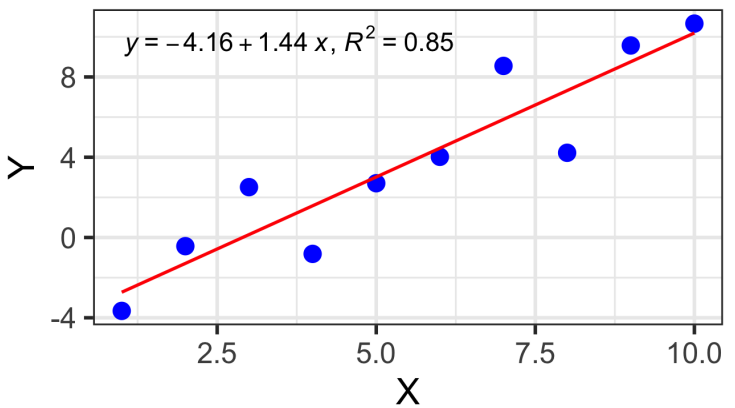
Multiple Regression

Week 4

Multiple Regression

- In **bivariate regresssion** we use X to predict Y:
  - $Y_i = \beta_0 + \beta_1 X + \varepsilon_i$
  - one **dependent variable** Y
    (the variable to be predicted)
  - one **independent variable** X
    (the variable we are using to predict Y)
  - N different observations of
    (X_i, Y_i), for $i = 1 \ldots N$
  - two model coefficients:
    - β_0 (intercept)
    - β_1 (slope)



Multiple Regression

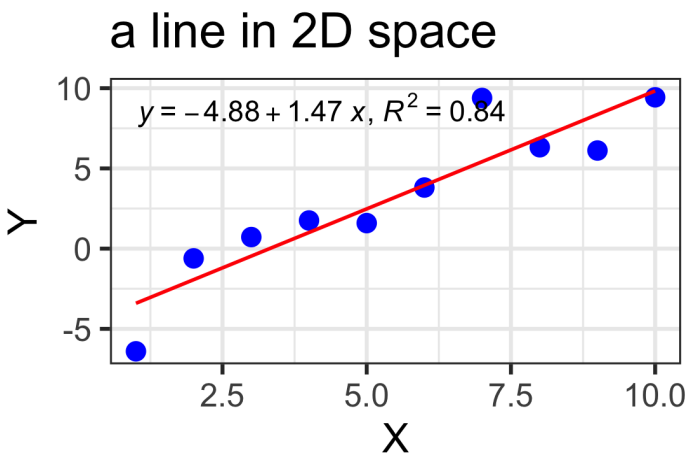
- In **Multiple Regression**: we use N *predictor variables* $X_1, X_2, \ldots X_N$ to predict Y
  - $Y_i = \beta_0 + \beta_1 X_{i1} + \beta_2 X_{i2} + \cdots + \beta_k X_{ik} + \varepsilon_i$
  - one **dependent variable** Y (the variable to be predicted)
  - K **independent variables** X_k, for $k = 1 \ldots K$
  - N different observations (X_{ik}, Y_i), for $i = 1 \ldots N$
  - $k + 1$ model coefficients β (*one slope for each* X_i plus a model intercept β_0)

$$Y_i = \beta_0 + \sum_{k=1}^{K} (\beta_k X_{ik}) + \varepsilon_i$$

(for $i = 1 \ldots N$ observations)

1 predictor

- $Y_i = \beta_0 + \beta_1 X + \varepsilon_i$
- one **dependent variable** Y
  (the variable to be predicted)
- one **independent variable** X
  (the variable we are using to predict Y)
- N different observations of
  (X_i, Y_i), for $i = 1 \ldots N$
- two model coefficients:
  - β_0 (intercept)
  - β_1 (slope)

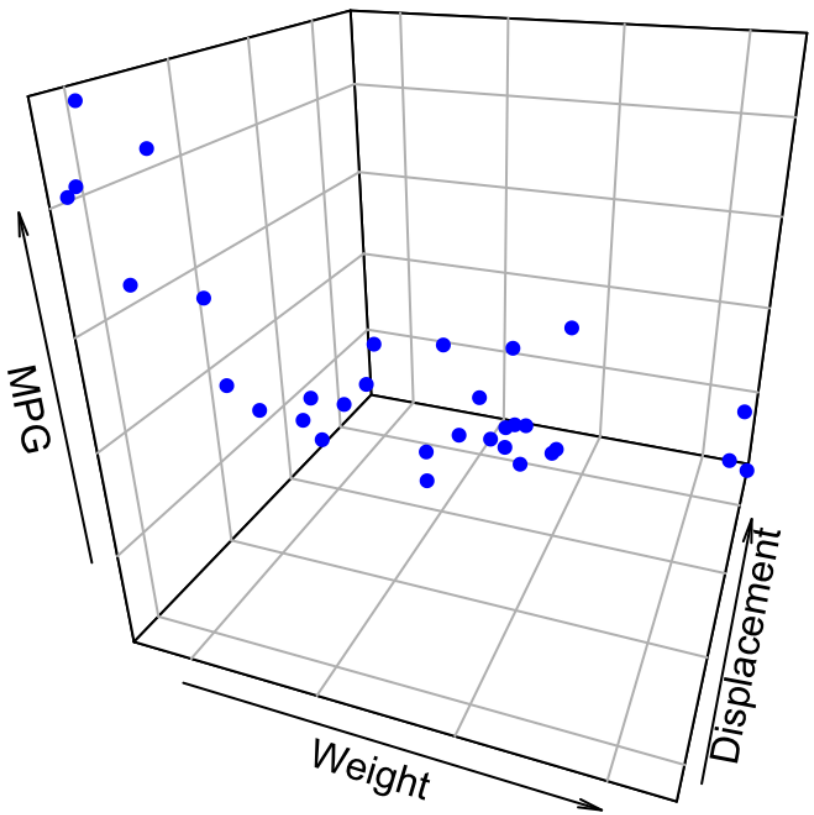


2 predictors

- $Y_i = \beta_0 + \beta_1 X_{i1} + \beta_2 X_{i2} + \varepsilon_i$
- Model a car's fuel efficiency (MPG) as a function of:
  - the weight of the car
  - the car's engine size
- Y: MPG of cars
- X_1: car weight
- X_2: engine size
- β_1: dependence of (**slope** of) MPG (Y) on car weight (X_1)
- β_2: dependence of (**slope** of) MPG (Y) on engine size (X_2)
- β_0: **intercept** — predicted MPG (Y) when car weight and engine size are both zero

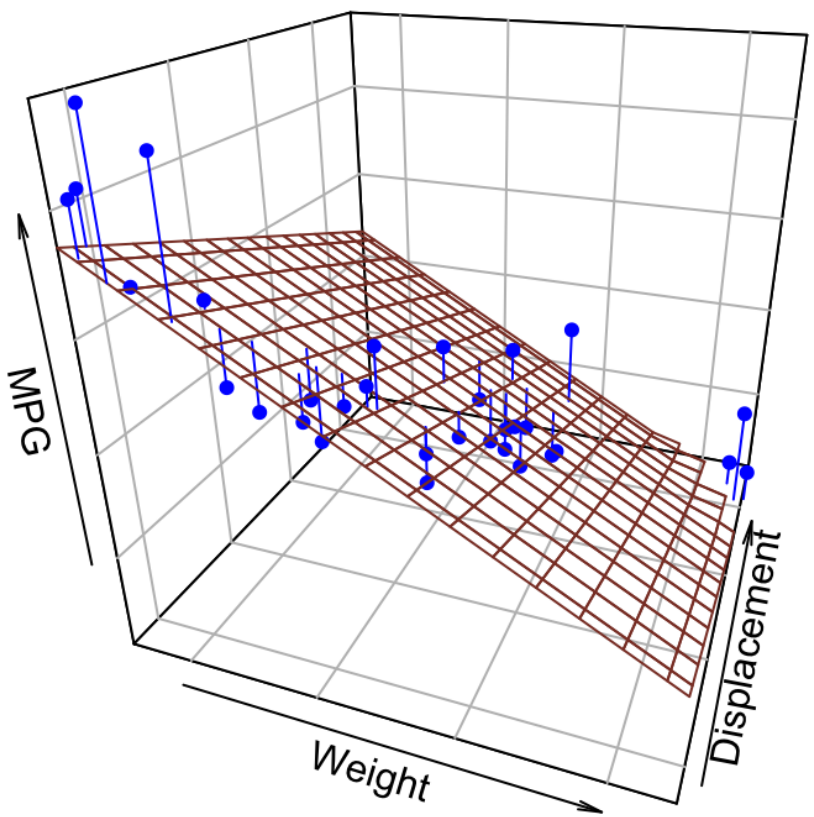
2 predictors

- $Y_i = \beta_0 + \beta_1 X_{i1} + \beta_2 X_{i2} + \varepsilon_i$
- `MPG ~ Weight + Displacement` (using the `mtcars` built-in dataset)



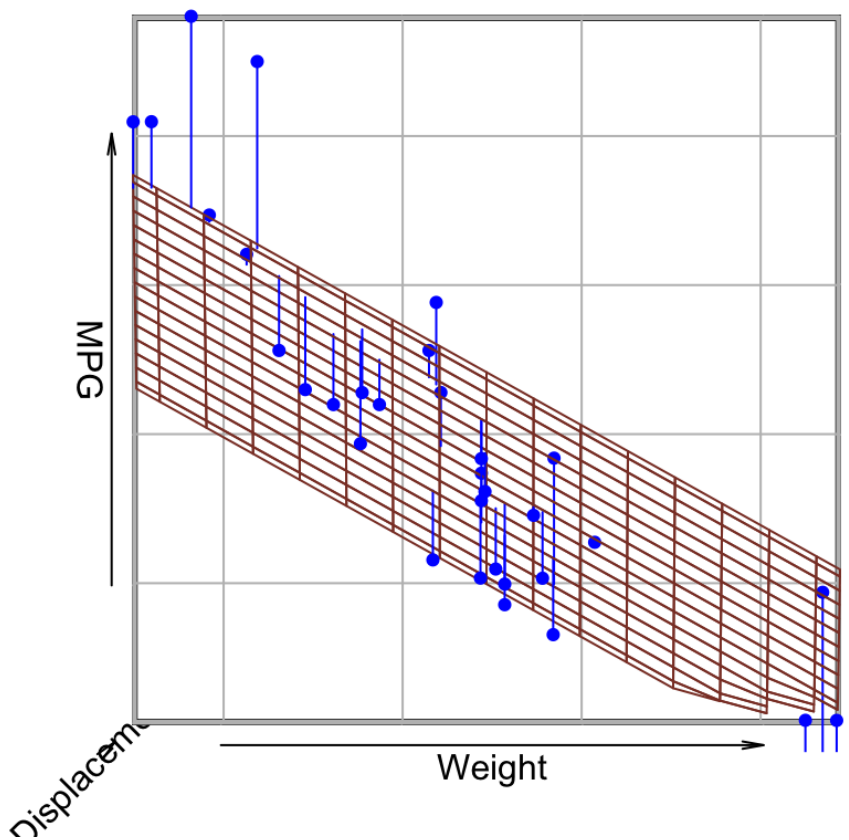
2 predictors

- $Y_i = \beta_0 + \beta_1 X_{i1} + \beta_2 X_{i2} + \varepsilon_i$
- `MPG ~ Weight + Displacement`



