

Exercise day 2 with solutions

Introduction to R for Basic Statistics

Exercise B: Reshaping data (Part II)

Consider the data we used for Exercise of day 1.

It is 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 over time among different treatment groups.

Question 0 Load data into R :

```
follicle<-read.csv("https://raw.githubusercontent.com/AMeddis/IntrotoR-for-Basic-Statistics/main/data_exercise/follicle.csv")

patients<-read.csv("https://raw.githubusercontent.com/AMeddis/IntrotoR-for-Basic-Statistics/main/data_exercise/patient.csv")
```

1. Consider Data set *follicle*.
2. Visualize the first lines of the data.
3. Print the summary of the data. Is there any missing values? If yes, how many at Day0 and how many at Day8?

```
head(follicle)
```

##	Number	Patient	Day0	Day2	Day4	Day6	Day8
## 1	1	1	101.4590	112.1605	135.1980	160.2315	161.500
## 2	2	1	89.8315	141.3770	165.4925	NA	NA
## 3	3	1	90.2835	116.9870	122.6500	127.7305	129.447
## 4	4	1	120.3145	148.8840	166.9970	170.0245	170.740
## 5	5	1	93.0085	112.3135	120.8550	120.9000	120.940
## 6	6	2	83.9085	100.3520	112.6875	NA	NA

```
summary(follicle)
```

##	Number	Patient	Day0	Day2
##	Min. : 1.00	Min. : 1.0	Min. : 48.32	Min. : 59.87
##	1st Qu.:18.25	1st Qu.: 4.0	1st Qu.: 62.74	1st Qu.: 81.50
##	Median :35.50	Median : 7.5	Median : 83.91	Median :105.03
##	Mean :35.50	Mean : 7.5	Mean : 84.70	Mean :106.85
##	3rd Qu.:52.75	3rd Qu.:11.0	3rd Qu.: 95.56	3rd Qu.:118.05
##	Max. :70.00	Max. :14.0	Max. :194.47	Max. :263.01
##			NA's :3	NA's :5
##	Day4	Day6	Day8	
##	Min. : 62.97	Min. : 71.34	Min. : 72.48	
##	1st Qu.: 96.96	1st Qu.:102.64	1st Qu.:103.78	
##	Median :120.51	Median :126.42	Median :129.45	
##	Mean :127.01	Mean :139.46	Mean :146.24	
##	3rd Qu.:147.24	3rd Qu.:172.66	3rd Qu.:176.93	

```
## Max. :299.65 Max. :304.94 Max. :318.88
## NA's :11 NA's :24 NA's :29
```

4. Use the command `table(dbf$patient)`, interpret the numbers.

```
table(follicle$Patient)
```

```
##
## 1 2 3 4 5 6 7 8 9 10 11 12 13 14
## 5 5 5 5 5 5 5 5 5 5 5 5 5 5
```

We have 5 follicles for each patient.

Question 1

1. Calculate mean and standard deviation of the diameter at Day0

```
mean(follicle$Day0, na.rm=TRUE)
```

```
## [1] 84.70384
```

```
sd(follicle$Day0, na.rm=TRUE)
```

```
## [1] 27.6819
```

2. When we encounter into missing, we are often interested in the *complete case analysis* where we exclude patients with missing observations:

2a. Use the `na.omit` function (excludes all rows that have one missing values) (Run the command `*db.CC<-na.omit(NameofDataFrame)**`)

2b. Check the dimension of the new data.frame

2c. Calculate mean and standard deviation of the diameter at Day0 from db.CC .

2d. Compare results with the ones in point 1. Did something change? If yes, Why?

```
db.CC<-na.omit(follicle)
dim(db.CC)
```

```
## [1] 41 7
```

```
mean(db.CC$Day0)
```

```
## [1] 91.08129
```

```
sd(db.CC$Day0)
```

```
## [1] 31.47671
```

We can see that mean and standard deviation are different respect to the ones calculated in point 1. This is because the `na.omit` function is excluding all rows with at least one missing observation. However if one missing was at day 6, this might not be missing at Day0. The mean calculation, with `na.rm=TRUE` is excluding only the missing at Day0, whereas the complete case consider only follicles that have all observed measurements (for all days)

Question 2 For each follicle the diameter was measured at day 0,2,4,6,8.

