

practicando.R

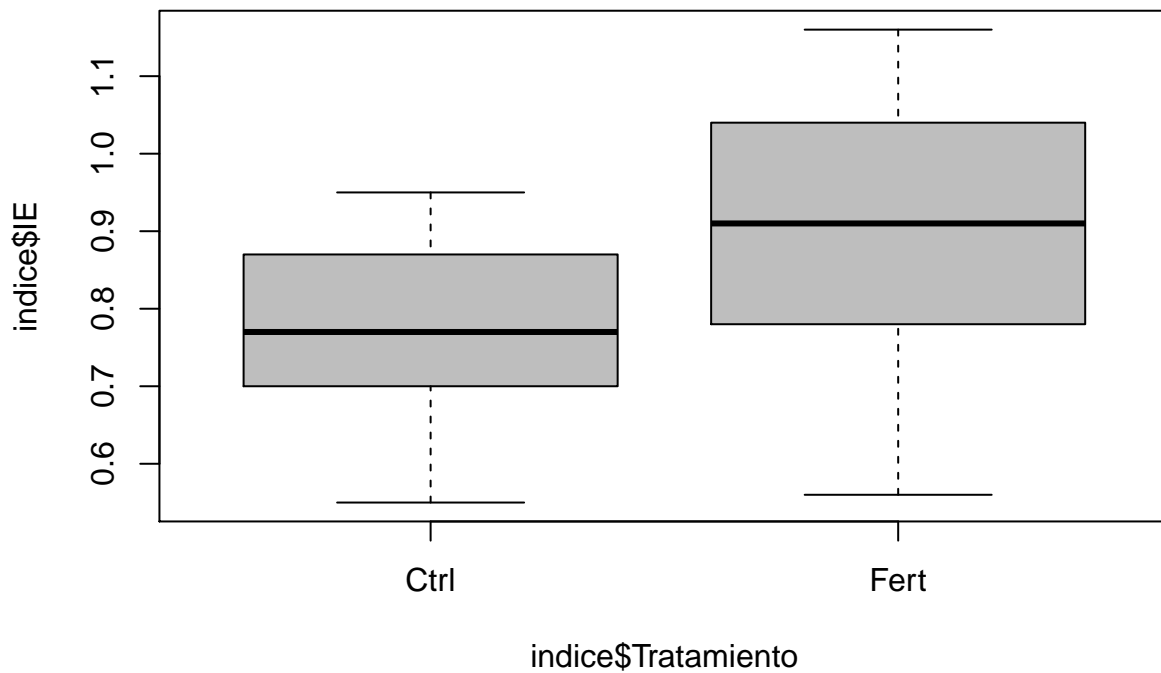
Usuario

2019-08-06

```
indice <- read.csv("C:/MCF202-2019/Datos/plantulas.csv", header = T)
head(indice)
```

```
##   planta   IE Tratamiento
## 1      1 0.80         Ctrl
## 2      2 0.66         Ctrl
## 3      3 0.65         Ctrl
## 4      4 0.87         Ctrl
## 5      5 0.63         Ctrl
## 6      6 0.94         Ctrl
```

```
boxplot(indice$IE ~ indice$Tratamiento, col="grey")
```



```
summary(indice)
```

```
##      planta      IE      Tratamiento
## Min.   : 1.00  Min.   :0.5500  Ctrl:21
## 1st Qu.:11.25  1st Qu.:0.7025  Fert:21
## Median :21.50  Median :0.7950
## Mean   :21.50  Mean   :0.8371
## 3rd Qu.:31.75  3rd Qu.:0.9375
```

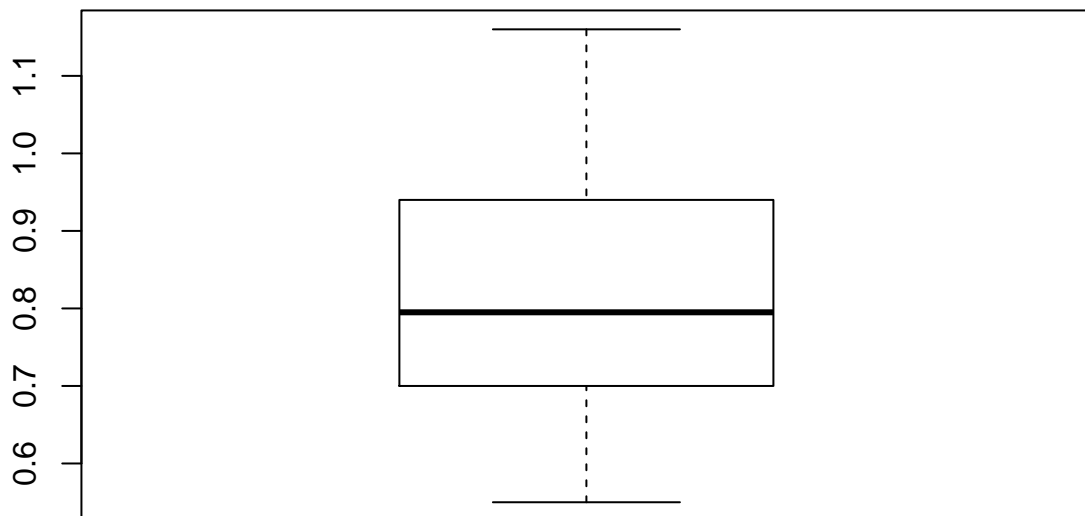
```
## Max. :42.00 Max. :1.1600
```

```
# T una muestra -----
```

```
