HW4_kmg0122

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2021 10 16

1.

2.

3.

```
library(tidyverse)
```

```
## Warning:   'tidyverse'  R   4.1.1
```

```
## -- Attaching packages --------------------------------------- tidyverse 1.3.1 --
```

```
## v ggplot2 3.3.5     v purrr   0.3.4
## v tibble  3.1.4     v dplyr   1.0.7
## v tidyr   1.1.3     v stringr 1.4.0
## v readr   2.0.1     v forcats 0.5.1
```

```
## Warning:   'ggplot2'  R   4.1.1
```

```
## Warning:   'tibble'  R   4.1.1
```

```
## Warning:   'tidyr'  R   4.1.1
```

```
## Warning:   'readr'  R   4.1.1
```

```
## Warning:   'purrr'  R   4.1.1
```

```
## Warning:   'dplyr'  R   4.1.1
```

```
## Warning:   'forcats'  R   4.1.1
```

```
## -- Conflicts ------------------------------------------ tidyverse_conflicts() --
## x dplyr::filter() masks stats::filter()
## x dplyr::lag()    masks stats::lag()
```

```
library(dplyr)
library(knitr)
```

```
## Warning:    'knitr'  R   4.1.1
```

```
library("data.table")
```

```
## Warning:    'data.table'  R   4.1.1
```

```
##
##          : 'data.table'
```

```
## The following objects are masked from 'package:dplyr':
##
##     between, first, last
```

```
## The following object is masked from 'package:purrr':
##
##     transpose
```

(a).

```
#load data
data.3.a<-read.csv("https://www2.isye.gatech.edu/~jeffwu/wuhamadabook/data/ThicknessGauge.dat",
                   header=F, skip=2, sep = " ")

#allocated names to the column
colnames(data.3.a)<-c("index", c("a1","a2","b1","b2","c1","c2"))

#made temporary data to merge by row.
data.temp.1 <- data.3.a %>% select(index,contains("1")) %>% rename(a=a1, b=b1, c=c1)

#added to index because its index also starts with 1.
data.temp.2 <- data.3.a %>% select(index,contains("2")) %>%
  rename(a=a2, b=b2, c=c2) %>% mutate(index=index+10)

dat.3.a <- bind_rows(data.temp.1, data.temp.2) %>%
  rename("Operator 1"=a,"Operator 2"= b, "Operator 3"=c)

kable(head(dat.3.a), caption="Wall Thickness")
```

Table 1: Wall Thickness

index	Operator 1	Operator 2	Operator 3
1	0.953	0.954	0.954
2	0.956	0.956	0.958
3	0.956	0.956	0.957
4	0.957	0.958	0.957

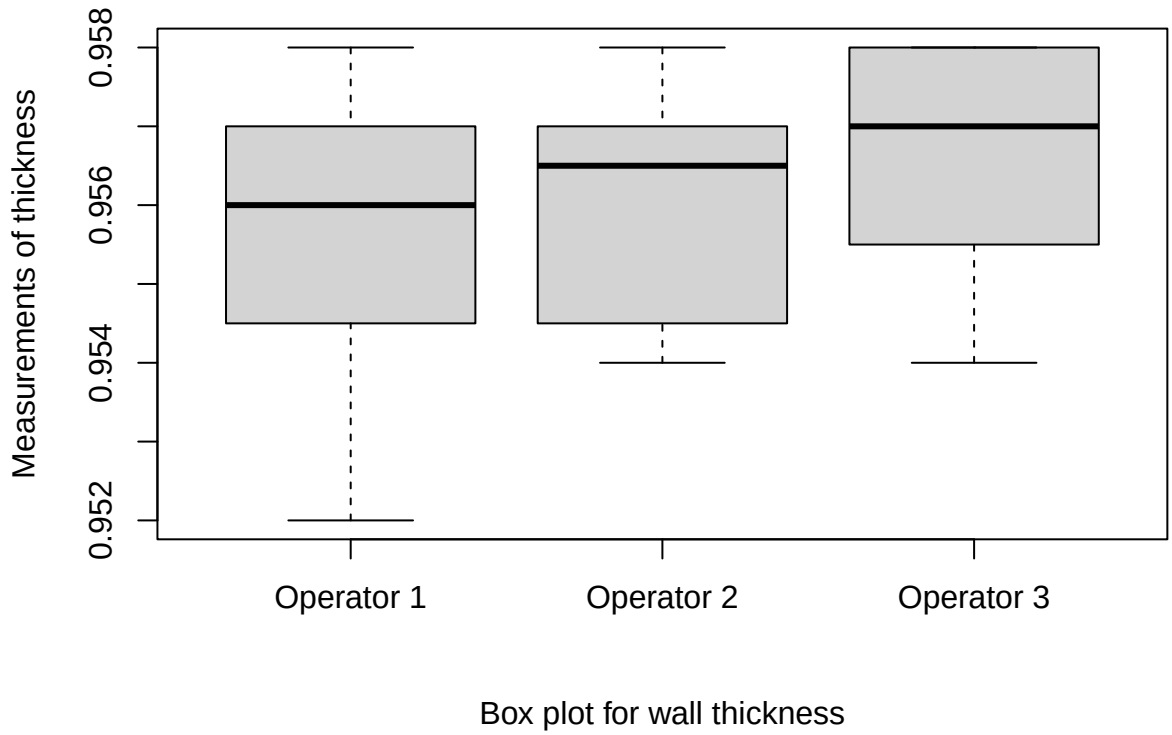
index	Operator 1	Operator 2	Operator 3
5	0.957	0.957	0.958
6	0.958	0.957	0.958

```
kable(summary(dat.3.a), caption="Wall Thickness Summary")
```

