

## Installing R and RStudio

We solve the computer exercises of this course using the statistical software R. R is widely used and freely distributed programming language that is particularly suitable for statistical analysis. You should be able to find R from every computer located in the Undergraduate Centre (Otakaari 1) or Maarintalo. The computer exercises of this course can be solved by using the basic R software, that you can download free of charge to your personal computer. There exists many different integrated development environments (IDE) for the R programming language. We recommend that you use the one called RStudio. RStudio is also free of charge. Note that, in order to use RStudio, you need the basic R software installed. Below are links for installing R and RStudio, respectively.

- Install R – <https://cran.r-project.org/>
- Install Rstudio – <https://www.rstudio.com/products/rstudio/download/>

## Demo Problem 1: Introduction to R

- a) Change your working directory. Try the commands `help(c)` and `help(matrix)`.
- b) Calculate the affine transformation  $\mathbf{y} = \mathbf{x}\mathbf{A}^{-1} + \mathbf{b}$ , where

$$\mathbf{A} = \begin{pmatrix} 2 & 1 & 5 \\ -2 & 7 & 0 \\ 5 & -8 & -1 \end{pmatrix}, \quad \mathbf{x}^T = \begin{pmatrix} 8 \\ -4 \\ 2 \end{pmatrix}, \quad \mathbf{b}^T = \begin{pmatrix} 3 \\ 10 \\ -19 \end{pmatrix}.$$

- c) Install the package `mvtnorm` and load the corresponding functions to your workspace. Set the seed to 123 using the command `set.seed(123)`. Generate 100 observations from a two dimensional normal distribution with expected value  $\boldsymbol{\mu}$  and covariance matrix  $\boldsymbol{\Sigma}$ , where

$$\boldsymbol{\mu} = \begin{pmatrix} 3 \\ 1 \end{pmatrix} \quad \text{and} \quad \boldsymbol{\Sigma} = \begin{pmatrix} 4 & 1 \\ 1 & 2 \end{pmatrix}.$$

Visualize the observations.

- d) Use the data from part c) and calculate the sample mean  $\bar{\mathbf{x}}$  and the sample covariance matrix  $\mathbf{S}_x$ . Calculate the eigenvalues and eigenvectors from the matrix  $\mathbf{S}_x$ . Verify from the data, that the following equations hold,

$$\begin{aligned} \text{Tr}(\mathbf{S}_x) &= \lambda_1 + \lambda_2 + \dots + \lambda_p \text{ and} \\ \text{Det}(\mathbf{S}_x) &= \lambda_1 \lambda_2 \dots \lambda_p, \end{aligned}$$

where  $\lambda_i$  are the eigenvalues of  $\mathbf{S}_x$ .

- e) Calculate the affine transformation  $\mathbf{y}_i = \mathbf{A}\mathbf{x}_i + \mathbf{b}$ , where

$$\mathbf{b} = \begin{pmatrix} 3 \\ 1 \end{pmatrix} \quad \text{and} \quad \mathbf{A} = \begin{pmatrix} 1 & 2 \\ 3 & 1 \end{pmatrix},$$

verify that  $\bar{\mathbf{y}} = \mathbf{A}\bar{\mathbf{x}} + \mathbf{b}$  and  $\mathbf{S}_y = \mathbf{A}\mathbf{S}_x\mathbf{A}^T$ . What does affine equivariance mean in practice?

- f) Upload the data from the file `data.txt` into your workspace. Create a function, that centers your data (removes the mean) and pairwise scatterplots the variables. Calculate the sample covariance and correlation matrices and the corresponding eigenvalues- and vectors.

## Solution

- a) Whenever you refer to a file with a relative path, you have to type the path relative to your working directory.

Path of the current working directory can be seen with the function `getwd`. The working directory can be set with the function `setwd`. In RStudio this can be done also by choosing from the upper panel: **Session** → **Set Working Directory** → **Choose Directory** (Ctrl + Shift + H).

```
setwd("~/teaching/multivariate/01week/markdown/")  
getwd()
```

```
## [1] "/home/perej/teaching/multivariate/01week/markdown"
```

Manual pages for functions, classes etc. can be found with the command `help` or `?`. You can comment code by starting a line with `#`.

```
# How do I create vectors?  
help(c)  
?c  
  
# How do I create matrices?  
help(matrix)  
?matrix
```

- b) First, create matrix  $A$  and vectors  $x$  and  $b$ . You can assign values to variables with either `=` or `<-`. Choose one and stick with it.