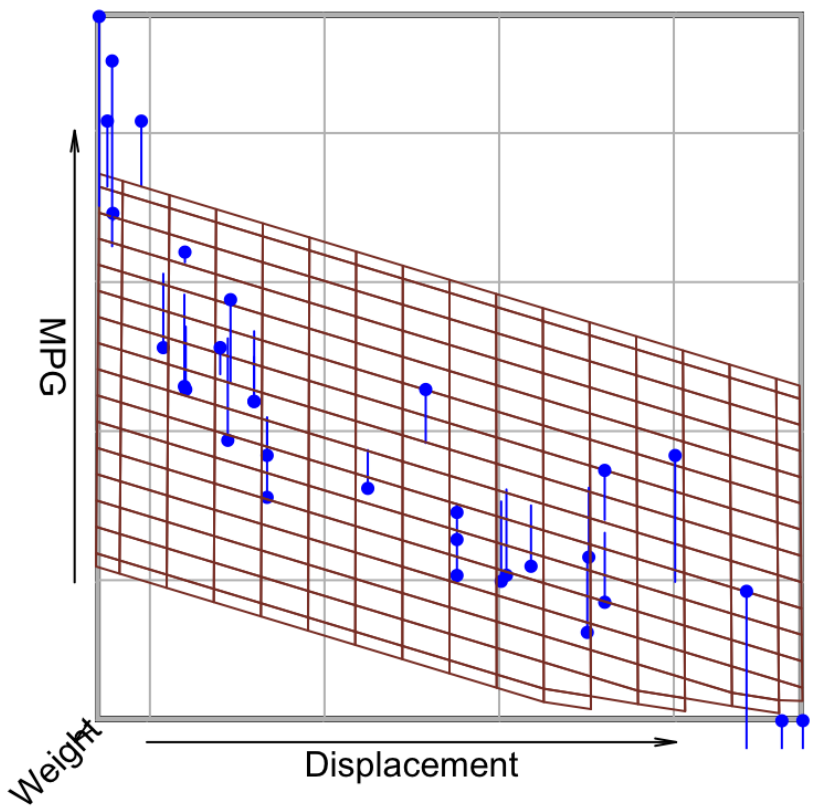
2 predictors

- $Y_i = \beta_0 + \beta_1 X_{i1} + \beta_2 X_{i2} + \varepsilon_i$
- `MPG ~ Weight + Displacement`
- value of β_1: MPG dependency (**slope**) on Weight



2 predictors

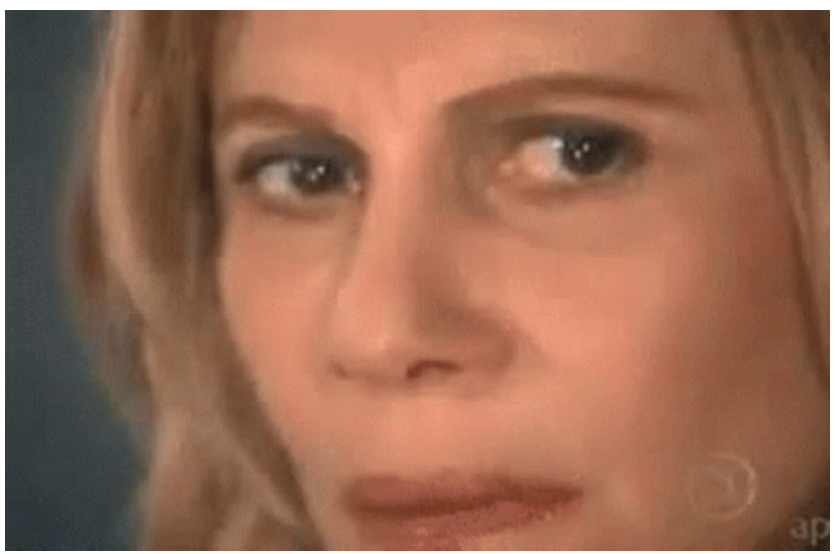
- $Y_i = \beta_0 + \beta_1 X_{i1} + \beta_2 X_{i2} + \varepsilon_i$
- `MPG ~ Weight + Displacement`
- value of β_2: MPG dependency (**slope**) on Displacement



K predictors

$$Y_i = \beta_0 + \sum_{k=1}^{K} (\beta_k X_{ik}) + \varepsilon_i$$

- sorry! I can't draw in > 3 dimensions



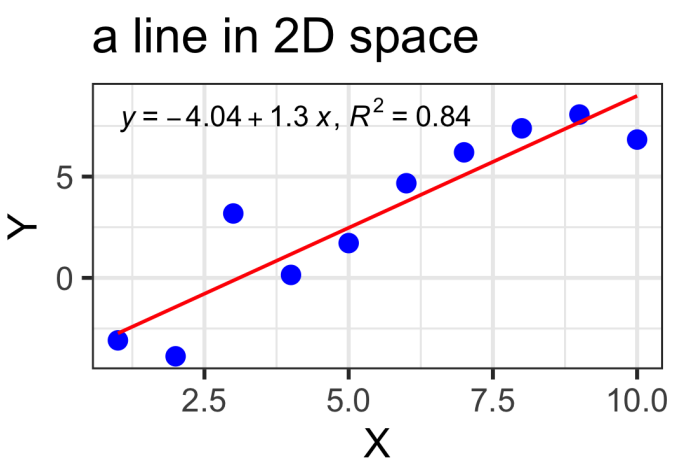
Multiple Regression

- **Multiple Regression**: we use N *predictor variables* $X_1, X_2, \ldots X_N$ to predict Y
  - $Y_i = \beta_0 + \beta_1 X_{i1} + \beta_2 X_{i2} + \cdots + \beta_k X_{ik} + \varepsilon_i$
  - one **dependent variable** Y (the variable to be predicted)
  - K **independent variables** X_k, for $k = 1 \ldots K$
  - N different observations (X_i, Y_i), for $i = 1 \ldots N$
  - $k + 1$ model coefficients β (*one slope for each* X_k plus a model intercept β_0)

$$Y_i = \beta_0 + \sum_{k=1}^{K} (\beta_k X_{ik}) + \varepsilon_i$$

1 predictor: a line in 2D

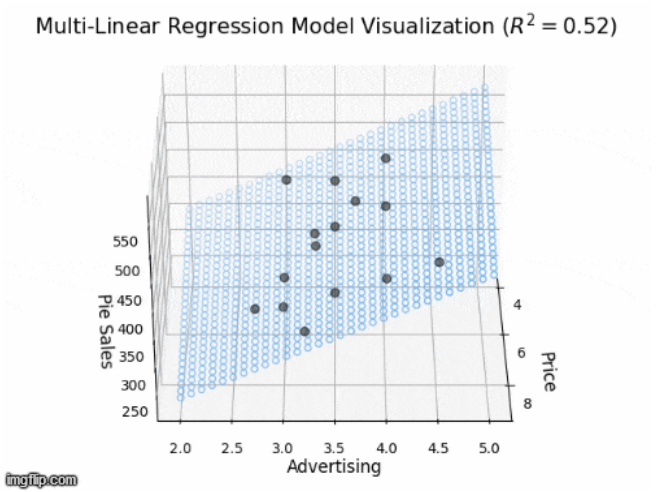
- $Y_i = \beta_0 + \beta_1 X + \varepsilon_i$
- one **dependent variable** Y
  (the variable to be predicted)
- one **independent variable** X
  (the variable we are using to predict Y)
- N different observations of
  (X_i, Y_i), for $i = 1 \ldots N$
- two model coefficients:
  - β_0 (intercept)
  - β_1 (slope)



2 predictors: a 2D plane in 3D

- $Y_i = \beta_0 + \beta_1 X_{i1} + \beta_2 X_{i2} + \varepsilon_i$
- Y: “Pie Sales”
- X_1: “Price”, X_2 is “Advertising”
- β_1: dependence of Pie Sales (Y) on Price (X_1)
- β_2: dependence of Pie Sales (Y) on Advertising (X_2)
- β_0: predicted Pie Sales (Y) when Price and Advertising are both zero

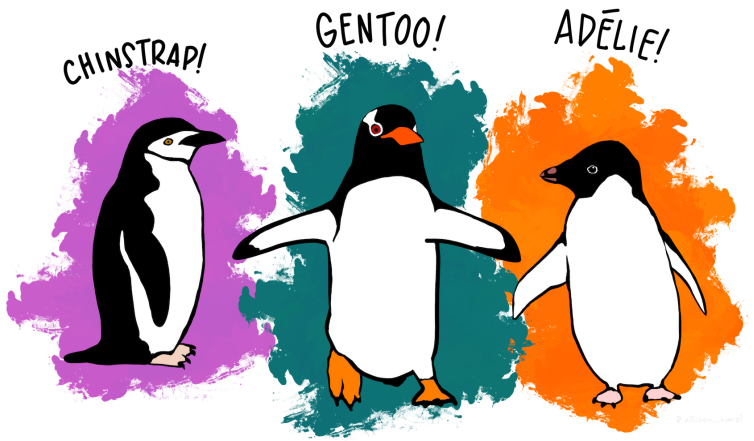
- a 2D plane in 3D space



An Example: palmerpenguins

```
1 library(palmerpenguins)
2 library(tidyverse)
```

The `penguins` data from the **palmerpenguins** package contains size measurements for 344 penguins from three species observed on three islands in the Palmer Archipelago, Antarctica.



An Example: palmerpenguins

```
1 glimpse(penguins)
```

```
Rows: 344
Columns: 8
$ species           <fct> Adelie, Adelie, Adelie, Adelie, Adelie, Adelie, Adel…
$ island            <fct> Torgersen, Torgersen, Torgersen, Torgersen, Torgerse…
$ bill_length_mm    <dbl> 39.1, 39.5, 40.3, NA, 36.7, 39.3, 38.9, 39.2, 34.1, …
$ bill_depth_mm     <dbl> 18.7, 17.4, 18.0, NA, 19.3, 20.6, 17.8, 19.6, 18.1, …
$ flipper_length_mm <int> 181, 186, 195, NA, 193, 190, 181, 195, 193, 190, 186…
$ body_mass_g       <int> 3750, 3800, 3250, NA, 3450, 3650, 3625, 4675, 3475, …
$ sex               <fct> male, female, female, NA, female, male, female, male…
$ year              <int> 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007, 2007…
```

- can we predict `body_mass_g` of `Adelie` penguins using a model that includes:
  - `flipper_length_mm`
  - `bill_length_mm`
  - `bill_depth_mm`

An Example: palmerpenguins

1. gather variables we need — `dplyr()`
2. examine correlations to get a first impression — `GGally::ggpairs()`
3. build a “full model” — `lm()`
4. check assumptions
5. refine the model (kick out non-useful X variables) — `step()`
6. interpret the model