t.test(indice$IE, mu= 0.85)
```

```
##  
## One Sample t-test  
##  
## data: indice$IE  
## t = -0.5049, df = 41, p-value = 0.6163  
## alternative hypothesis: true mean is not equal to 0.85  
## 95 percent confidence interval:  
## 0.7857153 0.8885704  
## sample estimates:  
## mean of x  
## 0.8371429
```

```
boxplot(indice$IE)
```



```
# Control -----
```

```
Ctrl <- subset(indice, Tratamiento == "Ctrl")
```

```
mean=mean(Ctrl$IE)
```

```
fivenum(Ctrl$IE)
```

```
## [1] 0.55 0.70 0.77 0.87 0.95
```

```
sd=sd(Ctrl$IE)
```

```
shapiro.test(Ctrl$IE)
```

```
##
```

```
## Shapiro-Wilk normality test
```

```
##
```

```
## data: Ctrl$IE
```

```
## W = 0.9532, p-value = 0.3908
```

```
ks.test(Ctrl$IE, "pnorm", mean, sd)
```

```
## Warning in ks.test(Ctrl$IE, "pnorm", mean, sd): ties should not be present
```

```
## for the Kolmogorov-Smirnov test
```

```
##
```

```
## One-sample Kolmogorov-Smirnov test
```

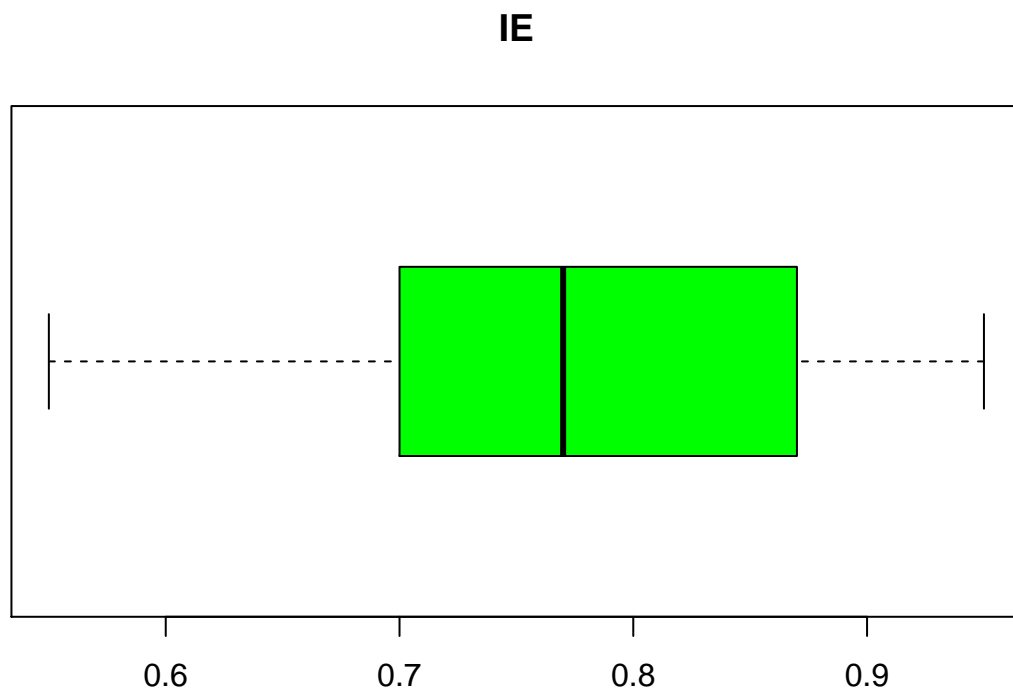
```
##
```

```
## data: Ctrl$IE
```

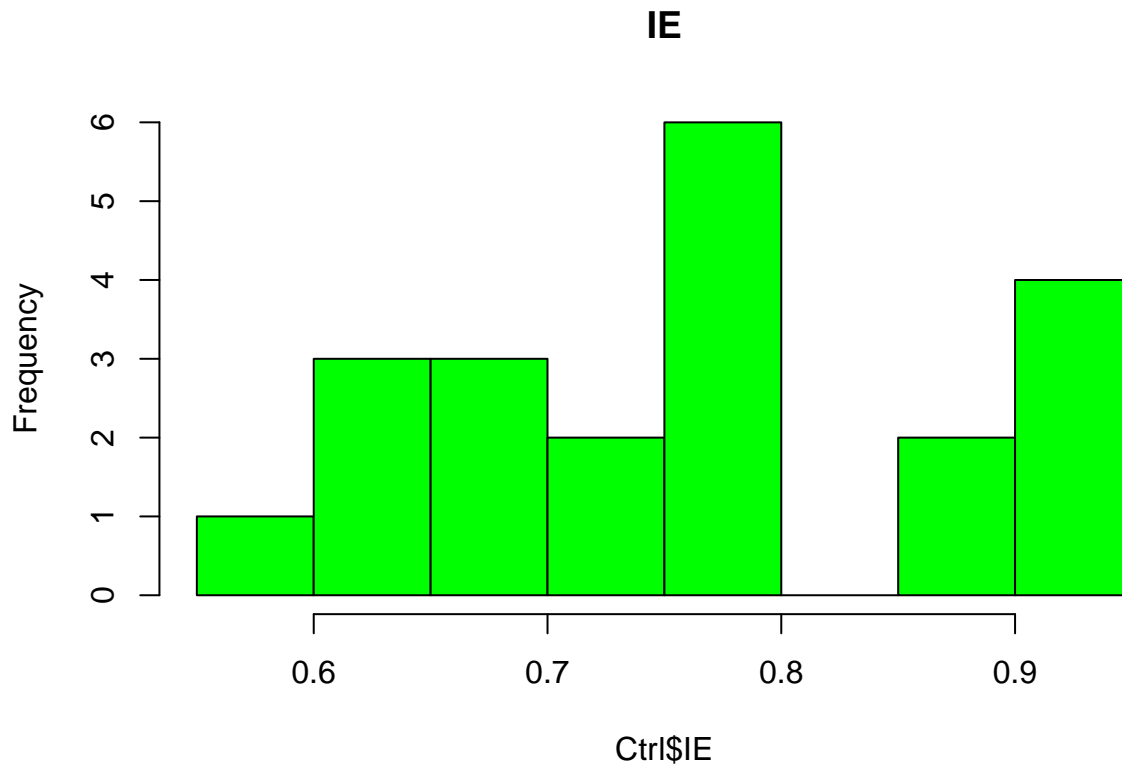
```
## D = 0.11991, p-value = 0.9233
```

```
## alternative hypothesis: two-sided
```

```
boxplot(Ctrl$IE, horizontal = TRUE, col= "green", main="IE")
```



```
hist(Ctrl$IE, col= "green", main="IE")
```



```
# Fertilizante -----
```

```
Fert <- subset(indice, Tratamiento == "Fert")
meanF=mean(Fert$IE)
fivenum(Fert$IE)
```

```
## [1] 0.56 0.78 0.91 1.04 1.16
```

```
sdF=sd(Fert$IE)
```

```
shapiro.test(Fert$IE)
```

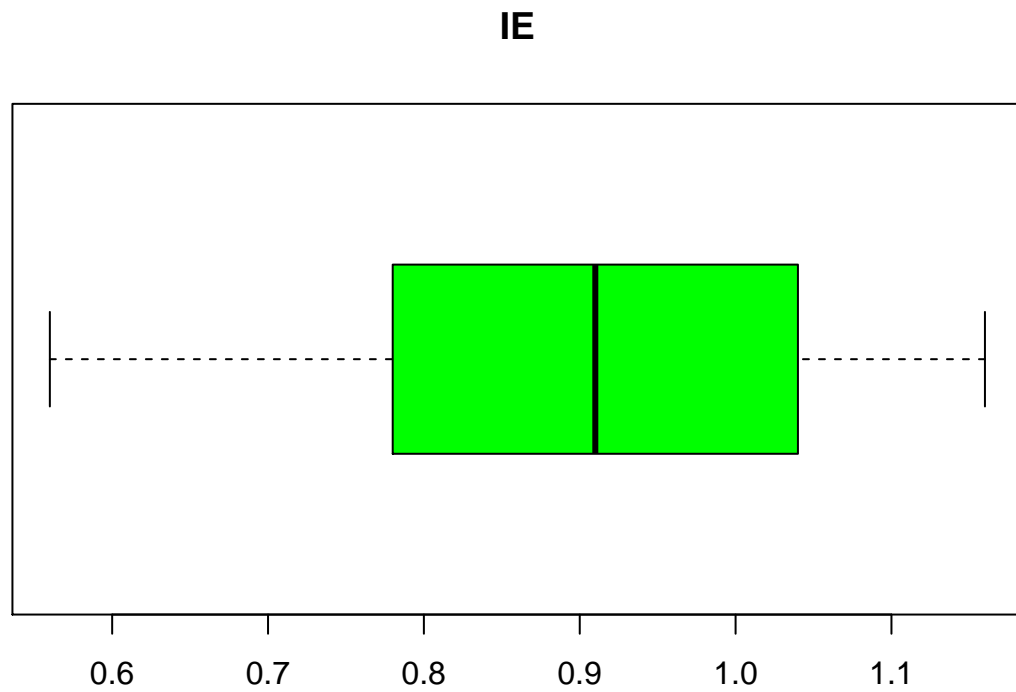
```
##
##  Shapiro-Wilk normality test
##
## data:  Fert$IE
## W = 0.95339, p-value = 0.3941
```

```
ks.test(Fert$IE, "pnorm", meanF, sdF)