1. Are the data in a wide or long format?

Data are in a wide format because we have one row for each follicle and several columns to indicate the measurement at different time points.

2. Convert data from wide to long. **Hint: You can use the function `reshape`**

```
db_long<-reshape(db.CC, direction="long",
                 idvar="Number",
                 varying=c("Day0", "Day2", "Day4", "Day6", "Day8"),
                 timevar="Day", v.names=c("diameter"),
                 times=c("0", "2", "4", "6", "8"))
```

3. How many rows would we expect for each Day? Is it correct? (You can use the command `table(db$Day)`)

```
table(db_long$Day)
```

```
##
##  0  2  4  6  8
## 41 41 41 41 41
```

We have 41 patients with complete data, thus we expect 41 observations for each day

Question 3 Descriptive at baseline (Day0). We would like to create one data set with all characteristics of patients at baseline.

1. Merge the data set obtained in Question 2 and *patient* to add baseline characteristics in the data.frame

```
db_all<-merge(db_long, patient, by="Patient")
```

2. Create a categorical variable for age considering the intervals: (19,30], (30,35], (35,40] (**Hint use the function `cut()`**)

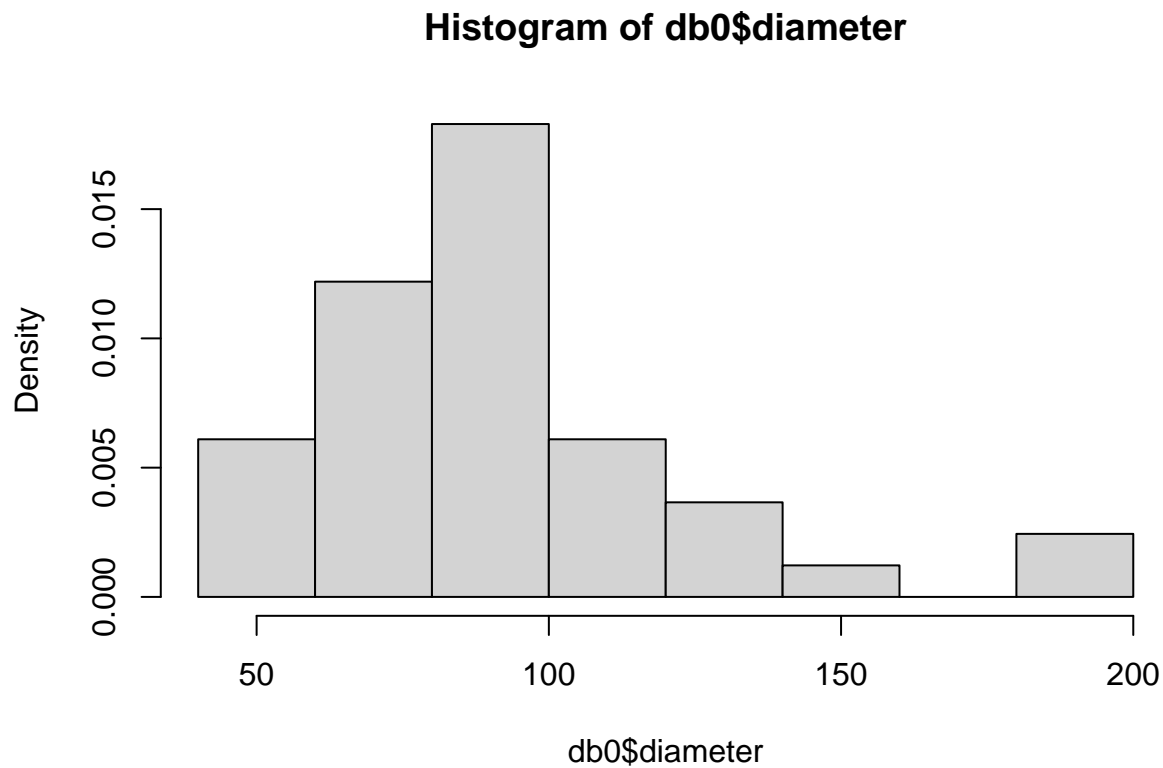
```
db_all$Age_group<-cut(db_all$Age, breaks=c(19,30,35,40))
```

