An Introduction to Machine Learning

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Contents

Chapter 1

About the course

1.1 Overview

Machine learning gives computers the ability to learn without being explicitly programmed. It encompasses a broad range of approaches to data analysis with applicability across the biological sciences. Lectures will introduce commonly used algorithms and provide insight into their theoretical underpinnings. In the practicals students will apply these algorithms to real biological data-sets using the R language and environment.

During this course you will learn about:

- Some of the core mathematical concepts underpinning machine learning algorithms: matrices and linear algebra; Bayes' theorem.
- Classification (supervised learning): partitioning data into training and test sets; feature selection; logistic regression; support vector machines; artificial neural networks; decision trees; nearest neighbours, cross-validation.
- Exploratory data analysis (unsupervised learning): dimensionality reduction, anomaly detection, clustering.

After this course you should be able to:

- Understand the concepts of machine learning.
- Understand the strengths and limitations of the various machine learning algorithms presented in this course.
- Select appropriate machine learning methods for your data.
- Perform machine learning in R.

1.2 Registration

Bioinformatics Training: An Introduction to Machine Learning

1.3 Prerequisites

- Some familiarity with R would be helpful.
- For an introduction to R see An Introduction to Solving Biological Problems with R course.

1.4 Github

bioinformatics-training/intro-machine-learning

1.5 License

GPL-3

1.6 Contact

If you have any **comments**, **questions** or **suggestions** about the material, please contact the authors: Sudhakaran Prabakaran, Matt Wayland and Chris Penfold.

1.7 Colophon

This book was produced using the **bookdown** package (Xie, 2017), which was built on top of R Markdown and **knitr** (Xie, 2015).

Chapter 2

Introduction

You can label chapter and section titles using `{#label}` after them, e.g., we can reference Chapter 2. If you do not manually label them, there will be automatic labels anyway, e.g., Chapter **??**.

Figures and tables with captions will be placed in `figure` and `table` environments, respectively.

```
par(mar = c(4, 4, .1, .1))
plot(pressure, type = 'b', pch = 19)
```

Reference a figure by its code chunk label with the `fig:` prefix, e.g., see Figure 2.1. Similarly, you can reference tables generated from `knitr::kable()`, e.g., see Table 2.1.

```
knitr::kable(
  head(iris, 20), caption = 'Here is a nice table!',
  booktabs = TRUE
)
```

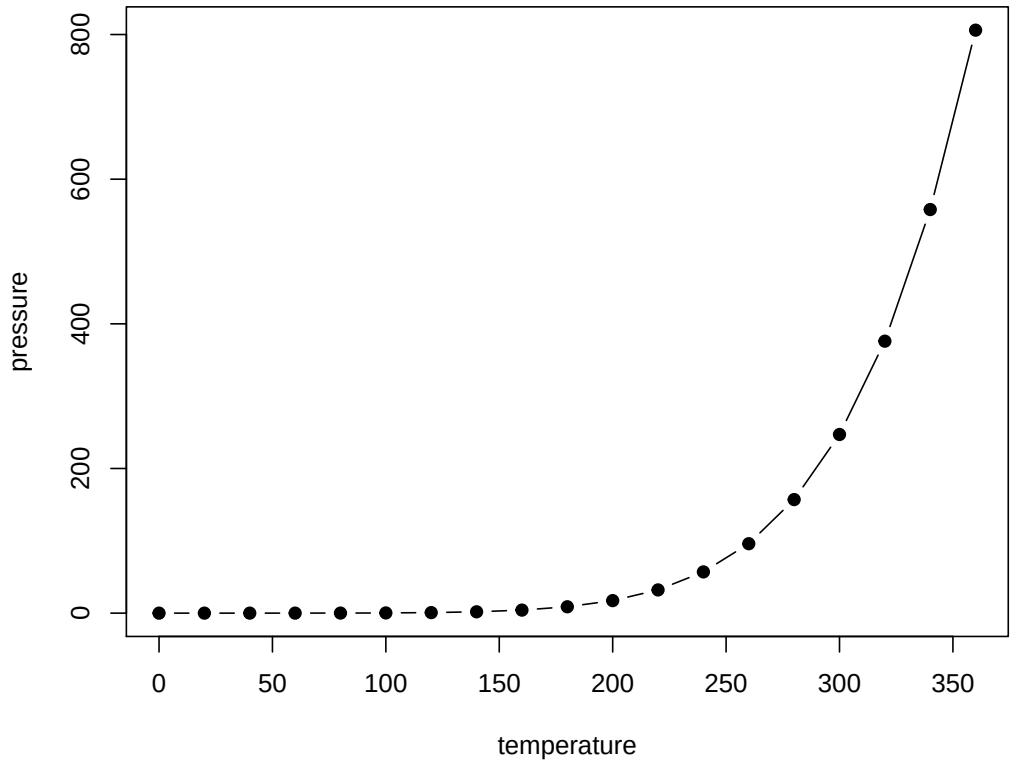

Figure 2.1: Here is a nice figure!

Table 2.1: Here is a nice table!

Sepal.Length	Sepal.Width	Petal.Length	Petal.Width	Species
5.1	3.5	1.4	0.2	setosa
4.9	3.0	1.4	0.2	setosa
4.7	3.2	1.3	0.2	setosa
4.6	3.1	1.5	0.2	setosa
5.0	3.6	1.4	0.2	setosa
5.4	3.9	1.7	0.4	setosa
4.6	3.4	1.4	0.3	setosa
5.0	3.4	1.5	0.2	setosa
4.4	2.9	1.4	0.2	setosa
4.9	3.1	1.5	0.1	setosa
5.4	3.7	1.5	0.2	setosa
4.8	3.4	1.6	0.2	setosa
4.8	3.0	1.4	0.1	setosa
4.3	3.0	1.1	0.1	setosa
5.8	4.0	1.2	0.2	setosa
5.7	4.4	1.5	0.4	setosa
5.4	3.9	1.3	0.4	setosa
5.1	3.5	1.4	0.3	setosa
5.7	3.8	1.7	0.3	setosa
5.1	3.8	1.5	0.3	setosa

Chapter 3

Linear models and matrix algebra

3.1 Exercises

Solutions to exercises can be found in appendix B

Chapter 4

Linear and non linear logistic regression

4.1 Exercises

Solutions to exercises can be found in appendix C.