```

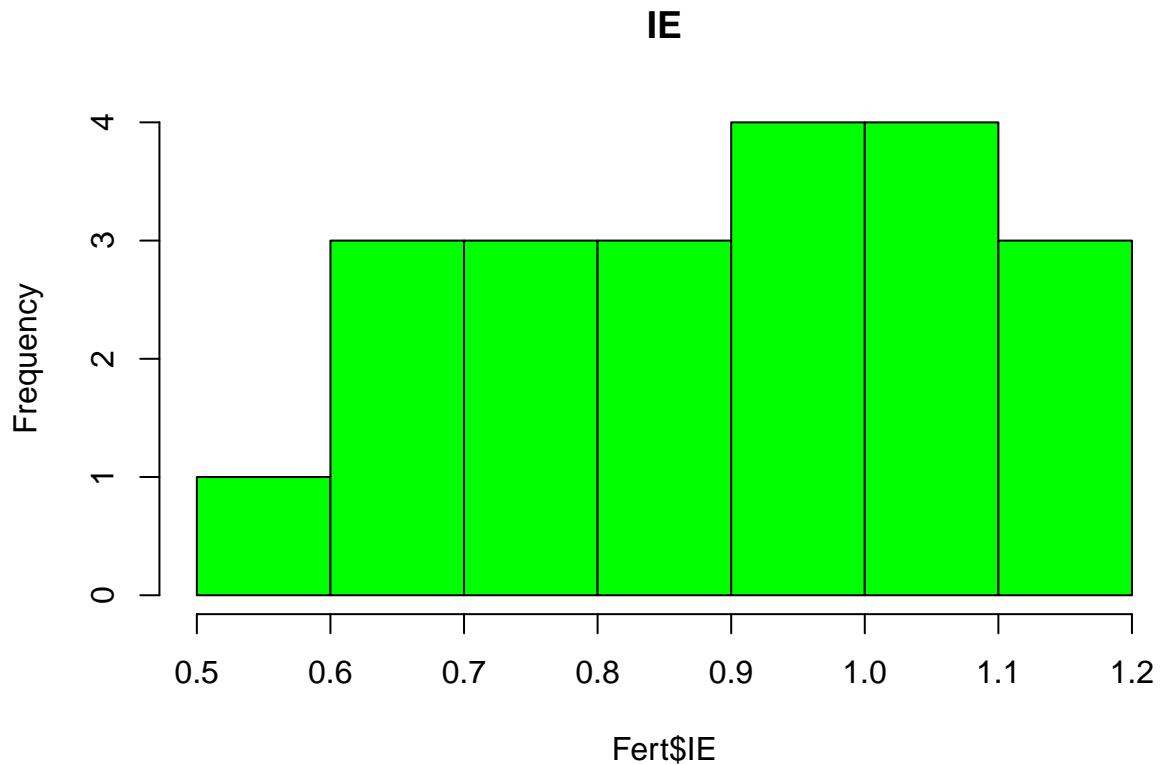
```
## Warning in ks.test(Fert$IE, "pnorm", meanF, sdF): ties should not be
## present for the Kolmogorov-Smirnov test
```

```
##
##  One-sample Kolmogorov-Smirnov test
##
## data:  Fert$IE
## D = 0.10776, p-value = 0.9677
```

```
## alternative hypothesis: two-sided  
boxplot(Fert$IE, horizontal = TRUE, col= "green", main="IE")
```



```
hist(Fert$IE, col= "green", main="IE")
```



```
# Normalidad de varianza -----
```

```
var.test(Ctrl$IE, Fert$IE)
```

```
##
## F test to compare two variances
##
## data: Ctrl$IE and Fert$IE
## F = 0.41068, num df = 20, denom df = 20, p-value = 0.05304
## alternative hypothesis: true ratio of variances is not equal to 1
## 95 percent confidence interval:
## 0.1666376 1.0121038
## sample estimates:
## ratio of variances
## 0.4106757
```

