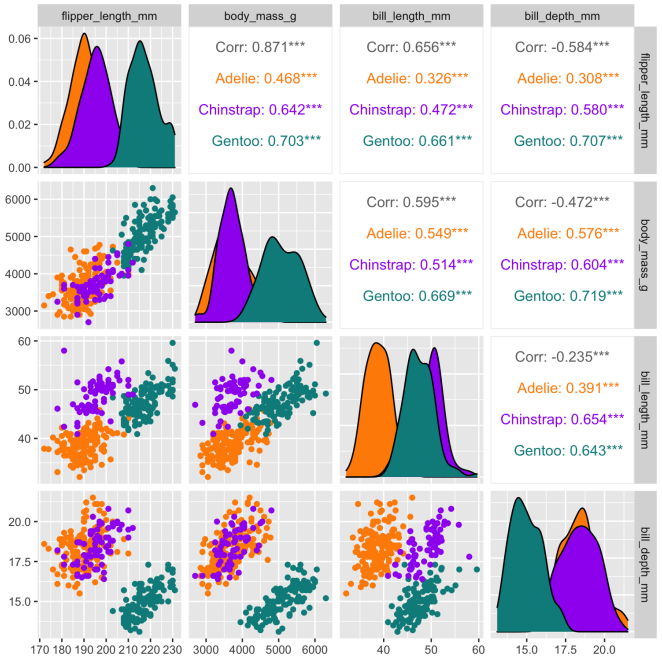
Result: a ggplot object...

```
library(GGally)
penguins %>%
  select(
    species,
    bill_depth_mm,
    bill_length_mm,
    flipper_length_mm,
    body_mass_g
  ) %>%
  ggpairs(
    columns = c(
      "flipper_length_mm", "body_mass_g",
      "bill_length_mm", "bill_depth_mm")
    )
```



Correlations between multiple variabeles visualized WITH COLOR!

```
penguins %>%
  select(
    species,
    bill_depth_mm,
    bill_length_mm,
    flipper_length_mm,
    body_mass_g
  ) %>%
  ggpairs(
    aes(color = species),
    columns = c(
      "flipper_length_mm", "body_mass_g",
      "bill_length_mm", "bill_depth_mm")) +
  scale_colour_manual(
    values = c("darkorange","purple","cyan4")) +
  scale_fill_manual(
    values = c("darkorange","purple","cyan4"))
```



2. t-test

First some descriptives

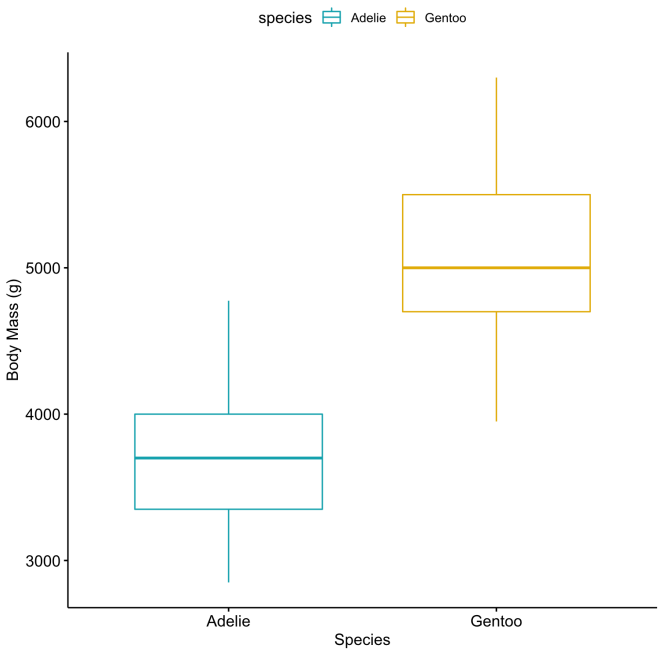
Compare Gentoo with Adelie penguins on `body_mass_g`

```
library(kableExtra)
penguins %>%
  select(
    species,
    body_mass_g
  ) %>%
  filter(
    species == 'Adelie' | species == 'Gentoo'
  ) %>%
  group_by(species) %>%
  summarize(
    count = n(),
    mean = mean(body_mass_g, na.rm = TRUE),
    sd = sd(body_mass_g, na.rm = TRUE)
  ) %>%
  kable()
```

species	count	mean	sd
Adelie	152	3700.662	458.5661
Gentoo	124	5076.016	504.1162

Create boxplots with `ggpubr` package

```
# install.packages(ggpubr)

library(ggpubr)
penguins %>%
  select(
    species,
    body_mass_g
  ) %>%
  filter(
    species == 'Adelie' | species == 'Gentoo'
  ) %>%
  ggboxplot(
    x = "species", y = "body_mass_g",
          color = "species", palette = c("#00AFBB", "#E7B800"),
        ylab = "Body Mass (g)", xlab = "Species")
```