3. Subset from the merged data only observation at baseline (Day 0)

```
db0<-subset(db_all, Day=="0")
```

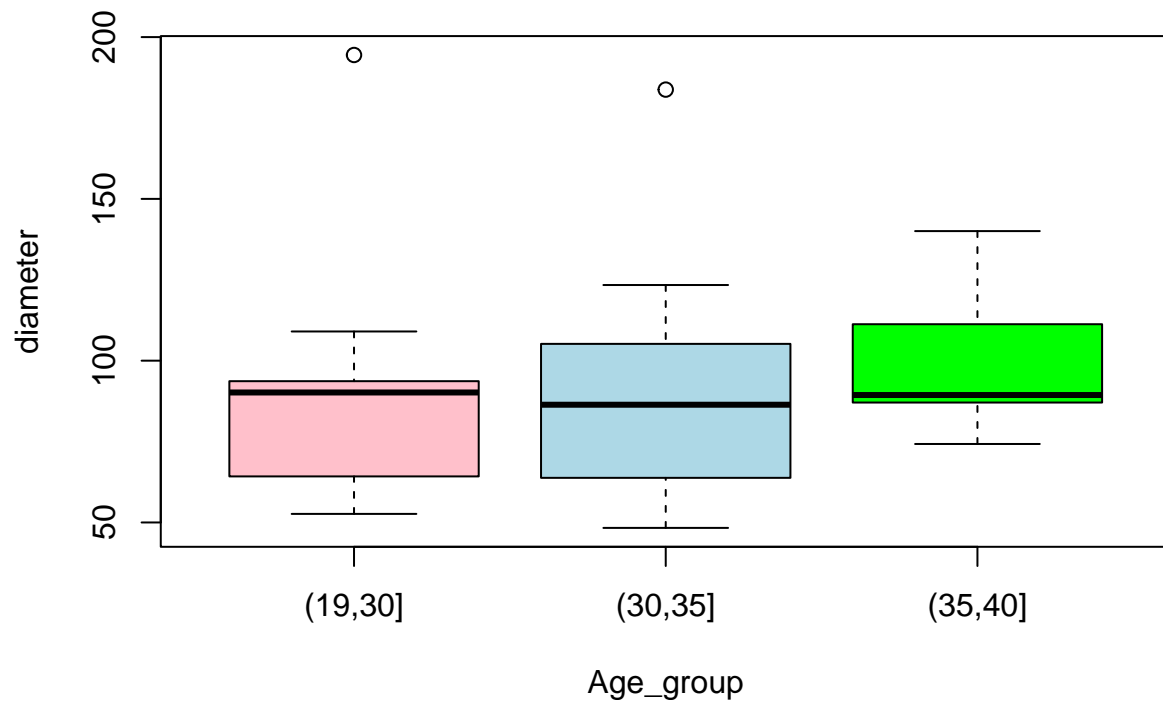
4. Plot the histogram for the density of diameter at Day0.

```
hist(db0$diameter, prob=TRUE)
```



5. Create a Boxplot of diameter at Day 0 by Age category.

```
boxplot(diameter~Age_group, db0, col=c("pink","lightblue","green"))
```



6. Create a table with the counts of follicles per disease and Treatment. Which is the most common disease?

```
table(db0$Disease, db0$Treatment)
```

```
##
##           FBS hPL HSA
## Brain_cancer      0  0  1
## Breast_cancer    26  0  0
## Chronic_myeloid_leukemia  4  0  0
## Mb_Hodgkin       0  5  0
## Neurological_cancer  3  0  0
## Sarcoma          0  0  2
```