Table 2: Wall Thickness Summary

index	Operator 1	Operator 2	Operator 3
Min. : 1.00	Min. :0.9520	Min. :0.9540	Min. :0.9540
1st Qu.: 5.75	1st Qu.:0.9547	1st Qu.:0.9547	1st Qu.:0.9557
Median :10.50	Median :0.9560	Median :0.9565	Median :0.9570
Mean :10.50	Mean :0.9557	Mean :0.9560	Mean :0.9566
3rd Qu.:15.25	3rd Qu.:0.9570	3rd Qu.:0.9570	3rd Qu.:0.9580
Max. :20.00	Max. :0.9580	Max. :0.9580	Max. :0.9580

```
#Draw box plot to compare each operator's distribution
boxplot(dat.3.a[,2:4], ylab = "Measurements of thickness",  sub="Box plot for wall thickness")
```



I used a box plot because it is a efficient way to describe and compare the distribution of each operators.

(b).

```
data.3.b<-read.csv("https://www2.isye.gatech.edu/~jeffwu/wuhamadabook/data/BrainandBodyWeight.dat",
                   header=F, sep=" ", skip=1)

#rename each column because dplyr cannot road data when column name is duplicated.
colnames(data.3.b)<-paste(rep(c("Body_Wt","Brain_Wt"),3),c(1,1,2,2,3,3),sep="_")

#made temporary data to merge by row.
data.temp.1<-data.3.b %>% select(contains("1")) %>%

  rename( Body_Wt=Body_Wt_1, Brain_Wt=Brain_Wt_1)
data.temp.2<-data.3.b %>% select(contains("2")) %>%

  rename( Body_Wt=Body_Wt_2, Brain_Wt=Brain_Wt_2)
data.temp.3<-data.3.b %>% select(contains("3")) %>%

  rename( Body_Wt=Body_Wt_3, Brain_Wt=Brain_Wt_3)

#bind data by row. bind_row merge data by row which have the
# same column name. And then omitted NA data.
dat.3.b<-bind_rows(data.temp.1,data.temp.2,data.temp.3) %>% na.omit()

kable(head(dat.3.b), caption="Body and Brain weight Data")
```

Table 3: Body and Brain weight Data

Body_Wt	Brain_Wt
3.385	44.5
0.480	15.5
1.350	8.1
465.000	423.0
36.330	119.5
27.660	115.0