Checking the assumptions of equal variances with `var.test()` function

```
p <- penguins %>%
  select(
    species,
    body_mass_g
  ) %>%
  filter(
    species == 'Adelie' | species == 'Gentoo'
  )

var.test(body_mass_g ~ species, data= p)
```

```
##
##     F test to compare two variances
##
## data:  body_mass_g by species
## F = 0.82745, num df = 150, denom df = 122, p-value
## alternative hypothesis: true ratio of variances is
## 95 percent confidence interval:
##  0.5875588 1.1583164
## sample estimates:
## ratio of variances
##          0.8274515
```


Perform unpaired t-test with `t.test()` function

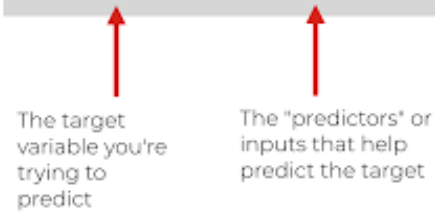
```
p <- penguins %>%
  select(
    species,
    body_mass_g
  ) %>%
  filter(
    species == 'Adelie' | species == 'Gentoo'
  )

t.test(body_mass_g ~ species, data= p, var.equal = TRUE)
```

```
##
##     Two Sample t-test
##
## data:  body_mass_g by species
## t = -23.614, df = 272, p-value < 2.2e-16
## alternative hypothesis: true difference in means b
## 95 percent confidence interval:
##  -1490.021 -1260.687
## sample estimates:
## mean in group Adelie mean in group Gentoo
##             3700.662             5076.016
```

3. Linear regression

lm()

```
lm(target ~ predictor, data = df )
```




```
Model1 <- lm(flipper_length_mm ~ body_mass_g,
             data = penguins)
```

Model results with `summary()`

```
summary(Model1)
```

```
##
## Call:
## lm(formula = flipper_length_mm ~ body_mass_g, data = penguins)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -23.7626  -4.9138   0.9891   5.1166  16.6392
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept) 1.367e+02  1.997e+00   68.47   <2e-16 ***
## body_mass_g 1.528e-02  4.668e-04   32.72   <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 6.913 on 340 degrees of freedom
##   (2 observations deleted due to missingness)
## Multiple R-squared:  0.759,    Adjusted R-squared:  0.7583
## F-statistic:  1071 on 1 and 340 DF,  p-value: < 2.2e-16
```


The `broom` package

Function: `tidy()`

Result: tidy dataset with information on **parameter estimates**

```
tidy(Model1,
     conf.int = TRUE,
     conf.level = .90)
```

```
## # A tibble: 2 × 7
##   term        estimate std.error statistic   p.value conf.low conf.high
##   <chr>          <dbl>     <dbl>     <dbl>     <dbl>    <dbl>     <dbl>
## 1 (Intercept) 137.      2.00          68.5 5.71e-201 133.      140.
## 2 body_mass_g   0.0153  0.000467      32.7 4.37e-107   0.0145    0.0160
```

The broom package + kable()


```
tidy(Model1,
     conf.int = TRUE,
     conf.level = .90) %>%
  kable()
```

term	estimate	std.error	statistic	p.value	conf.low	conf.high
(Intercept)	136.7295593	1.9968354	68.47312	0	133.4360836	140.0230350
body_mass_g	0.0152759	0.0004668	32.72223	0	0.0145059	0.0160459