```
# #Prueba T de student -----
```

```
t.test(Ctrl$IE, Fert$IE, var.equal=T)
```

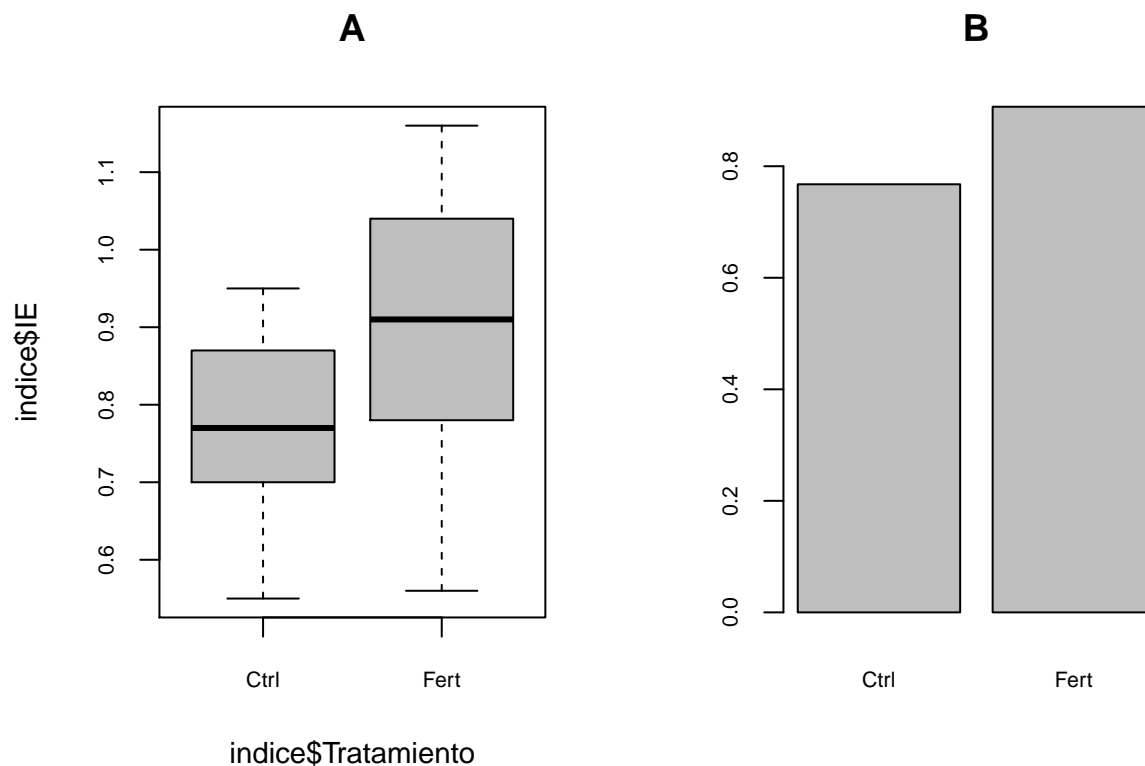
```
##
## Two Sample t-test
##
## data: Ctrl$IE and Fert$IE
## t = -2.9813, df = 40, p-value = 0.004868
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
```

```
## -0.23331192 -0.04478332
## sample estimates:
## mean of x mean of y
## 0.7676190 0.9066667
```

```
t.test(Ctrl$IE, Fert$IE)
```

```
##
## Welch Two Sample t-test
##
## data: Ctrl$IE and Fert$IE
## t = -2.9813, df = 34.056, p-value = 0.00527
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -0.23382707 -0.04426816
## sample estimates:
## mean of x mean of y
## 0.7676190 0.9066667
```

```
op <- par(mfrow=c(1,2), cex.axis=.7, cex.lab=.9)
boxplot(indice$IE ~ indice$Tratamiento, col="grey", main="A")