Chapter 5

Nearest neighbours

5.1 Example one

5.2 Example two

5.3 Exercises

Solutions to exercises can be found in appendix D.

Chapter 6

Decision trees and random forests

6.1 Exercises

Solutions to exercises can be found in appendix E.

Chapter 7

Support vector machines

7.1 Exercises

Solutions to exercises can be found in appendix F

Chapter 8

Artificial neural networks

8.1 Exercises

Solutions to exercises can be found in appendix G.

Chapter 9

Dimensionality reduction

9.1 Linear Dimensionality Reduction

9.1.1 Principle Component Analysis

9.1.2 Horeshoe effect

9.2 Nonlinear Dimensionality Reduction

9.2.1 t-SNE

9.2.2 Gaussian Process Latent Variable Models

9.2.3 GPLVMs with informative priors

9.3 Exercises

Solutions to exercises can be found in appendix H.

Chapter 10

Clustering

10.1 Introduction

What is clustering - add figure showing idea of minimizing intra-cluster variation and maximizing inter-cluster variation.

Hierarchic (produce dendrogram) vs partitioning methods

- Hierarchic agglomerative
- k-means
- DBSCAN

10.2 Distance metrics

dist function cor as.dist(1-cor(x))

Minkowski distance:

$$distance\,(x, y, p) = \left(\sum_{i=1}^{n} abs(x_i - y_i)^p \right)^{1/p} \tag{10.1}$$

Graphical explanation of euclidean, manhattan and max (Chebyshev?)

10.2.1 Image segmentation

10.3 Hierarchic agglomerative

Get to see clusters for all number of clusters k

produce step by step figure to show how objects are linked

10.3.1 Linkage algorithms

Make one section panel of three dendrograms one table

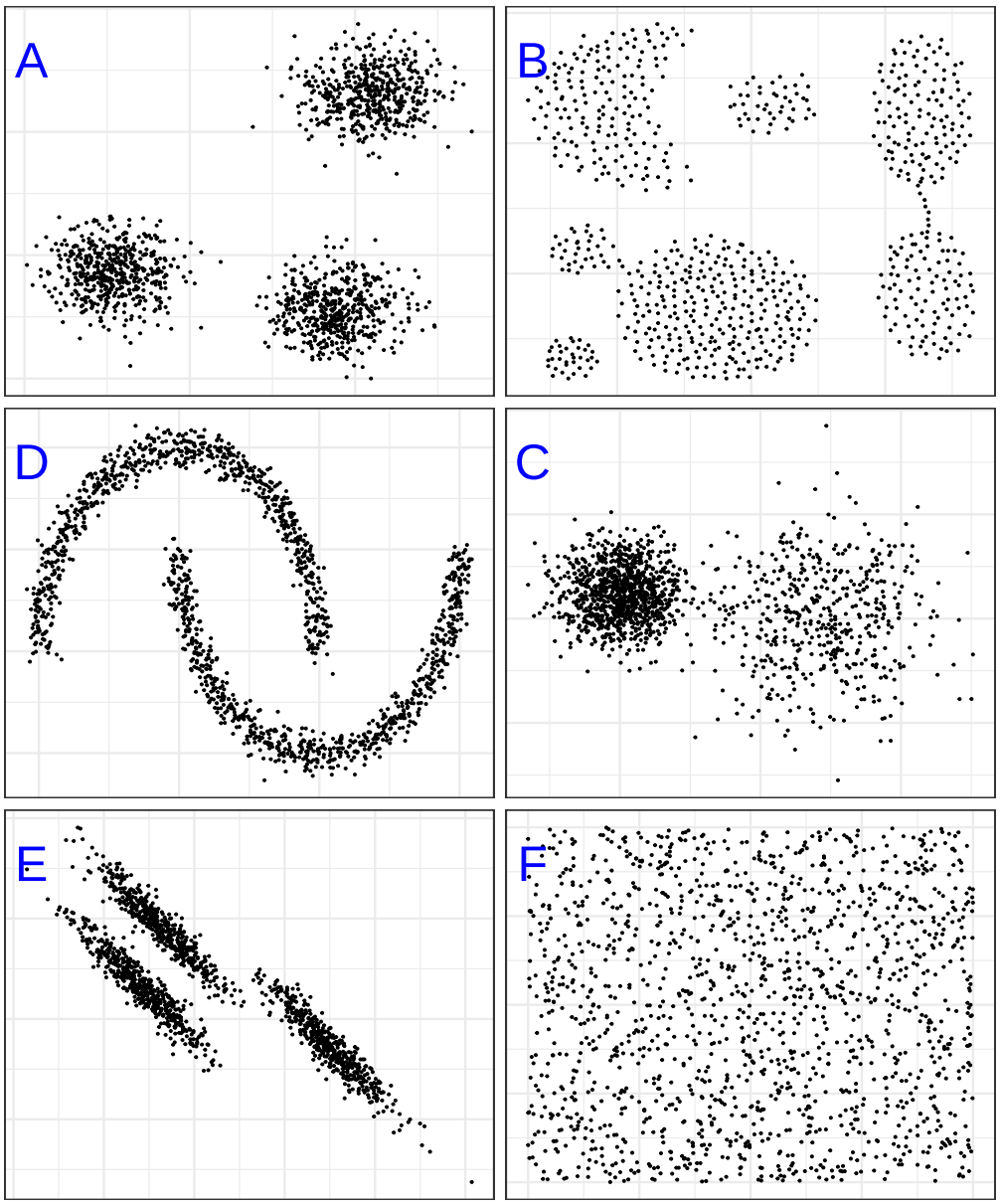

Figure 10.1: Example clusters. **A**, *blobs*; **B**, *aggregation* [@Gionis2007]; **C**, *noisy moons*; **D**, *different density*; **E**, *anisotropic distributions*; **F**, *no structure*.