We create vectors  $x$  and  $b$  in two ways. First, with command `c` and then as a row vector with command `matrix`.

```
a <- matrix(c(2, 1, 5, -2, 7, 0, 5, -8, -1), nrow = 3, byrow = TRUE)  
x1 <- c(8, -4, 2)  
b1 <- c(3, 10, -19)  
  
x2 <- matrix(x1, nrow = 1, byrow = TRUE)  
b2 <- matrix(b1, nrow = 1, byrow = TRUE)
```

Matrix multiplication can be performed with the operator `%*%` and inverse matrix can be computed with the function `solve`. Both variables `y1` and `y2` give the right result. This is because according to the documentation of `%*%`, vectors are interpreted as row or column vectors such that arguments are conformable. If you want to be explicit about dimensions of vectors use the function `matrix`.

```
y1 <- x1 %*% solve(a) + b1  
y2 <- x2 %*% solve(a) + b2  
  
all(y1 == y2)
```

```
## [1] TRUE
```

```
y1
```

```
##           [,1]      [,2]      [,3]  
## [1,] 3.774775 11.45946 -17.12613
```

For example, the following code gives an error.

```
x3 <- matrix(x1, ncol = 1, byrow = FALSE)  
b3 <- matrix(b1, ncol = 1, byrow = FALSE)  
  
x3 %*% solve(a) + b3
```

- c) If there is some functionality that is not implemented in base R there is most probably a package for it. You can install packages with the function `install.packages`. Note that the package name has to

be given as a character string for the function `install.packages`. For example, the package `mvtnorm` that is required for this exercise session can be installed with the following line of code.

```
install.packages("mvtnorm")
```

Once the package is installed you can use functionality inside the package by specifying the correct namespace and using double colon `::` between the namespace and the function. Below we use the function `rmvnorm` from the package `mvtnorm`.

```
mvtnorm::rmvnorm(3, rep(0, 2))
```

Namespaces are a useful concept since there can be functions with the same name in different packages. For example function `lag` can be found at least in two different packages.

```
?stats::lag  
?dplyr::lag
```

Instead of specifying the namespace one can attach the package with the function `library`. For an example, see following lines of code.

```
library(mvtnorm)  
rmvnorm(3, rep(0, 2))
```

If you decide to attach packages it is a good practice to put `library` commands at the top of your script, instead of scattering them all around.

Next, we create a sample of size  $n = 100$  from multivariate normal distribution with location vector  $\mu$  and covariance matrix  $\Sigma$ . With function `head` you can see the first few observations.

```
mu <- c(3, 1)  
sigma <- matrix(c(4, 1, 1, 2), byrow = TRUE, ncol = 2)  
n <- 100  
  
set.seed(123)  
x <- rmvnorm(n, mu, sigma)  
head(x)
```

```
##           [,1]      [,2]  
## [1,] 1.823028  0.5149745  
## [2,] 6.103696  1.5613434  
## [3,] 3.766090  3.4096342  
## [4,] 3.535096 -0.6118415  
## [5,] 1.508960  0.1794479  
## [6,] 5.527988  1.8617391
```

Figure 1 should look similar if you set seed to 123 before creating the sample.

```
plot(x, pch = 20, xlab = expression("X"[1]), ylab = expression("X"[2]),  
      main = expression(paste("Sample from ", "N(", mu, ", ", " ", Sigma, ")")))
```