barplot(tapply(indice$IE, list(indice$Tratamiento), mean ), beside=T, main="B")
```



```
# T dos muestras -----
semillas <-read.csv("C:/MCF202-2019/Datos/semillas.csv", header = T)
head(semillas)
```

```
## Kilogramos tiempo
## 1      9 T2010
## 2      8 T2010
## 3      6 T2010
## 4      9 T2010
## 5      9 T2010
## 6      7 T2010

# T2010 -----

T2010 <- subset(semillas, tiempo == "T2010")

mean2010=mean(T2010$Kilogramos)
fivenum(T2010$Kilogramos)

## [1] 3.0 5.0 6.0 7.5 9.0
sd2010=sd(T2010$Kilogramos)

shapiro.test(T2010$Kilogramos)

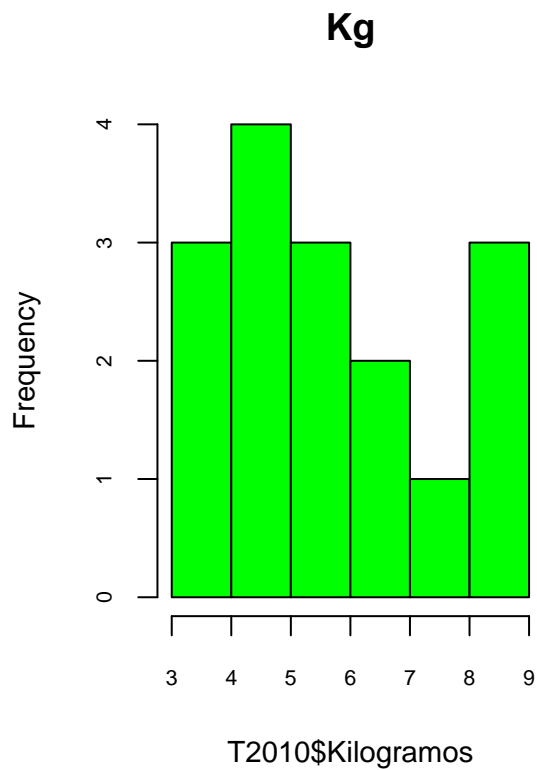
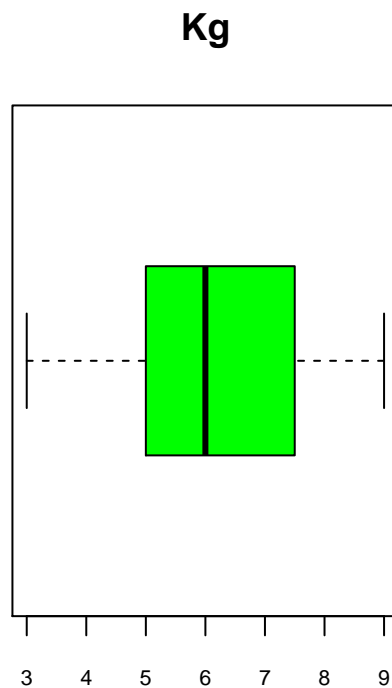
##
## Shapiro-Wilk normality test
##
## data:  T2010$Kilogramos
## W = 0.92998, p-value = 0.2436

ks.test(T2010$Kilogramos, "pnorm", mean2010, sd2010)