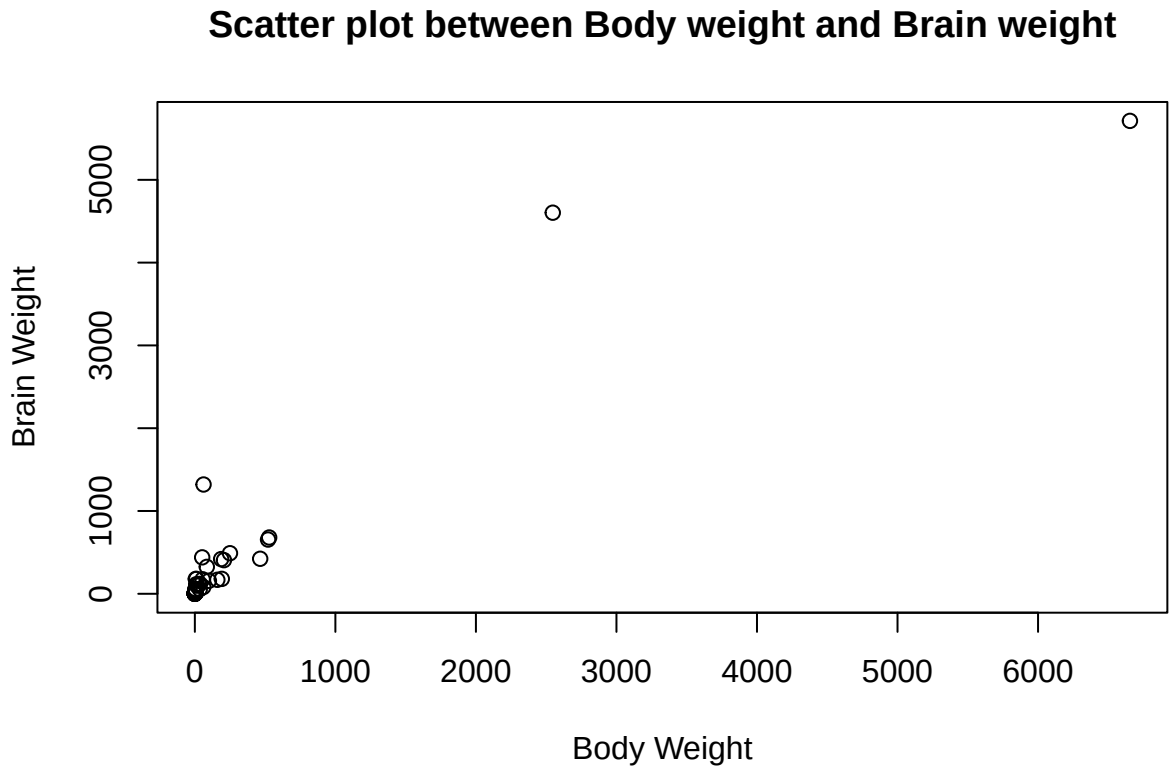
```
kable(summary(dat.3.b), caption="Summary")
```

Table 4: Summary

Body_Wt	Brain_Wt
Min. : 0.005	Min. : 0.10
1st Qu.: 0.600	1st Qu.: 4.25
Median : 3.342	Median : 17.25
Mean : 198.790	Mean : 283.13
3rd Qu.: 48.202	3rd Qu.: 166.00
Max. :6654.000	Max. :5712.00

```r
#Draw scatter plot to see if there is any relationship between Body weight and Brain weight

plot(dat.3.b$Body_Wt, dat.3.b$Brain_Wt, xlab="Body Weight",
     ylab="Brain Weight", main="Scatter plot between Body weight and Brain weight")
```



Since there was NA values, I omitted them. I drew scatter plot to see if there is any relatioship between body weight and brain weight. In the plot, there are two outliers. It seems that the reason for this may be some problem in data unit.

(c).

```r
data.3.c<-fread("http://www2.isye.gatech.edu/~jeffwu/wuhamadabook/data/LongJumpData.dat",
                sep=" ", fill=T, skip=1,
                col.names = c(paste0(rep(c("year", "Long_Jump"),4),c(1,1,2,2,3,3,4,4))))

#made temporary data to merge by row.
data.temp.1<-data.3.c %>% select(contains("1")) %>%
  rename(year=year1, Long_Jump=Long_Jump1) %>%
  mutate(year=year+1900)
data.temp.2<-data.3.c %>% select(contains("2")) %>%
  rename(year=year2, Long_Jump=Long_Jump2) %>%
  mutate(year=year+1900)
data.temp.3<-data.3.c %>% select(contains("3")) %>%
  rename(year=year3, Long_Jump=Long_Jump3) %>%
```

```
  mutate(year=year+1900)
data.temp.4<-data.3.c %>% select(contains("4")) %>%
  rename(year=year4, Long_Jump=Long_Jump4) %>%
  mutate(year=year+1900)

# data merge
dat.3.c<-bind_rows(data.temp.1,data.temp.2,data.temp.3, data.temp.4)

# data summary
kable(summary(dat.3.c), caption="Summary")
```