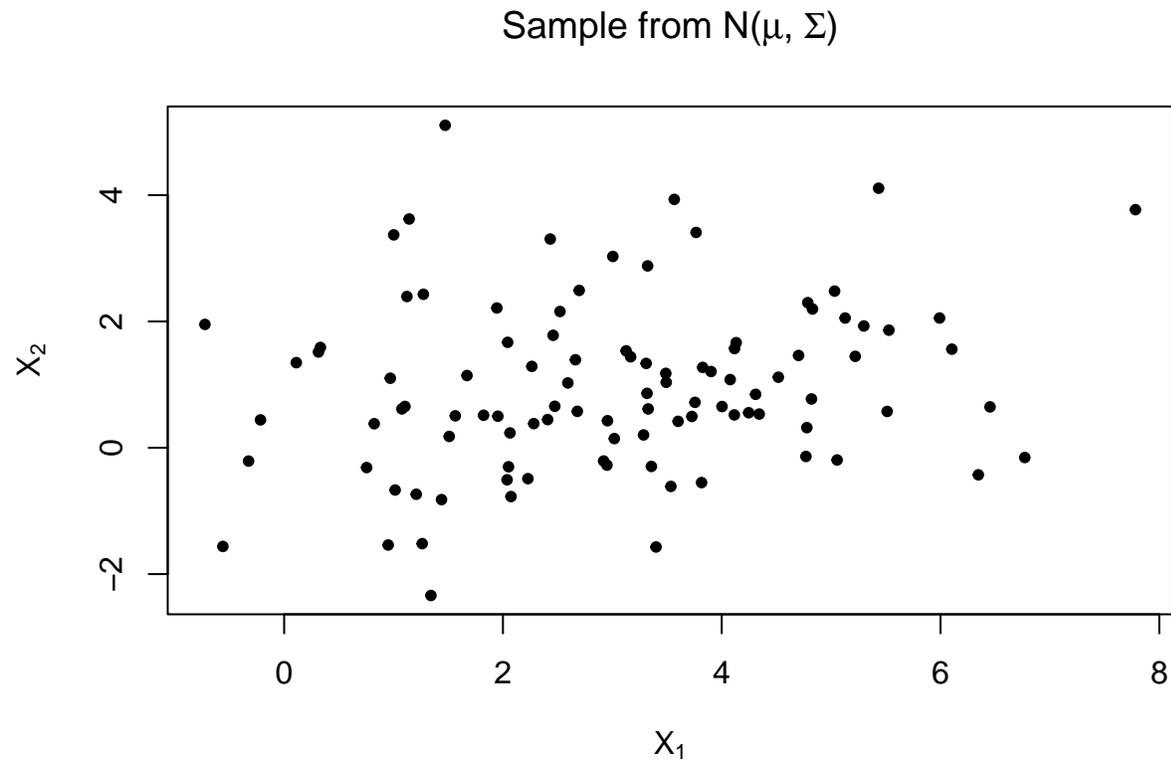


Figure 1: Scatter plot of a sample from a bivariate normal distribution.

d) There are a couple of ways to calculate the sample mean vector.

```
x_mean1 <- apply(x, 2, mean) # Apply function "mean" to every column
x_mean2 <- colMeans(x)
all(x_mean1 == x_mean2)
```

```
## [1] TRUE
```

```
x_mean1
```

```
## [1] 3.004655 0.970002
```

One can use the function `cov` to calculate the sample covariance.

```
x_cov <- cov(x)
x_cov
```

```
##           [,1]      [,2]
## [1,] 3.0744739 0.4545397
## [2,] 0.4545397 1.8184535
```

Next, let us calculate eigenvalues and eigenvectors of sample covariance matrix  $S_x$ . Columns of variable `eigvec` contain the eigenvectors.

```
eig <- eigen(x_cov)
eigval <- eig$values
eigvec <- eig$vectors
eigval
```

```
## [1] 3.221708 1.671220
```

```
eigvec
```

```
##          [,1]      [,2]
## [1,] -0.9513361  0.3081552
## [2,] -0.3081552 -0.9513361
```

Lastly, let us verify that

$$\text{Tr}(\mathbf{S}_x) = \lambda_1 + \lambda_2$$

and that

$$\text{Det}(\mathbf{S}_x) = \lambda_1 \lambda_2.$$

```
sum(diag(x_cov)) - sum(eigval)
```

```
## [1] 0
```

```
det(x_cov) - prod(eigval)
```

```
## [1] -1.776357e-15
```

e) First, let us create matrix  $\mathbf{A}$  and vector  $\mathbf{b}$ .

```
b <- c(3, 1)
a <- matrix(c(1, 2, 3, 1), byrow = TRUE, ncol = 2)
```