Most patients have breast cancer and they have all being treated with FBS

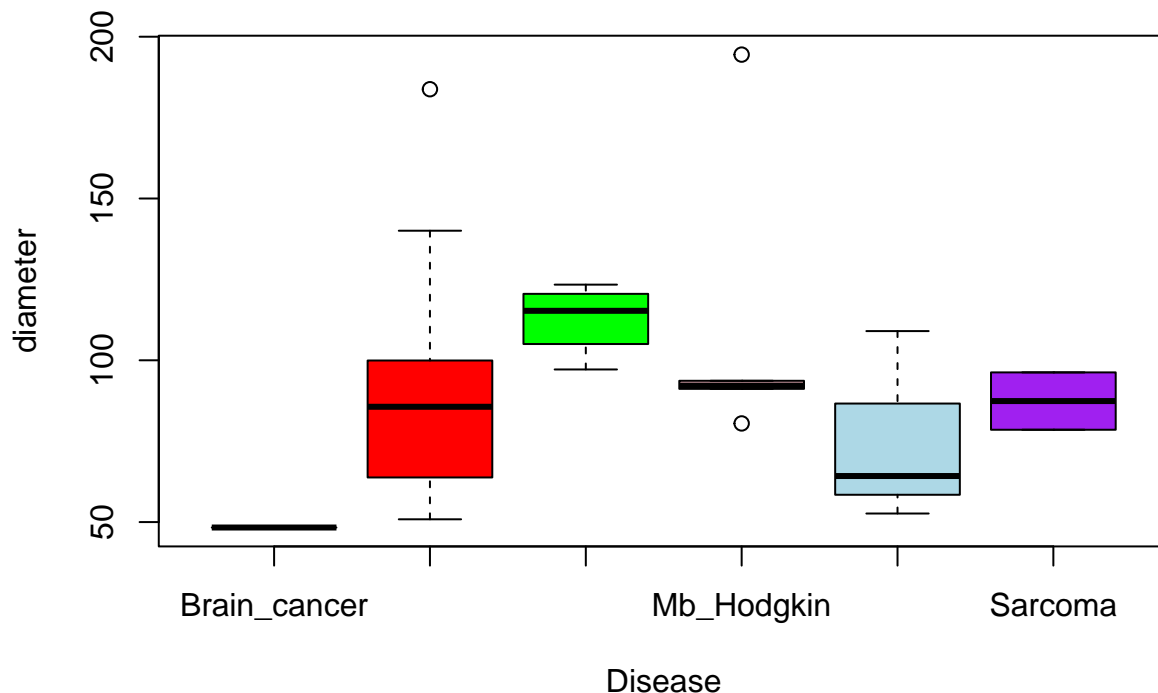
7. Print the mean of diameter at Day0 by Disease (use *tapply()* or *aggregate()*).

7a. Would you say that the follicle diameter is dependent on the disease? 7b. Show the boxplot of diameter at time 0 by Disease.

```
tapply(db0$diameter,db0$Disease,mean,na.rm=TRUE)
```

```
##           Brain_cancer           Breast_cancer Chronic_myeloid_leukemia
##           48.32000           87.77877           112.77750
##           Mb_Hodgkin       Neurological_cancer           Sarcoma
##           110.39300           75.30000           87.39500
```

```
boxplot(diameter~Disease, db0, col=c("gray","red","green","pink","lightblue","purple"))
```



Question 4 : We are interested in the follicle growth over time. We can calculate the diameter difference from time 0 at each time point:

1. Take the subset observations at Day 0. Create a data.frame with only columns *Number* and *diameter*

```
day0<-db0[, c("Number","diameter")]
```

2. Rename the variable of diameter into *diameter0*

```
colnames(day0)<-c("Number","diameter0")
```

3. Merge this data.frame and the long format of your data set (created in Question 3.1) by *Number*.

```
db_join=merge(db_all,day0, by="Number")
```

4. Create a new variable “diam.change” for the difference of diameter at each time point.

```
db_join$diam.change<-db_join$diameter-db_join$diameter0
```

