Lab #1 - solutions

Vittorio Zampinetti[*] Mauro Gasparini[†]

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Lab 1 (with solutions)

Iris Dataset

Download the dataset at this link (https://archive.ics.uci.edu/ml/datsets/iris) (look for the `iris.data` file) and place the file together with your R script (for simplicity). At that web page, you can also get some information regarding the origin and nature of the data.

The dataset is available as Comma-Separated Values (CSV) file, which is nothing but a plain text file where each row is a row of a table and every column is separated by a comma. To make it look more like a CSV file, rename it from `iris.data` to `iris.csv`.

Import data

Now we're ready to import the data in R and view it as a table.

> Hint: use `read_csv()` function from the `readr` library. Check the function arguments. Also, you might need to manually add the column names. To check which column names should be added and in which order, check under **"attribute information"** on the dataset reference page linked above.

```r
library(tidyverse) # we will use tibble, dplyr, ggplot, readr, ...
```

```r
iris_df <- read_csv("./datasets/iris.csv",
  col_names = c(
    "sepal_length", "sepal_width",
    "petal_length", "petal_width", "class"
  )
)
```

```
## Rows: 150 Columns: 5
## -- Column specification ----------------------------------------------------------------------------
## Delimiter: ","
## chr (1): class
## dbl (4): sepal_length, sepal_width, petal_length, petal_width
##
## i Use `spec()` to retrieve the full column specification for this data.
## i Specify the column types or set `show_col_types = FALSE` to quiet this message.
```

```r
iris_df
```

```
## # A tibble: 150 x 5
```

[*] Politecnico di Torino, vittorio.zampinetti@polito.it
[†] Politecnico di Torino, mauro.gasparini@polito.it

```
##    sepal_length sepal_width petal_length petal_width class
##           <dbl>       <dbl>        <dbl>       <dbl> <chr>
##  1          5.1         3.5          1.4         0.2 Iris-setosa
##  2          4.9         3            1.4         0.2 Iris-setosa
##  3          4.7         3.2          1.3         0.2 Iris-setosa
##  4          4.6         3.1          1.5         0.2 Iris-setosa
##  5          5           3.6          1.4         0.2 Iris-setosa
##  6          5.4         3.9          1.7         0.4 Iris-setosa
##  7          4.6         3.4          1.4         0.3 Iris-setosa
##  8          5           3.4          1.5         0.2 Iris-setosa
##  9          4.4         2.9          1.4         0.2 Iris-setosa
## 10          4.9         3.1          1.5         0.1 Iris-setosa
## # ... with 140 more rows
```

Answer these questions:

- How many observations does the dataset consist of?
- Which are the different classes?

```
iris_df %>%
  nrow()
```

```
## [1] 150
```

```
iris_df %>%
  pull(class) %>%
  unique()
```

```
## [1] "Iris-setosa"     "Iris-versicolor" "Iris-virginica"
```

Exploratory Data Analysis (EDA)

First compute the mean and standard deviation of each measure for each class separately.

```
iris_df %>%
  group_by(class) %>%
  summarize(
    msl = mean(sepal_length), msw = mean(sepal_width),
    mpl = mean(petal_length), mpw = mean(petal_width),
    ssl = sd(sepal_length), ssw = sd(sepal_width),
    spl = sd(petal_length), spw = sd(petal_width)
  )
```

```
## # A tibble: 3 x 9
##   class             msl   msw   mpl   mpw   ssl   ssw   spl   spw
##   <chr>           <dbl> <dbl> <dbl> <dbl> <dbl> <dbl> <dbl> <dbl>
## 1 Iris-setosa      5.01  3.42  1.46 0.244 0.352 0.381 0.174 0.107
## 2 Iris-versicolor  5.94  2.77  4.26 1.33  0.516 0.314 0.470 0.198
## 3 Iris-virginica   6.59  2.97  5.55 2.03  0.636 0.322 0.552 0.275
```

- What can you infer? Is there any measure which is more indicative of a certain class?

You can also plot the empirical distribution of the four measures separately, in order to better visualize how far (or close) they are from each other.

- Plot the distributions of the four measures in a 2x2 grid, differentiating the types with color encoding (optional).

  Hint: You can use `melt()` from the `reshape2` library to transform the dataset, and then plot the various densities with color encoding on the four measures.

