STAT 210

Applied Statistics and Data Analysis: Homework 2 - Solution

Due on Sep. 21/2025

You cannot use artificial intelligence tools to solve this homework.

Show complete solutions to get full credit. Writing code is not enough to answer a question. Your comments are more important than the code. Do not write comments in chunks. Label your graphs appropriately

Question 1

You will need the file weights.txt. This file has (simulated) data on an experiment to test the effects of two different types of diet. The set has 100 observations (50 males and 50 females), and there are three types of diet, coded as 1, 2, and 3. The first type (coded 1) corresponds to the control group and has subjects who did not change their usual diet during the eight weeks that the experiment lasted. The other two groups (coded 2 and 3) correspond to the diets that are being tested. The weight is measured in kilograms and the height in centimeters.

- (a) Read the file weights.txt and store it in an object called data1. Look at the structure of data1 using the function str. Check whether there are missing values in the file using the function is.na.
- (b) The columns pre_weight and post_weight have the weight for the subjects before starting the diet and eight weeks after following the diet, respectively. Create a new column in data1 called diff that has the difference in weights (final weight minus initial weight).
- (c) Using the function subset, create a new data frame named data1b that has the variables gender, age, height, diet, and diff in data1. Using data1b and the function tapply, calculate mean and standard deviation for diff according to diet. Compare these results and comment.
- (d) Using data1b and the function tapply, calculate mean and standard deviation for diff according to diet and gender. Compare these results and comment.
- (e) Use the function split on the file data1 with argument gender and store the result in an object called d1. What type of object is d1? Use the function quantile on the variable height on each of the components of d1 to get a summary of the height for the different genders classes. Store the results in two vectors named q11 and q12. Calculate q12/q11 and interpret the result.
- (f) The body mass index (BMI) is defined as a person's weight in kilograms divided by the square of height in meters. Add a column named bmi to the data frame data1 with the value of this index for each subject using the weight before the experiment started. Count how many subjects have BMI above 30.

Solution:

```
data1 <- read.table('weights.txt', header = T)
str(data1)</pre>
```

```
## 'data.frame':
                    100 obs. of 7 variables:
                       1 2 3 4 5 6 7 8 9 10 ...
##
   $ subject
                 : int
                        "F" "F" "F" "F" ...
## $ gender
                 : chr
## $ age
                       50 30 43 36 43 41 24 24 57 45 ...
                 : int
   $ height
                 : int
                        169 170 175 162 173 157 170 153 161 168 ...
                       76 70 73 65 75 42 68 41 43 66 ...
## $ pre weight : int
                       1 1 1 1 1 1 1 1 1 1 ...
  $ diet
                 : int
## $ post_weight: num 74.4 73.6 75.3 65.6 77.7 ...
```

There are seven variables in the data frame. The first, subject is just an index. The we have gender, age, height, pre_weight, which is the weight before the experiment started, diet, and post_weight, which is the weight after dieting for eight weeks.

We check for NA's:

```
sum(is.na(data1))
```

[1] 0

There are none.

(b) We create the new column in the data frame and use str to chack:

```
data1$diff <- data1$post_weight - data1$pre_weight
str(data1)</pre>
```

```
## 'data.frame':
                    100 obs. of 8 variables:
                        1 2 3 4 5 6 7 8 9 10 ...
## $ subject
                 : int
                        "F" "F" "F" "F" ...
   $ gender
                 : chr
## $ age
                 : int
                        50 30 43 36 43 41 24 24 57 45 ...
## $ height
                        169 170 175 162 173 157 170 153 161 168 ...
                 : int
## $ pre_weight : int
                        76 70 73 65 75 42 68 41 43 66 ...
                        1 1 1 1 1 1 1 1 1 1 ...
   $ diet
                 : int
                       74.4 73.6 75.3 65.6 77.7 ...
## $ post_weight: num
## $ diff
                       -1.6 3.645 2.259 0.648 2.666 ...
                 : num
```

