Lab 2: Starting multiple linear regression

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1 Lab activities

In this lab you will work with a data set on biometric features of FORE224-STAT202 students. Students recorded their weight_kg (response variable in kg), and the following predictors: height_cm (in cm),sex, handspan_cm (distance in cm between the tips of their thumb and little finger), finger2_cm (length of index in cm) and finger4_cm (length of annular in cm). We will ignore sex in this lab.

Remember to create a folder for this assignment and to create a new project in that folder. This way R will know where to read files from and where to save output files.

In this assignment you will read a MS Excel file, for which you will need to use the read_excel() function from the readxl package. If you do not have the package installed go to Tools - Install packages in RStudio to install it.

Your script will need to start with the following code:

library(tidyverse)
library(readxl)
library(performance)

- 1. Read the biometrics.xlsx file and assign it to the name biomet.
- 2. Create a scatterplot where weight_kg is the response and height_cm is the predictor. Note: all the scatterplots in this assignment must use theme theme_bw().
- 3. Remove the two outliers using code, also remove any observations that have missing values, and take a sample of size 150 observations. Assign the sample to a data frame called my_biom. You will use my_biom for the following questions. Remember to use set.seed() with your student number before taking the sample.
- 4. Create a series of scatterplots between weight_kg, height_cm, handspan_cm and finger2_cm and write a 50-word comment on the relationships you observe between the variables, including direction (positive, negative) and strength. This requires either creating plots one at the time or just one scatterplot matrix. For the latter you'll need the ggpairs() function of the GGally package.

- 5. Fit five different linear regression models (call them m1, m2 ... m5) using weight_kg as the response variable and using height_cm, handspan_cm, finger2_cm, height_cm + handspan_cm and height_cm + handspan_cm + finger2_cm as predictors. Notice the changes of goodness of fit when moving from models with 1, 2 and 3 predictors. Have a look at R-squared, Adjusted R-squared and residual standard errors for the models. Write a 50-word comment on the improvement of fit when moving from m1 through m5.
- 6. Compare models m4 and m5 using the anova(m4, m5) function. Which model fits best?
- 7. Considering the best model, have a look at any potential outliers. Use the check_model() function to visualize the distribution of residuals. Write 50 words explaining what you learned about the residuals of your model.
- 8. Now we will use the tricarpa.csv data set. Read it in R and name the data frame tricarpa.
- 9. Reset the random seed to your student ID number and take a sample of 900 observations, called this sample my_tri.
- 10. Produce a scatterplot of MOE vs acoustic_velocity; that is, MOE in the y-axis and acoustic_velocity in the x-axis. This time we want both axes to go all the way to 0. You can add + $\limsup(y = c(0, 18))$ to the plot. Use something similar to change the scale of x, taking into account the ranges of the variables.
- 11. Fit a linear regression model of MOE vs acoustic_velocity and explain the meaning of the regression coefficients (using the values you estimated) in the context of the problem.
- 12. Create a new variable in my_tri, called c_acoustic, which is the centered version of acoustic_velocity. Produce a scatterplot of MOE vs c_acoustic, with the y axis going all the way to 0.
- 13. Fit a linear regression model of MOE vs c_acoustic and explain the meaning of the regression coefficients (using the values you estimated) in the context of the problem. Refer to the plots produced in items 10- and 12- to help in your answer.
- 14. Create a Word file with your graphs, code and answers and submit it in Learn. For each question present question, your code/figures and your comments.