Table 5: Summary

year	Long_Jump
Min. :1896	Min. :249.8
1st Qu.:1921	1st Qu.:295.4
Median :1950	Median :308.1
Mean :1945	Mean :310.3
3rd Qu.:1971	3rd Qu.:327.5
Max. :1992	Max. :350.5
NA's :2	NA's :2

```
#drop NA values
dat.3.c <- dat.3.c %>% na.omit()

kable(head(dat.3.c), caption="Body and Brain weight Data")
```

Table 6: Body and Brain weight Data

year	Long_Jump
1896	249.75
1900	282.88
1904	289.00
1908	294.50
1912	299.25
1920	281.50

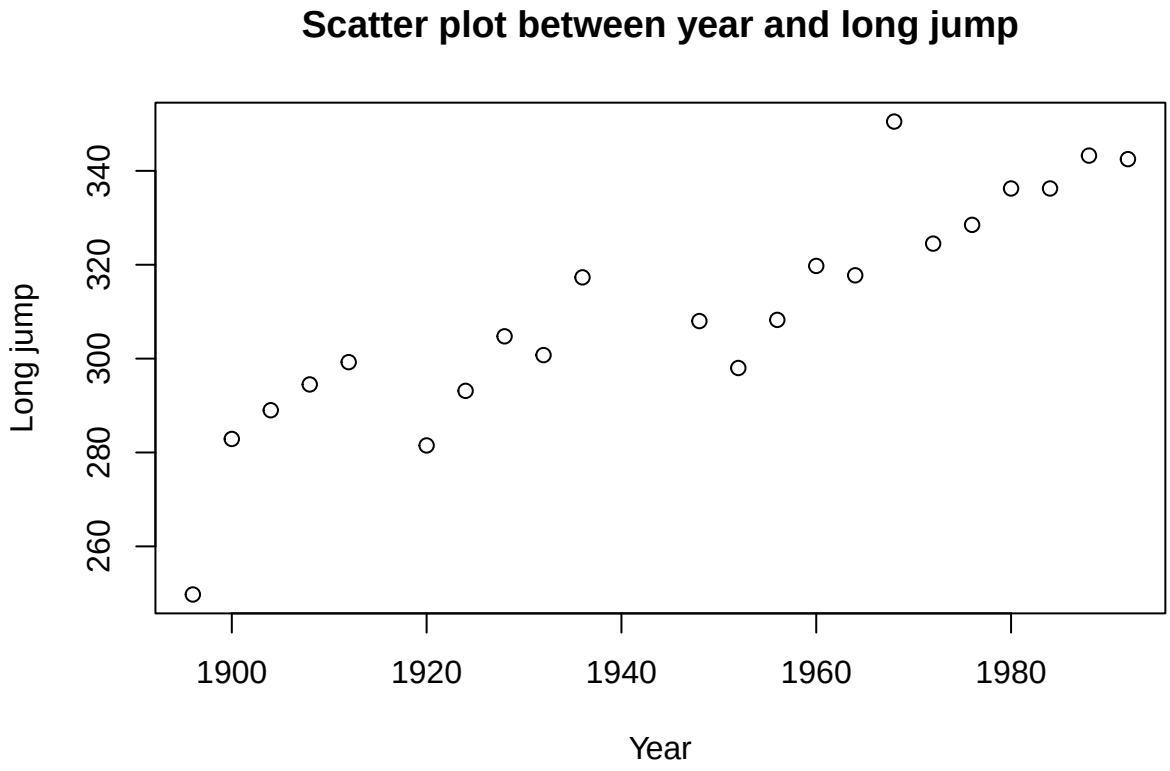
```
#check that NA values disappear
kable(summary(dat.3.c), caption="Summary")
```

Table 7: Summary

year	Long_Jump
Min. :1896	Min. :249.8
1st Qu.:1921	1st Qu.:295.4
Median :1950	Median :308.1
Mean :1945	Mean :310.3
3rd Qu.:1971	3rd Qu.:327.5

year	Long_Jump
Max. :1992	Max. :350.5

```
#scatter plot
plot(dat.3.c$year, dat.3.c$Long_Jump, xlab="Year",
     ylab="Long jump", main="Scatter plot between year and long jump")
```



I drew scatter plot to see if there is any relatioship between the year and long jump. It seems that as time goes, the performance of long jump increases.