1. Gather variables

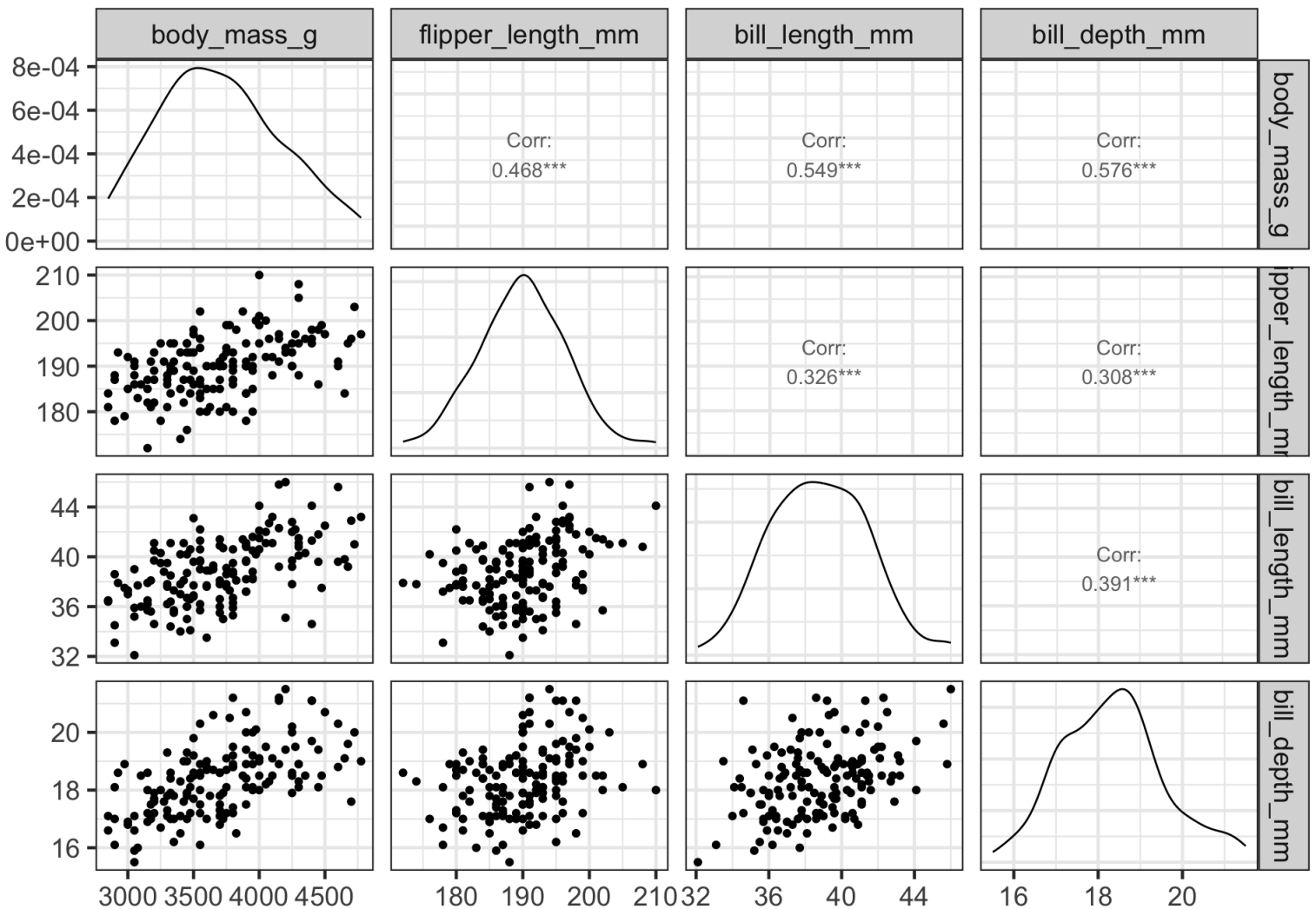
```r
pdata <- penguins %>%
  filter(species == "Adelie") %>%
  select(body_mass_g, flipper_length_mm, bill_length_mm, bill_depth_mm) %>%
  drop_na() # skips rows containing NA values (indicating missing data)
glimpse(pdata)
```

```
Rows: 151
Columns: 4
$ body_mass_g       <int> 3750, 3800, 3250, 3450, 3650, 3625, 4675, 3475, 4250…
$ flipper_length_mm <int> 181, 186, 195, 193, 190, 181, 195, 193, 190, 186, 18…
$ bill_length_mm    <dbl> 39.1, 39.5, 40.3, 36.7, 39.3, 38.9, 39.2, 34.1, 42.0…
$ bill_depth_mm     <dbl> 18.7, 17.4, 18.0, 19.3, 20.6, 17.8, 19.6, 18.1, 20.2…
```

- we have 151 observations (penguins)
- each has 4 variables
- we want to predict `body_mass_g` based on the other three
  - `flipper_length_mm`, `bill_length_mm`, and `bill_depth_mm`

2. Look at correlation matrix

```
1 library(GGally)  # you will first need to install.packages("GGally") once
2 ggpairs(pdata) + theme_bw(base_size=18)
```



3. Build a full model

- "full" means we include all independent variables X_k in the model

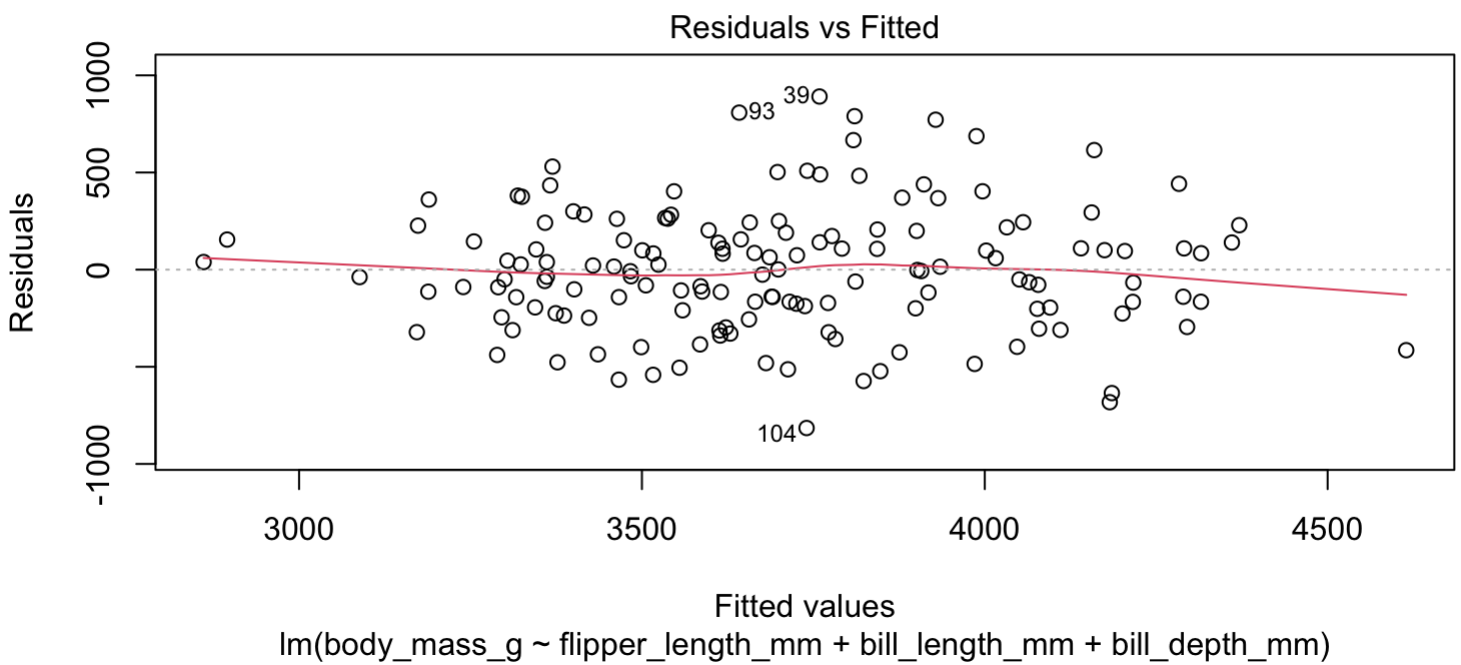
```
mod.full <- lm(body_mass_g ~ flipper_length_mm + bill_length_mm + bill_depth_mm, data=pdata)
summary(mod.full)
```

```
Call:
lm(formula = body_mass_g ~ flipper_length_mm + bill_length_mm +
    bill_depth_mm, data = pdata)

Residuals:
    Min      1Q  Median      3Q     Max
-815.12 -200.33   -7.35  201.02  891.03

Coefficients:
                  Estimate Std. Error t value Pr(>|t|)
(Intercept)       -4341.302    795.117  -5.460 1.98e-07 ***
flipper_length_mm    17.421      4.385   3.973 0.000111 ***
bill_length_mm       55.368     11.133   4.973 1.81e-06 ***
bill_depth_mm       140.895     24.216   5.818 3.58e-08 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 324.9 on 147 degrees of freedom
Multiple R-squared:  0.5082,    Adjusted R-squared:  0.4982
F-statistic: 50.63 on 3 and 147 DF,  p-value: < 2.2e-16
```

4. Check assumptions

- check the **linearity** assumption
- plot the fitted values against the residuals—no obvious indication of non-linearity

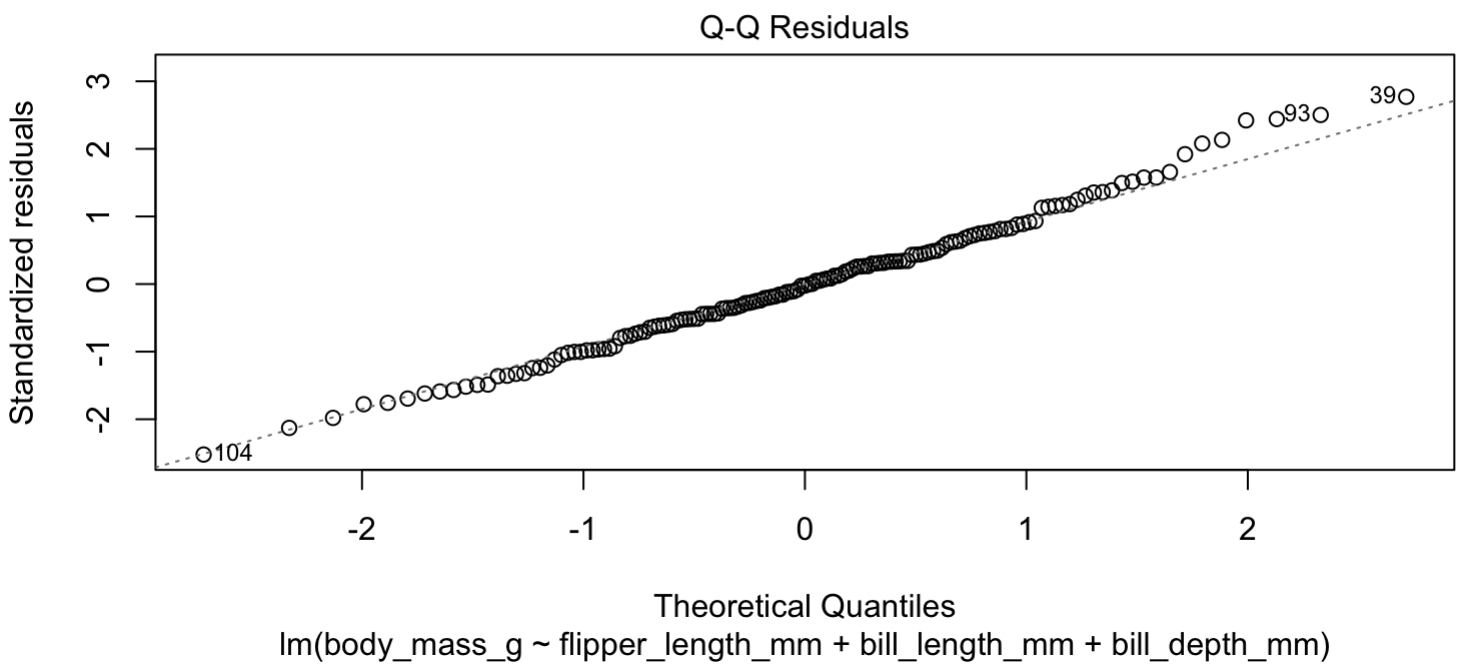
```
1  plot(mod.full, 1) # 1 means plot residuals
```