Table 10.1: Example distance matrix

	A	B	C	D
B	2			
C	6	5		
D	10	10	5	
E	9	8	3	4

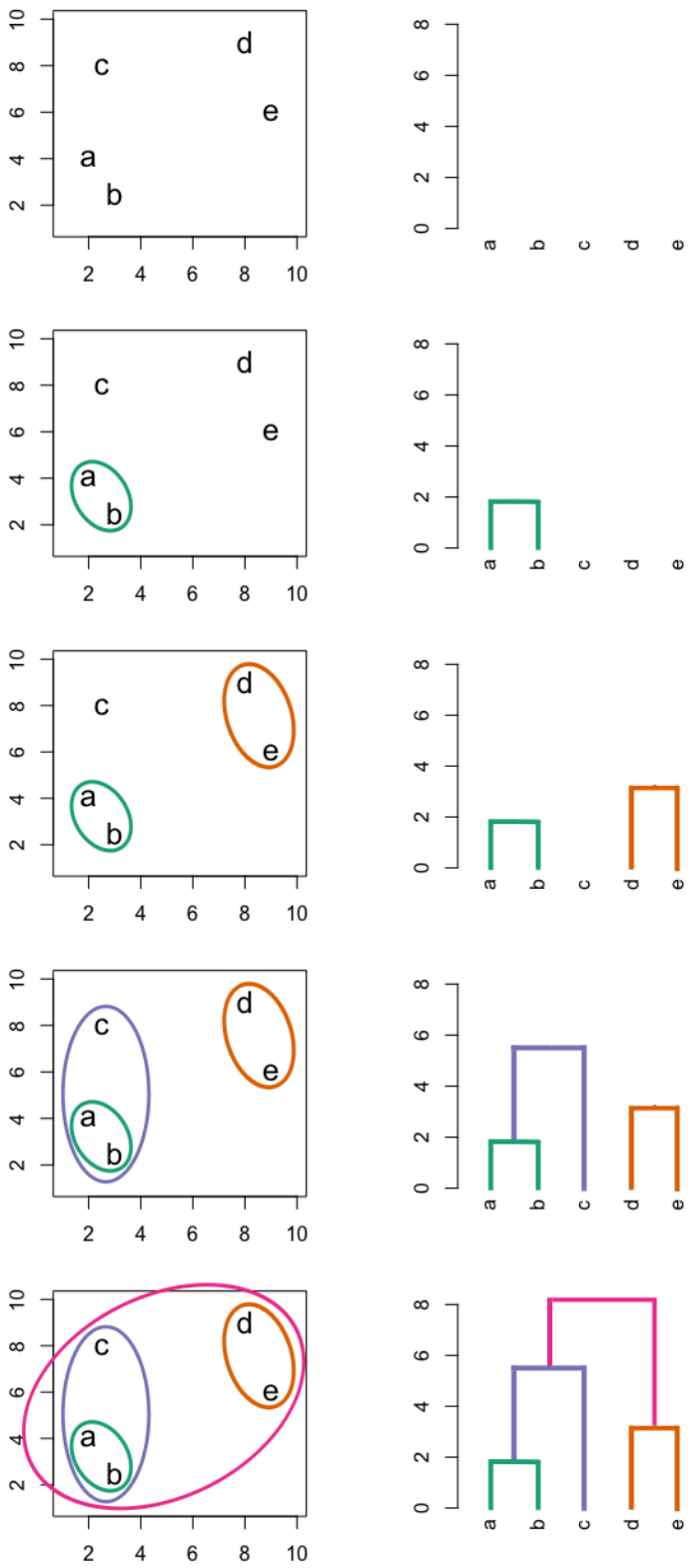

Figure 10.2: Building a dendrogram using hierarchic agglomerative clustering.

Table 10.2: Merge distances for objects in the example distance matrix using three different linkage methods.

Groups	Single	Complete	Average
A,B,C,D,E	0	0	0
(A,B),C,D,E	2	2	2
(A,B),(C,E),D	3	3	3
(A,B)(C,D,E)	4	5	4.5
(A,B,C,D,E)	5	10	8

Single linkage - nearest neighbours linkage Complete linkage - furthest neighbours linkage Average linkage - UPGMA (Unweighted Pair Group Method with Arithmetic Mean)

10.3.2 Example: clustering synthetic data sets

10.3.2.1 Step-by-step instructions

1. Load required packages.

```
library(RColorBrewer)
library(dendextend)
```

```
##
## ---------------------
## Welcome to dendextend version 1.5.2
## Type citation('dendextend') for how to cite the package.
##
## Type browseVignettes(package = 'dendextend') for the package vignette.
## The github page is: https://github.com/talgalili/dendextend/
##
## Suggestions and bug-reports can be submitted at: https://github.com/talgalili/dendextend/issues
## Or contact: <tal.galili@gmail.com>
##
##  To suppress this message use:  suppressPackageStartupMessages(library(dendextend))
## ---------------------
```

```
##
## Attaching package: 'dendextend'
```

```
## The following object is masked from 'package:ggdendro':
##
##     theme_dendro
```

```
## The following object is masked from 'package:stats':
##
##     cutree
```

```
library(ggplot2)
library(GGally)
```

