

Exercise day 1 with solutions

Introduction to R for Basic Statistics

Exercise A: Reshaping the data and descriptive

For this exercise we will work with a subset of “follicle” data, collected from patients with cancer that had OTC (ovarian tissue cryopreservation). Follicles were cultured for 8 days and the diameter was collected every 2 days. The aim of the study was to compare the follicles growth among different treatment groups.

Information are collected in two data sets.

Data set *follicle* with:

- Patient: patient ID
- Number: follicle ID
- Day_x: follicle diameter at Day x
- AMH: Anti-Mullerian hormone concentration

Data set *patient* with:

- Patient ID
- Type of Disease
- Age at Day 0
- Treatment: Treatment group for the follicle growth

Question 1 Download both data sets and load them into R.

```
db_follicle<-read.csv("~/Desktop/KVN2021/Course/IntrotoR/data_exercise/db_follicle.csv")
db_pat<-read.csv("~/Desktop/KVN2021/Course/IntrotoR/data_exercise/patient.csv")
```

Consider the data set *patient*.

1. How many Patients?

To check how many patients are included in the study we can check the dimension of the data frame where each line is referred to one patient.

```
dim(db_pat)
```

```
## [1] 14 4
```

```
nrow(db_pat)
```

```
## [1] 14
```

We have 14 patients in total

2. Visualize the first lines of the data and print a summary of the data. What is the data type of each variable?

We can visualize the first 6 lines of the data using the function head()

```
head(db_pat)
```

```
## Patient Disease Treatment Age
## 1 1 Breast_cancer FBS 31.6
```

```
## 2      2      Breast_cancer      FBS 29.4
## 3      3 Neurological_cancer      FBS 19.3
## 4      4 Rheumatoid_arthritis      FBS 20.3
## 5      5      Mb_Hodgkin          hPL 29.8
## 6      6      Sarcoma             HSA 19.7
```

```
summary(db_pat)
```

```
##      Patient      Disease      Treatment      Age
## Min.   : 1.00 Length:14      Length:14      Min.   :19.30
## 1st Qu.: 4.25 Class :character Class :character 1st Qu.:29.50
## Median : 7.50 Mode  :character Mode  :character Median :31.40
## Mean   : 7.50                                     Mean  :29.74
## 3rd Qu.:10.75                                     3rd Qu.:32.25
## Max.   :14.00                                     Max.   :37.10
```

Patient and Age are quantitative and are either numerical or integer, while Disease is a categorical variables and is listed as character.

Question 2

Disease is *character*, can we understand from the summary how many different diseases are in the data?

1. Would it be better if Disease were of a different type? If yes, which one?

For easier representation it is better to have factor for categorical variables, thus we can transform Disease into factor.

2. Transform them into factor. You can use the function `factor()` in **R**.

```
db_pat$Disease<-factor(db_pat$Disease)
```

3. Print the summary of the data, can you see any difference?

```
summary(db_pat)
```

```
##      Patient      Disease      Treatment
## Min.   : 1.00 Brain_cancer      :1 Length:14
## 1st Qu.: 4.25 Breast_cancer      :8 Class :character
## Median : 7.50 Chronic_myeloid_leukemia:1 Mode  :character
## Mean   : 7.50 Mb_Hodgkin          :1
## 3rd Qu.:10.75 Neurological_cancer      :1
## Max.   :14.00 Rheumatoid_arthritis :1
##      Sarcoma             :1
##      Age
## Min.   :19.30
## 1st Qu.:29.50
## Median :31.40
## Mean   :29.74
## 3rd Qu.:32.25
## Max.   :37.10
##
```

The summary now shows the different levels of Disease with the number of observations in that category.

4. Create a new variable *Cancer* that groups the Disease into *Breast cancer* and *Others*:

```
db_pat$Cancer<-ifelse(db_pat$Disease=="Breast_cancer", "Breast_cancer", "Others")
```

we use the *ifelse* function to create the variable *Cancer* which write “Breast cancer” when the condition is verified and “Others” otherwise. This creates a character variable.