4. Check assumptions

- check the **normality** assumption
- produce a Q-Q plot—no obvious indication of non-linearity

```
1 plot(mod.full, 2) # 2 means Q-Q plot
```



4. Check assumptions

- check the **normality** assumption
- conduct a `shapiro.test()` on the residuals
- H_0 is that the population residuals are normally distributed
- p = 0.6645 so we do not reject H_0
- no evidence we have violated the normality assumption

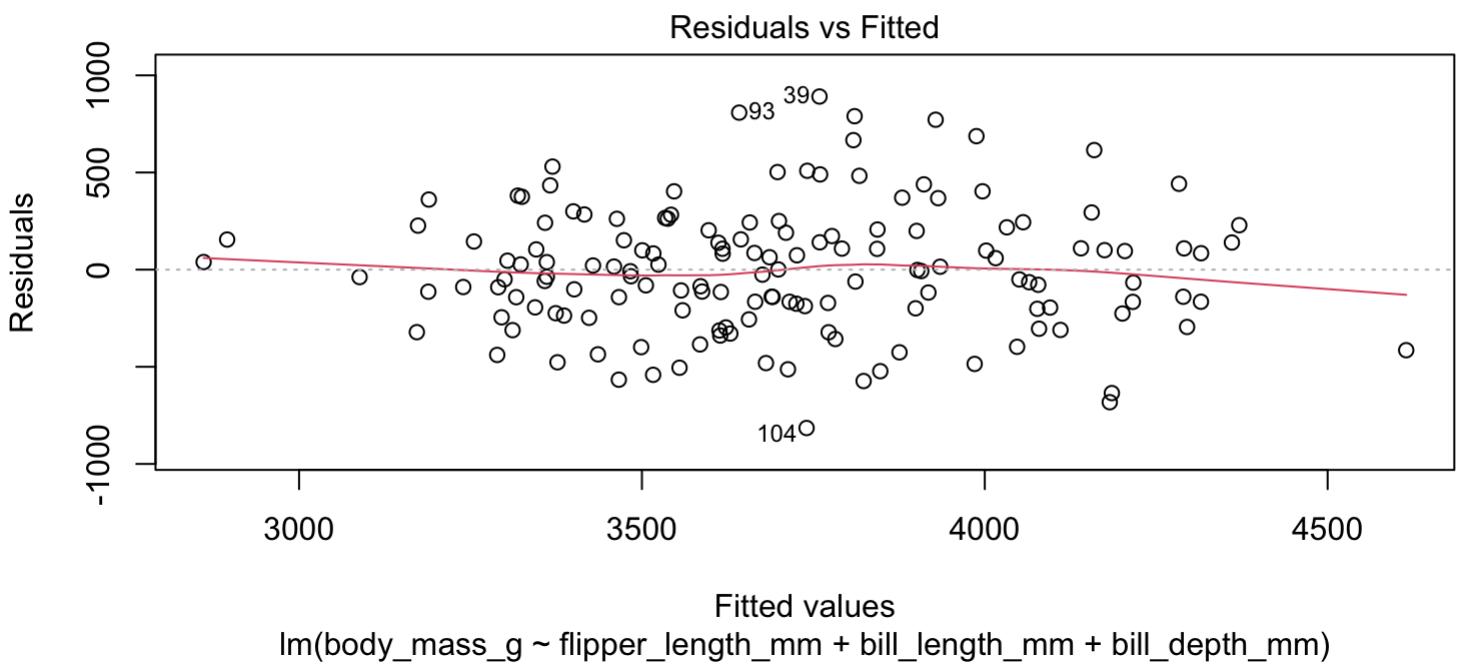
```
1 shapiro.test(residuals(mod.full))
```

```
    Shapiro-Wilk normality test

data:  residuals(mod.full)
W = 0.99291, p-value = 0.6645
```

4. Check assumptions

- check the **homoscedasticity** assumption
- look at plot of residuals—no sign of variance change across range

```
1  plot(mod.full, 1) # 1 means plot residuals
```



4. Check assumptions

- check the **homoscedasticity** assumption
- conduct a non-constant variance test (`ncvTest()` in the `car` package)
- H_0 is that the population residuals have constant variance
- p = 0.11762 so we do not reject H_0
- no evidence of violation of homoscedasticity

```
1 library(car) # you may first have to `install.packages("car")` once
2 ncvTest(mod.full)
```

```
Non-constant Variance Score Test
Variance formula: ~ fitted.values
Chisquare = 2.448791, Df = 1, p = 0.11762
```

4. Collinearity

- See Navarro 15.9.6 for ways to check for collinearity
- variance inflation factors VIFs
- familiarize yourself with the concept if not the details

5. Interpret the model

```
> summary(mod.full)

Call:
lm(formula = body_mass_g ~ flipper_length_mm + bill_length_mm +
    bill_depth_mm, data = pdata)

Residuals:
    Min      1Q  Median      3Q     Max
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Coefficients:
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---
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> summary(mod.full)

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bill_length_mm       55.368     11.133   4.973 1.81e-06 ***
bill_depth_mm       140.895     24.216   5.818 3.58e-08 ***
---
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Residual standard error: 324.9 on 147 degrees of freedom
Multiple R-squared:  0.5082,    Adjusted R-squared:  0.4982
F-statistic: 50.63 on 3 and 147 DF,  p-value: < 2.2e-16
```

5. Interpret the model

- Let's use the `broom` package to `tidy` the model object into a `tibble`
- why??
- so that we can more easily **plot** the coefficients (slopes) and their confidence intervals
- why?
- we dont' have to … but it's a nicer way of visualizing them compared to a table

```
library(broom) # you will need to first install.packages("broom") once
mod.tidy <- tidy(mod.full, conf.int=TRUE, conf.level=0.95)
mod.tidy
```

```
# A tibble: 4 × 7
  term              estimate std.error statistic      p.value conf.low conf.high
  <chr>                <dbl>     <dbl>     <dbl>        <dbl>    <dbl>     <dbl>
1 (Intercept)        -4341.     795.       -5.46 0.000000198  -5913.     -2770.
2 flipper_length_mm     17.4      4.39      3.97 0.000111          8.76      26.1
3 bill_length_mm        55.4     11.1       4.97 0.00000181       33.4       77.4
4 bill_depth_mm        141.      24.2       5.82 0.0000000358     93.0      189.
```

5. Interpret the model

- let's remove the `(Intercept)` term from the model output
- why?
- in a multiple regression the intercept is not so informative
- we're mainly interested in the **slopes** — the effect of **flipper length**, **bill length**, and **bill depth** on penguin **weight**

```
mod.conf <- mod.tidy %>% filter(term != "(Intercept)")
mod.conf
```

```
# A tibble: 3 × 7
  term              estimate std.error statistic      p.value conf.low conf.high
  <chr>                <dbl>     <dbl>     <dbl>        <dbl>    <dbl>     <dbl>
1 flipper_length_mm     17.4      4.39      3.97 0.000111          8.76      26.1
2 bill_length_mm        55.4     11.1       4.97 0.00000181       33.4       77.4
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```

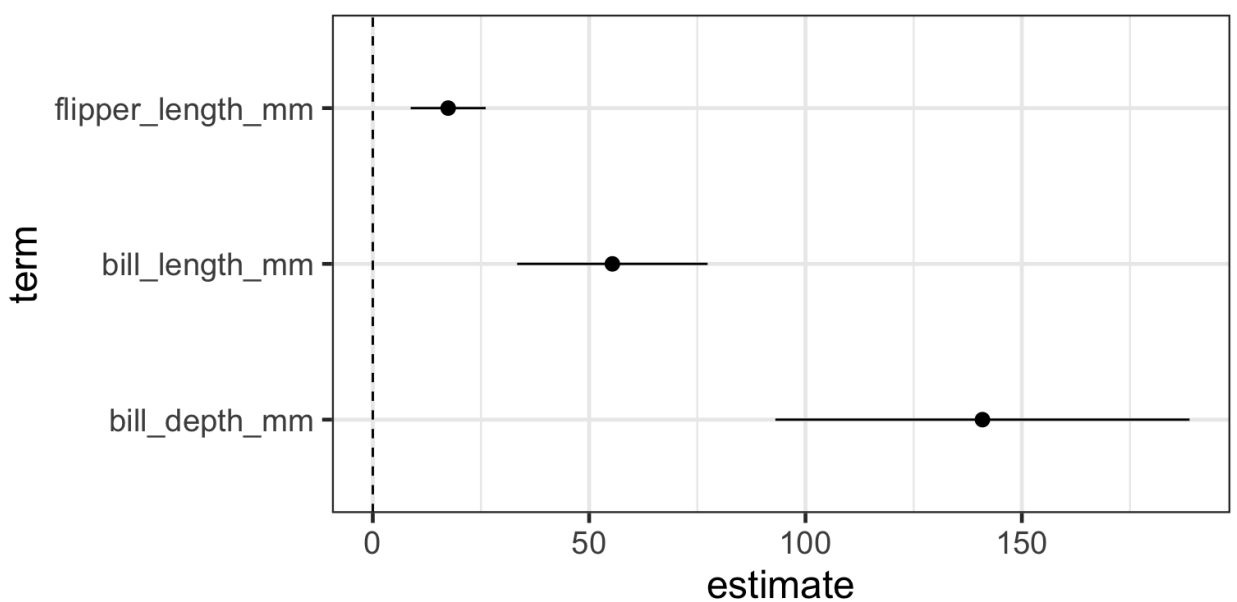
5. Interpret the model

