Instructions

- Clear the environment
- Open a new R Script called `day4_exercise_script` where you will do the exercise and later save in the `day4` project directory.
- Add the purpose of the file and the author [MANDATORY]
- Here are the main activities for this excercise
    1) Load the `rio`, `lubridate`,`epikit`, `janitor`, `infer` and `tidyverse` package
    2) Load the blood *class presusure data* from Mohammed's study. Use the `import` function.
    3) Clean a string variable
    4) Explore the distribution of all continuous variables using density, bar and boxplots
    5) Plot frequency bar plots
    6) Compare means and proportions

1 Importing the dataset into R

- Save the *BP_measure.xlsx* in the `Data` folder
- Import the dataset into R using the `import` function

2 Data cleaning

- Clean the `syst_diast` variable to separate the diastolic and systolic measurements.
- Create a new variable (name it `hr_cat`) that classifies `hr` as *high* or *low* using a cutt-off of 72.

Plotting graphs

- Make a *boxplot* that compares `hr` by `age_cat`
- Make a *boxplot* that compares `hr` by `sex`. Make this one horizontal.
- Make a *bar graph* that shows the fequencies of male and female respondents

Data summaries

- Make data summaries that shows the mean `hr` by sex. Hint: use `group_by()` and `summarise()`
- Make data summaries that shows the mean `hr` by age_cat.

Comparison of means and proportions

- Compare mean `hr` between males and females and interpret.

HINT: **Helper code**

```
# example of comparing means

t.test(data=dataframe ,
       hr_cat_variable ~ hr_cat_variable)
```

- Compare proportions of or respondents with high `hr` in males and females. Use the variable `hr_cat`. Interpret.

HINT: **Helper code**

```
# example of comparing proportions

infer::prop_test(dataframe ,
                 hr_cat_variable ~ sex)
```

Reshaping

- Use `select()` to select *age_cat*, *sex* and *hr* and put then in an object named *hr_sex*
- Use `pivot_wider()` to reshape *hr_sex* and put the resulting dataset in an object named *hr_sex_wider*, where the new columns will be *male* and *female*

HINT: **Helper code**

```r
# example of reshaping from long to wide
hr_sex_wider <- hr_sex %>%
  pivot_wider(names_from = ,
              values_from = )
```