Introduction to the case study

UNSUPERVISED LEARNING IN R

Hank Roark
Senior Data Scientist at Boeing

Objectives

- Complete analysis using unsupervised learning
- Reinforce what you've already learned
- Add steps not covered before (e.g., preparing data, selecting good features for supervised learning)
- Emphasize creativity

Example use case

- Human breast mass data:
  - Ten features measured of each cell nuclei
  - Summary information is provided for each group of cells
  - Includes diagnosis: benign (not cancerous) and malignant (cancerous)

[1] Source: K. P. Bennett and O. L. Mangasarian: "Robust Linear Programming Discrimination of Two Linearly Inseparable Sets"

Analysis

- Download data and prepare data for modeling
- Exploratory data analysis (# observations, # features, etc.)
- Perform PCA and interpret results
- Complete two types of clustering
- Understand and compare the two types
- Combine PCA and clustering

Review: PCA in R

```r
pr.iris <- prcomp(x = iris[-5],
                  scale = FALSE,
                  center = TRUE)
summary(pr.iris)
```

```
Importance of components:
                          PC1     PC2    PC3     PC4
Standard deviation     2.0563 0.49262 0.2797 0.15439
Proportion of Variance 0.9246 0.05307 0.0171 0.00521
Cumulative Proportion  0.9246 0.97769 0.9948 1.00000
```

Unsupervised learning is open-ended

- Steps in this use case are only one example of what can be done
- There are other approaches to analyzing this dataset

Let's practice!

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PCA review and next steps

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Review thus far

- Downloaded data and prepared it for modeling
- Exploratory data analysis
- Performed principal component analysis

Next steps

- Complete hierarchical clustering
- Complete k-means clustering
- Combine PCA and clustering
- Contrast results of hierarchical clustering with diagnosis
- Compare hierarchical and k-means clustering results
- PCA as a pre-processing step for clustering

Review: hierarchical clustering in R

```r
# Calculates similarity as Euclidean distance between observations
s <- dist(x)

# Returns hierarchical clustering model
hclust(s)
```

```
Call:
hclust(d = s)

Cluster method   : complete
Distance         : euclidean
Number of objects: 50
```

Review: k-means in R

```
# k-means algorithm with 5 centers, run 20 times
kmeans(x, centers = 5, nstart = 20)
```

- One observation per row, one feature per column
- k-means has a random component
- Run algorithm multiple times to improve odds of the best model

Let's practice!

