

R Assignment 6

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```
# 1st Part of 19.1
# h0: All means are equal // Ha: One mean is not equal

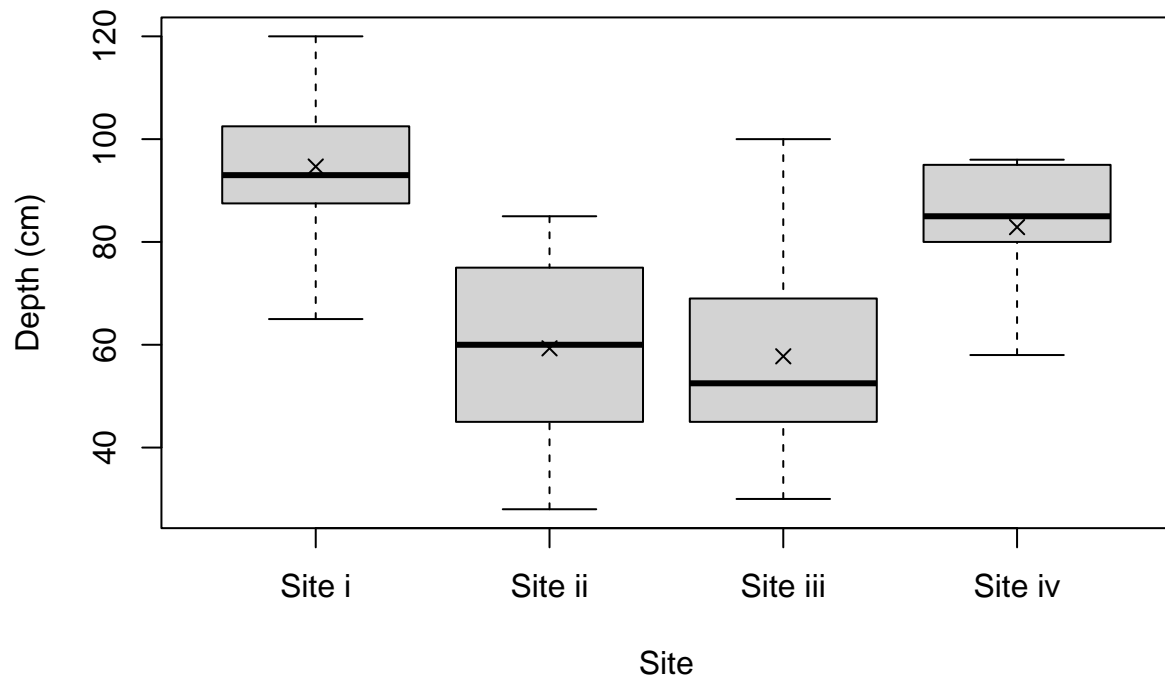
# Create a data frame with the depth and site columns
info <- data.frame(
  "depth" = c(
    93, 120, 65, 105, 115, 82, 99, 87, 100, 90, 78, 95, 93, 88, 110, 85,
    45, 80, 28, 75, 70, 65, 55, 50, 40, 100, 75, 65, 40, 73, 65, 50, 30,
    45, 50, 45, 55, 96, 58, 95, 90, 65, 80, 85, 95, 82
  ),
  "site" = c(
    rep("Site i", 15),
    rep("Site ii", 10),
    rep("Site iii", 12),
    rep("Site iv", 9)
  )
)