The broom package

Function: `glance()`

Result: tidy dataset with information on **model fit**

```
glance(Model1)
```

```
## # A tibble: 1 × 12
##   r.squared adj.r.squ…¹ sigma stati…²   p.value    df logLik   AIC   BIC devia…³
##       <dbl>       <dbl> <dbl>   <dbl>     <dbl> <dbl>  <dbl> <dbl> <dbl>   <dbl>
## 1     0.759       0.758  6.91   1071. 4.37e-107     1 -1146. 2297. 2309.  16250.
## # … with 2 more variables: df.residual <int>, nobs <int>, and abbreviated
## #   variable names ¹adj.r.squared, ²statistic, ³deviance
```

The broom package

Function: `augment()`

Result: add information to the dataset based on the model like **fitted values**, **residuals**, ...

```
augment(Model1)
```

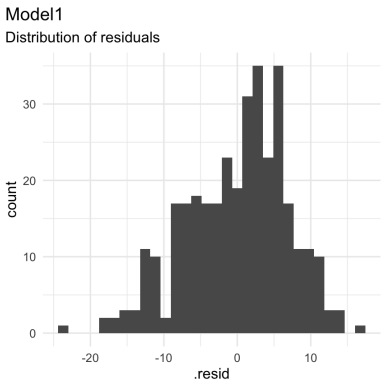
```
## # A tibble: 342 × 9
##    .rownames flipper_len…¹ body_…² .fitted .resid    .hat .sigma .cooksd .std.…³
##    <chr>              <int>   <int>   <dbl>  <dbl>   <dbl>  <dbl>   <dbl>   <dbl>
##  1 1                    181    3750    194. -13.0  0.00385   6.89 6.88e-3  -1.89
##  2 2                    186    3800    195.  -8.78 0.00366   6.91 2.97e-3  -1.27
##  3 3                    195    3250    186.   8.62 0.00705   6.91 5.57e-3   1.25
##  4 5                    193    3450    189.   3.57 0.00550   6.92 7.41e-4   0.518
##  5 6                    190    3650    192.  -2.49 0.00431   6.92 2.81e-4  -0.360
##  6 7                    181    3625    192. -11.1  0.00444   6.90 5.78e-3  -1.61
##  7 8                    195    4675    208. -13.1  0.00395   6.89 7.19e-3  -1.91
##  8 9                    193    3475    190.   3.19 0.00533   6.92 5.73e-4   0.462
##  9 10                   190    4250    202. -11.7  0.00293   6.89 4.19e-3  -1.69
## 10 11                   186    3300    187.  -1.14 0.00663   6.92 9.14e-5  -0.165
## # … with 332 more rows, and abbreviated variable names ¹flipper_length_mm,
## #   ²body_mass_g, ³.std.resid
```


The broom package to check some assumptions

Functions: `augment()` + `geom_histogram()`

Result: Are the residuals normally distributed?

```
augment(Model1) %>%
  select(.resid) %>%
  ggplot(
    aes(
      x = .resid
    )
  ) +
  geom_histogram() +
  theme_minimal() +
  labs(
    title = "Model1",
    subtitle = "Distribution of residuals"
  ) +
  theme(plot.title.position = "plot")
```

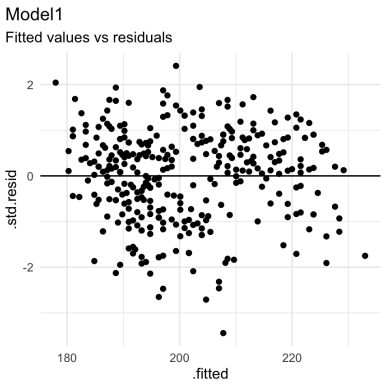


The broom package to check some assumptions

Functions: `augment()` + `geom_point()`

Resultaat: Homoscedasticity?

```
augment(Model1) %>%
  select(.fitted, .std.resid) %>%
  ggplot(
    aes(
      x = .fitted,
      y = .std.resid
    )
  ) +
  geom_point() +
  theme_minimal() +
  labs(
    title = "Model1",
    subtitle = "Fitted values vs residuals"
  ) + geom_hline(yintercept = 0) +
  theme(plot.title.position = "plot")
```