```
mod.conf
```

```
# A tibble: 3 × 7
  term              estimate std.error statistic      p.value conf.low conf.high
  <chr>                <dbl>     <dbl>     <dbl>        <dbl>    <dbl>     <dbl>
1 flipper_length_mm     17.4      4.39      3.97 0.000111         8.76      26.1
2 bill_length_mm        55.4     11.1       4.97 0.00000181      33.4       77.4
3 bill_depth_mm        141.      24.2       5.82 0.0000000358    93.0      189.
```

- plot model coefficients (slopes) relative to zero

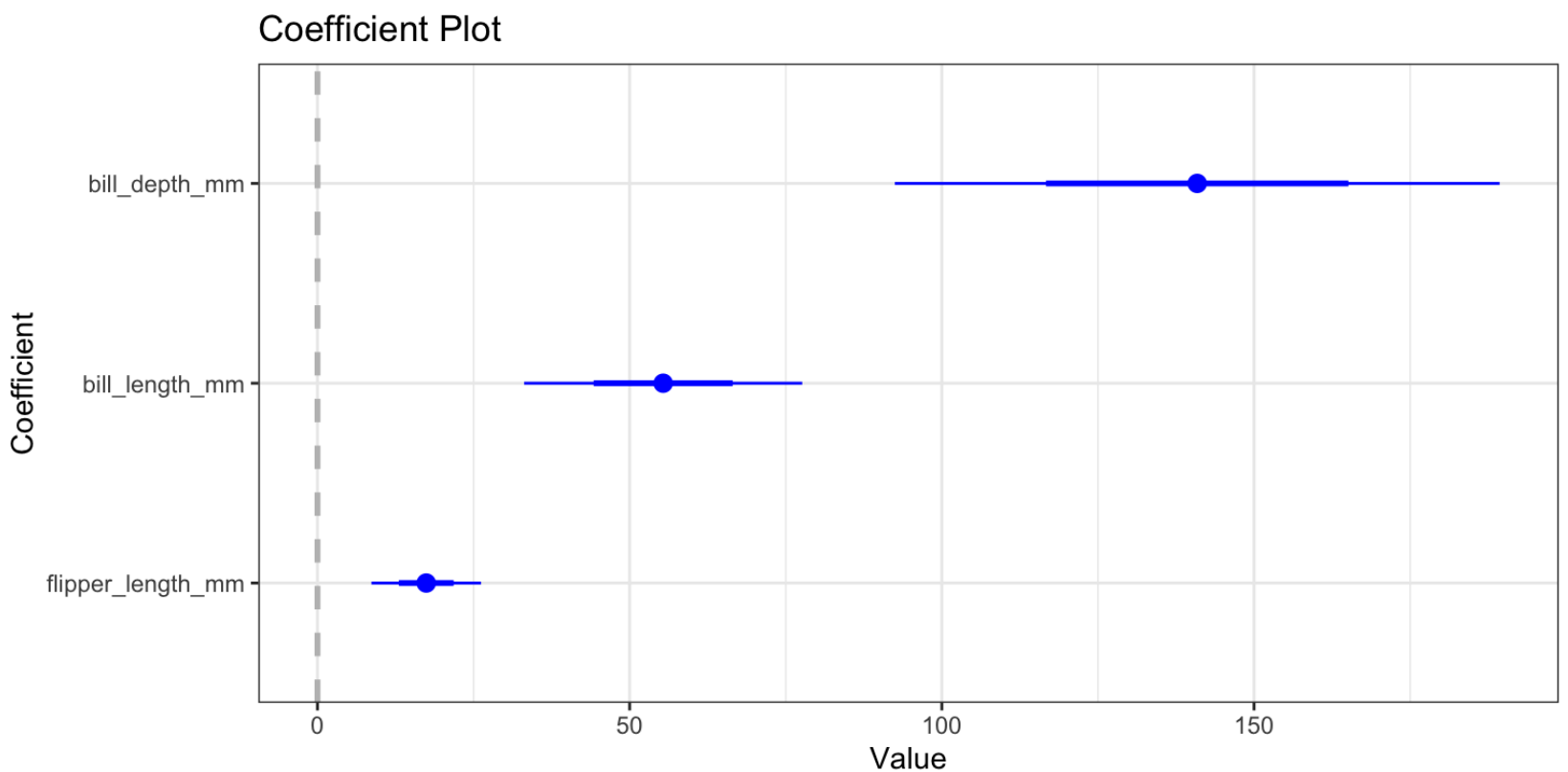
```
ggplot(mod.conf, mapping=aes(x=term, y=estimate, ymin=conf.low, ymax=conf.high)) +
  geom_pointrange() + geom_hline(yintercept=0, linetype=2, size=0.5) + coord_flip() + theme_bw(base_size=18)
```



5. Interpet the model

- OR: You can use the `coefplot` package to more easily plot coefficients and their confidence intervals
- just pass it your `lm()` model object

```
1 mod.full <- lm(body_mass_g ~ flipper_length_mm + bill_length_mm + bill_depth_mm, data=pdata)
2 library(coefplot) # you will have to install.packages("coefplot") once
3 coefplot(mod.full, intercept=FALSE) + theme_bw()
```



6. Refine the model

```
1 mod.full <- lm(body_mass_g ~ flipper_length_mm + bill_length_mm + bill_depth_mm, data=pdata)
```

- We have our “full model”
- “full” because it includes all of our predictor (X) variables
- Q: is this the “best” model?
- Q: do we need all 3 variables?
- Q: do all three variables explain **unique** portions of the variance in `body_mass_g`?
  - **collinearity** (see Chapter 9 of OpenIntroStats, & Chapter 15.9.6 / 15.10 of Learning Statistics with R)

6. Refine the model

```
1 mod.full <- lm(body_mass_g ~ flipper_length_mm + bill_length_mm + bill_depth_mm, data=pdata)
```

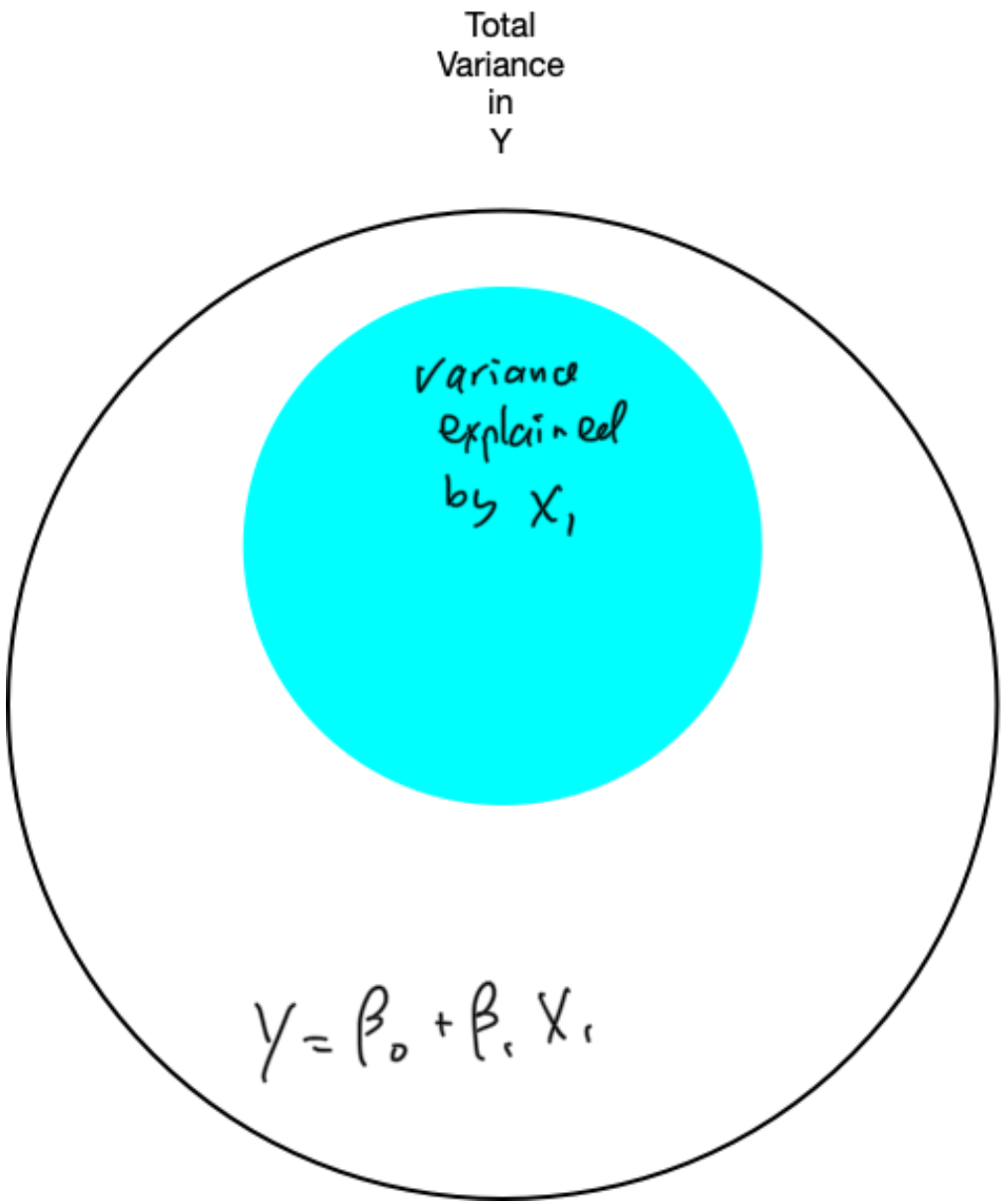
- principle of **parsimony** in science
  - all other things being (almost) equal, a model with fewer predictor variables is better than a model with many predictor variables
  - simpler explanations (models) are preferred to complex ones

6. Refine the model

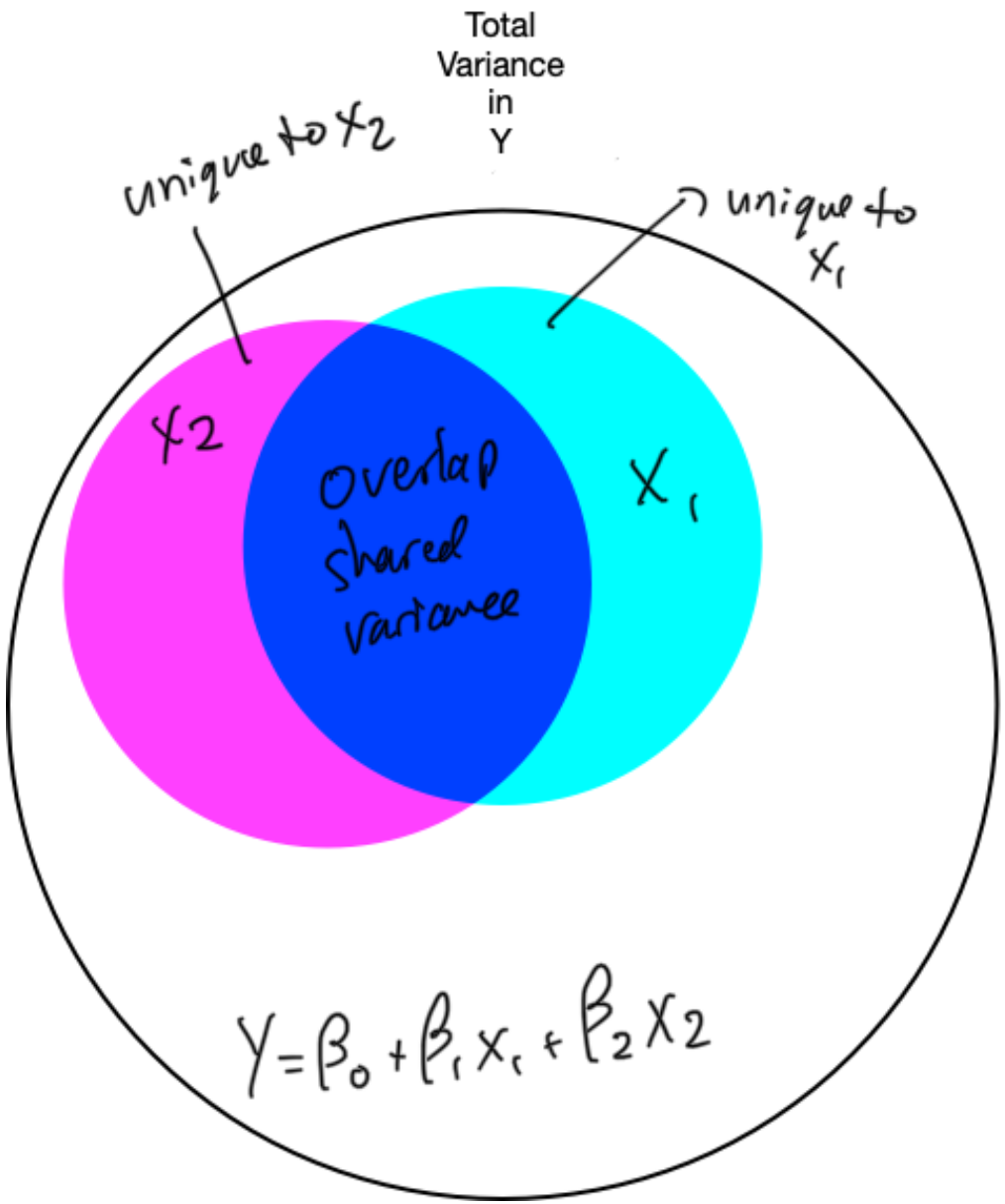
```
1 mod.full <- lm(body_mass_g ~ flipper_length_mm + bill_length_mm + bill_depth_mm, data=pdata)
```

- statistical/mathematical reasons
  - often multiple predictor variables (X_k) are correlated with each other
  - adding multiple correlated variables to a model doesn't help much
  - each time you add an X variable you have to "pay" using a **degree of freedom**
  - fewer degrees of freedom in your model means a larger denominator in your F or t ratios
  - then it's more difficult to reliably say a model coefficient is significant (different from zero)

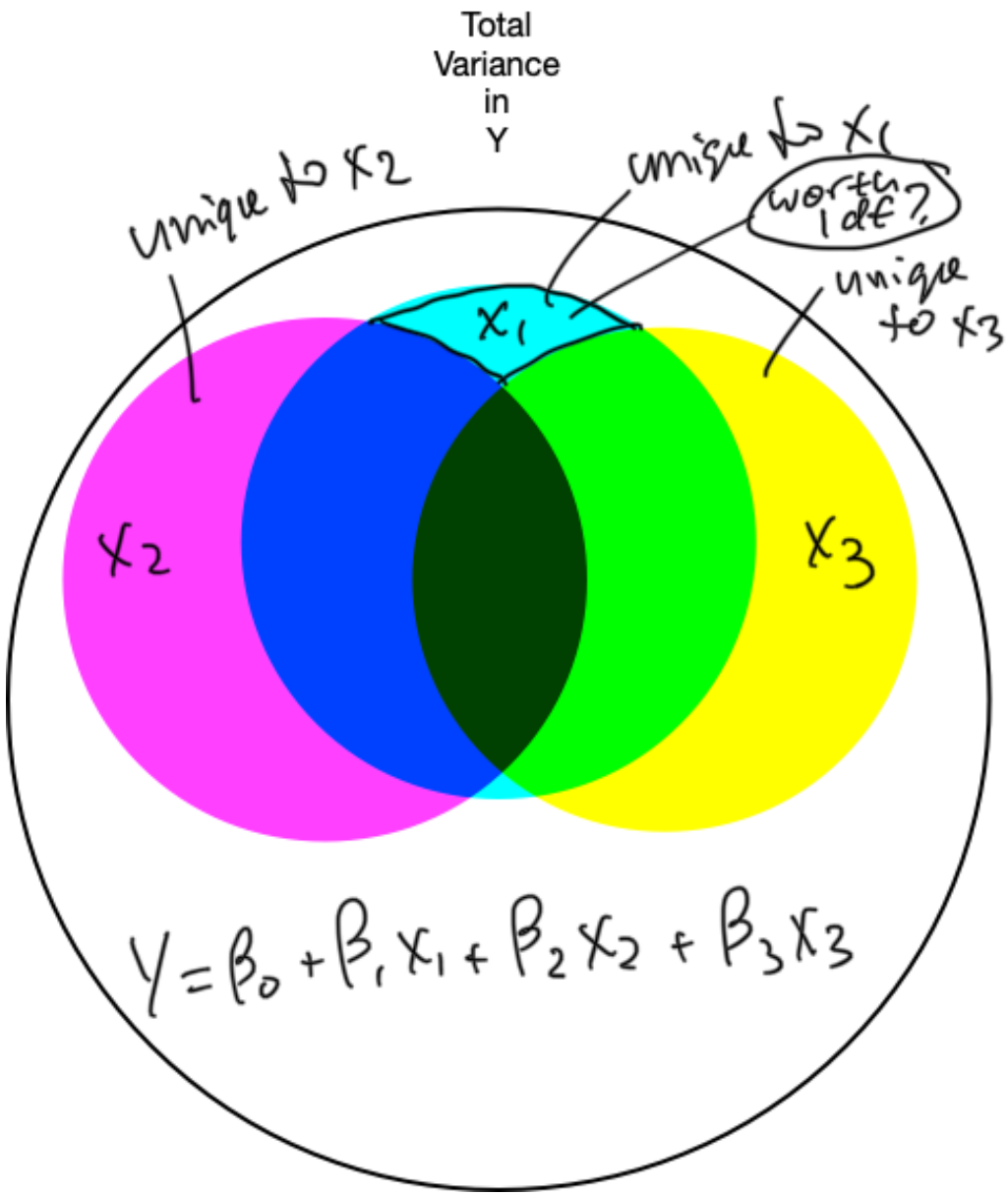
6. Refine the model: unique variance



6. Refine the model: unique variance



6. Refine the model: unique variance



6. Refine the model