# Convert site to a factor
info$site <- factor(info$site)

# Calculate the mean depth for each site
infomean <- tapply(info$depth, info$site, mean)

# Create a boxplot and add mean values as points
boxplot(info$depth ~ info$site,
        xlab = "Site",
        ylab = "Depth (cm)",
        main = "Boxplot of Depth by cm by Site")
points(1:4, infomean, pch = 4)
```

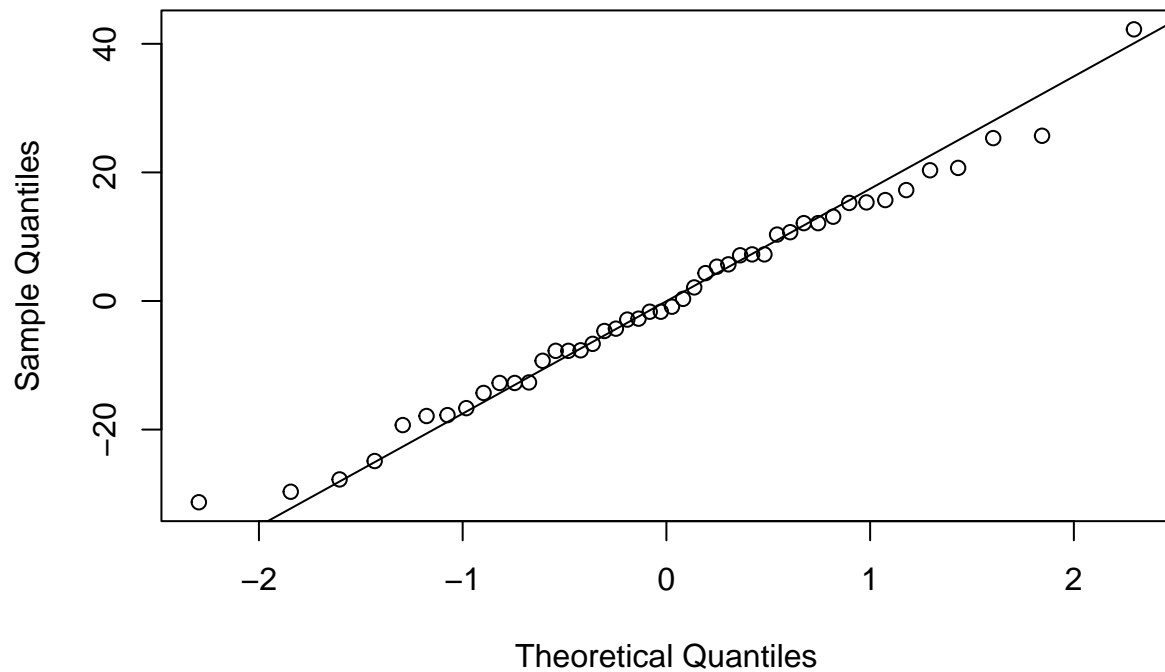
Boxplot of Depth by cm by Site



```
# Center the depth values by subtracting the mean depth for each site  
infomeancn <- info$depth - infomean[info$site]
```

```
# Check the normality assumption by creating a normal QQ plot  
qqnorm(infomeancn)  
qqline(infomeancn)
```

Normal Q-Q Plot



```
# Check the equality of variances using the ratio of the maximum to minimum standard deviation
info.sds <- tapply(info$depth, info$site, sd)
max(info.sds)/min(info.sds)
```

```
## [1] 1.399928
```

```
# Run an ANOVA test and print the summary
infoaov <- aov(depth ~ site, info)
summary(infoaov)
```

```
##           Df Sum Sq Mean Sq F value    Pr(>F)
## site         3  12397    4132   15.14 7.99e-07 ***
## Residuals   42   11465     273
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
# Close the plot device
dev.off()
```

```
## null device
##           1
```

```
# 2nd Part of 19.1
# Diagnosis checking what suits an ANOVA analysis
# Sepal.Length ----
```