We can avoid having any for loops by doing matrix operations and using the function `sweep`. Function `sweep` is quite similar to `apply`. For example, below are two ways to sum vector  $\mathbf{b}$  to each row of  $\mathbf{A}$ .

```
test1 <- sweep(a, 2, b, "+")
test2 <- t(apply(a, 1, "+", b))
all(test1 == test2)
```

```
## [1] TRUE
```

```
test1
```

```
##      [,1] [,2]
## [1,]    4    3
## [2,]    6    2
```

Below is another example where we sum vector  $\mathbf{b}$  to each column of  $\mathbf{A}$ .

```
test1 <- sweep(a, 1, b, "+")
test2 <- apply(a, 2, "+", b)
all(test1 == test2)
```

```
## [1] TRUE
```

```
test1
```

```
##      [,1] [,2]
## [1,]    4    5
## [2,]    4    2
```

Now that we have introduced function `sweep`, let us perform the affine transformations. Notice that

$$\mathbf{X}\mathbf{A}^T + \mathbf{1}_{100}\mathbf{b}^T = \begin{pmatrix} (\mathbf{A}\mathbf{x}_1 + \mathbf{b})^T \\ (\mathbf{A}\mathbf{x}_2 + \mathbf{b})^T \\ \vdots \\ (\mathbf{A}\mathbf{x}_{100} + \mathbf{b})^T \end{pmatrix}, \quad (1)$$

where  $\mathbf{1}_{100} \in \mathbb{R}^{100}$  is a column vector of ones.

```
# First way
y1 <- sweep(x %*% t(a), 2, b, "+")

# Second way
ones <- rep(1, n)
y2 <- x %*% t(a) + ones %*% t(b)

all(y1 == y2)
```

```
## [1] TRUE
```

Lastly, let us check that  $\bar{\mathbf{y}} = \mathbf{A}\bar{\mathbf{x}} + \mathbf{b}$  and  $\mathbf{S}_y = \mathbf{A}\mathbf{S}_x\mathbf{A}^T$ . We can use any matrix norm  $\|\cdot\|$  to check that two matrices  $\mathbf{X}, \mathbf{Y} \in \mathbb{R}^{n \times m}$  are equal. This works since

$$\mathbf{X} = \mathbf{Y} \iff \|\mathbf{X} - \mathbf{Y}\| = 0.$$

We can choose to use, e.g., Frobenius norm.

```
norm(colMeans(y1) - (a %*% colMeans(x) + b), type = "F")
```

```
## [1] 8.881784e-16
```

```
norm(cov(y1) - (a %*% cov(x) %*% t(a)), type = "F")
```

```
## [1] 3.552714e-15
```

f) Be sure that you know the path to the data with respect to the working directory. For example, in this case `data.txt` is located in a different directory than the R script.

```
getwd()
```

```
## [1] "/home/perej/teaching/multivariate/01week/markdown"
```

```
data <- read.table("../data/data.txt", sep = "\t", header = FALSE)
head(data)
```

```
##           V1           V2           V3           V4
## 1 0.04301325 0.39287882 0.3078980 0.8659341
## 2 0.07597216 0.16503982 0.9537341 0.6011355
## 3 0.82452548 0.60148149 0.7152086 0.9866722
## 4 0.56774748 0.81009764 0.7085845 0.8704875
## 5 0.57517488 0.12338534 0.3329567 0.9171741
## 6 0.81746640 0.08863711 0.6017773 0.2063420
```

Here we create the function that plots the pairwise scatter plots and centers the data. Additionally, Figure 2 shows the resulting plot.

```
center <- function(x) {
  pairs(x, pch = 19, col = "midnightblue", gap = 0, upper.panel = NULL,
        cex.labels = 1)
  sweep(x, 2, colMeans(x), "-")
}

data_center <- center(data)
```