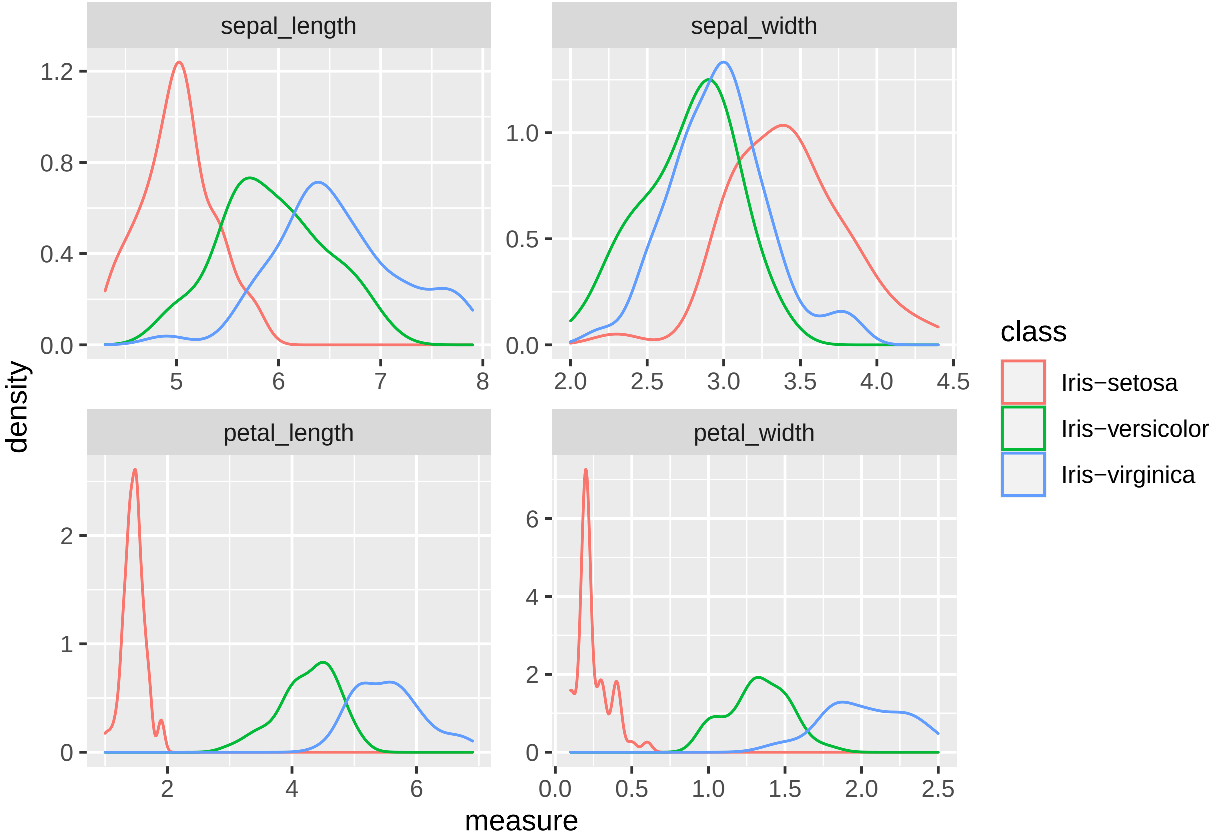
```
library(reshape2)
```

```
##
## Attaching package: 'reshape2'

## The following object is masked from 'package:tidyr':
##
##     smiths
```

```
iris_df %>%
  melt(value.name = "measure") %>% # collapse all measures in one col
  # then add a column with the measure name
  ggplot() +
  geom_density(aes(measure, color = class)) +
  facet_wrap(vars(variable), nrow = 2, scales = "free")
```

```
## Using class as id variables
```



We can also visualize the four measures on a set of plots that shows the correlation between variables, two-by-two. This is easily done with a pair plot.

- Draw a pair plot (optional).

  Hint: install the package with `install.packages("GGally")` and load it with `library(GGally)`, then read the help document of the `ggpairs()` function. You can also use R base `pairs()` function.