```
# Load the iris dataset
mydata <- iris
```

```
# Print the dataset
mydata
```

##	Sepal.Length	Sepal.Width	Petal.Length	Petal.Width	Species
## 1	5.1	3.5	1.4	0.2	setosa
## 2	4.9	3.0	1.4	0.2	setosa
## 3	4.7	3.2	1.3	0.2	setosa
## 4	4.6	3.1	1.5	0.2	setosa
## 5	5.0	3.6	1.4	0.2	setosa
## 6	5.4	3.9	1.7	0.4	setosa
## 7	4.6	3.4	1.4	0.3	setosa
## 8	5.0	3.4	1.5	0.2	setosa
## 9	4.4	2.9	1.4	0.2	setosa
## 10	4.9	3.1	1.5	0.1	setosa
## 11	5.4	3.7	1.5	0.2	setosa
## 12	4.8	3.4	1.6	0.2	setosa
## 13	4.8	3.0	1.4	0.1	setosa
## 14	4.3	3.0	1.1	0.1	setosa
## 15	5.8	4.0	1.2	0.2	setosa
## 16	5.7	4.4	1.5	0.4	setosa
## 17	5.4	3.9	1.3	0.4	setosa
## 18	5.1	3.5	1.4	0.3	setosa
## 19	5.7	3.8	1.7	0.3	setosa
## 20	5.1	3.8	1.5	0.3	setosa
## 21	5.4	3.4	1.7	0.2	setosa
## 22	5.1	3.7	1.5	0.4	setosa
## 23	4.6	3.6	1.0	0.2	setosa
## 24	5.1	3.3	1.7	0.5	setosa
## 25	4.8	3.4	1.9	0.2	setosa
## 26	5.0	3.0	1.6	0.2	setosa
## 27	5.0	3.4	1.6	0.4	setosa
## 28	5.2	3.5	1.5	0.2	setosa
## 29	5.2	3.4	1.4	0.2	setosa
## 30	4.7	3.2	1.6	0.2	setosa
## 31	4.8	3.1	1.6	0.2	setosa
## 32	5.4	3.4	1.5	0.4	setosa
## 33	5.2	4.1	1.5	0.1	setosa
## 34	5.5	4.2	1.4	0.2	setosa
## 35	4.9	3.1	1.5	0.2	setosa
## 36	5.0	3.2	1.2	0.2	setosa
## 37	5.5	3.5	1.3	0.2	setosa
## 38	4.9	3.6	1.4	0.1	setosa
## 39	4.4	3.0	1.3	0.2	setosa
## 40	5.1	3.4	1.5	0.2	setosa
## 41	5.0	3.5	1.3	0.3	setosa
## 42	4.5	2.3	1.3	0.3	setosa

## 43	4.4	3.2	1.3	0.2	setosa
## 44	5.0	3.5	1.6	0.6	setosa
## 45	5.1	3.8	1.9	0.4	setosa
## 46	4.8	3.0	1.4	0.3	setosa
## 47	5.1	3.8	1.6	0.2	setosa
## 48	4.6	3.2	1.4	0.2	setosa
## 49	5.3	3.7	1.5	0.2	setosa
## 50	5.0	3.3	1.4	0.2	setosa
## 51	7.0	3.2	4.7	1.4	versicolor
## 52	6.4	3.2	4.5	1.5	versicolor
## 53	6.9	3.1	4.9	1.5	versicolor
## 54	5.5	2.3	4.0	1.3	versicolor
## 55	6.5	2.8	4.6	1.5	versicolor
## 56	5.7	2.8	4.5	1.3	versicolor
## 57	6.3	3.3	4.7	1.6	versicolor
## 58	4.9	2.4	3.3	1.0	versicolor
## 59	6.6	2.9	4.6	1.3	versicolor
## 60	5.2	2.7	3.9	1.4	versicolor
## 61	5.0	2.0	3.5	1.0	versicolor
## 62	5.9	3.0	4.2	1.5	versicolor
## 63	6.0	2.2	4.0	1.0	versicolor
## 64	6.1	2.9	4.7	1.4	versicolor
## 65	5.6	2.9	3.6	1.3	versicolor
## 66	6.7	3.1	4.4	1.4	versicolor
## 67	5.6	3.0	4.5	1.5	versicolor
## 68	5.8	2.7	4.1	1.0	versicolor
## 69	6.2	2.2	4.5	1.5	versicolor
## 70	5.6	2.5	3.9	1.1	versicolor
## 71	5.9	3.2	4.8	1.8	versicolor
## 72	6.1	2.8	4.0	1.3	versicolor
## 73	6.3	2.5	4.9	1.5	versicolor
## 74	6.1	2.8	4.7	1.2	versicolor
## 75	6.4	2.9	4.3	1.3	versicolor
## 76	6.6	3.0	4.4	1.4	versicolor