(c) New data frame:

```
data1b <- subset(data1, select = c('gender', 'age', 'height', 'diet', 'diff'))
str(data1b)</pre>
```

```
## 'data.frame': 100 obs. of 5 variables:
## $ gender: chr "F" "F" "F" ...
## $ age : int 50 30 43 36 43 41 24 24 57 45 ...
## $ height: int 169 170 175 162 173 157 170 153 161 168 ...
## $ diet : int 1 1 1 1 1 1 1 1 ...
## $ diff : num -1.6 3.645 2.259 0.648 2.666 ...
```

We create the vectors with mean and standard deviation.

```
(diff_mn <- tapply(data1b$diff, data1$diet, mean))</pre>
```

```
## 1 2 3
## 0.3076043 0.2291316 -1.2873649

(diff_sd <- tapply(data1b$diff, data1$diet, sd))</pre>
```

```
## 1 2 3
## 2.5301875 3.6408409 0.9576384
```

We see that the average difference for diets 1 and 2 is positive and small, while the difference for diet 3 is

negative and above one kilogram. Regarding the standard deviation, it is smaller for subjects that followed diat 3 than for the other two diets.

(d) The means and standard deviations according to diet and gender are

```
tapply(data1b$diff, data1[,c(2,6)], mean)
##
         diet
## gender
                                         3
                    1
##
          1.0094958 0.2901713 -1.328099
        M -0.3529995 0.1642768 -1.246631
##
tapply(data1b$diff, data1[,c(2,6)], sd)
##
         diet.
## gender
                                      3
##
        F 2.076769 4.058366 1.0064372
##
        M 2.793558 3.271363 0.9354238
```

With diet 1, females have an average positive gain of weight of about one kilogram while men lose about 350 grams. For diet 2, the results for both genders are similar, they are positive and small. Finally, for diet 3 both values are negative and similar, with a loss of about 1.3 kilograms.

Regarding the standard deviation, the values for males and females are similar for all diets, but there are differences between diets, with diet 3 having the smalled standard deviation, while diet 2 has the largest.

(e) We use split:

```
d1 <- split(data1, data1$gender)</pre>
str(d1)
## List of 2
    $ F:'data.frame':
                         50 obs. of 8 variables:
##
     ..$ subject
                    : int [1:50] 1 2 3 4 5 6 7 8 9 10 ...
##
     ..$ gender
                    : chr [1:50] "F" "F" "F" "F" ...
##
     ..$ age
                     : int [1:50] 50 30 43 36 43 41 24 24 57 45 ...
##
                    : int [1:50] 169 170 175 162 173 157 170 153 161 168 ...
     ..$ height
##
     ..$ pre weight : int [1:50] 76 70 73 65 75 42 68 41 43 66 ...
##
                     : int [1:50] 1 1 1 1 1 1 1 1 1 1 ...
     ..$ diet
##
     ..$ post weight: num [1:50] 74.4 73.6 75.3 65.6 77.7 ...
##
     ..$ diff
                    : num [1:50] -1.6 3.645 2.259 0.648 2.666 ...
    $ M:'data.frame':
                        50 obs. of 8 variables:
##
##
     ..$ subject
                    : int [1:50] 51 52 53 54 55 56 57 58 59 60 ...
                    : chr [1:50] "M" "M" "M" "M" ...
##
     ..$ gender
                     : int [1:50] 50 39 48 46 54 44 42 27 42 49 ...
##
     ..$ age
##
     ..$ height
                    : int [1:50] 193 172 182 167 188 181 181 177 163 179 ...
##
     ..$ pre_weight : int [1:50] 100 62 92 43 112 81 88 84 41 66 ...
     ..$ diet
                    : int [1:50] 1 1 1 1 1 1 1 1 1 1 ...
     ..$ post_weight: num [1:50] 97.3 61.4 91.9 42.7 108.3 ...
##
     ..$ diff
                    : num [1:50] -2.691 -0.6187 -0.0856 -0.3228 -3.7141 ...
##
```