(d).

```
data.3.d<-fread("http://www2.isye.gatech.edu/~jeffwu/wuhamadabook/data/tomato.dat")
```

```
## Warning in fread("http://www2.isye.gatech.edu/~jeffwu/wuhamadabook/data/
## tomato.dat"): Detected 3 column names but the data has 4 columns (i.e. invalid
## file). Added 1 extra default column name for the first column which is guessed
## to be row names or an index. Use setnames() afterwards if this guess is not
## correct, or fix the file write command that created the file to create a valid
## file.
```

```
data.temp.1 <- data.3.d[,c(1,2)] %>% separate(`10000`, c("y1", "y2", "y3"), sep=",") %>%
  mutate(Density=rep(10000,2))
```

```
## Warning: Expected 3 pieces. Additional pieces discarded in 1 rows [2].
```

```
data.temp.2 <- data.3.d[,c(1,3)] %>% separate(`20000`, c("y1", "y2", "y3"), sep=",") %>%
  mutate(Density=rep(20000,2))
data.temp.3 <- data.3.d[,c(1,4)] %>% separate(`30000`, c("y1", "y2", "y3"), sep=",") %>%
  mutate(Density=rep(30000,2))

dat.3.d <-bind_rows(data.temp.1, data.temp.2, data.temp.3 )
dat.3.d <-dat.3.d %>% rename(variety=V1) %>%
  gather(key="Try", value = "yields", y1, y2, y3) %>% select(-Try)

#change yields to numeric variable
dat.3.d<-dat.3.d %>% mutate(yields=as.numeric(yields),
                            variety=as.factor(variety),
                            Density=as.factor(Density))

#print data
kable(head(dat.3.d), caption="Tomato yield")
```

Table 8: Tomato yield

variety	Density	yields
Ife#1	10000	16.1
PusaEarlyDwarf	10000	8.1
Ife#1	20000	16.6
PusaEarlyDwarf	20000	12.7
Ife#1	30000	20.8
PusaEarlyDwarf	30000	14.4