## 77	6.8	2.8	4.8	1.4	versicolor
## 78	6.7	3.0	5.0	1.7	versicolor
## 79	6.0	2.9	4.5	1.5	versicolor
## 80	5.7	2.6	3.5	1.0	versicolor
## 81	5.5	2.4	3.8	1.1	versicolor
## 82	5.5	2.4	3.7	1.0	versicolor
## 83	5.8	2.7	3.9	1.2	versicolor
## 84	6.0	2.7	5.1	1.6	versicolor
## 85	5.4	3.0	4.5	1.5	versicolor
## 86	6.0	3.4	4.5	1.6	versicolor
## 87	6.7	3.1	4.7	1.5	versicolor
## 88	6.3	2.3	4.4	1.3	versicolor
## 89	5.6	3.0	4.1	1.3	versicolor
## 90	5.5	2.5	4.0	1.3	versicolor
## 91	5.5	2.6	4.4	1.2	versicolor
## 92	6.1	3.0	4.6	1.4	versicolor
## 93	5.8	2.6	4.0	1.2	versicolor
## 94	5.0	2.3	3.3	1.0	versicolor
## 95	5.6	2.7	4.2	1.3	versicolor
## 96	5.7	3.0	4.2	1.2	versicolor

## 97	5.7	2.9	4.2	1.3	versicolor
## 98	6.2	2.9	4.3	1.3	versicolor
## 99	5.1	2.5	3.0	1.1	versicolor
## 100	5.7	2.8	4.1	1.3	versicolor
## 101	6.3	3.3	6.0	2.5	virginica
## 102	5.8	2.7	5.1	1.9	virginica
## 103	7.1	3.0	5.9	2.1	virginica
## 104	6.3	2.9	5.6	1.8	virginica
## 105	6.5	3.0	5.8	2.2	virginica
## 106	7.6	3.0	6.6	2.1	virginica
## 107	4.9	2.5	4.5	1.7	virginica
## 108	7.3	2.9	6.3	1.8	virginica
## 109	6.7	2.5	5.8	1.8	virginica
## 110	7.2	3.6	6.1	2.5	virginica
## 111	6.5	3.2	5.1	2.0	virginica
## 112	6.4	2.7	5.3	1.9	virginica
## 113	6.8	3.0	5.5	2.1	virginica
## 114	5.7	2.5	5.0	2.0	virginica
## 115	5.8	2.8	5.1	2.4	virginica
## 116	6.4	3.2	5.3	2.3	virginica
## 117	6.5	3.0	5.5	1.8	virginica
## 118	7.7	3.8	6.7	2.2	virginica
## 119	7.7	2.6	6.9	2.3	virginica
## 120	6.0	2.2	5.0	1.5	virginica
## 121	6.9	3.2	5.7	2.3	virginica
## 122	5.6	2.8	4.9	2.0	virginica
## 123	7.7	2.8	6.7	2.0	virginica
## 124	6.3	2.7	4.9	1.8	virginica
## 125	6.7	3.3	5.7	2.1	virginica
## 126	7.2	3.2	6.0	1.8	virginica
## 127	6.2	2.8	4.8	1.8	virginica
## 128	6.1	3.0	4.9	1.8	virginica
## 129	6.4	2.8	5.6	2.1	virginica
## 130	7.2	3.0	5.8	1.6	virginica
## 131	7.4	2.8	6.1	1.9	virginica
## 132	7.9	3.8	6.4	2.0	virginica
## 133	6.4	2.8	5.6	2.2	virginica
## 134	6.3	2.8	5.1	1.5	virginica
## 135	6.1	2.6	5.6	1.4	virginica
## 136	7.7	3.0	6.1	2.3	virginica
## 137	6.3	3.4	5.6	2.4	virginica
## 138	6.4	3.1	5.5	1.8	virginica
## 139	6.0	3.0	4.8	1.8	virginica
## 140	6.9	3.1	5.4	2.1	virginica
## 141	6.7	3.1	5.6	2.4	virginica
## 142	6.9	3.1	5.1	2.3	virginica
## 143	5.8	2.7	5.1	1.9	virginica
## 144	6.8	3.2	5.9	2.3	virginica
## 145	6.7	3.3	5.7	2.5	virginica
## 146	6.7	3.0	5.2	2.3	virginica
## 147	6.3	2.5	5.0	1.9	virginica
## 148	6.5	3.0	5.2	2.0	virginica
## 149	6.2	3.4	5.4	2.3	virginica
## 150	5.9	3.0	5.1	1.8	virginica