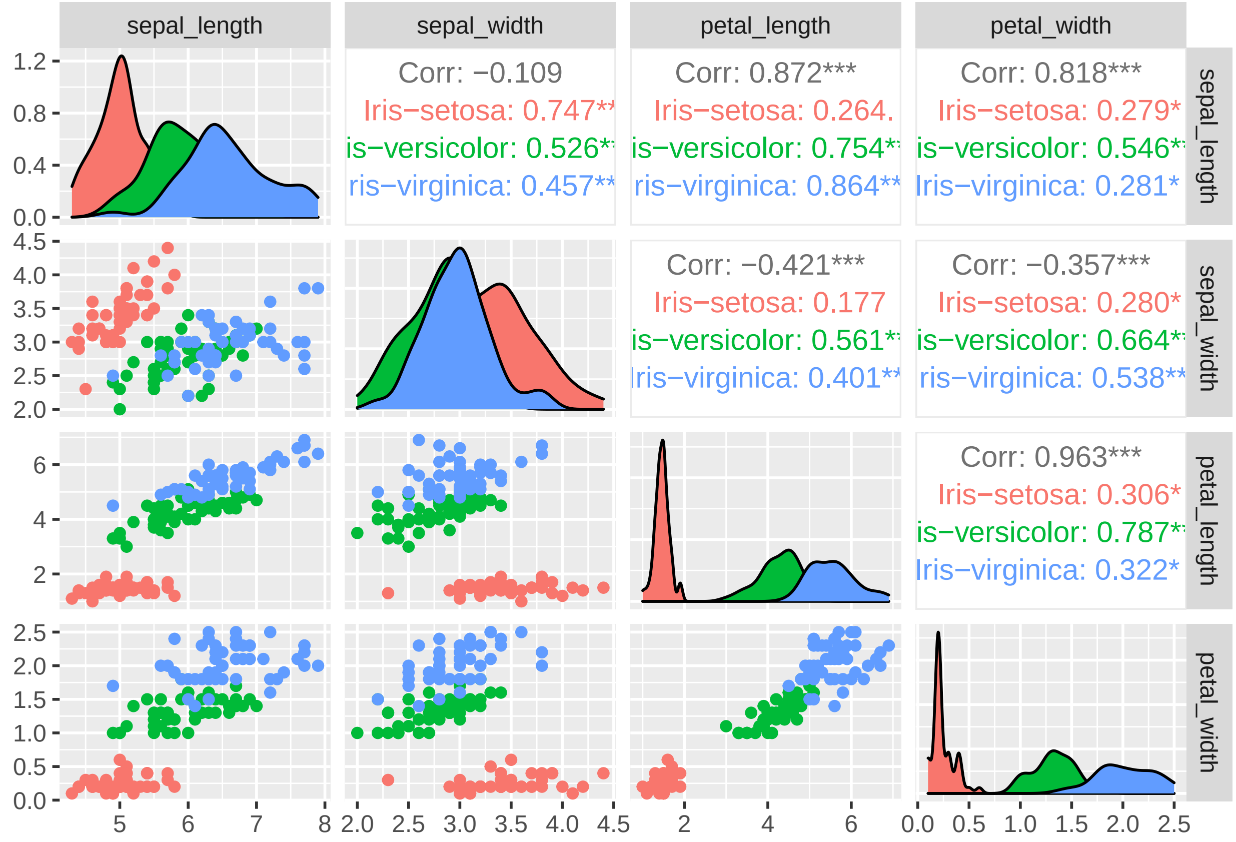
```
library(GGally)
```

```
## Registered S3 method overwritten by 'GGally':
##   method from
##   +.gg   ggplot2
```

```
iris_df %>%
  ggpairs(mapping = aes(color = class), columns = 1:4)
```

```
##

## plot: [1,1] [==>-----------------------------------------------] 6% est: 0s
## plot: [1,2] [=====>--------------------------------------------] 12% est: 0s
## plot: [1,3] [========>-----------------------------------------] 19% est: 0s
## plot: [1,4] [===========>--------------------------------------] 25% est: 0s
## plot: [2,1] [===============>----------------------------------] 31% est: 0s
## plot: [2,2] [==================>-------------------------------] 38% est: 0s
## plot: [2,3] [=====================>----------------------------] 44% est: 0s
## plot: [2,4] [========================>-------------------------] 50% est: 0s
## plot: [3,1] [===========================>----------------------] 56% est: 0s
## plot: [3,2] [==============================>-------------------] 62% est: 0s
## plot: [3,3] [=================================>----------------] 69% est: 0s
## plot: [3,4] [=====================================>------------] 75% est: 0s
## plot: [4,1] [========================================>---------] 81% est: 0s
## plot: [4,2] [===========================================>------] 88% est: 0s
## plot: [4,3] [==============================================>---] 94% est: 0s
## plot: [4,4] [==================================================]100% est: 0s
```



Confidence intervals

Let's make our decision more statistically relevant. Select only one class, the Setosa type, and one measure, petal length.

Now build a 95% CI around the mean value of the Setosa petal length. Assume σ unknown.