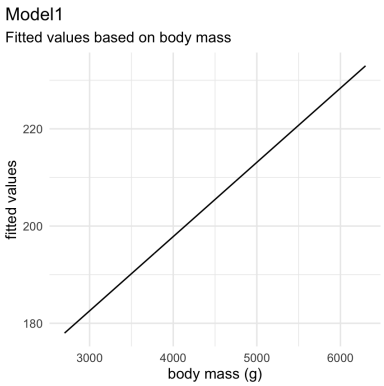


broom package to visualise model results

Functions: `augment()` + `geom_line()`

Result: Plot of the fitted regression model (the line)

```
augment(Model1) %>%
  select(.fitted, body_mass_g) %>%
  ggplot(
    aes(
      x = body_mass_g,
      y = .fitted
    )
  ) +
  geom_line() +
  theme_minimal() +
  labs(
    title = "Model1",
    subtitle = "Fitted values based on body m
    x = "body mass (g)",
    y = "fitted values"
  )  +
  theme(plot.title.position = "plot")
```



Multivariate regression

```
Model2 <- lm(
  flipper_length_mm ~ body_mass_g + sex + species,
  data = penguins
)

tidy(Model2) %>%
  kable()
```

term	estimate	std.error	statistic	p.value
(Intercept)	164.5887169	3.1836146	51.698694	0.0000000
body_mass_g	0.0065499	0.0009308	7.036742	0.0000000
sexmale	2.4777215	0.8540581	2.901116	0.0039696
speciesChinstrap	5.5444400	0.7852051	7.061136	0.0000000
speciesGentoo	18.0213174	1.4424942	12.493165	0.0000000

Model comparison

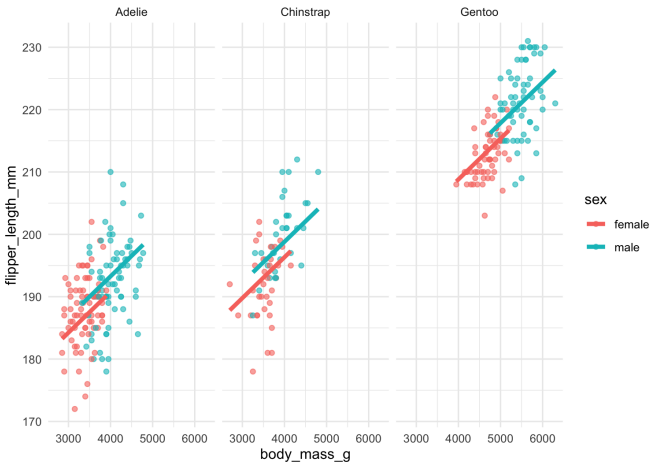
Model fit of multiple models:

```
M1_info <- glance(Model1) %>% select(r.squared, AIC, BIC)
M2_info <- glance(Model2) %>% select(r.squared, AIC, BIC)

M1_info %>% rbind(M2_info) %>% kable()
```

r.squared	AIC	BIC
0.7589925	2297.035	2308.540
0.8562944	2068.357	2091.206

Visualize this model

```
augment(Model2) %>%
  ggplot() +
  geom_point(
    aes(x = body_mass_g,
        y = flipper_length_mm,
        color = sex),
    alpha = .6
  ) +
  geom_line(
    aes(
      x = body_mass_g,
      y = .fitted,
      color = sex,
    ),
    size = 1.5
  ) +
  facet_wrap(.~species) +
  theme_minimal()
```



Some cool stuff with the `sjPlot` package

For instance, create an html-table with the estimates of two models: `Model1` & `Model2`