```r
mod.full <- lm(body_mass_g ~ flipper_length_mm + bill_length_mm + bill_depth_mm, data=pdata)
```

- recall the significance test of the model “as a whole”:

$$F = \frac{MS_{mod}}{MS_{res}}$$

$$MS_{mod} = \frac{SS_{mod}}{df_{mod}}$$

$$MS_{res} = \frac{SS_{res}}{df_{res}}$$

6. Refine the model

- recall the significance test of the model “as a whole”:

$$F = \frac{MS_{mod}}{MS_{res}}$$

big F → small p → more significant

$$MS_{mod} = \frac{SS_{mod}}{df_{mod}}$$

$SS_{mod} = SS_{tot} - SS_{resid}$

K = # predictors in model = # X variables = # model parameters to estimate = # slopes

$df_{mod} \Rightarrow$ K, the # of X variables (predictors)

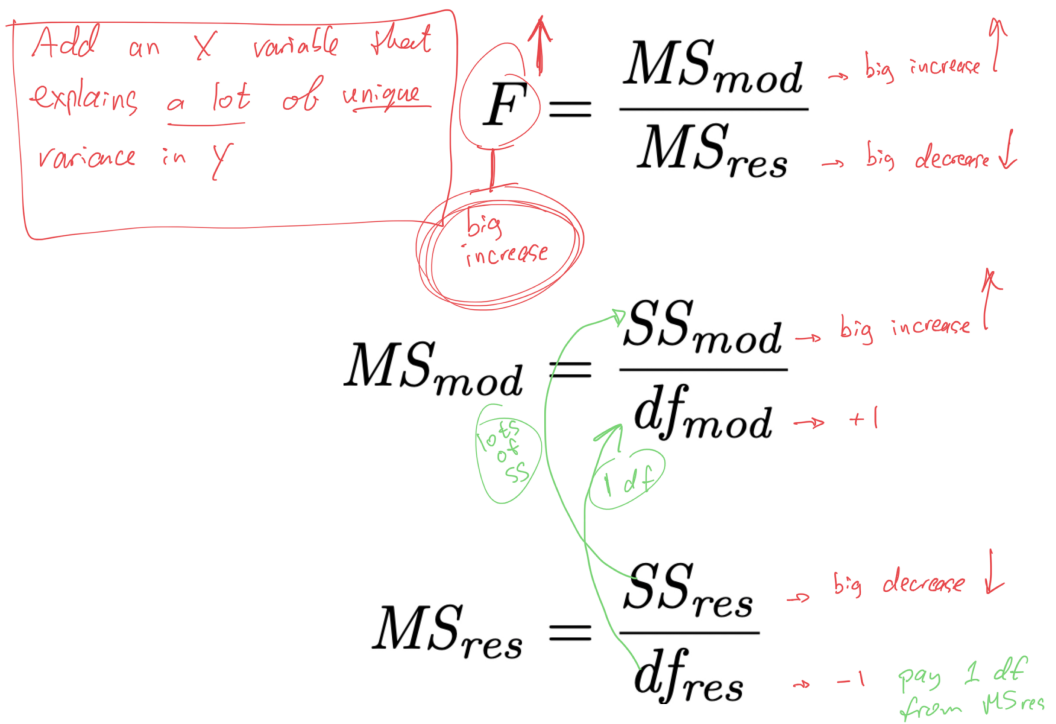
$$MS_{res} = \frac{SS_{res}}{df_{res}}$$

$SS_{res} \Rightarrow$ leftover (unexplained) SS

$df_{res} \Rightarrow N - K - 1$ (N: # observations; K: # X variables)

6. Refine the model

- recall the significance test of the model “as a whole”:



6. Refine the model

- recall the significance test of the model “as a whole”:

Add an X variable that explains hardly any unique variance in Y

$$F = \frac{MS_{mod}}{MS_{res}}$$

→ small increase or even decrease

→ small decrease or even increase

no change or even a decrease!

$$MS_{mod} = \frac{SS_{mod}}{df_{mod}}$$

→ v. small increase

→ +1

v-small SS

1 df

$$MS_{res} = \frac{SS_{res}}{df_{res}}$$

→ v. small decrease

→ −1 pay 1 df

6. Refine the model

- when we add an X variable to the model,
- we “pay” by taking 1 df out of MSres
- smaller MSres denominator means larger MSres
- larger MSres means smaller F
- smaller F means larger p
- larger p means less significant

$$F = \frac{MS_{mod}}{MS_{res}}$$

big enough to offset

-1 df

$$MS_{mod} = \frac{SS_{mod}}{df_{mod}}$$

1 df

$$MS_{res} = \frac{SS_{res}}{df_{res}}$$

- if we are to “pay” 1 df from the MSres denominator, to make it **worth it**,
  - the X variable should explain a lot of unique variance in Y
  - it should increase SSmod and decrease SSres **enough** to offset the increase in MSres caused by the removal of 1 df

6. Refine the model

```
1 mod.full <- lm(body_mass_g ~ flipper_length_mm + bill_length_mm + bill_depth_mm, data=pdata)
```

- if we are to "pay" 1 df from the MSres denominator, to make it **worth it**,
  - the X variable should explain **enough** unique variance in Y
  - it should increase SSmod and decrease SSres **enough** to offset the change in MSres caused by the removal of 1 df
- how much is "**enough**"?
- how much unique variance does an X variable need to explain in order to offset having to "pay" with 1 df from the error term (from MSres)?

$$F = \frac{MS_{mod}}{MS_{res}}$$

big enough to offset

-1 df

$$MS_{mod} = \frac{SS_{mod}}{df_{mod}}$$

1 df

$$MS_{res} = \frac{SS_{res}}{df_{res}}$$

6. Refine the model

- There exist several reasonable ways of quantitatively assessing whether or not to include a variable in your model:
  - adjusted R^2
  - Akaike information criterion (**AIC**) (this is used by default in R's `step()` function)
  - p-values for individual coefficients
  - F-tests
- all share same procedural concept—compare:
  - **full model** containing all X variables with
  - **reduced model** in which the X variable being tested is removed
- Q: is the full model *better than* the reduced model?

6. Refine the model: Adj. R^2