Wrap-up and review

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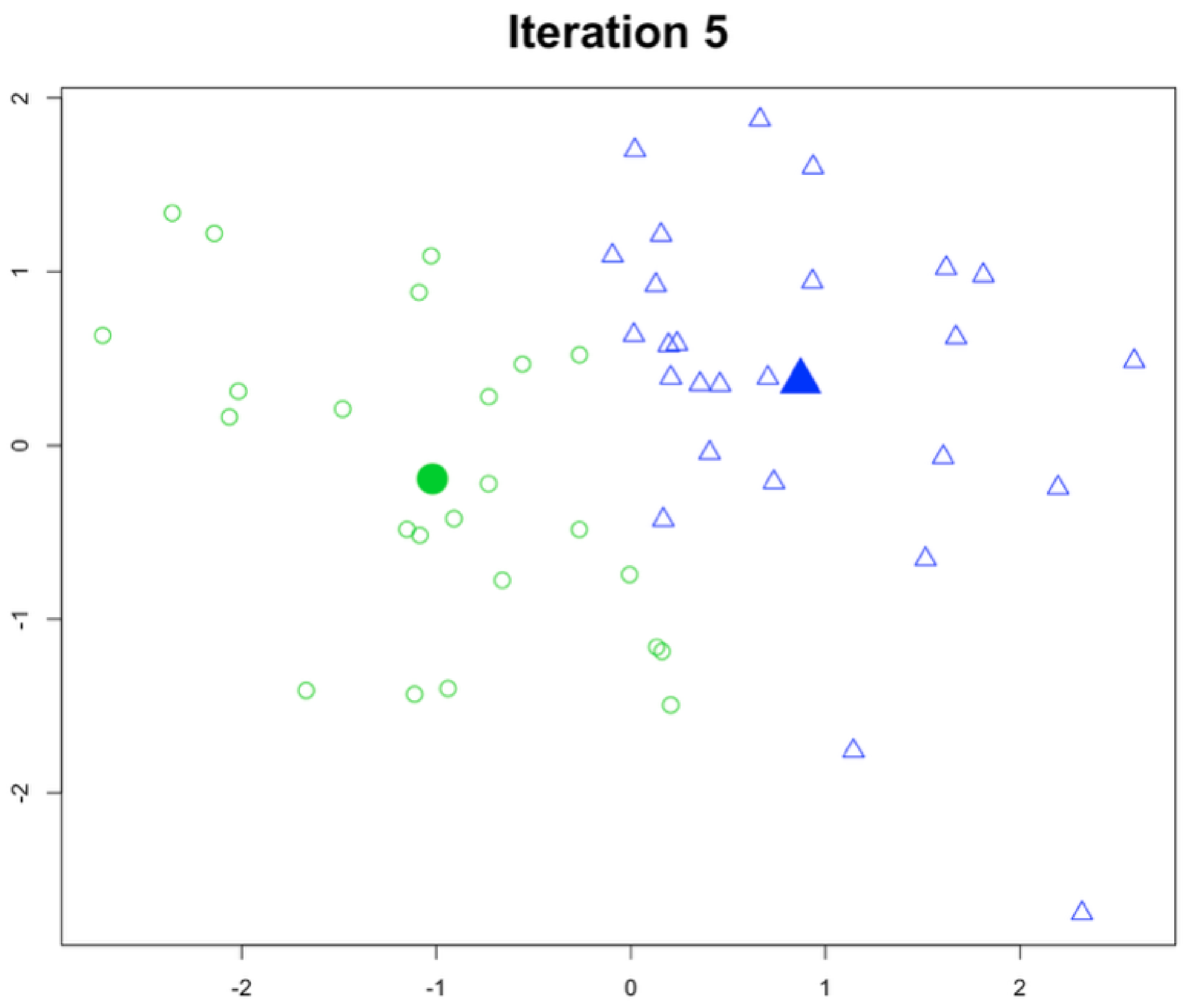
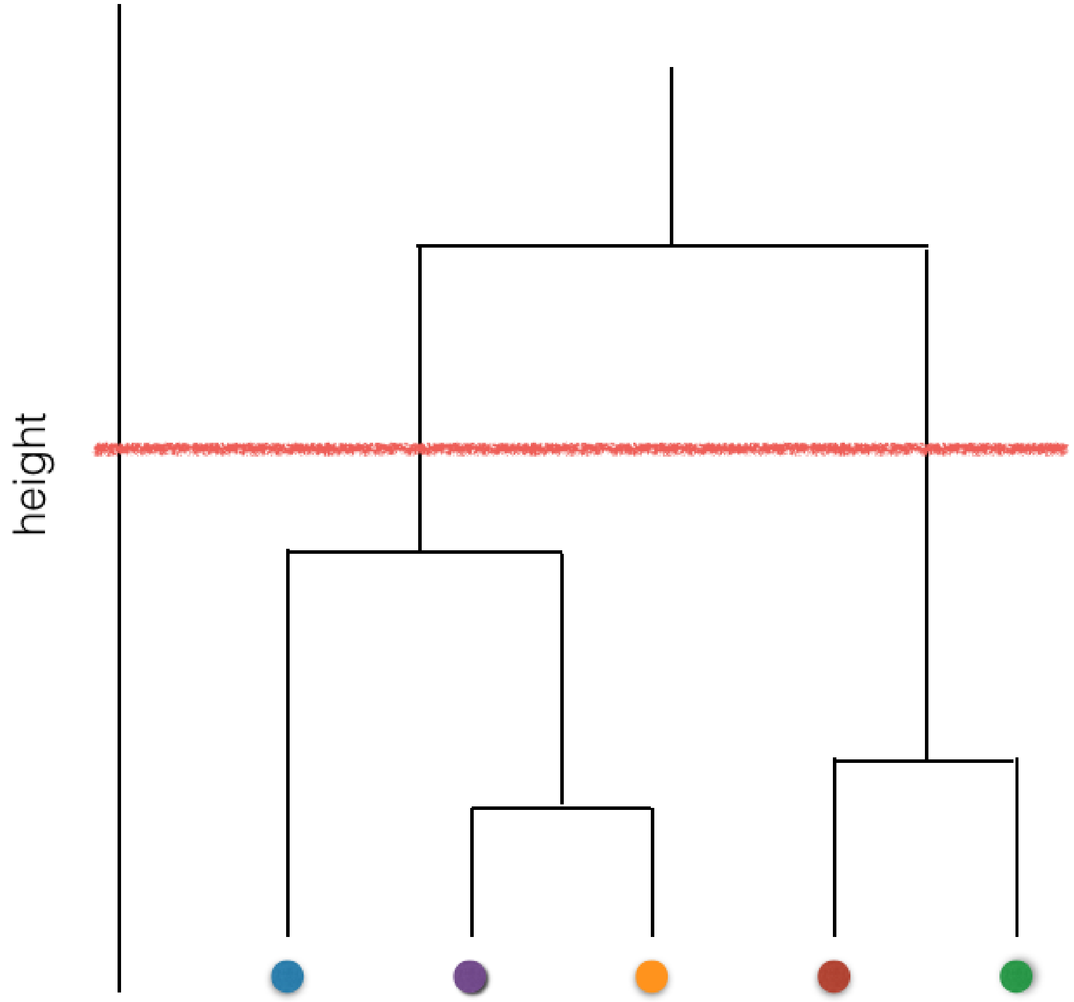
Case study wrap-up