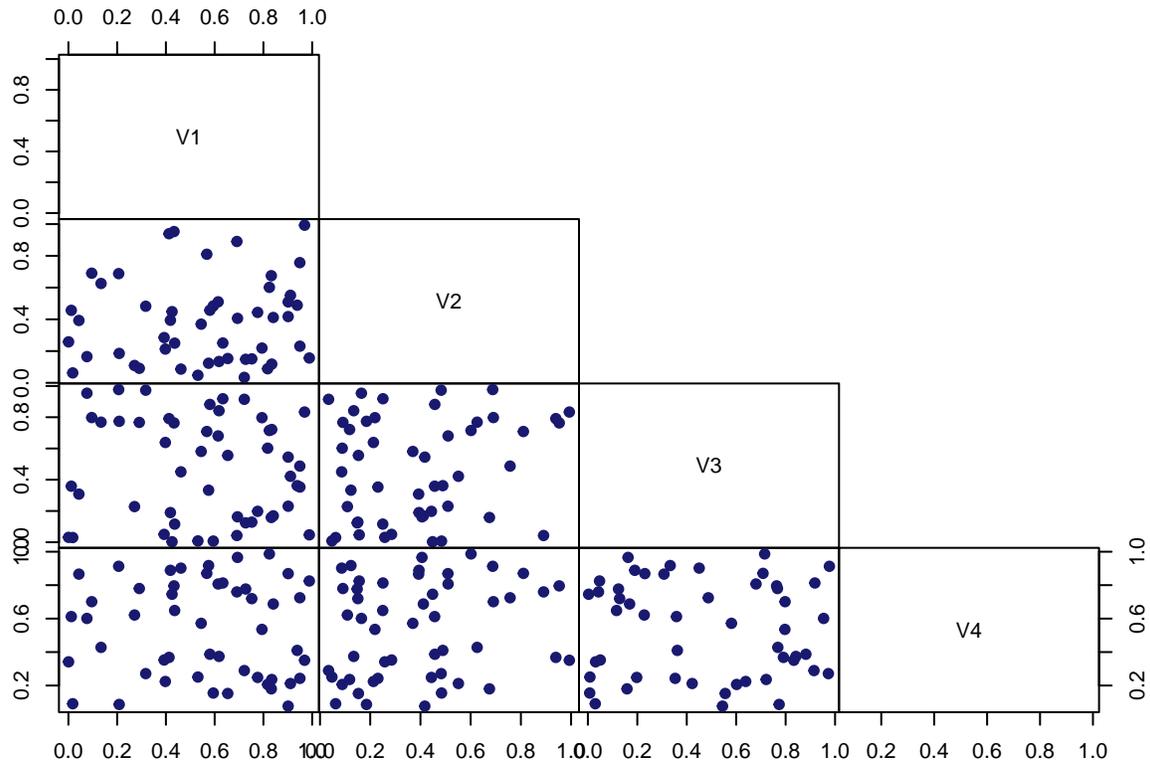


Figure 2: Scatter plot of variables.

```
colMeans(data_center)
```

```
##           V1           V2           V3           V4  
## -1.887379e-17  1.221245e-17 -1.665335e-18 -2.109424e-17
```

Lastly, we calculate sample covariance, sample correlation and the corresponding eigenvalues and eigenvectors.

```
center_cov <- cov(data_center)  
center_cor <- cor(data_center)  
eigen(center_cov)$values
```

```
## [1] 0.11163469 0.08903608 0.08697829 0.05218629
```

```
eigen(center_cov)$vectors
```

```
##           [,1]      [,2]      [,3]      [,4]  
## [1,] -0.24232756  0.51237112  0.76290091  0.3110231  
## [2,]  0.30797566  0.55314104  0.04145492 -0.7729602  
## [3,]  0.91739205 -0.09949153  0.23313028  0.3068282  
## [4,]  0.06942745  0.64931676 -0.60159285  0.4600583
```

```
eigen(center_cor)$values
```

```
## [1] 1.2367328 1.0762947 1.0211537 0.6658188
```

```
eigen(center_cor)$vectors
```

```
##           [,1]      [,2]      [,3]      [,4]
## [1,] -0.02338207  0.7717167 -0.5016233  0.3902315
## [2,]  0.72821948  0.2244426 -0.1739016 -0.6237629
## [3,]  0.47737240 -0.5465891 -0.4787554  0.4941145
## [4,]  0.49118760  0.2352002  0.6992321  0.4631307
```

## Demo Problem 2: The Eigenvalues of a Symmetric Matrix

Show that the eigenvalues of a real valued symmetric matrix are always real valued.