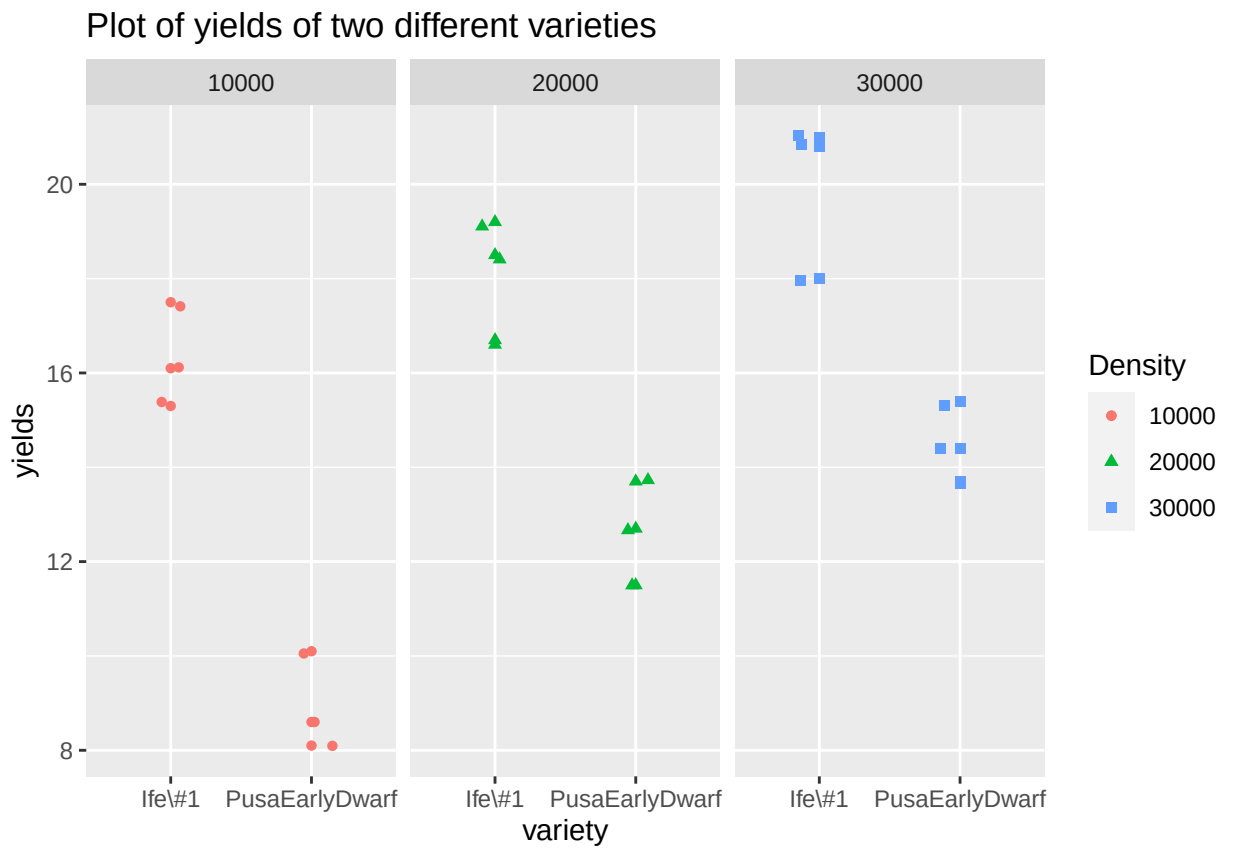
```
#check summary
kable(summary(dat.3.d), caption="Summary")
```

Table 9: Summary

variety	Density	yields
Ife#1 :9	10000:6	Min. : 8.10
PusaEarlyDwarf:9	20000:6	1st Qu.:12.95
NA	30000:6	Median :15.35
NA	NA	Mean :15.07
NA	NA	3rd Qu.:17.88
NA	NA	Max. :21.00

```
#plot
dat.3.d %>% ggplot(aes(x=variety, y=yields,
           group=Density,
           shape=Density,
```

```
          color=Density)) +
          geom_point() +
          ggtitle("Plot of yields of two different varieties") +
          geom_point(position=position_jitter(h=0.1, w=0.2)) +
          facet_grid(~factor(Density))
```



I drew plot like above because I want to compare each variety's difference in yield depending on Density. It seems that Ife#1 :9 has better yield than PusaEarlyDwarf:9.

(e).

```
data.3.e<-fread("https://www2.isye.gatech.edu/~jeffwu/wuhamadabook/data/LarvaeControl.dat")

#add age colunm and rename number with treatment
data.temp.age1<-data.3.e[,c(1:6)] %>% rename(Trt1=`1`, Trt2=`2`, Trt3=`3`, Trt4=`4`, Trt5=`5`) %>%
  mutate(age=rep(1,8))
data.temp.age2 <- data.3.e[,c(1,7:11)] %>%
  rename(Trt1=` 1`, Trt2=`2`, Trt3=`3`, Trt4=`4`, Trt5=`5`) %>%
  mutate(age=rep(2,8))

#merge data
dat.3.e <- bind_rows(data.temp.age1, data.temp.age2) %>%

  gather(key="Treatment", value="Counts", Trt1, Trt2, Trt3, Trt4, Trt5) %>%
```

```
  mutate(Treatment=substring(Treatment,4), age=as.factor(age), Block=as.factor(Block))

#print data
kable(head(dat.3.e), caption="Larvae Counts")
```