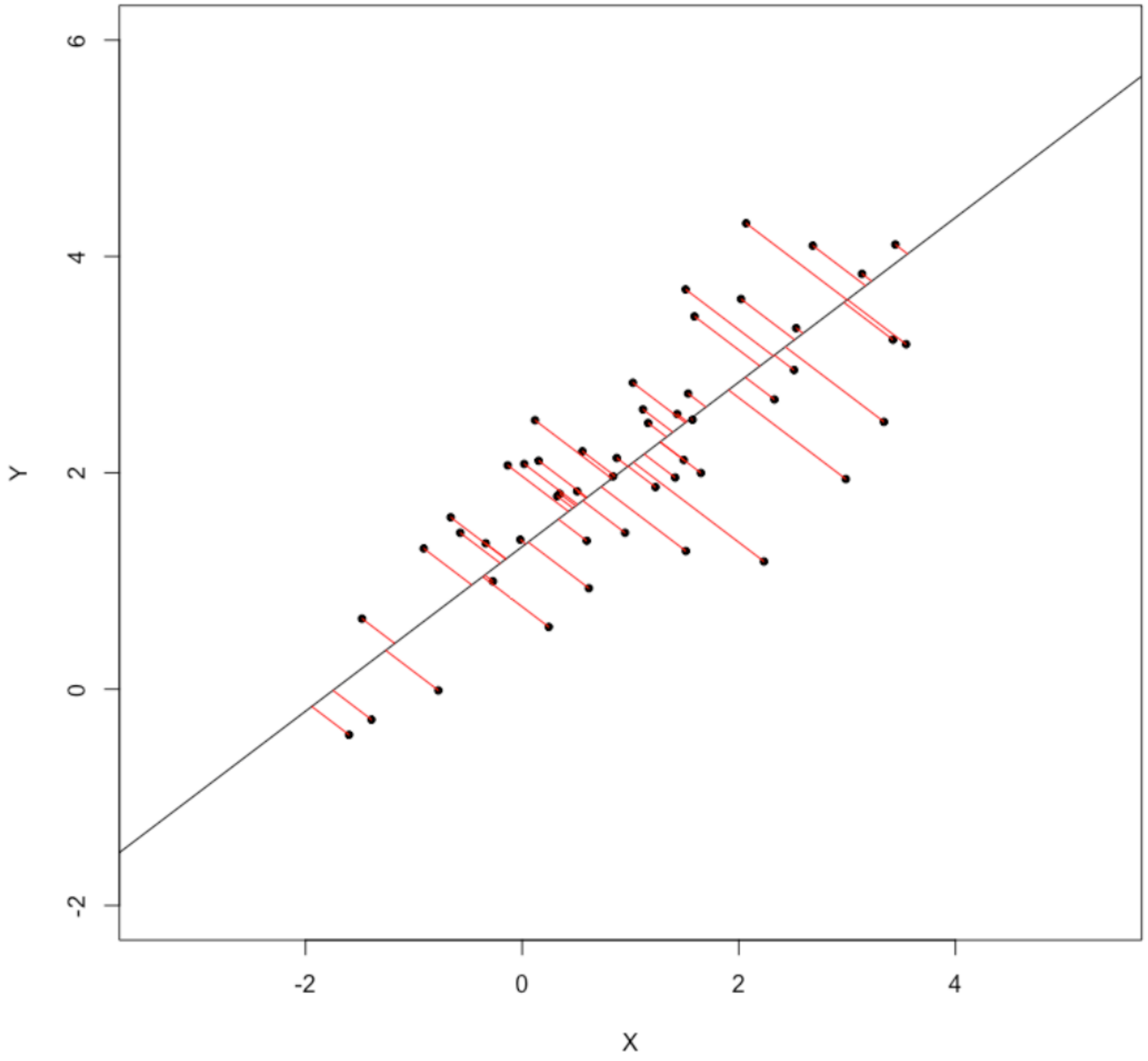
- Entire data analysis process using unsupervised learning
- Creative approach to modeling
- Prepared to tackle real world problems