Question 3

Age is a continuous covariate:

1. Show min,max and mean for age.

To check their min,max and mean value we could use the summary function, otherwise we use min,max and mean separately

```
summary(db_pat$Age)
```

```
##      Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
##    19.30  29.50   31.40   29.74   32.25   37.10
```

```
min(db_pat$Age)
```

```
## [1] 19.3
```

```
max(db_pat$Age)
```

```
## [1] 37.1
```

```
mean(db_pat$Age)
```

```
## [1] 29.74286
```

2. Calculate the mean of age by cancer group (you can use **aggregate** or **tapply**)

When using *aggregate()*

```
aggregate(Age~Cancer, db_pat, mean)
```

```
##           Cancer      Age
## 1 Breast_cancer 32.91250
## 2           Others 25.51667
```

When using *tapply()*

```
tapply(db_pat$Age, db_pat$Cancer, mean)
```

```
## Breast_cancer      Others
##      32.91250      25.51667
```

3. Create a new variable in the data.frame for a categorical variable for age with the median as cut-off for the two categories

3a. Use the function *cut* in **R**. Run the command *str(NameofDatabase)*, of which type is the new categorical variable?

```
db_pat$age.cat<-cut(db_pat$Age, breaks=c(15,32,40), labels=c("<32",">32"))
str(db_pat)
```

```
## 'data.frame':   14 obs. of  6 variables:
## $ Patient   : int  1 2 3 4 5 6 7 8 9 10 ...
## $ Disease   : Factor w/ 7 levels "Brain_cancer",...: 2 2 5 6 4 7 1 2 2 3 ...
## $ Treatment: chr  "FBS" "FBS" "FBS" "FBS" ...
## $ Age       : num  31.6 29.4 19.3 20.3 29.8 19.7 32.1 34.8 37.1 31.9 ...
## $ Cancer    : chr  "Breast_cancer" "Breast_cancer" "Others" "Others" ...
## $ age.cat   : Factor w/ 2 levels "<32",">32": 1 1 1 1 1 1 2 2 2 1 ...
```

From the internal structure of the data.frame we can notice that age.cat created by the cut function is a factor

3b. Use the function *ifelse* in **R**. Run the command *str(NameofDatabase)*, of which type is the new categorical variable?

```
db_pat$age.cat2<-ifelse(db_pat$Age<32, "<32", ">=32")
str(db_pat)
```

```
## 'data.frame':  14 obs. of  7 variables:
## $ Patient   : int  1 2 3 4 5 6 7 8 9 10 ...
## $ Disease   : Factor w/ 7 levels "Brain_cancer",...: 2 2 5 6 4 7 1 2 2 3 ...
## $ Treatment: chr  "FBS" "FBS" "FBS" "FBS" ...
## $ Age       : num  31.6 29.4 19.3 20.3 29.8 19.7 32.1 34.8 37.1 31.9 ...
## $ Cancer    : chr  "Breast_cancer" "Breast_cancer" "Others" "Others" ...
## $ age.cat   : Factor w/ 2 levels "<32", ">32": 1 1 1 1 1 1 2 2 2 1 ...
## $ age.cat2  : chr  "<32" "<32" "<32" "<32" ...
```

From the internal structure of the data.frame we can notice that age.cat2 created by the ifelse function is a character

4. Create a Table to count how many patients belong to each age group.

```
table(db_pat$age.cat)
```

```
##
## <32 >32
##    9    5
```

5. Show the proportion of patients by cancer group (use *prop.table*)

```
prop.table(table(db_pat$Cancer))
```

```
##
## Breast_cancer    Others
##    0.5714286    0.4285714
```

Question 4

1. Show the proportions of patients in each Cancer group

```
prop.table(table(db_pat$Cancer))
```

```
##
## Breast_cancer    Others
##    0.5714286    0.4285714
```

Consider only patients with Breast cancer.

2. Subset data for Breast cancer patients

```
db_BC<-subset(db_pat, Cancer=="Breast_cancer")
```

3. Show the number of patients for each Age group

```
table(db_BC$age.cat)
```

```
##
## <32 >32
##    4    4
```

4. Calculate mean and standard deviation for Age

```
mean(db_BC$Age)
```

```
## [1] 32.9125
```

```
sd(db_BC$Age)
```

```
## [1] 2.700496
```