

**9a**

```
data(iris)
```

```
# Use only the numeric columns for clustering (exclude the Species column)
```

```
iris_data <- iris[, -5]
```

```
# Standardize the data
```

```
iris_scaled <- scale(iris_data)
```

```
# Compute the distance matrix
```

```
distance_matrix <- dist(iris_scaled, method = "euclidean")
```

```
# Perform hierarchical clustering using the "complete" linkage method
```

```
hc_complete <- hclust(distance_matrix, method = "complete")
```

```
# Plot the dendrogram
```

```
plot(hc_complete, main = "Hierarchical Clustering Dendrogram", xlab = "", sub = "", cex =
0.6)
```

```
# Cut the tree to form 3 clusters
```

```
clusters <- cutree(hc_complete, k = 3)
```

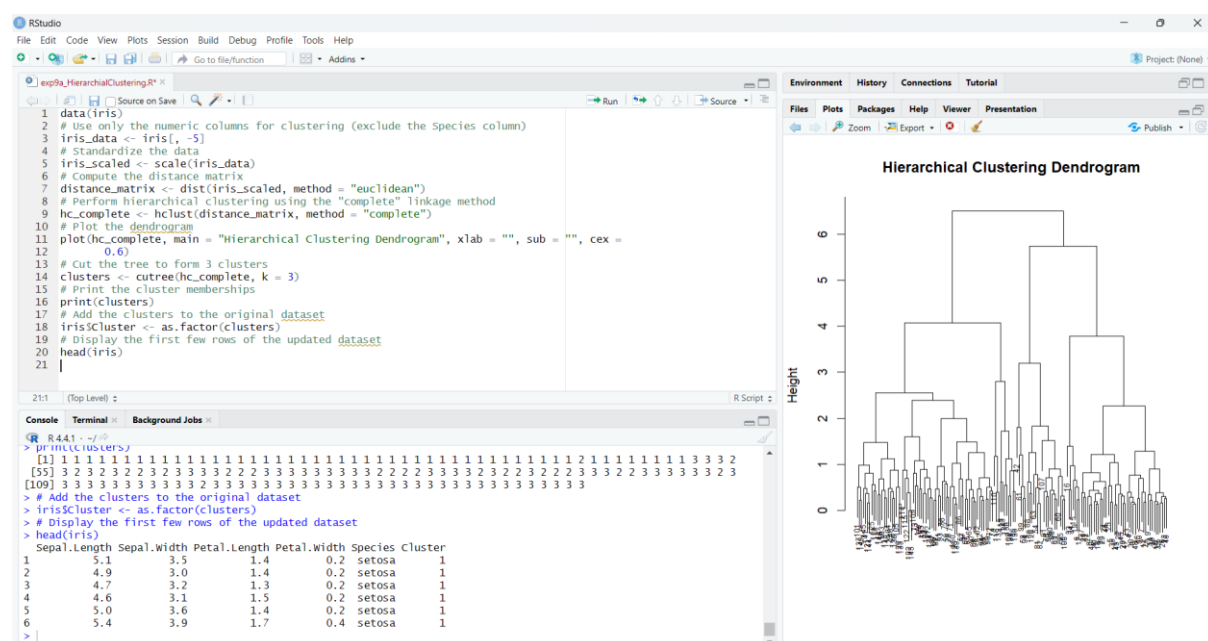
```
print(clusters)
```

```
# Add the clusters to the original dataset
```

```
iris$Cluster <- as.factor(clusters)
```

```
# Display the first few rows of the updated dataset
```

```
head(iris)
```



9b

```
data(iris)

iris_data <- iris[, -5]

# Standardize the data
iris_scaled <- scale(iris_data)

set.seed(123) # For reproducibility

k <- 3 # Number of clusters

# Perform K-Means clustering
kmeans_result <- kmeans(iris_scaled, centers = k, nstart = 25)

# Print the K-Means result
print(kmeans_result)

# Print the cluster centers
print(kmeans_result$centers)

iris$Cluster <- as.factor(kmeans_result$cluster)

head(iris)

# Plot the clusters

library(ggplot2)

ggplot(iris, aes(x = Sepal.Length, y = Sepal.Width, color = Cluster)) +

  geom_point(size = 3) +

  labs(title = "K-Means Clustering of Iris Dataset", x = "Sepal Length", y = "Sepal Width")
```