2. Retrieve a palette of eight colours.

```
cluster_colours <- brewer.pal(8,"Dark2")
```

3. Read in data for **blobs** example.

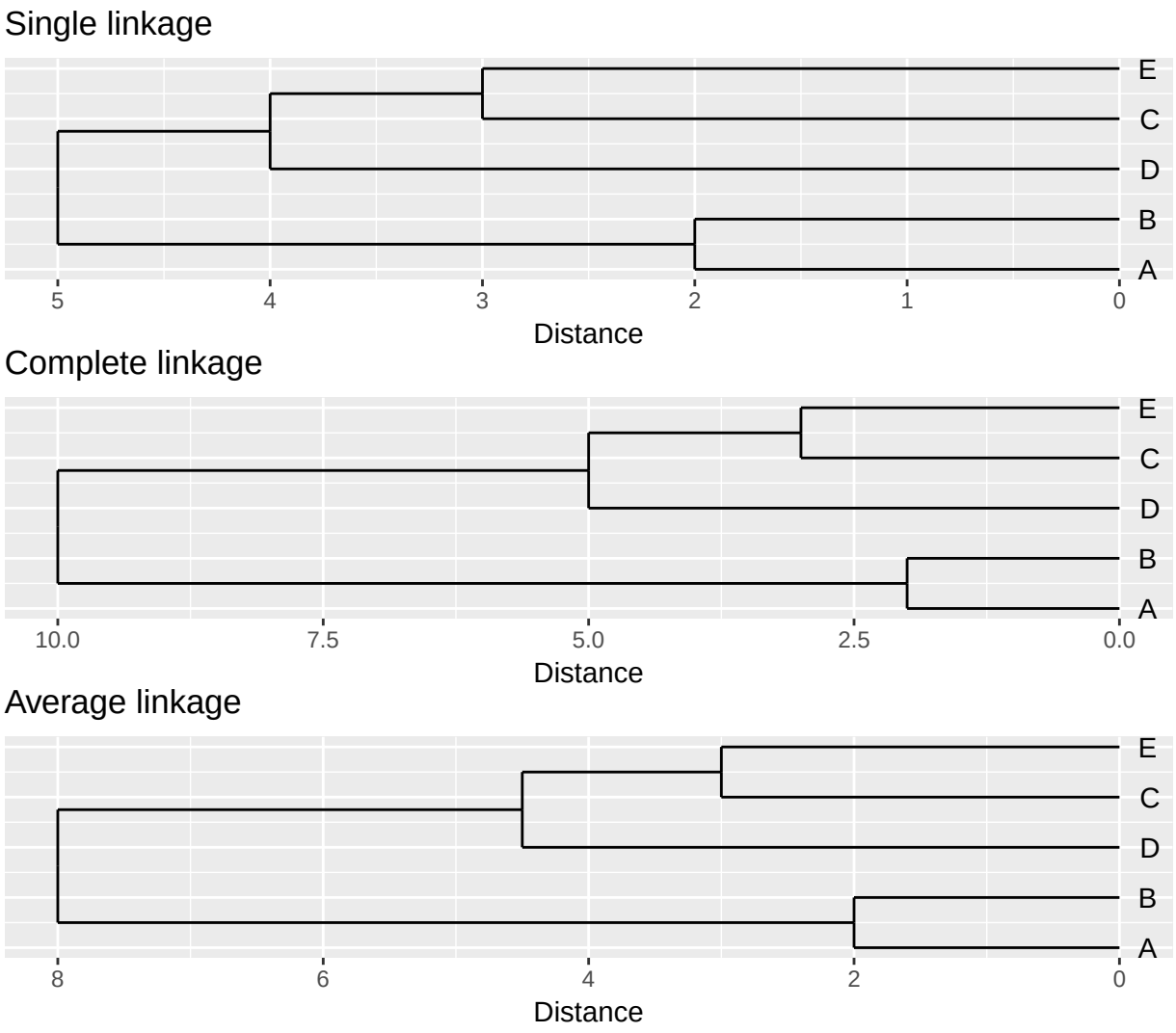

Figure 10.3: Dendrograms for the example distance matrix using three different linkage methods.

```
blobs <- read.csv("data/example_clusters/blobs.csv", header=F)
```

4. Create distance matrix using Euclidean distance metric.

```
d <- dist(blobs[,1:2])
```

5. Perform hierarchical clustering using the **average** agglomeration method and convert the result to an object of class **dendrogram**. A **dendrogram** object can be edited using the advanced features of the **dendextend** package.

```
dend <- as.dendrogram(hclust(d, method="average"))
```

6. Cut the tree into three clusters

```
clusters <- cutree(dend,3,order_clusters_as_data=F)
```

7. The vector **clusters** contains the cluster membership (in this case *1*, *2* or *3*) of each observation (data point) in the order they appear on the dendrogram. We can use this vector to colour the branches of the dendrogram by cluster.

```
dend <- color_branches(dend, clusters=clusters, col=cluster_colours[1:3])
```

8. We can use the **labels** function to annotate the leaves of the dendrogram. However, it is not possible to create legible labels for the 1,500 leaves in our example dendrogram, so we will set the label for each leaf to an empty string.

```
labels(dend) <- rep("", length(blobs[,1]))
```

9. If we want to plot the dendrogram using **ggplot**, we must convert it to an object of class **ggdend**.

```
ggd <- as.ggdend(dend)
```

10. The **nodes** attribute of **ggd** is a data.frame of parameters related to the plotting of dendogram nodes. The **nodes** data.frame contains some NAs which will generate warning messages when **ggd** is processed by **ggplot**. Since we are not interested in annotating dendrogram nodes, the easiest option here is to delete all of the rows of **nodes**.

```
ggd$nodes <- ggd$nodes[!(1:length(ggd$nodes[,1])),]
```

11. We can use the cluster membership of each observation contained in the vector **clusters** to assign colours to the data points of a scatterplot. However, first we need to reorder the vector so that the cluster memberships are in the same order that the observations appear in the data.frame of observations. Fortunately the names of the elements of the vector are the indices of the observations in the data.frame and so reordering can be accomplished in one line.

```
clusters <- clusters[order(as.numeric(names(clusters)))]
```

12. We are now ready to plot a dendrogram and scatterplot. We will use the **ggmatrix** function from the **GGally** package to place the plots side-by-side.

```
plotList <- list(ggplot(ggd),
                 ggplot(blobs, aes(V1,V2)) +
                   geom_point(col=cluster_colours[clusters], size=0.2)
                 )

pm <- ggmatrix(
  plotList, nrow=1, ncol=2, showXAxisPlotLabels = F, showYAxisPlotLabels = F,
  xAxisLabels=c("dendrogram", "scatter plot")
) + theme_bw()
```