### Solution

Let  $A$  be a symmetric real valued  $p \times p$  matrix ( $A = A^T$ ). Note that, if the symmetry condition is dropped,  $A$  can have complex valued eigenvalues and -vectors. Let  $\lambda_i$  be the  $i$ th eigenvalue and  $v_i$  the corresponding eigenvector of  $A$ .

**Definition 1** (Eigenvalues and eigenvectors). A scalar  $\lambda_i$  is called an eigenvalue of  $p \times p$  matrix  $A$  if there is a nontrivial solution  $v_i$  to

$$Av_i = \lambda_i v_i,$$

where  $v_i$  is called an eigenvector corresponding to the eigenvalue  $\lambda_i$ .

Here, trivial solutions are obtained if  $v_i = 0$  (zero vector) since every scalar  $\lambda_i$  would then satisfy the equation above. First, we take the complex conjugate from both sides,

$$\begin{aligned} \overline{(Av_i)} &= \overline{(\lambda_i v_i)} \\ \Rightarrow A\bar{v}_i &= \bar{\lambda}_i \bar{v}_i, \end{aligned}$$

since  $A$  is real valued. Then, we multiply the above with  $v_i^T$  from the left side

$$\begin{aligned} v_i^T A\bar{v}_i &= v_i^T \bar{\lambda}_i \bar{v}_i \\ v_i^T A^T \bar{v}_i &= v_i^T \bar{\lambda}_i \bar{v}_i \\ (Av_i)^T \bar{v}_i &= \bar{\lambda}_i v_i^T \bar{v}_i \\ \lambda_i v_i^T \bar{v}_i &= \bar{\lambda}_i v_i^T \bar{v}_i \\ \Rightarrow (\lambda_i - \bar{\lambda}_i) v_i^T \bar{v}_i &= 0. \end{aligned}$$

Thus we must have that  $\lambda_i - \bar{\lambda}_i = 0$  or  $v_i^T \bar{v}_i = 0$ . However, note that  $v_i^T \bar{v}_i = \langle v_i, v_i \rangle$  is the canonical hermitian inner product. By properties of inner product we have

- $\langle v_i, v_i \rangle \geq 0$  and
- $\langle v_i, v_i \rangle = 0$  if and only if  $v_i = 0$ .

Remember that by definition of eigenvectors we assume that  $v_i \neq 0$ . Thus the option  $v_i^T \bar{v}_i = 0$  is not possible. That is, we must have  $\lambda_i = \bar{\lambda}_i$ .

*Remark.* Real *nonsymmetric* matrices can have complex eigenvalues. For example, consider matrix

$$A = \begin{pmatrix} 1 & -1 \\ 1 & 1 \end{pmatrix}.$$

```
a <- matrix(c(1, -1, 1, 1), ncol = 2, byrow = TRUE)
eigen(a)$values
```

```
## [1] 1+1i 1-1i
```

Thus the assumption of symmetricity cannot be dropped from the claim of the exercise.

## Homework Problem 1: Functions

In this exercise do not use the built-in functions `cov`, `cor`, `cov2cor` or any additional R packages.

- a) Create an R function that takes a data matrix  $\mathbf{X} \in \mathbb{R}^{n \times p}$ ,  $n > p$ , as an argument and returns the unbiased estimator of the covariance matrix.
- b) Create an R function that takes a full-rank covariance matrix  $\mathbf{A} \in \mathbb{R}^{p \times p}$  as an argument and returns the square root of the inverse matrix such that  $\mathbf{A}^{-\frac{1}{2}} \mathbf{A}^{-\frac{1}{2}} = \mathbf{A}^{-1}$ .
- c) Create an R function that takes a full-rank covariance matrix  $\mathbf{A}$  as an argument and returns the corresponding correlation matrix.