Object d1 is a list with two components, which correspond to the two values for gender: F and M. Each component is a data frame with all the information included in data1 for the corresponding value of gender. Hence, each component has 50 observations.

```
ql1 <- quantile(d1$'F'$height)
ql2 <- quantile(d1$'M'$height)
ql2/ql1</pre>
```

```
##
         0%
                  25%
                           50%
                                     75%
                                              100%
## 1.053691 1.037267 1.066265 1.076923 1.066298
```

The function quantile gives the minimum, maximum, and quartile values for the sample. We observe that the ratio of the male to female values is always greater than one by between 3.7 and 7.7 %.

(f) Since the height is in centimeters, we need to divide by 100:

```
data1$bmi <- data1$pre_weight/(data1$height/100)^2</pre>
str(data1)
##
   'data.frame':
                     100 obs. of 9 variables:
##
    $ subject
                         1
                           2 3 4 5 6 7 8 9 10 ...
                  : int
                         "F" "F" "F" "F" ...
##
    $ gender
                  : chr
    $ age
                   int
                         50 30 43 36 43 41 24 24 57 45 ...
                         169 170 175 162 173 157 170 153 161 168 ...
##
    $ height
                  : int
                         76 70 73 65 75 42 68 41 43 66 ...
##
    $ pre_weight : int
##
                         1 1 1 1 1 1 1 1 1 1 ...
    $ diet
                  : int
                         74.4 73.6 75.3 65.6 77.7 ...
    $ post_weight: num
##
    $ diff
                  : num
                         -1.6 3.645 2.259 0.648 2.666
    $ bmi
                         26.6 24.2 23.8 24.8 25.1 ...
                  : num
How many are above 30:
sum(data1$bmi> 30)
```

[1] 10

Ten out of 100 have BMI over 30.

Question 2

- (a) Create two matrices. The first, called m1, has dimension 3×5 and the components are values simulated from a binomial distribution with size 15 and probability 0.25. The second, called m2, has dimension 5×3 and the components are values simulated from a Poisson distribution with parameter 3. Create also a vector v1 of length three from a negative binomial distribution with parameters size = 2 and prob = 0.25.
- (b) Create a list named hwlist that has as a first component m1, second component m2, and third component v1. The names of these components should be item1, item2, and item3, respectively. Use the function rm to remove m1, m2, and v1 from the working environment.
- (c) Using matrix multiplication, multiply item1 times item2 and store the result in hwlist under the name item4. Multiply item1 and item2 also in the reverse order, but do not store the outcome.
- (d) Denote the transpose of a matrix M by M^t . Verify that

$$(\mathtt{item1} \star \mathtt{item2})^t = (\mathtt{item1})^t \star (\mathtt{item2})^t$$

where \star denotes standard matrix multiplication, and verify this relation also for the product of the matrices in the reverse order.

- (e) The matrix item4 has dimension 3×3 . Add an identity matrix of dimension 3 to item4 and store it in the same position.
- (f) Solve the system of equations item4 $\star x = item3$. Verify that you have obtained the correct solution.
- (g) Find the inverse of item4 and call it item4 inv. Verify that item4 inv is indeed the inverse of item4, and that multiplying item4_inv × item3 gives the solution to the system of equations in (f).