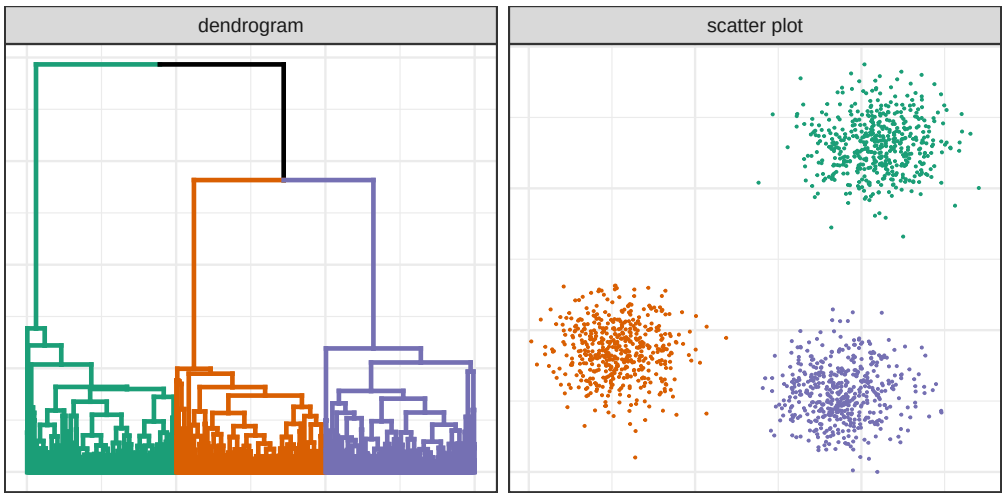

Figure 10.4: Hierarchical clustering of the blobs data set.

```
pm
```

10.3.2.2 Clustering of other synthetic data sets

```
aggregation <- read.table("data/example_clusters/aggregation.txt")
noisy_moons <- read.csv("data/example_clusters/noisy_moons.csv", header=F)
diff_density <- read.csv("data/example_clusters/different_density.csv", header=F)
aniso <- read.csv("data/example_clusters/aniso.csv", header=F)
no_structure <- read.csv("data/example_clusters/no_structure.csv", header=F)

hclust_plots <- function(data_set, n){
  d <- dist(data_set[,1:2])
  dend <- as.dendrogram(hclust(d, method="average"))
  clusters <- cutree(dend,n,order_clusters_as_data=F)
  dend <- color_branches(dend, clusters=clusters, col=cluster_colours[1:n])
  clusters <- clusters[order(as.numeric(names(clusters)))]
  labels(dend) <- rep("", length(data_set[,1]))
  ggd <- as.ggdend(dend)
  ggd$nodes <- ggd$nodes[!(1:length(ggd$nodes[,1])),]
  plotPair <- list(ggplot(ggd),
    ggplot(data_set, aes(V1,V2)) +
      geom_point(col=cluster_colours[clusters], size=0.2))
  return(plotPair)
}

plotList <- c(
  hclust_plots(aggregation, 7),
  hclust_plots(noisy_moons, 2),
  hclust_plots(diff_density, 2),
  hclust_plots(aniso, 3),
  hclust_plots(no_structure, 3)
)
```

```
pm <- ggmatrix(
  plotList, nrow=5, ncol=2, showXAxisPlotLabels = F, showYAxisPlotLabels = F,
  xAxisLabels=c("dendrogram", "scatter plot"),
  yAxisLabels=c("aggregation", "noisy moons", "different density", "anisotropic", "no structure")
) + theme_bw()

pm
```

10.3.3 Example: gene expression profiling of human tissues

10.3.3.1 Basics

Load required libraries

```
library(RColorBrewer)
library(dendextend)
```

Load data

```
load("data/tissues_gene_expression/tissuesGeneExpression.rda")
```

Inspect data

```
table(tissue)
```

```
## tissue
##  cerebellum       colon endometrium hippocampus      kidney       liver
##          38          34          15          31          39          26
##    placenta
##           6
```

```
dim(e)
```

```
## [1] 22215   189
```

Compute distance between each sample

```
d <- dist(t(e))
```

perform hierarchical clustering

```
hc <- hclust(d, method="average")
plot(hc, labels=tissue, cex=0.5, hang=-1, xlab="", sub="")
```

10.3.3.2 Colour labels

use dendextend library to plot dendrogram with colour labels

```
tissue_type <- unique(tissue)
dend <- as.dendrogram(hc)
dend_colours <- brewer.pal(length(unique(tissue)),"Dark2")
names(dend_colours) <- tissue_type
labels(dend) <- tissue[order.dendrogram(dend)]
labels_colors(dend) <- dend_colours[tissue][order.dendrogram(dend)]
labels_cex(dend) = 0.5
plot(dend, horiz=T)
```