Types of clustering





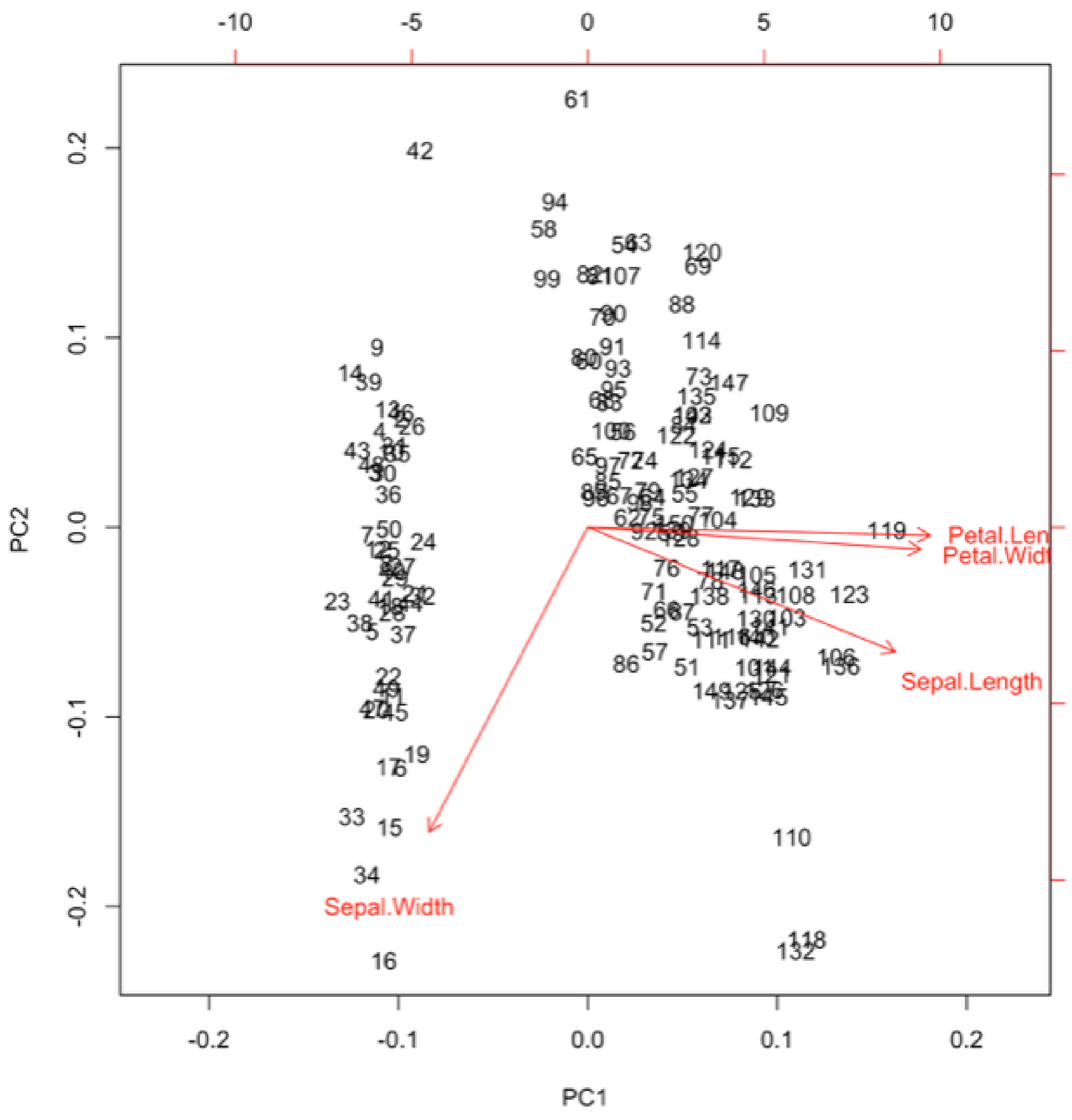
Dimensionality reduction

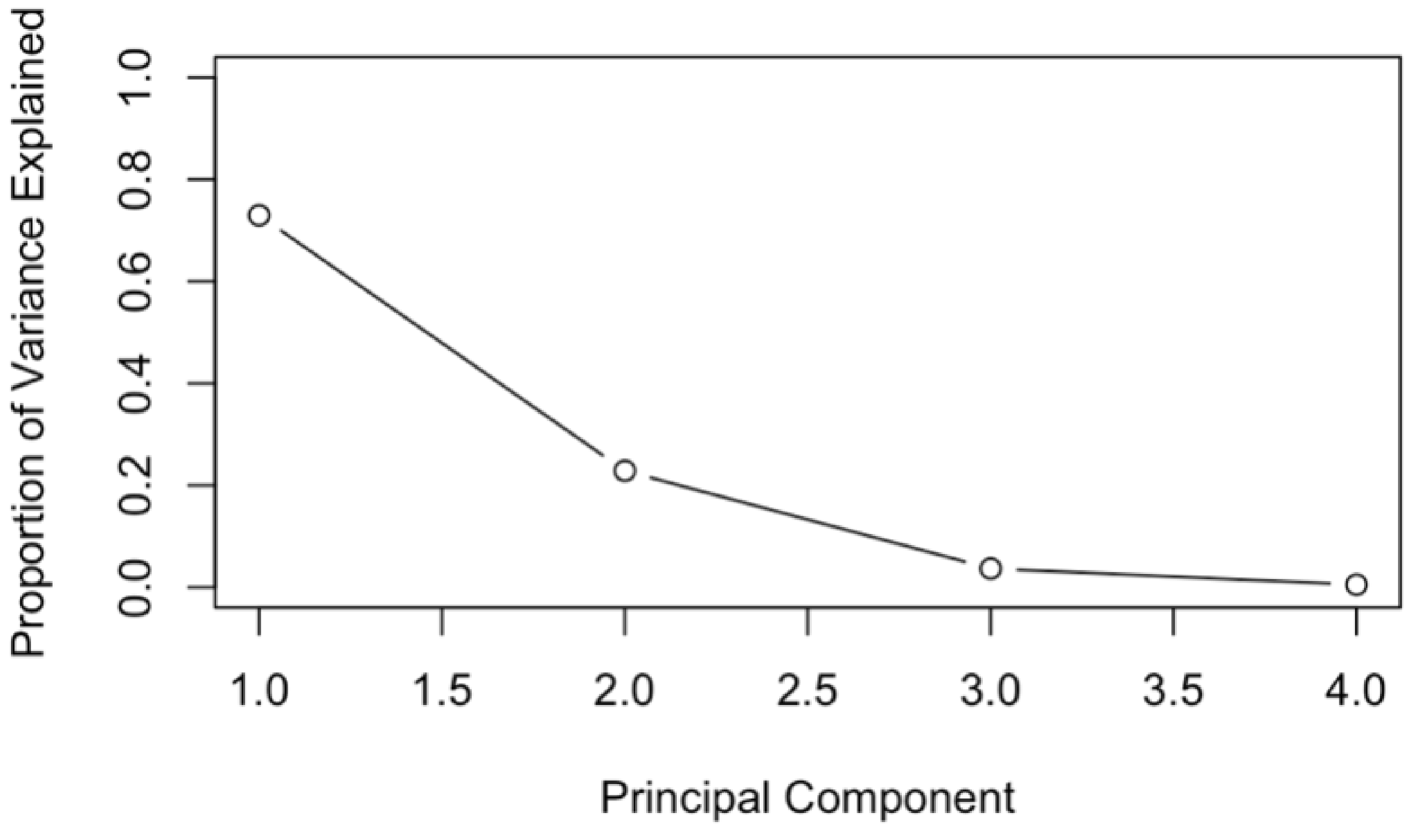


Model selection

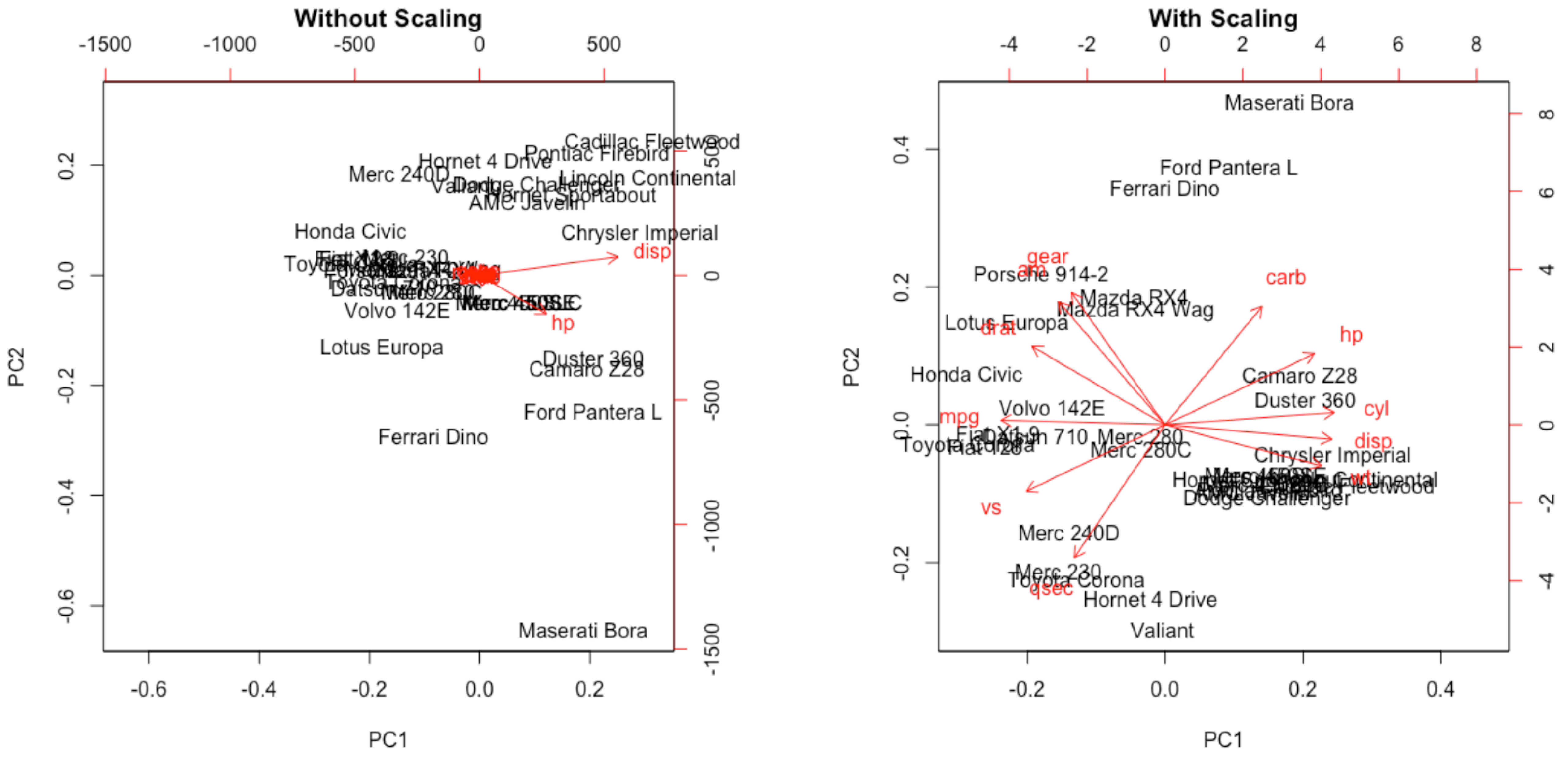
```r
# Initialize total within sum of squares error: wss
wss <- 0

# Look over 1 to 15 possible clusters
for (i in 1:15) {
  # Fit the model: km.out
  km.out <- kmeans(pokemon, centers = i, nstart = 20, iter.max = 50)
  # Save the within cluster sum of squares
  wss[i] <- km.out$tot.withinss
}

# Produce a scree plot
plot(1:15, wss, type = "b",
     xlab = "Number of Clusters",
     ylab = "Within groups sum of squares")
```

