

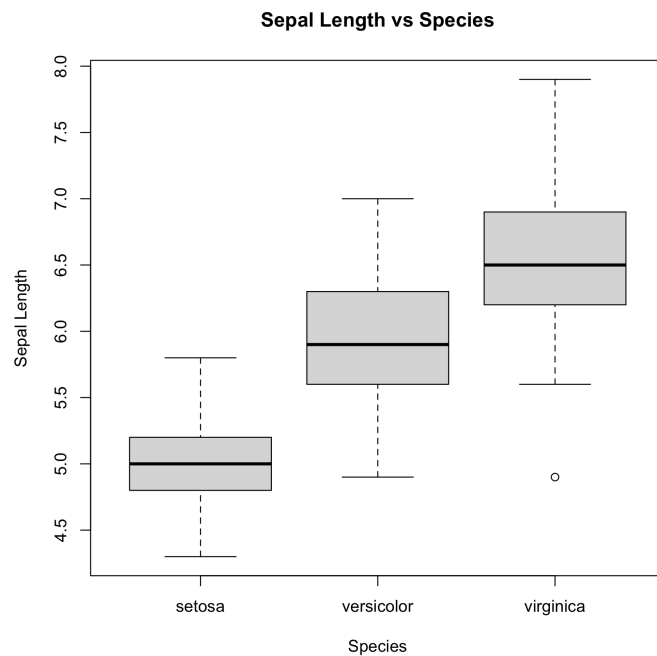
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Module 8 Exercise: Box Plots

i. The entire R code used when creating the box plot in (1)

```
boxplot(Sepal.Length~Species, data=iris, main="Sepal Length vs Species", ylab="Sepal Length")
```

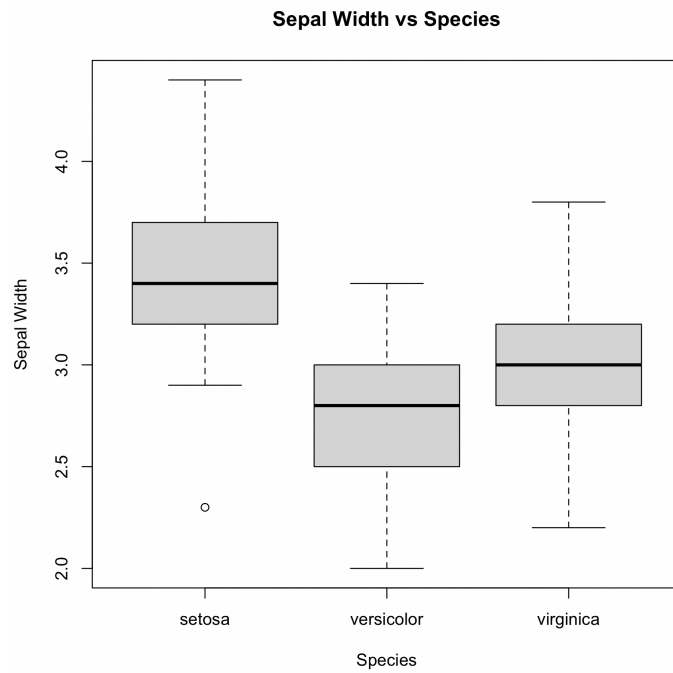
ii. Screenshot of the box plot created in (1)



iii. The entire R code used when creating the box plot in (2)

```
boxplot(Sepal.Width~Species, data=iris, main="Sepal Width vs Species", ylab="Sepal Width")
```

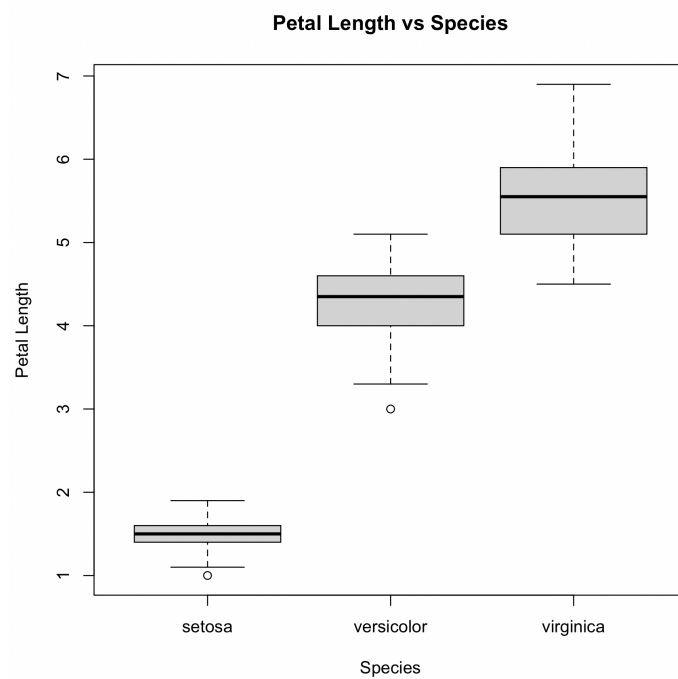
iv. Screenshot of the box plot created in (2)



v. The entire R code used when creating the box plot in (3)

```
boxplot(Petal.Length~Species, data=iris, main="Petal Length vs Species", ylab="Petal Length")
```

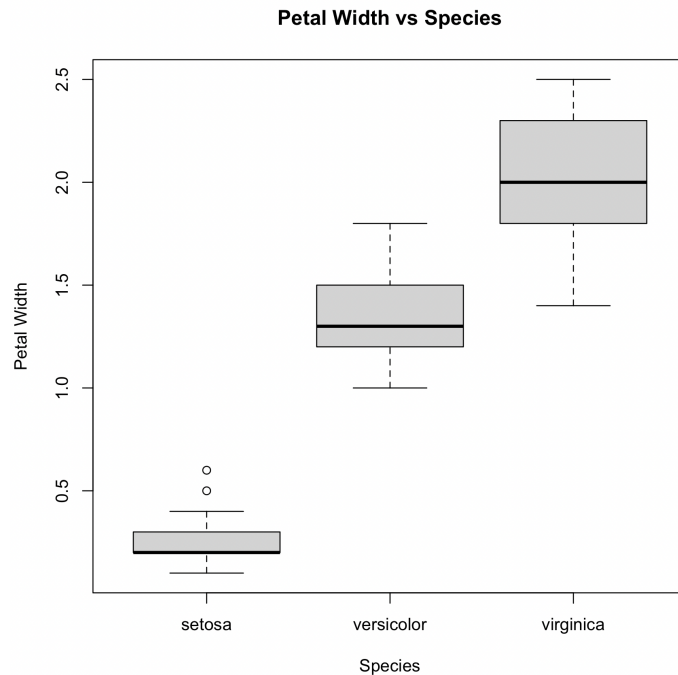
vi. Screenshot of the box plot created in (3)



vii. **The entire R code used when creating the box plot in (4)**

```
boxplot(Petal.Width~Species, data=iris, main="Petal Width vs Species", ylab="Petal Width")
```

viii. **Screenshot of the box plot created in (4)**



ix. **How you would identify the species a certain sample of an iris flower would belong to, based on these plots**

By analyzing the plots and comparing a sample's sepal length, sepal width, petal length, and petal width to the distribution ranges for each iris species, we can deduce the sample's likely species. For instance, if all measurements align with the "versicolor" species' ranges, the sample probably belongs to "versicolor".