## Warning in ks.test(T2010$Kilogramos, "pnorm", mean2010, sd2010): ties
## should not be present for the Kolmogorov-Smirnov test

##
## One-sample Kolmogorov-Smirnov test
##
## data:  T2010$Kilogramos
## D = 0.16135, p-value = 0.7991
## alternative hypothesis: two-sided

boxplot(T2010$Kilogramos, horizontal = TRUE, col= "green", main="Kg")
hist(T2010$Kilogramos, col= "green", main="Kg")
```

```
# 2013 -----
```

```
T2013 <- subset(semillas, tiempo == "T2013")
```

```
mean2013=mean(T2013$Kilogramos)
```

```
fivenum(T2013$Kilogramos)
```

```
## [1] 3.0 4.0 5.0 7.5 9.0
```

```
sd2013=sd(T2013$Kilogramos)
```

```
shapiro.test(T2013$Kilogramos)
```

```
##
```

```
## Shapiro-Wilk normality test
```

```
##
```

```
## data: T2013$Kilogramos
```

```
## W = 0.9158, p-value = 0.1444
```

```
ks.test(T2013$Kilogramos, "pnorm", mean2013, sd2013)
```

```
## Warning in ks.test(T2013$Kilogramos, "pnorm", mean2013, sd2013): ties
```

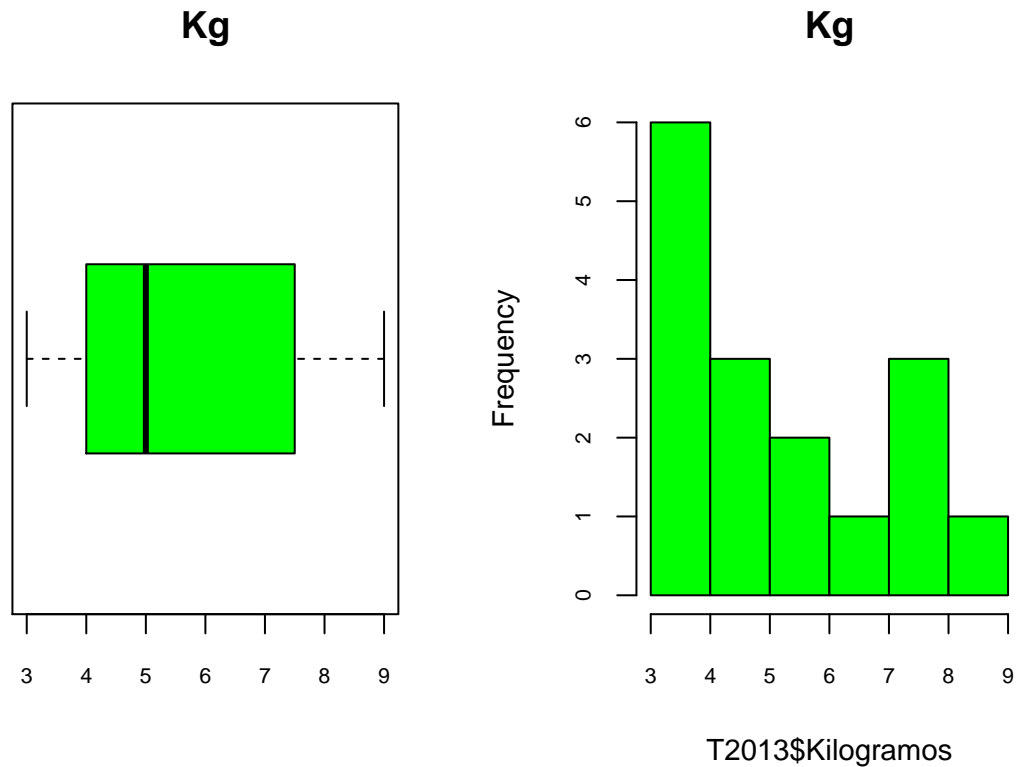
```
## should not be present for the Kolmogorov-Smirnov test
```

```
##
```

```
## One-sample Kolmogorov-Smirnov test
```

```
##
```

```
## data: T2013$Kilogramos
## D = 0.17708, p-value = 0.6973
## alternative hypothesis: two-sided
boxplot(T2013$Kilogramos, horizontal = TRUE, col= "green", main="Kg")
hist(T2013$Kilogramos, col= "green", main="Kg")
```



```
# Paired t-test -----
```

```
test.tiempo <- t.test(semillas$Kilogramos ~ semillas$tiempo, paired=TRUE)
test.tiempo
```

```
##
## Paired t-test
##
## data: semillas$Kilogramos by semillas$tiempo
## t = 1.5927, df = 15, p-value = 0.1321
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -0.1902958 1.3152958
## sample estimates:
## mean of the differences
## 0.5625
```