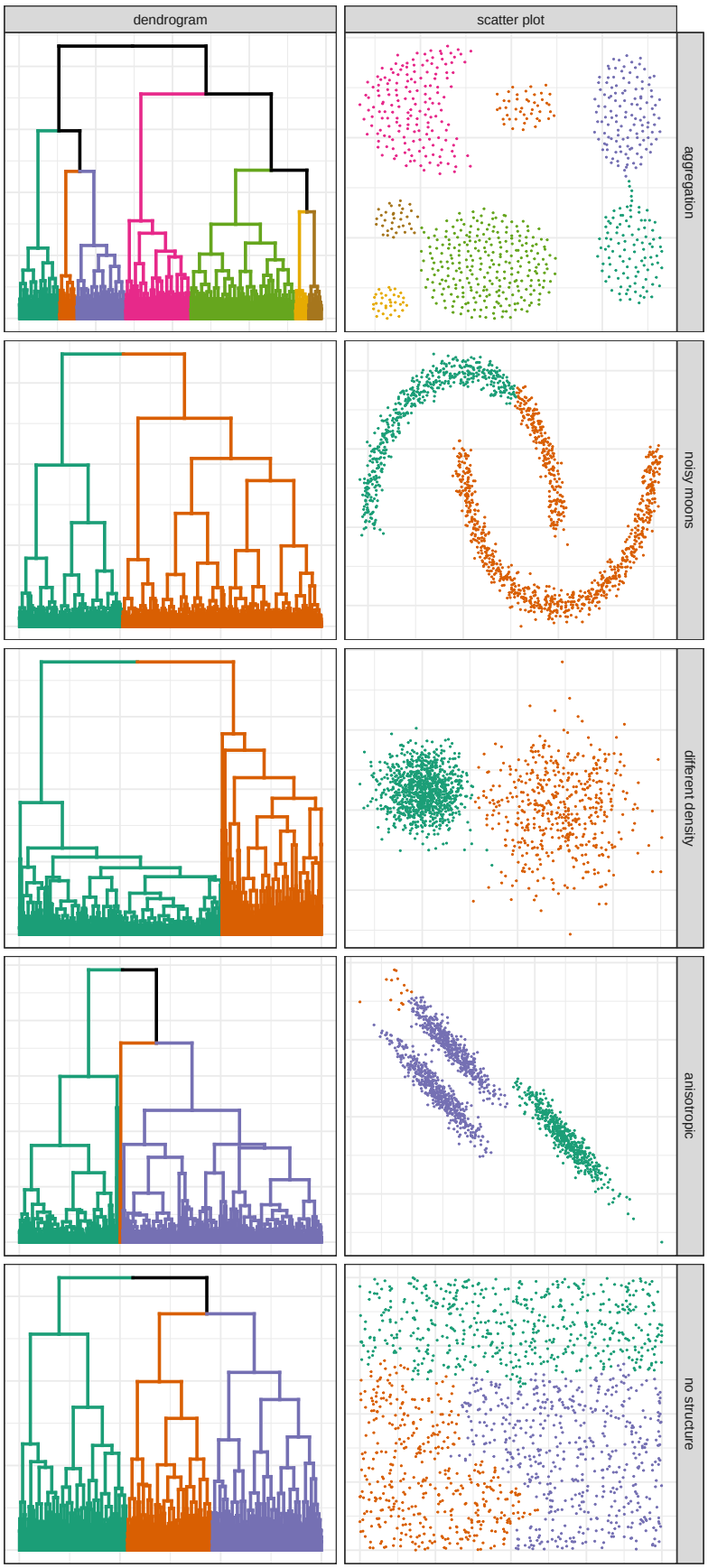

Figure 10.5: Hierarchical clustering of synthetic data-sets.

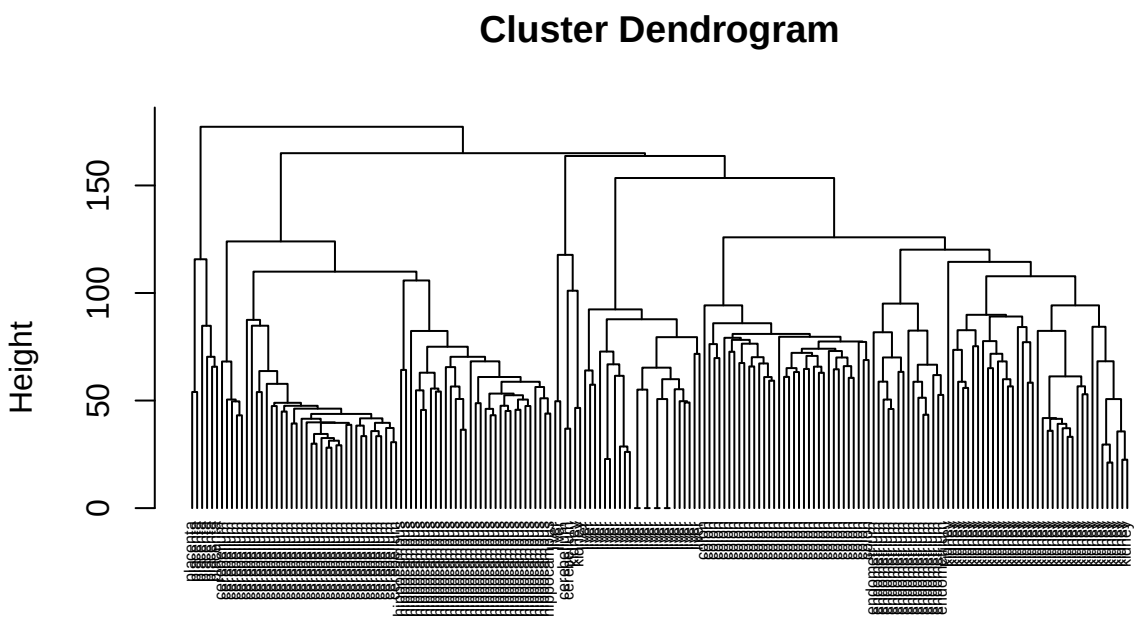

Figure 10.6: Clustering of tissue samples based on gene expression profiles.

10.3.3.3 Defining clusters by cutting tree

Define clusters by cutting tree at a specific height

```
plot(dend, horiz=T)
abline(v=125, lwd=2, lty=2, col="blue")
```

```
hclusters <- cutree(dend, h=125)
table(tissue, cluster=hclusters)
```

```
##              cluster
## tissue         1  2  3  4  5  6
##   cerebellum   0 36  0  0  2  0
##   colon        0  0 34  0  0  0
##   endometrium 15  0  0  0  0  0
##   hippocampus  0 31  0  0  0  0
##   kidney      37  0  0  0  2  0
##   liver        0  0  0 24  2  0
##   placenta     0  0  0  0  0  6
```

Select a specific number of clusters.

```
plot(dend, horiz=T)
abline(v = heights_per_k.dendrogram(dend)["8"], lwd = 2, lty = 2, col = "blue")
```

```
hclusters <- cutree(dend, k=8)
table(tissue, cluster=hclusters)
```

```
##              cluster
## tissue         1  2  3  4  5  6  7  8
##   cerebellum   0 31  0  0  2  0  5  0
##   colon        0  0 34  0  0  0  0  0
##   endometrium  0  0  0  0  0 15  0  0
##   hippocampus  0 31  0  0  0  0  0  0
```

