

# Biostatistics: Theory and Applications in R (Virtual)

## Week3\_Session2\_R\_training3

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**Prof Dr Mohammed Abu Sayed Arfin Khan**

Department of Forestry and Environmental Science

Shahjalal University of Science and Technology, Sylhet

+8801917174537, [khan-for@sust.edu](mailto:khan-for@sust.edu), [nobelarfin@yahoo.com](mailto:nobelarfin@yahoo.com)

[Homepage](#) | [Google scholar](#) | [Researchgate](#) | [ORCID](#) | [Publons](#) | [BayCEER](#)

## #Creating a subset

**#Set the working directory- getwd()/ setwd("Y:/")**

getwd()

setwd("C:/Users/Fahmida Sultana/Desktop/R training/R\_training\_Class\_03")

**#install openxlsx package or xlsx package**

library(openxlsx)

library(readxl)

**#####import data set from xlsx file**

study\_1 <- read.xlsx("Tree\_height.xlsx")

str(study\_1)

study\_2 <- read\_excel("Tree\_height.xlsx", sheet = "study\_2")

str(study\_2)

**###Import csv file**

study\_3 <- read.csv("C:/Users/Fahmida Sultana/Desktop/R  
training/R\_training\_Class\_03/Tree\_height1.csv")

str(study\_3)

**#read the data file**

str(study\_1)           #to see the data frame

unique(study\_1\$year)   # to see the the all year

range(study\_1\$year)   # to see the range of the year column

sort(study\_1\$year)    # to see the all input in year column

#study\_1[1,]           # see the 1st row

study\_1[,5]           # see the 5th column

**# create a subset from the main file study\_1 with the year > 2007**

unique(study\_1\$year)   # year- 2005 2006 2007 2008 2009 2010

A <- subset(study\_1, study\_1\$year > 2007)

unique(A\$year)        # check the data, all the year 2005, 2006, 2007 are not included in the subset

unique(study\_1\$year)# but all year are available in the main file

**# create a subset from the main file study\_1 with the year > 2005 & year < 2010**

A2 <- subset(study\_1, study\_1\$year > 2005 & study\_1\$year < 2010)

```
unique(A2$year)
```

### **#Task**

**# please create a subset named A3 from the main file study\_1 with the year <2009**

**# create a subset from the main file study\_1 with the control treatment**

**# selecting a treatment**

```
B<- subset(study_1, study_1$treatment== "Control") # selecting a treatment
unique(B$treatment)
```

**# delete a treatment**

```
C<- subset(study_1, study_1$treatment!= "Control") # deleting a treatment
unique(C$treatment)
```

**# delete multiple treatments**

```
D<- subset(study_1, study_1$treatment!= "Control" & study_1$treatment!= "Drought")
unique(D$treatment)
str(D)
```

### **#Task**

**#create a subset named E by deleting the "Drought" and "Rain" treatments**

## **#Create scatter plot with trend line (lm)**

```
library(plotrix)
```

```
??plotrix
```

```
study_2 <- read_excel("Tree_height.xlsx", sheet = "study_2")
str(study_2)
```

```
par(mfrow=c(1,1))
```

```
plot(study_2$Elevation_m, study_2$Diameter_cm, pch=9, col="blue")
abline(lm((Diameter_cm) ~ (Elevation_m), data =study_2 ))
```

```
plot(study_2$Height_m, study_2$Diameter_cm, pch=16, col="red")
abline(lm((Height_m) ~ (Elevation_m), data =study_2))
```

**# check the available symbols and colors for R figures**

```
?pch
```

```
?colors
```

```
demo("colors")
```

```
Return #Hit <Return> to start
```

Return #Hit <Return> to see next plot: Return

## #par() function

#Subsequent figures will be drawn in

#by rows (mfrow) or columns (mfc) respectively.

### #plot 2 figure in one row

```
par(mfrow=c(1,2)) # back to normal
plot(study_2$Elevation_m, study_2$Diameter_cm, pch=9, col="blue")
plot(study_2$Height_m, study_2$Diameter_cm, pch=16, col="red")
```

### #plot 2 figure in one column

```
par(mfrow=c(2,1))
plot(study_2$Elevation_m, study_2$Diameter_cm, pch=9, col="blue")
plot(study_2$Height_m, study_2$Diameter_cm, pch=16, col="red")
```

## #Create barplot

```
library(sciplot)
str(study_2)
par(mfrow = c(1,1))
bargraph.CI(x.factor = study_area, response=species_richness, ylim= c(0,50), ylab = "No of Species", xlab
= "Study area", las = 1, data =study_2,col = c("black", "red", "green"), main = "p=0.05")
```

## #Create barplot by group

```
str(study_1)
bargraph.CI(x.factor = treatment, group= plant, response=biomass, ylim= c(0,200), ylab = "Biomass",
xlab = "Treatment", las = 1, data =study_1,legend = T, col = c("red", "green"), main = "p=0.05")
```

## #Create line plot

```
str(study_1)

par(mfrow=c(1,1))
lineplot.CI((year), biomass,ylim=c(50,300), xlab="Year",ylab="Biomass",x.cont=T,legend=T,
data=study_1, main = "")
```

## #Create line plot by group

```
par(mfrow=c(1,1))
lineplot.CI((year), biomass, group=treatment,ylim=c(50,300),
xlab="Year",ylab="Biomass",x.cont=T,legend=T, data=study_1, main = "")
```

## #Week3\_Session2\_R Task

**## To do ##**

**#####**

**# Use the study\_2 data set to create the following scatter plot plot:**

**# \* plot diameter\_cm against Height\_m with filled red circles**

**# \* Add a background color green to a plot**

**# \* increase the size of the circle by 3**

**# \* change the text of the axislabels to include what was measured plus the units of measurement**

**# \* give the plot the heading "My Own Plot"**

**# \* export the plot to a PDF file**

**#####Hints#####**

**#library(plotrix), library**

**#pch=16, filled circle**

**#col="red", color**

**#cex= 2, size**

**#plot\_bg(col="green"), background**

**#xlab="Height (m)", x axis label**

**#ylab="Diameter (cm)", y axis label**

**#main = "My Own Plot"), plot name**