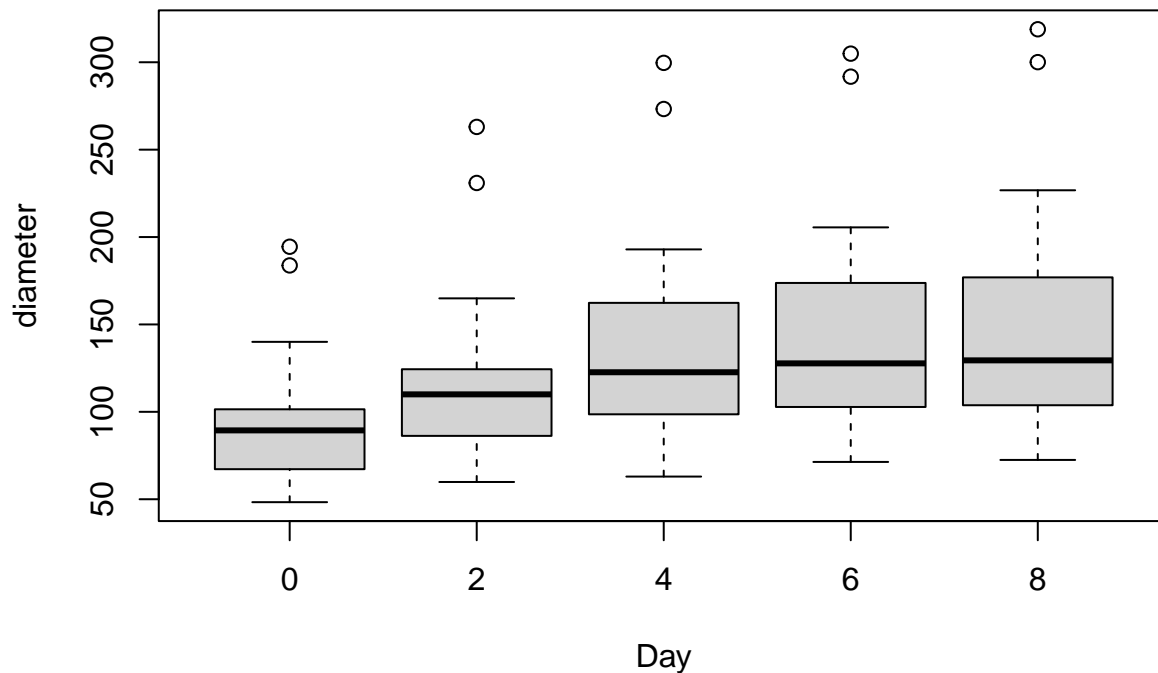
```
head(db_join)
```

```
##   Number Patient Day diameter      Disease Treatment  Age Age_group diameter0
## 1      1      1    0 101.4590 Breast_cancer      FBS  31.6  (30,35]   101.4590
## 2      1      1    4 135.1980 Breast_cancer      FBS  31.6  (30,35]   101.4590
## 3      1      1    2 112.1605 Breast_cancer      FBS  31.6  (30,35]   101.4590
## 4      1      1    6 160.2315 Breast_cancer      FBS  31.6  (30,35]   101.4590
## 5      1      1    8 161.5000 Breast_cancer      FBS  31.6  (30,35]   101.4590
## 6      3      1    4 122.6500 Breast_cancer      FBS  31.6  (30,35]    90.2835
##   diam.change
## 1      0.0000
## 2     33.7390
## 3     10.7015
## 4     58.7725
## 5     60.0410
## 6     32.3665
```

Question 5: Descriptive of diameter change over time

1. Show the Boxplot of diameter by Day. Would you say that the diameter is growing over time?

```
boxplot(diameter~Day , db_join)
```



2. Calculate the median diameter change by Day and Treatment (save the results, you need them for the next step). **use aggregate with formula: diam.change~Day + Treatment**