Formally, we want to find x_l, x_u s.t.

$$P(x_l \leq \bar{X} \leq x_u) = 95\%\,.$$

- Find such CI, using only R base operators (`mean`, `sd`).

To do this, remember that

- $\frac{(\bar{X}-\mu_0)\sqrt{n}}{s} \sim T(n-1)$ where s is the sample standard deviation
- `qt()` is the R function for the t-distribution quantile
- Validate your result by using `t.test()` to get the CI.

```
setosa_petal_length <- iris_df %>%
  filter(class == "Iris-setosa") %>%
  pull(petal_length)

nspl <- length(setosa_petal_length)
crit_t <- qt(.975, nspl - 1)
mu0 <- mean(setosa_petal_length)
se <- sd(setosa_petal_length) / sqrt(nspl)
delta <- crit_t * se

ci <- c(mu0 - delta, mu0 + delta)
ci
```

```
## [1] 1.414689 1.513311
```

With `t.test`

```
t.test(setosa_petal_length, mu = mu0, conf.level = 0.95)
```

```
##
##  One Sample t-test
##
## data:  setosa_petal_length
## t = 0, df = 49, p-value = 1
## alternative hypothesis: true mean is not equal to 1.464
## 95 percent confidence interval:
##  1.414689 1.513311
## sample estimates:
## mean of x
##     1.464
```

Compare this confidence interval to the mean and std-dev values you got for each class for the petal length measure.

- Do you think the petal length is a good measure to differentiate between Setosa and the other two types? Why?

P-value

Imagine you get measurements in terms of all 4 indicators of 5 iris flowers belonging to the same class, but you don't know which. These are the observations.

```
x_sample <- tibble(
  sepal_length = c(4.738759, 5.545983, 5.389729, 4.549803, 5.896723),
  sepal_width = c(3.132478, 3.537232, 3.217107, 3.190097, 3.636949),
  petal_length = c(1.220472, 1.321923, 1.573662, 1.289875, 1.705737),
  petal_width = c(0.23, 0.09, 0.33, 0.22, 0.18)
)
```

- Just looking at the values of the petal length, can you take advantage of the CI you just computed in order to make a guess about the class of these flowers? (Setosa or not Setosa)

To make this guess more statistically relevant, we have to quantify our confidence.

- What is the *p-value* of this sample, only looking at the petal length, against the null hypothesis that the samples are coming from the Setosa type?

  Remember that the *p-value* is defined as

$$P\left(T \geq \frac{(\bar{\mathbf{x}} - \mu_0)\sqrt{n}}{s} | \mu = \mu_0\right)$$

- Based on the value you found, what can you say about the class of this sample?

```
# manually
nx <- nrow(x_sample)
t_stat <- (mean(x_sample$petal_length) - mu0) * sqrt(nx) /
  sd(x_sample$petal_length)
pt(t_stat, df = nx - 1, lower.tail = FALSE)
```

```
## [1] 0.6619335
```

```
# with t-test
t.test(x_sample$petal_length, mu = mu0)
```

```
##
##  One Sample t-test
##
## data:  x_sample$petal_length
## t = -0.44983, df = 4, p-value = 0.6761
## alternative hypothesis: true mean is not equal to 1.464
## 95 percent confidence interval:
##  1.165161 1.679506
## sample estimates:
## mean of x
##  1.422334
```

Now take this other sample:

```
y_sample <- tibble(
  sepal_length = c(6.303990, 6.705969, 7.795044, 7.015665, 7.056670),
  sepal_width = c(3.152411, 2.499612, 3.293934, 3.275724, 2.843923),
  petal_length = c(6.356729, 5.975576, 4.998114, 5.423811, 5.382871),
  petal_width = c(1.589342, 2.305014, 2.260900, 2.185519, 1.589370)
)
```

- What is the *p-value*?

- Is it higher or lower than 0.025?
- Could we guess the answer to this last question without computing it?

```
# manually
ny <- nrow(y_sample)
t_stat <- (mean(y_sample$petal_length) - mu0) * sqrt(ny) / sd(y_sample$petal_length)
pt(t_stat, df = ny - 1, lower.tail = FALSE)
```

```
## [1] 3.231502e-05
```

```
# with t-test
t.test(y_sample$petal_length, mu = mu0)
```

```
##
##  One Sample t-test
##
## data:  y_sample$petal_length
## t = 17.36, df = 4, p-value = 6.463e-05
## alternative hypothesis: true mean is not equal to 1.464
## 95 percent confidence interval:
##  4.961539 6.293302
## sample estimates:
## mean of x
##   5.62742
```