Function: `tab_model()`

```
library(sjPlot)
tab_model(Model1, Model2)
```

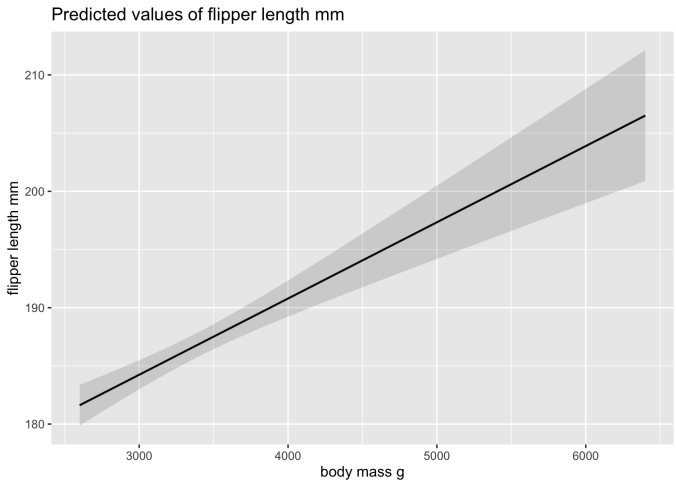
	flipper length mm			flipper length mm		
Predictors	*Estimates*	*CI*	*p*	*Estimates*	*CI*	*p*
(Intercept)	136.73	132.80 – 140.66	**<0.001**	164.59	158.33 – 170.85	**<0.001**
body mass g	0.02	0.01 – 0.02	**<0.001**	0.01	0.00 – 0.01	**<0.001**
sex [male]				2.48	0.80 – 4.16	**0.004**
species [Chinstrap]				5.54	4.00 – 7.09	**<0.001**
species [Gentoo]				18.02	15.18 – 20.86	**<0.001**
Observations	342			333		
R^2 / R^2 adjusted	0.759 / 0.758			0.856 / 0.855		

Some cool stuff with the `sjPlot` package

Create a plot of predicted values based on the effect of `body_mass_g`

Function: plot_model() with `type = "pred"` specifically to plot **predicted values**

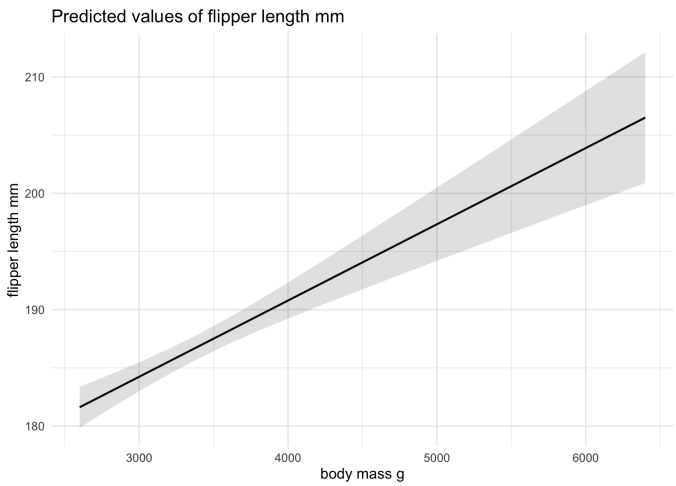
```
plot_model(Model2, type = "pred", terms = "body_mass_g")
```



Some cool stuff with the `sjPlot` package

Function: `plot_model()` creates a **`ggplot` object**! So we can customize it!

```
plot_model(Model2, type = "pred", terms = "body_mass_g") +
  theme_minimal()
```

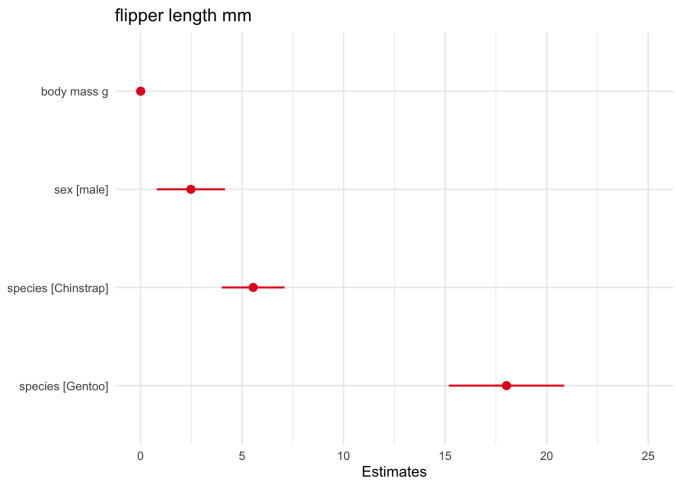


Some cool stuff with the `sjPlot` package

Create a plot of the different parameter estimates in the model

Function: plot_model() without a `type =` argument

```
plot_model(Model2) +
  theme_minimal()
```



Other Statistical Modelling in R

- Structural Equation Modelling: `lavaan`
- Multilevel analyses: `lme4`
- Cluster Analyses: `mclust`
- Factor Analyses (or PCA) & reliability analyses (e.g., Cronbach's alpha): `psych`
- Item Response Theory models: `ltm` or `sirt`
- Bayesian analyses (using MCMC): `brms`