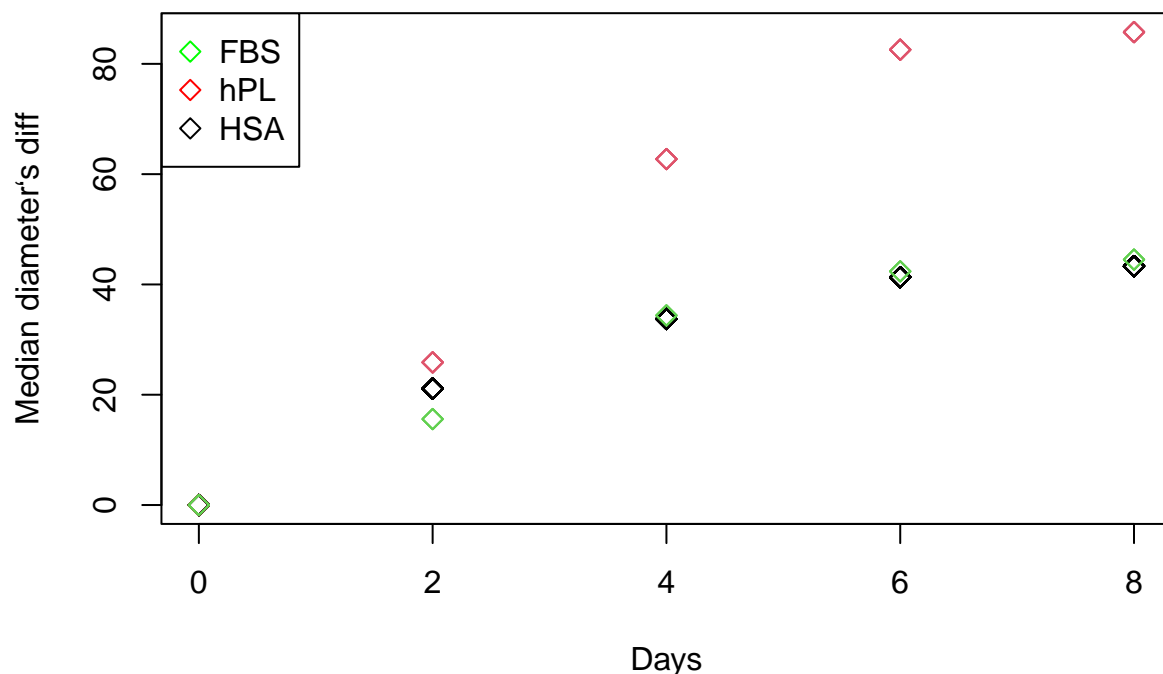
```
db_median<-aggregate(diam.change~ Day + Treatment, db_join, median)
```

3. Plot the diameter growth over time by treatment group:

- 2a. rename the column “diam.change” from the data.frame obtained in the previous point with “median.change”
- 2b. merge the data set with the one obtained in Question 4 (after creating diam.change)
- 2c. create a plot (with points) of the difference from time 0 at varying of days:
 - define the color by Treatment group
 - precise as name of axis: x= "Days", y="median diameter's diff"
 - add the legend

```
colnames(db_median)[3]<-"median.change"
db_join2<-merge(db_join,db_median, by=c("Day","Treatment"))

plot(db_join2$Day, db_join2$median.change,
     col=as.factor(db_join2$Treatment), pch=5,
     xlab="Days", ylab="Median diameter`s diff")
legend("topleft", c("FBS","hPL","HSA"), col=c("green","red","black"), pch=c(5,5,5))
```



4. (Optional) Calculate the relative change for the diameter($(\text{diameter} - \text{diameter0})/\text{diameter0}$) and re-create the same plot:

```
db_join$diam.Rchange<-(db_join$diameter-db_join$diameter0)/(db_join$diameter0)
db_medianR<-aggregate(diam.Rchange~ Day + Treatment, db_join, median)

colnames(db_median)[3]<-"median.Rchange"
db_join2<-merge(db_join,db_median, by=c("Day","Treatment"))
```

```
plot(db_join2$Day, db_join2$median.Rchange,
     col=as.factor(db_join2$Treatment), pch=5,
     xlab="Days", ylab="Median diameter`s relative change")
legend("topleft", c("FBS", "hPL", "HSA"), col=c("green", "red", "black"), pch=c(5,5,5))
```

