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# Load libraries
library(cluster)
library(factoextra)
library(datasets)

# Load data
data(iris)
iris_data <- iris[, 1:4] # use only numeric features

# Scale data for better clustering performance
iris_scaled <- scale(iris_data)

# -----
# Step 1: Find optimal number of clusters
# -----

# Silhouette method
fviz_nbclust(iris_scaled, pam, method = "silhouette") +
  labs(subtitle = "Silhouette method for optimal k (K-Medoids)")

# Gap statistic method (optional but more robust)
set.seed(123)
fviz_nbclust(iris_scaled, pam, method = "gap_stat") +
  labs(subtitle = "Gap statistic method")

# -----
# Step 2: Apply K-Medoids clustering
# -----

# Suppose optimal k = 3 (as expected for Iris)
set.seed(123)
pam_model <- pam(iris_scaled, k = 3)

# -----
# Step 3: Evaluate and visualize
# -----

# Cluster summary
pam_model

# Visualize clusters
fviz_cluster(pam_model, geom = "point", data = iris_scaled) +
  labs(title = "K-Medoids Clustering on Iris Data")

```

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# Compare with actual species  
table(pam_model$clustering, iris$Species)
```