Solution:

(a) Matrices and vector:

```
set.seed(2468)
(m1 \leftarrow matrix(rbinom(15, size = 15, prob = 0.25), ncol = 5))
         [,1] [,2] [,3] [,4] [,5]
##
## [1,]
                 6
                      4
                            3
## [2,]
            4
                      2
                                 5
                 2
                            1
## [3,]
            3
                 3
                      5
(m2 \leftarrow matrix(rpois(15, 3), ncol = 3))
        [,1] [,2] [,3]
## [1,]
            5
                 2
## [2,]
            2
## [3,]
            1
                      4
                 1
## [4,]
            2
                 2
                      1
## [5,]
            9
                 2
                      5
(v1 <- rnbinom(3, size = 2, prob = 0.25))
## [1] 11 4 15
 (b)
hwlist <- list(item1 = m1, item2 = m2, item3 = v1)
str(hwlist)
## List of 3
## $ item1: int [1:3, 1:5] 4 4 3 6 2 3 4 2 5 3 ...
## $ item2: int [1:5, 1:3] 5 2 1 2 9 2 4 1 2 2 ...
## $ item3: int [1:3] 11 4 15
Remove original objects. We check with 1s that the objects are no longer in the working directory.
rm(m1, m2, v1)
ls()
## [1] "d1"
                  "data1"
                             "data1b" "diff_mn" "diff_sd" "hwlist" "ql1"
## [8] "q12"
 (c) Matrix multiplications:
(hwlist$item4 <- hwlist$item1 %*% hwlist$item2)</pre>
         [,1] [,2] [,3]
## [1,]
           60
                46
                     77
## [2,]
                30
                     58
          73
## [3,]
           37
                27
                     53
In the reverse order
(hwlist$item2 %*% hwlist$item1)
        [,1] [,2] [,3] [,4] [,5]
##
## [1,]
                           20
          37
                43
                     39
                                23
## [2,]
          42
                38
                     46
                           16
                                30
## [3,]
          20
                20
                     26
                            8
                                11
## [4,]
          19
                19
                     17
                           9
                                15
## [5,]
          59
                73
                     65
                           34
                                33
```

(d) Verify the relation: t(hwlist\$item1 %*% hwlist\$item2) ## [,1] [,2] [,3] ## [1,] ## [2,] ## [3,] t(hwlist\$item2) %*% t(hwlist\$item1) ## [,1] [,2] [,3] ## [1,] ## [2,] ## [3,] In the reverse order: t(hwlist\$item2 %*% hwlist\$item1) [,1] [,2] [,3] [,4] [,5] ## ## [1,] ## [2,] ## [3,] ## [4,] ## [5,] t(hwlist\$item1) %*% t(hwlist\$item2) [,1] [,2] [,3] [,4] [,5] ## ## [1,] ## [2,] ## [3,] ## [4,] ## [5,] (e) (hwlist\$item4 <- hwlist\$item4 + diag(3))</pre> [,1] [,2] [,3] ## ## [1,] ## [2,] ## [3,] (f) We use solve to find the solution (x <- solve(hwlist\$item4, hwlist\$item3))</pre> ## [1] -0.3007154 -1.0547695 1.0112083 To verify that this is the solution, we multiply item4 by xhwlist\$item4 %*% x [,1] ## ## [1,] ## [2,] ## [3,]

(g) The inverse is also obtained using the function solve:

```
(item4_inv <- solve(hwlist$item4))</pre>
                 [,1]
                               [,2]
                                            [,3]
## [1,] -0.008585056  0.032193959 -0.02233704
## [2,] 0.142766296 -0.035373609 -0.16558029
## [3,] -0.065500795 -0.004372019 0.11661367
We check that this is the inverse. To make the result clearer, we round the value to 14 digits
round(hwlist$item4 %*% item4_inv, 14)
        [,1] [,2] [,3]
##
## [1,]
            1
                 0
## [2,]
            0
                 1
                       0
## [3,]
            0
                 0
                       1
round(item4_inv %*% hwlist$item4, 14)
        [,1] [,2] [,3]
## [1,]
           1
                 0
## [2,]
            0
                 1
                       0
## [3,]
            0
                 0
                       1
Verify solution to system of equations:
item4_inv %*% hwlist$item3
##
               [,1]
## [1,] -0.3007154
## [2,] -1.0547695
## [3,] 1.0112083
Recall the {\tt x} is
## [1] -0.3007154 -1.0547695 1.0112083
```

and we see that they are equal.