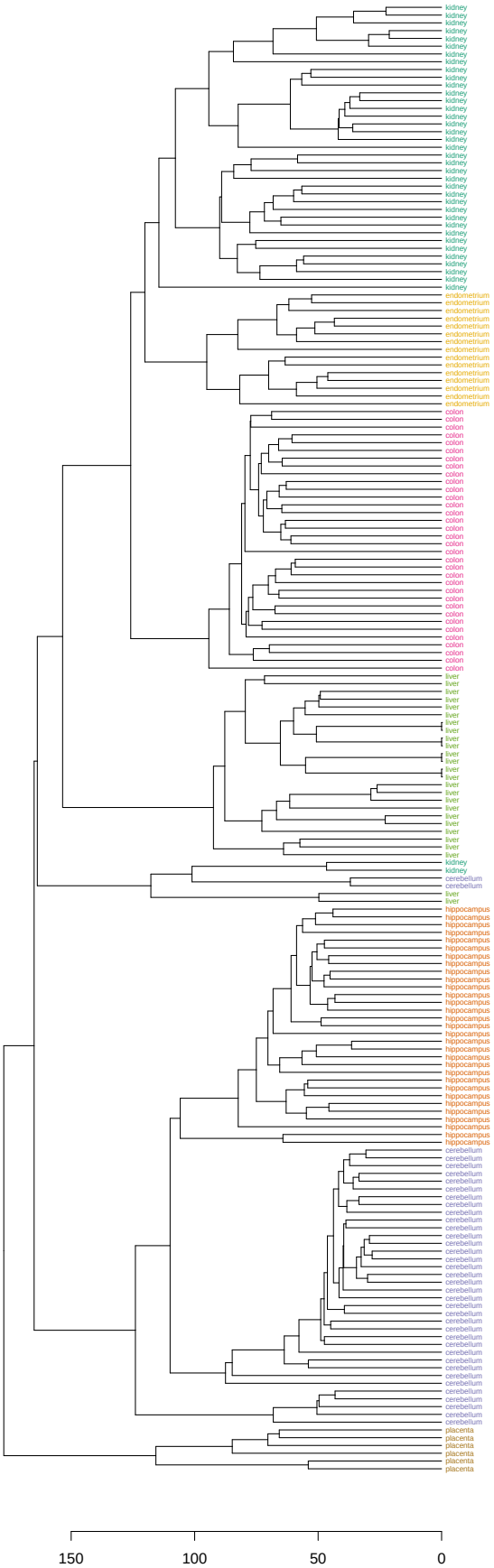

Figure 10.7: Clustering of tissue samples based on gene expression profiles with labels coloured by tissue type.

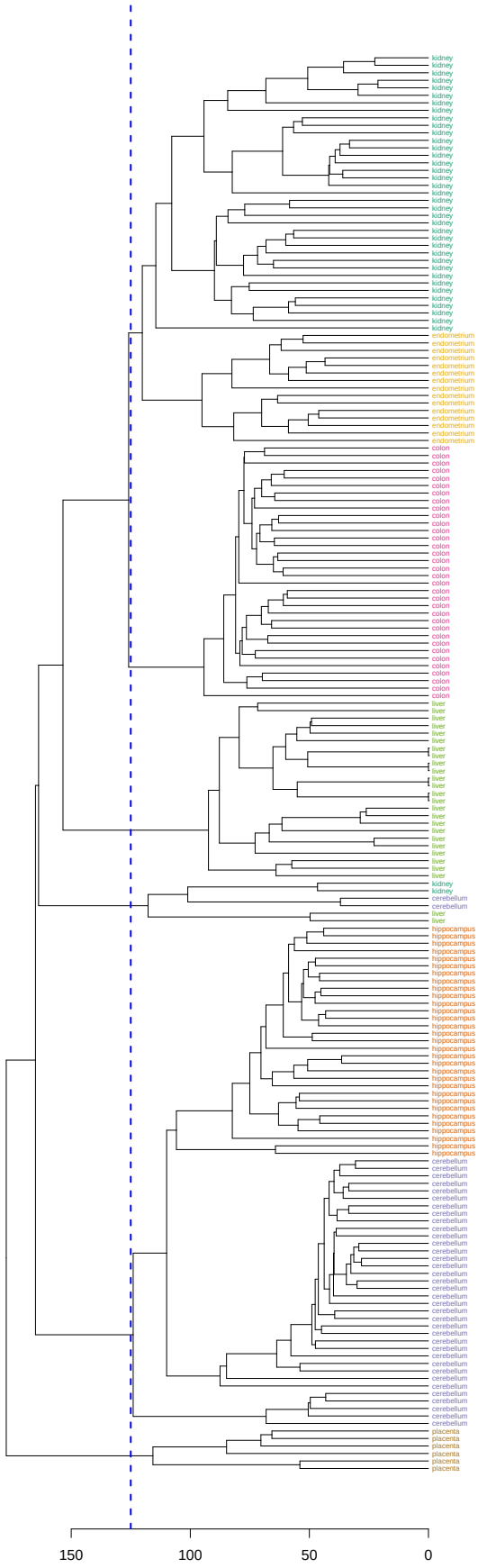

Figure 10.8: Clusters found by cutting tree at a height of 125

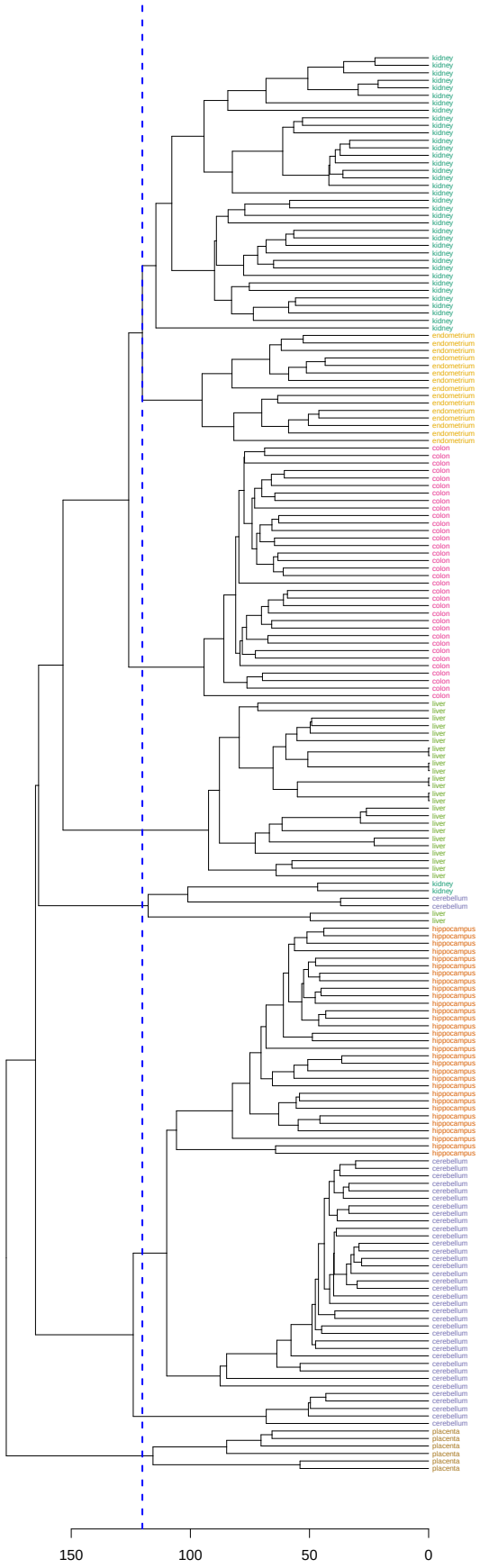

Figure 10.9: Selection of eight clusters from the dendogram

```
##   kidney      37  0  0  0  2  0  0  0
##   liver        0  0  0 24  2  0  0  0
##   placenta     0  0  0  0  0  0  0  6
```