Interpreting PCA results





Importance of scaling data



Course review

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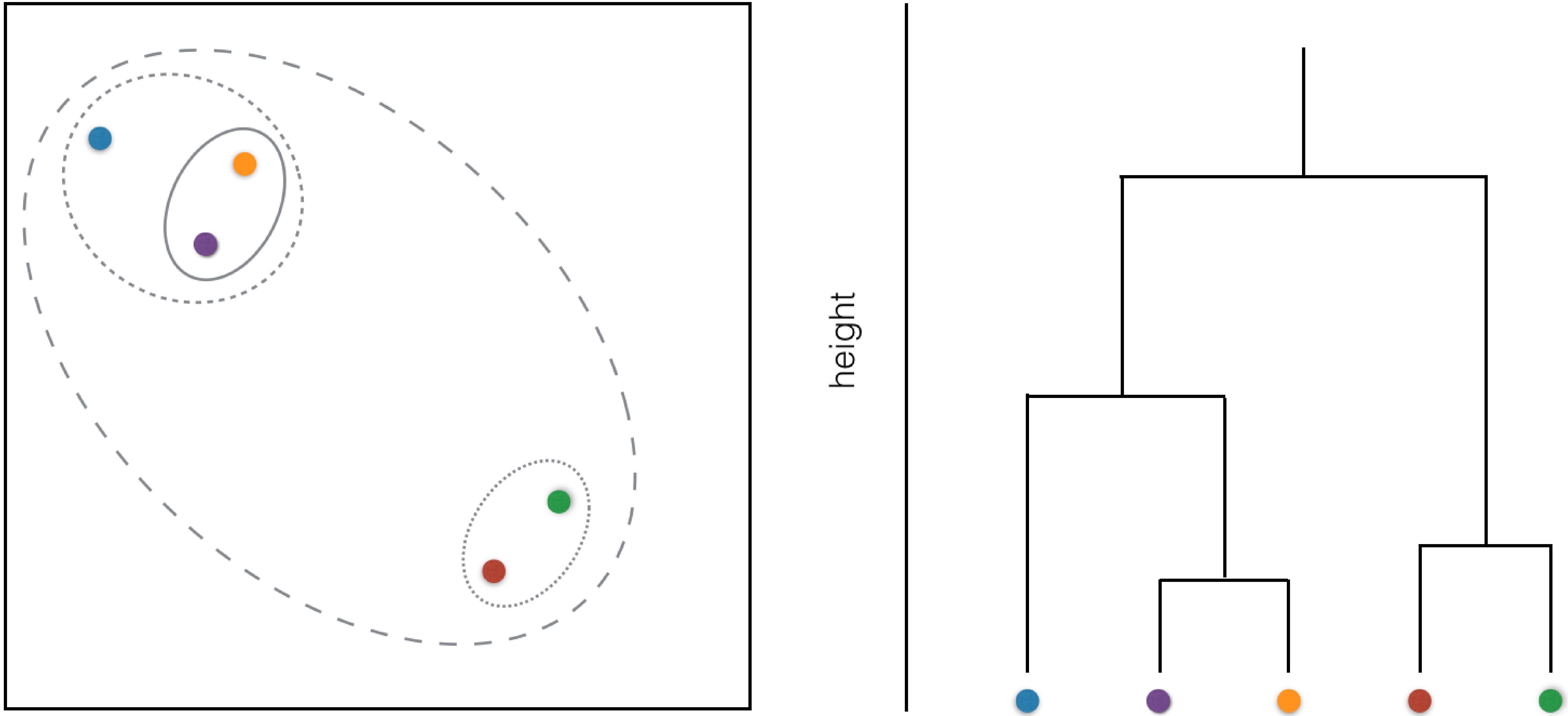
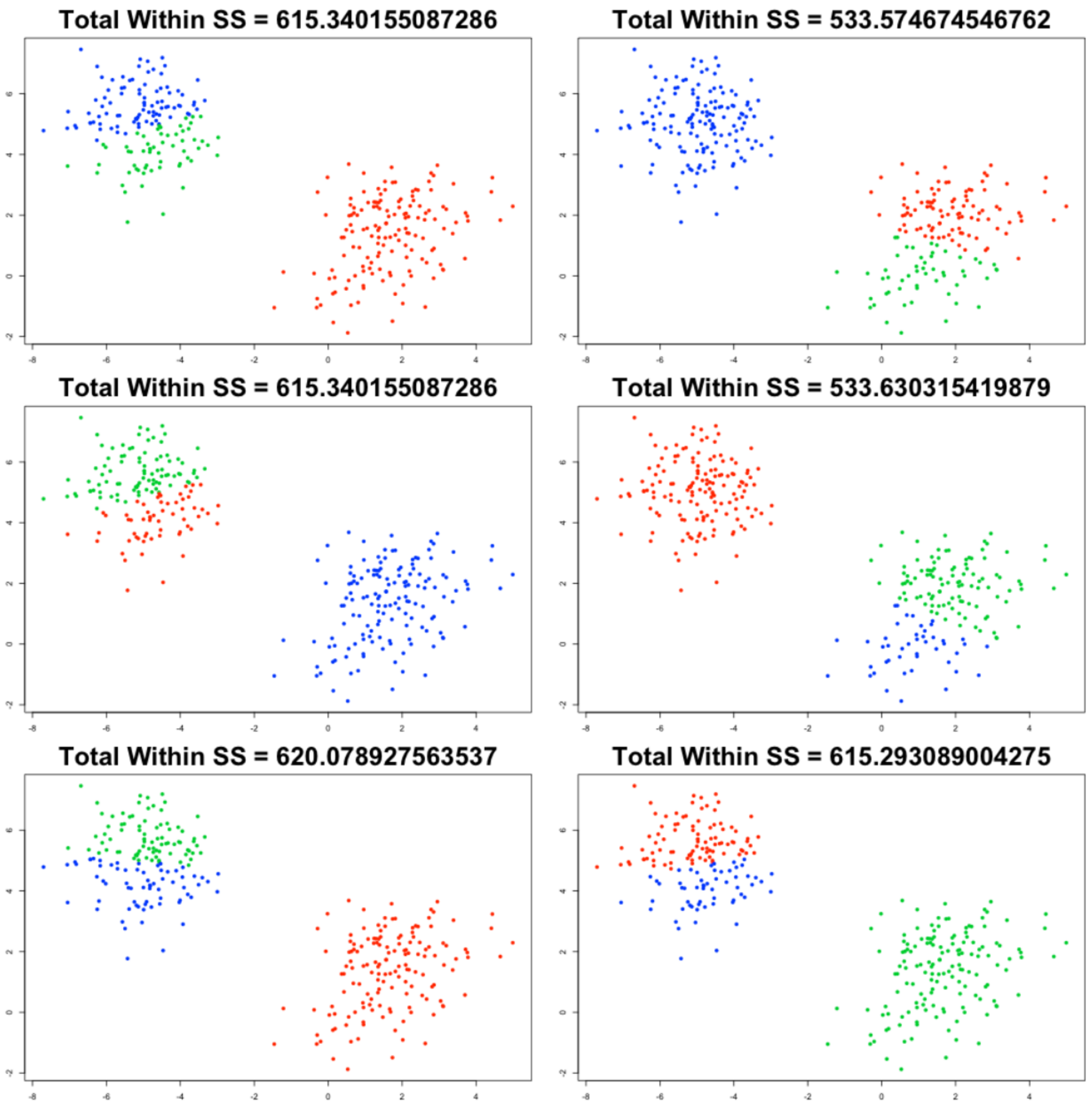
Dendrogram