```
# Check normality using Shapiro-Wilk test for each variable  
shapiro.test(mydata$Sepal.Length)
```

```
##  
## Shapiro-Wilk normality test  
##  
## data: mydata$Sepal.Length  
## W = 0.97609, p-value = 0.01018
```

```
shapiro.test(mydata$Sepal.Width)
```

```
##  
## Shapiro-Wilk normality test  
##  
## data: mydata$Sepal.Width  
## W = 0.98492, p-value = 0.1012
```

```
shapiro.test(mydata$Petal.Length)
```

```
##  
## Shapiro-Wilk normality test  
##  
## data: mydata$Petal.Length  
## W = 0.87627, p-value = 7.412e-10
```

```
shapiro.test(mydata$Petal.Width)
```

```
##  
## Shapiro-Wilk normality test  
##  
## data: mydata$Petal.Width  
## W = 0.90183, p-value = 1.68e-08
```

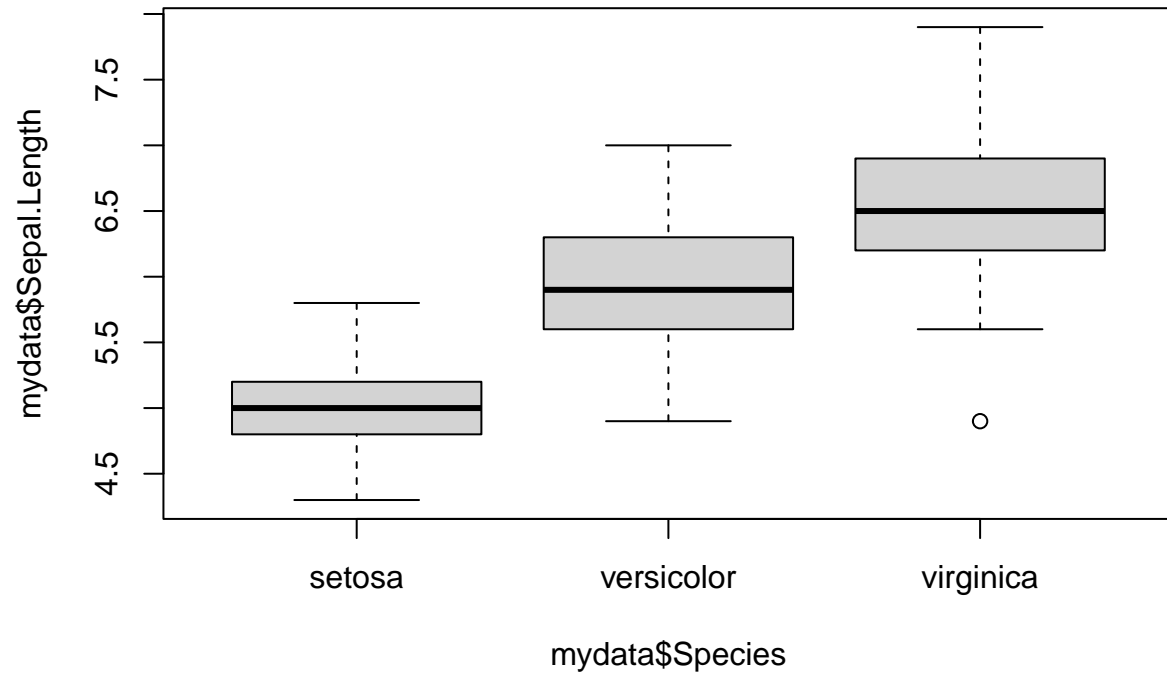
```
# Set plot margins
```