Table 10: Larvae Counts

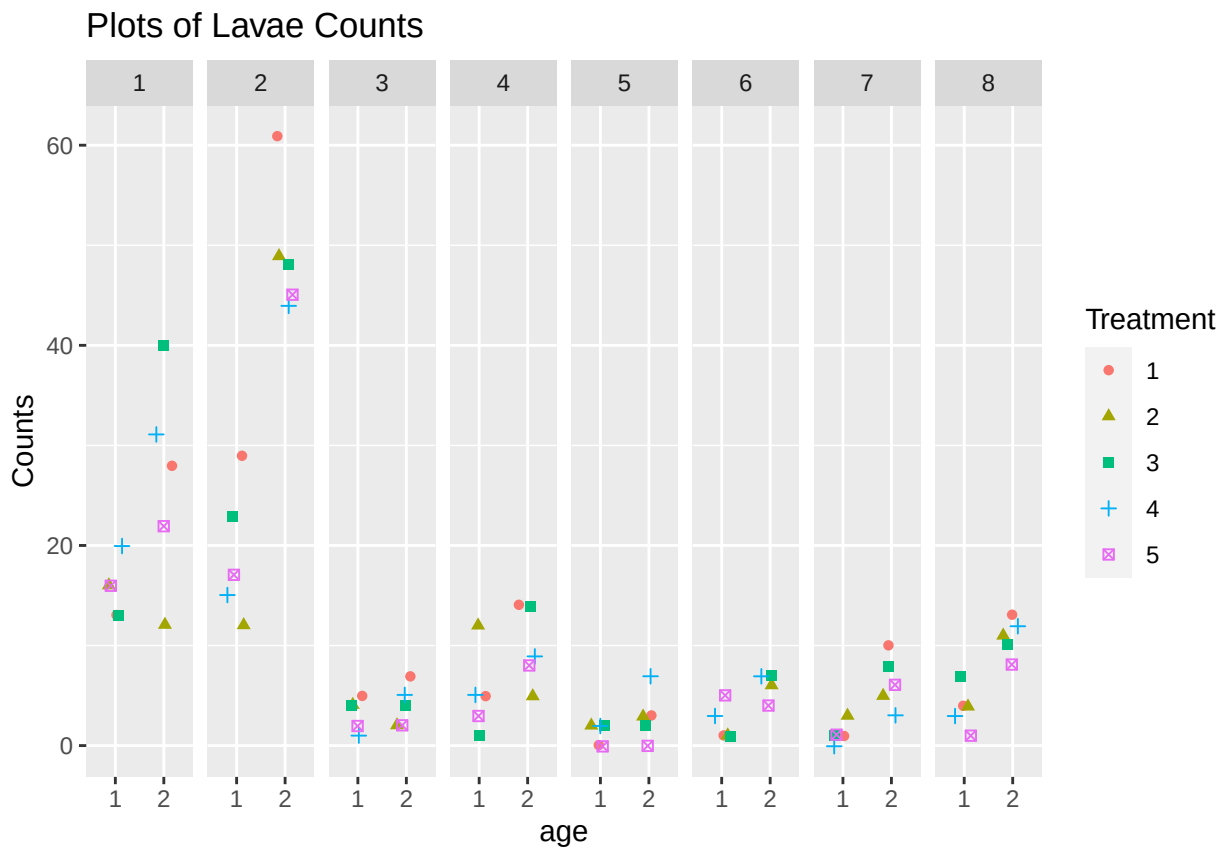
Block	age	Treatment	Counts
1	1	1	13
2	1	1	29
3	1	1	5
4	1	1	5
5	1	1	0
6	1	1	1

```
#check summary
kable(summary(dat.3.e), caption="Summary")
```

Table 11: Summary

Block	age	Treatment	Counts
1 :10	1:40	Length:80	Min. : 0.00
2 :10	2:40	Class :character	1st Qu.: 2.75
3 :10	NA	Mode :character	Median : 5.50
4 :10	NA	NA	Mean :10.50
5 :10	NA	NA	3rd Qu.:13.00
6 :10	NA	NA	Max. :61.00
(Other):20	NA	NA	NA

```
#plot
dat.3.e %>% ggplot(aes(x=age, y=Counts,
           group=Treatment,
           shape=Treatment,
           color=Treatment)) +
           geom_point(position=position_jitter(h=0.1, w=0.2)) +
  ggtitle("Plots of Lavae Counts") +
           facet_grid(~Block)
```



I drew plot like above because I want to compare each age's difference in counts depending on Treatment. I drew plots for each block and used shape option for treatment. It seems that age two group has more counts than age one group. Density.