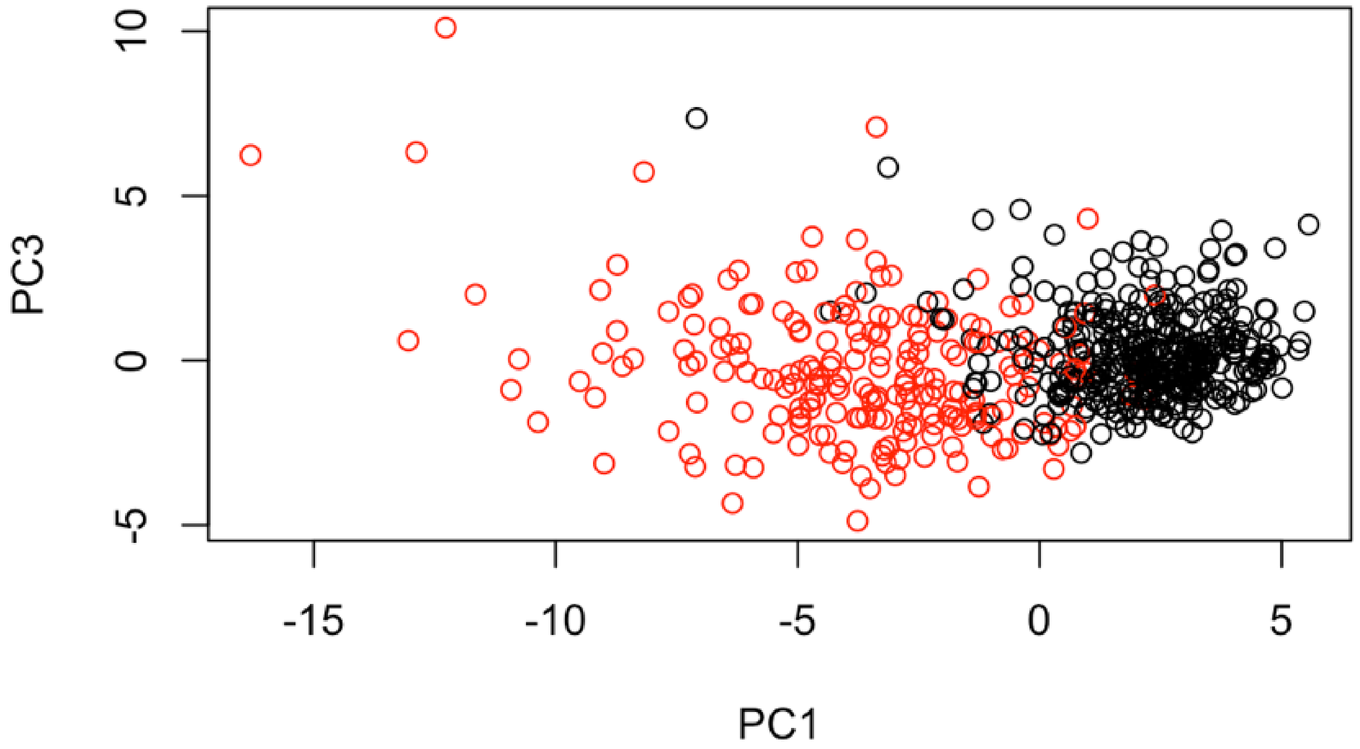


Strengths and weaknesses of each algorithm



Course review

```r
# Repeat for components 1 and 3
plot(wisc.pr$x[, c(1, 3)], col = (diagnosis + 1),
     xlab = "PC1", ylab = "PC3")
```



Hone your skills!