```
par(mar=c(5, 4, 4, 2) + 0.1)
```

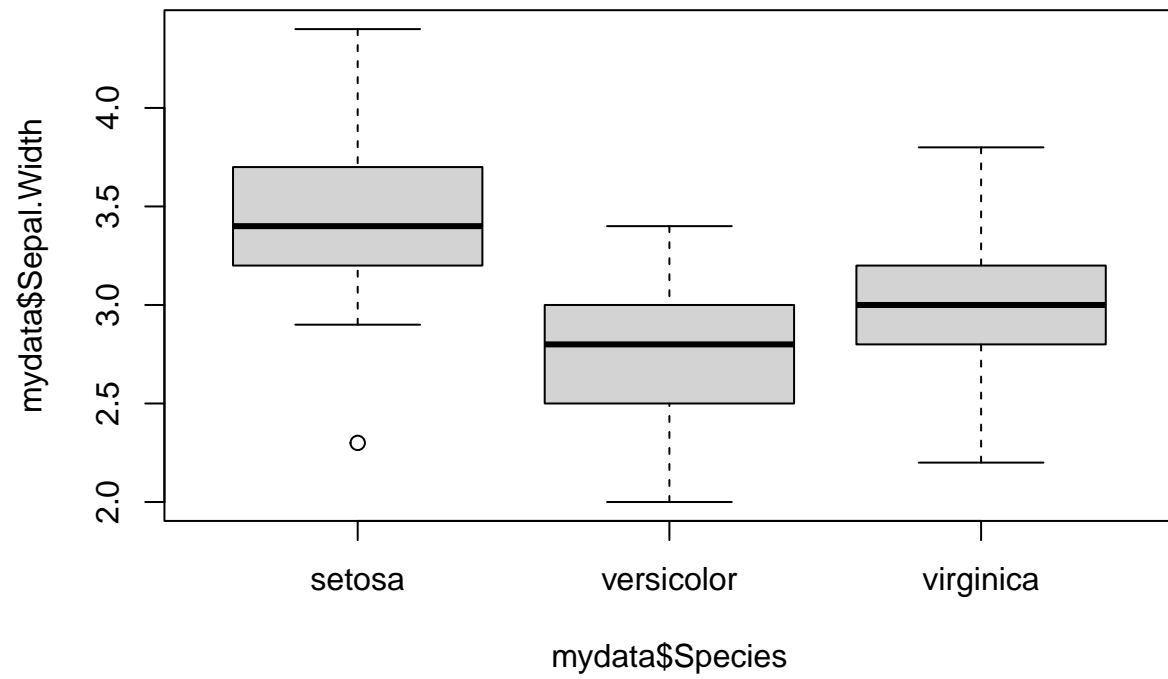
```
# Save boxplots for each variable grouped by species as a PDF file
```