```
> summary(mod.full)

Call:
lm(formula = body_mass_g ~ flipper_length_mm + bill_length_mm +
    bill_depth_mm, data = pdata)

Residuals:
    Min      1Q  Median      3Q     Max
-815.12 -200.33   -7.35  201.02  891.03

Coefficients:
                   Estimate Std. Error t value Pr(>|t|)
(Intercept)       -4341.302    795.117  -5.460 1.98e-07 ***
flipper_length_mm    17.421      4.385   3.973 0.000111 ***
bill_length_mm       55.368     11.133   4.973 1.81e-06 ***
bill_depth_mm       140.895     24.216   5.818 3.58e-08 ***
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Residual standard error: 324.9 on 147 degrees of freedom
Multiple R-squared:  0.5082,    Adjusted R-squared:  0.4982
F-statistic: 50.63 on 3 and 147 DF,  p-value: < 2.2e-16
```

$$R^2 = 1 - \frac{SS_{res}}{SS_{tot}}$$

$$\text{adj.}R^2 = 1 - \left(\frac{SS_{res}}{SS_{tot}} \times \frac{N-1}{N-K-1} \right)$$

- adding predictors to model will always increase R^2
- takes into account the number of parameters (X variables) K
- adj. R^2 will only increase if the new X variable improves the model performance **more than what you'd expect by chance**

6. Refine the model: Adj. R^2

- start with a full model:

```
mod.full <- lm(body_mass_g ~ flipper_length_mm + bill_length_mm + bill_depth_mm, data=pdata)
summary(mod.full)$adj.r.squared
```

```
[1] 0.4981588
```

- then remove a variable (`bill_depth_mm`) and see what effect it has on adjusted r-squared

```
mod.red <- lm(body_mass_g ~ flipper_length_mm + bill_length_mm, data=pdata)
summary(mod.red)$adj.r.squared
```

```
[1] 0.3867675
```

- adj. R^2 goes down when we remove `bill_depth_mm` to the model so we should keep it, it's "worth it"

Refine the model: AIC

$$AIC \approx \frac{SS_{res}}{\hat{\sigma}^2} + 2K$$

- better models have low SS_{res} and smallest K
- lower AIC values are better

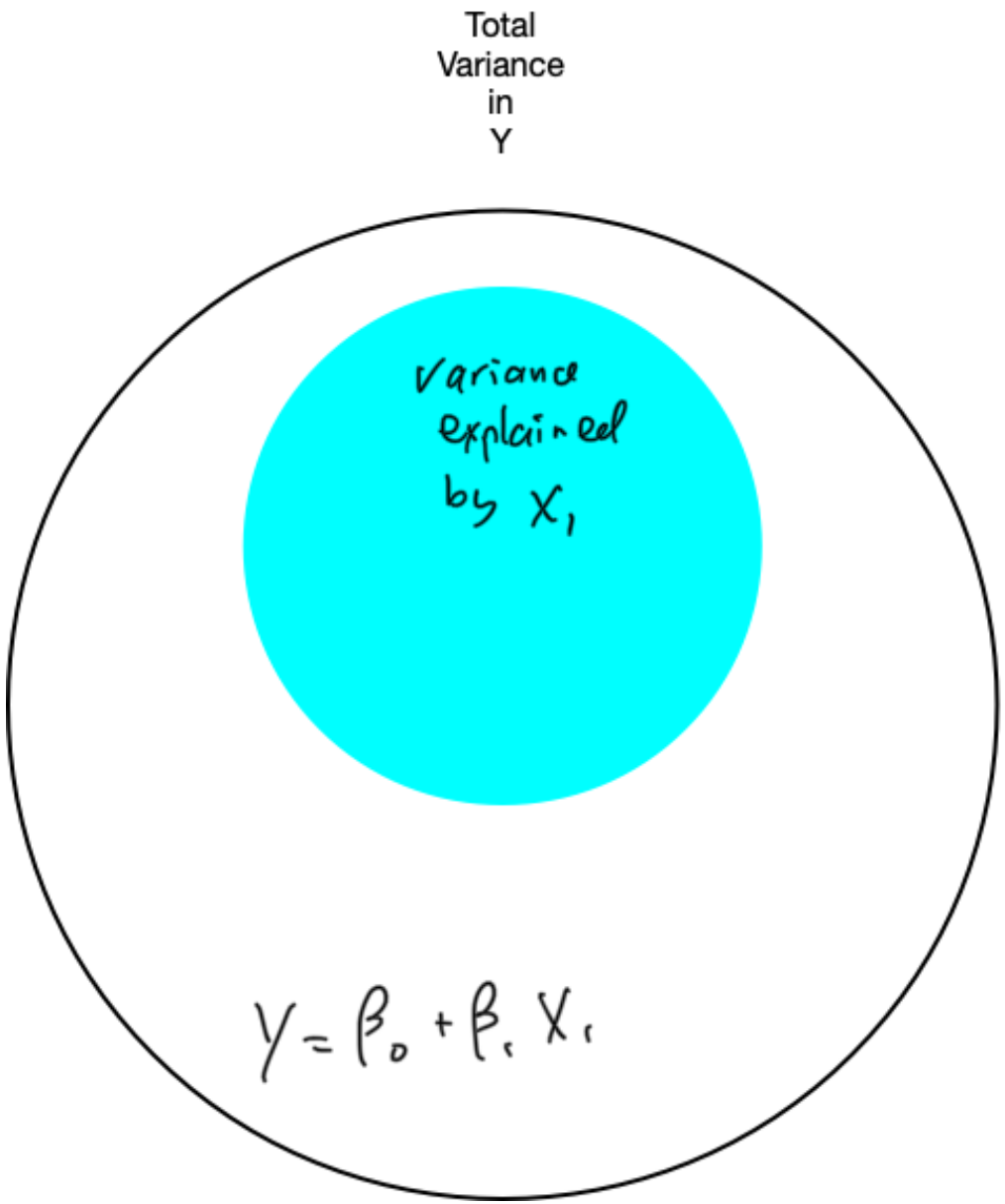
6. Refine the model: AIC

- start with a full model:

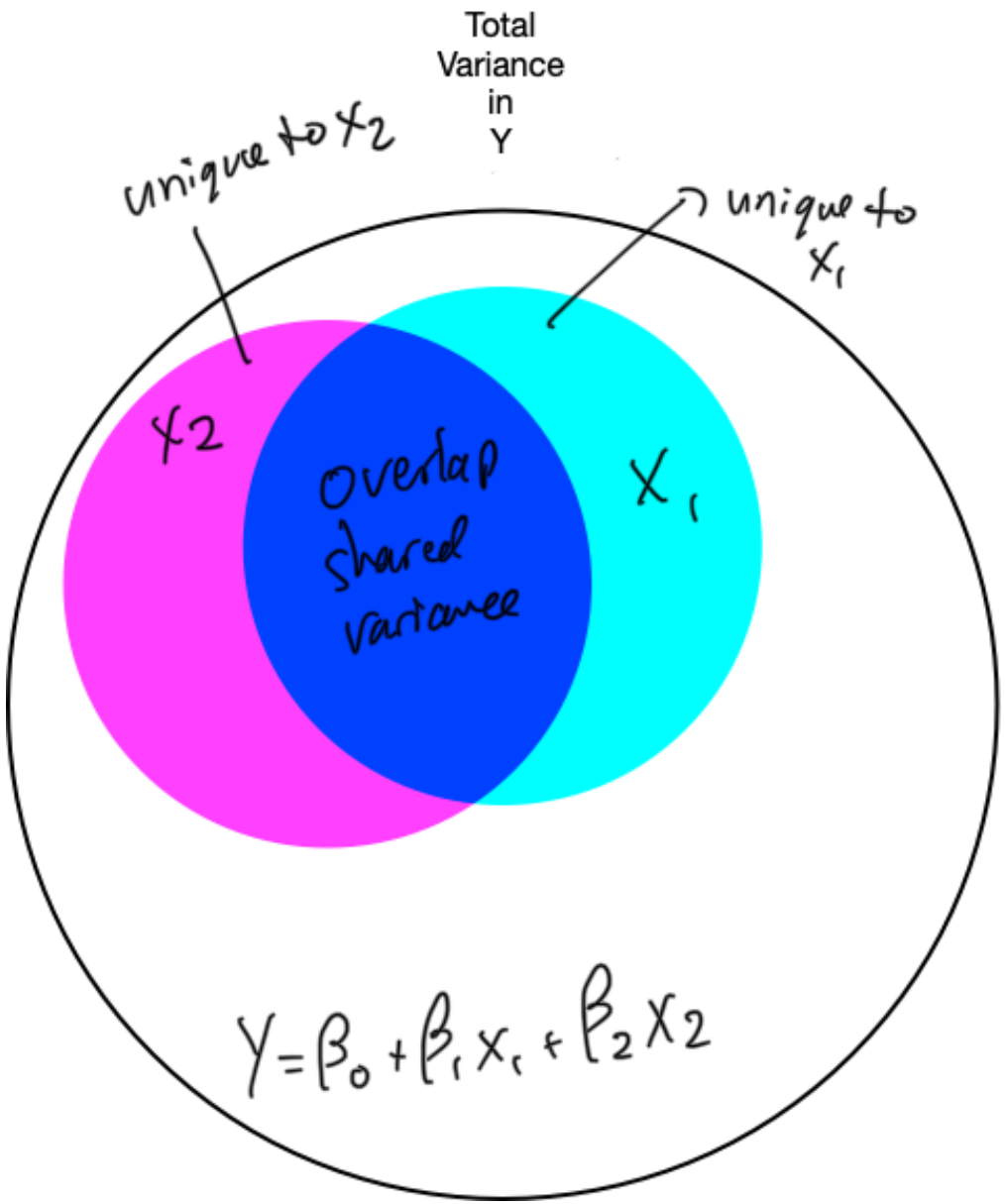
```
1 mod.full <- lm(body_mass_g ~ flipper_length_mm + bill_length_mm + bill_depth_mm, data=pdata)
```

- use R's `step()` function to test competing models and look at **AIC** measure
- `step()` can do 3 flavours of model refinement:
  - forward: start with an empty model and add variables one at a time
  - backward: start with a full model and remove variables one at a time
  - "both": allow `step()` to add or remove variables at each step
- why "both"???

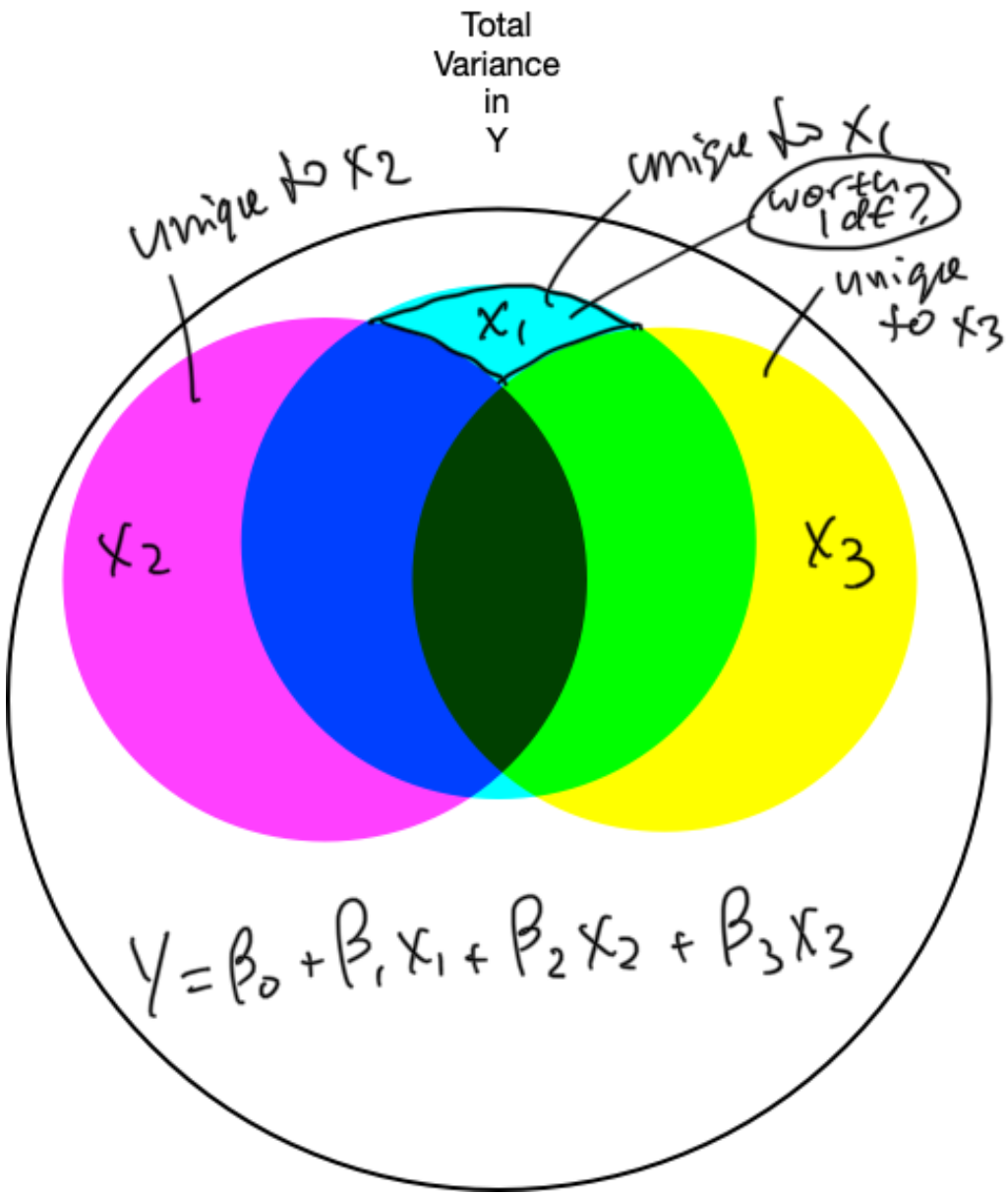
6. Refine the model: unique variance



6. Refine the model: unique variance



6. Refine the model: unique variance



6. Refine the model: AIC (live demo)

- define a full model

```
1 mod.full <- lm(body_mass_g ~ flipper_length_mm + bill_length_mm + bill_depth_mm, data=pdata)
```

- define an empty model (no variables, only an intercept)

```
1 mod.0 <- lm(body_mass_g ~ 1, data=pdata)
```

- issue the `step()` command, start with empty model

```
1 mod.refined <- step(mod.0, scope=list(lower=mod.0, upper=mod.full), direction="both")
```

- you'll see a long list of output (try this in your own RStudio session)
- `step()` starts with `mod.0` and adds the best single variable that most reduces AIC
- then next best variable
- then checks to see if dropping any variables currently in the model helps
- then checks to see if new variables not in the model helps
- keeps going until no more improvements are possible

6. Refine the model: AIC (live demo)

- define a full model

```
1 mod.full <- lm(body_mass_g ~ flipper_length_mm + bill_length_mm + bill_depth_mm, data=pdata)
```

- define an empty model (no variables, only an intercept)

```
1 mod.0 <- lm(body_mass_g ~ 1, data=pdata)
```

- issue the `step()` command, start with full model

```
1 mod.refined <- step(mod.full, scope=list(lower=mod.0, upper=mod.full), direction="both")
```

- this time `step()` starts with a full model and checks if dropping any single variable improves (reduces) AIC
- it finds out nope! dropping any single variable only makes things worse
- so it stops

6. Refine the model

- AIC, p-values, Adj. R^2, forward, backward, steps, …
- how to decide what to do?
- **no single correct answer**
- these are different approaches to achieve the same outcome
- always a gray zone
- report what you did, make sure things make sense
- in homeworks / exams I will specify what procedure I would like

Prediction

- We can use the model to make predictions
- A new penguin is observed:
  - `flipper_length_mm = 200 mm`
  - `bill_length_mm = 46 mm`
  - `bill_depth_mm = 22 mm`
- how much does it weigh according to our model?

Prediction

- create a tibble with the new penguin's data

```
1 newP <- tibble(flipper_length_mm=200, bill_length_mm=46, bill_depth_mm=22)
```

- use `predict()` to predict the value of `body_mass_g`

```
1 predict(mod.refined, newP)
```

```
       1
4789.586
```

- the penguin is predicted to weigh 4789.586 g
- standard error of the estimate is 324.9 g
  from `summary(mod.refined)`

Linear Models

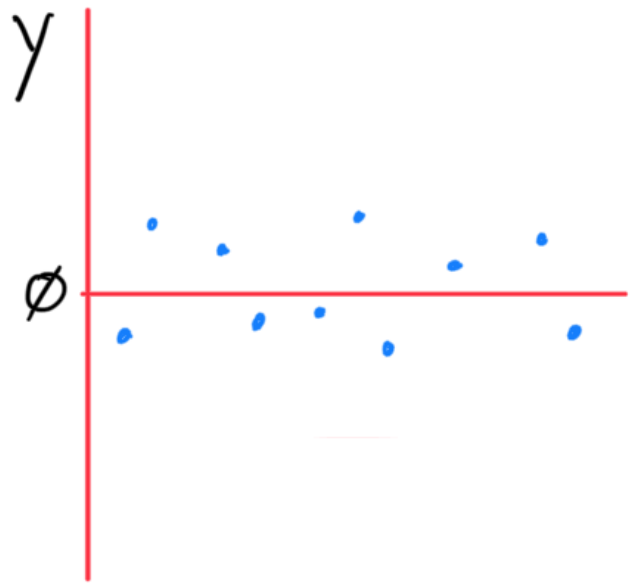
- $Y_i = \varepsilon_i$
- $Y_i = \beta_0 + \varepsilon_i$
- $Y_i = \beta_0 + \beta_1 X_{i1} + \varepsilon_i$
- $Y_i = \beta_0 + \beta_1 X_{i1} + \beta_2 X_{i2} + \varepsilon_i$
- $Y_i = \beta_0 + \beta_1 X_{i1} + \beta_2 X_{i2} + \beta_3 X_{i3} + \varepsilon_i$
- $Y_i = \beta_0 + \beta_1 X_{i1} + \beta_2 X_{i2} + \beta_3 X_{i3} + \beta_4 X_{i4} + \varepsilon_i$

Linear Models

- $Y_i = \varepsilon_i$
- $Y_i = \beta_0 + \varepsilon_i$
- $Y_i = \beta_0 + \beta_1 X_{i1} + \varepsilon_i$
- $Y_i = \beta_0 + \sum_{k=1}^{K} (\beta_k X_{ik}) + \varepsilon_i$

Linear Models

$$Y_i = \epsilon_i$$



$$Y_i = \beta_0 + \epsilon_i$$

$$Y_i = \beta_0 + \beta_1 X_{i1} + \epsilon_i$$

$$Y_i = \beta_0 + \sum_{k=1}^{K} (\beta_k X_{ik}) + \epsilon_i$$

Linear Models

$$Y_i = \epsilon_i$$

$$Y_i = \beta_0 + \epsilon_i$$

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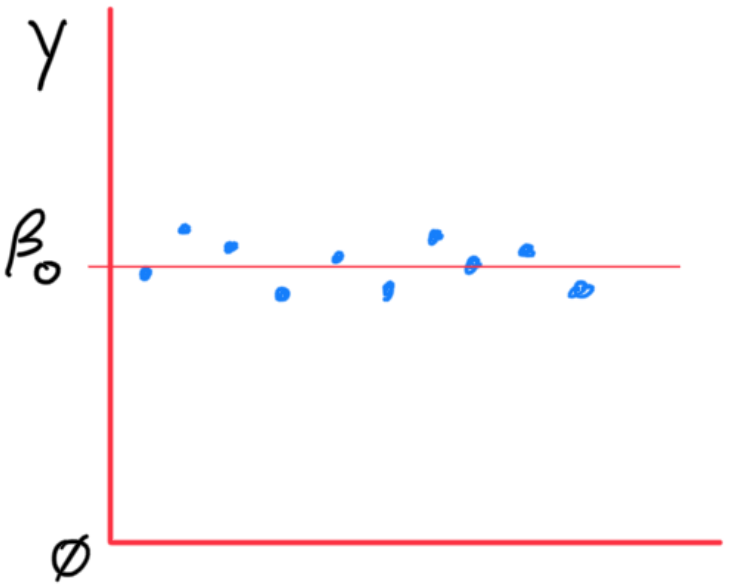

Linear Models

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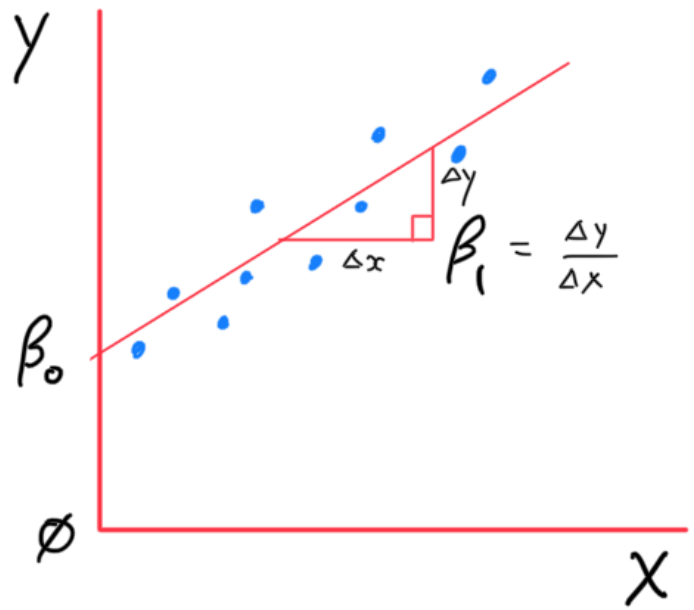

Linear Models

$$Y_i = \epsilon_i$$

$$Y_i = \beta_0 + \epsilon_i$$

$$Y_i = \beta_0 + \beta_1 X_{i1} + \epsilon_i$$

$$Y_i = \beta_0 + \sum_{k=1}^{K} (\beta_k X_{ik}) + \epsilon_i$$