```
pdf("myplot.pdf", width = 8, height = 4)
```

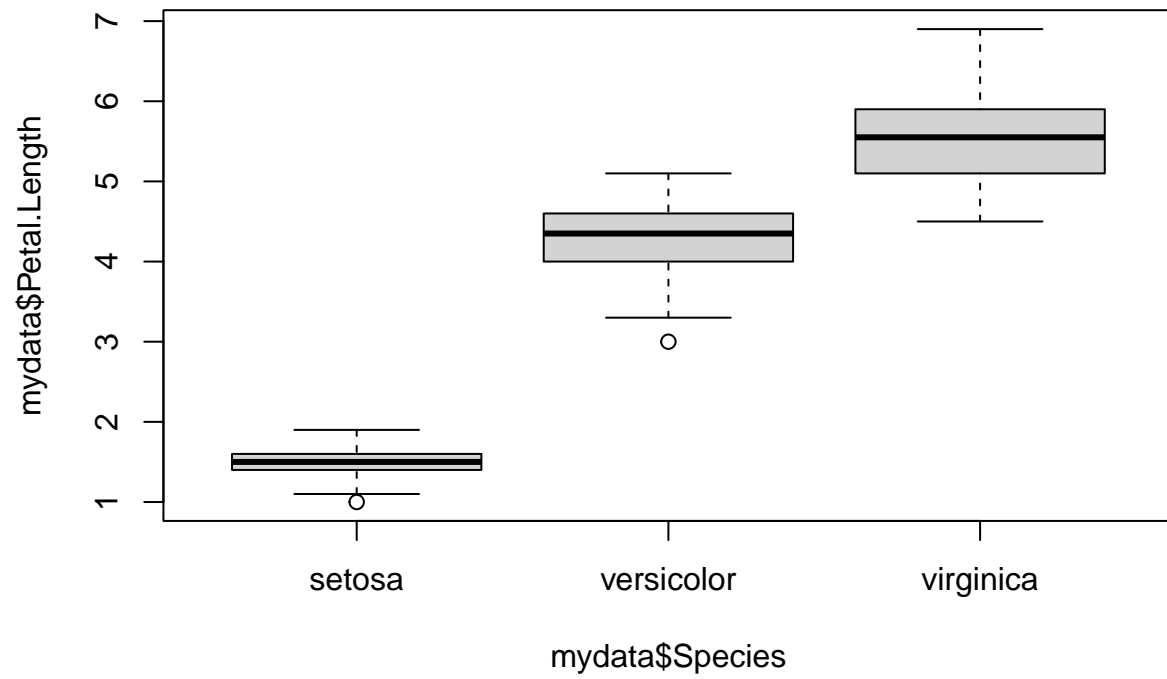
```
boxplot(mydata$Sepal.Length~mydata$Species)
```



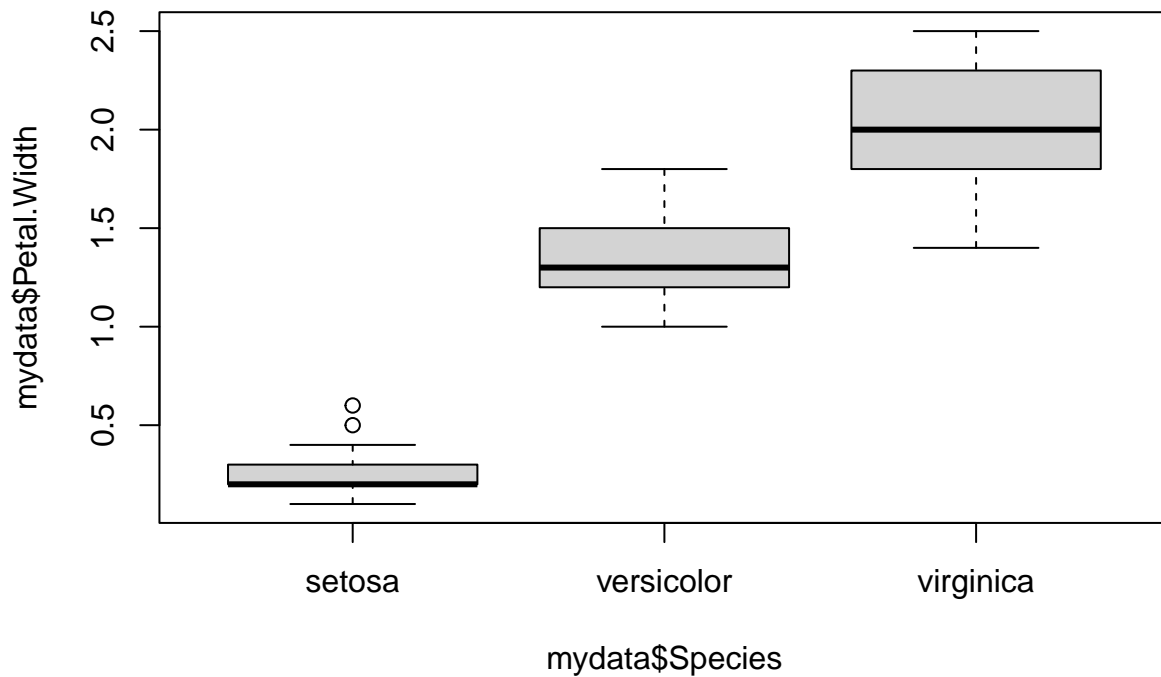

```
boxplot(mydata$Sepal.Width~mydata$Species)
```



```
{boxplot(mydata$Petal.Length~mydata$Species)}
```



```
{boxplot(mydata$Petal.Width~mydata$Species)}
```



```
{dev.off()}
```

```
## pdf
## 3
```

```
# Run an ANOVA test on Sepal.Width grouped by species and print the summary
anova=aov(mydata$Sepal.Width~mydata$Species)
summary(anova)
```

```
##              Df Sum Sq Mean Sq F value Pr(>F)
## mydata$Species  2  11.35    5.672   49.16 <2e-16 ***
## Residuals     147   16.96    0.115
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
# As the p-value is less than the significance level 0.05, we can conclude that there are significant d
```