10.3.3.4 Heatmap

Base R provides a **heatmap** function, but we will use the more advanced **heatmap.2** from the **gplots** package.

```
library(gplots)
```

```
##
## Attaching package: 'gplots'
```

```
## The following object is masked from 'package:stats':
##
##     lowess
```

Define a colour palette (also known as a lookup table).

```
heatmap_colours <- colorRampPalette(brewer.pal(9, "PuBuGn"))(100)
```

Calculate the variance of each gene.

```
geneVariance <- apply(e,1,var)
```

Find the row numbers of the 40 genes with the highest variance.

```
idxTop40 <- order(-geneVariance)[1:40]
```

Define colours for tissues.

```
tissueColours <- palette(brewer.pal(8, "Dark2"))[as.numeric(as.factor(tissue))]
```

Plot heatmap.

```
heatmap.2(e[idxTop40,], labCol=tissue, trace="none",
          ColSideColors=tissueColours, col=heatmap_colours)
```

10.4 K-means

10.4.1 Algorithm

Pseudocode

to illustrate range of different types of data that can be clustered - image segmentation

The default setting of the **kmeans** function is to perform a maximum of 10 iterations and if the algorithm fails to converge a warning is issued. The maximum number of iterations is set with the argument **iter.max**.

10.4.2 Choosing initial cluster centres

```
library(RColorBrewer)
point_shapes <- c(15,17,19)
point_colours <- brewer.pal(3,"Dark2")
point_size = 1.5
```

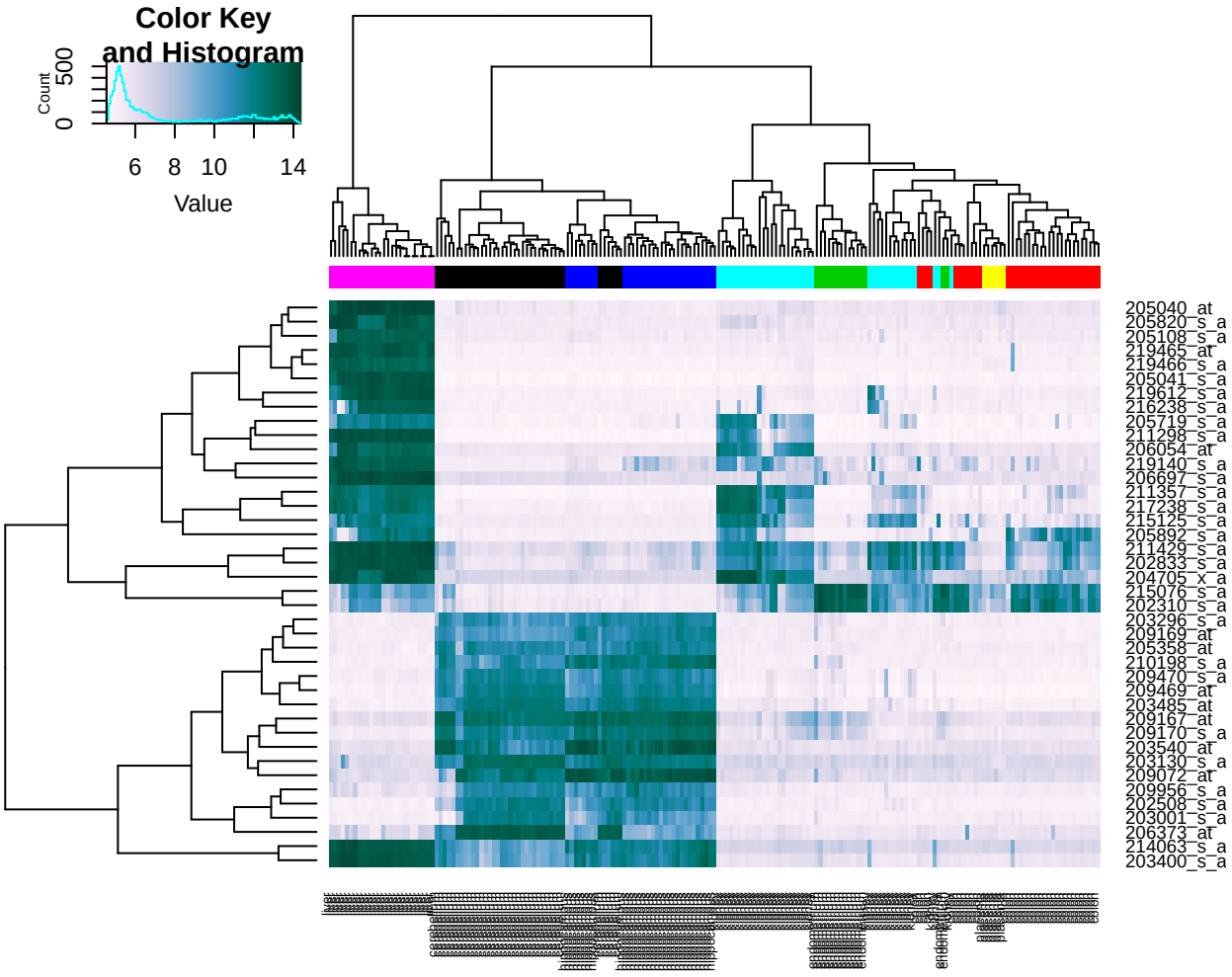

Figure 10.10: Heatmap of the expression of the 40 genes with the highest variance.

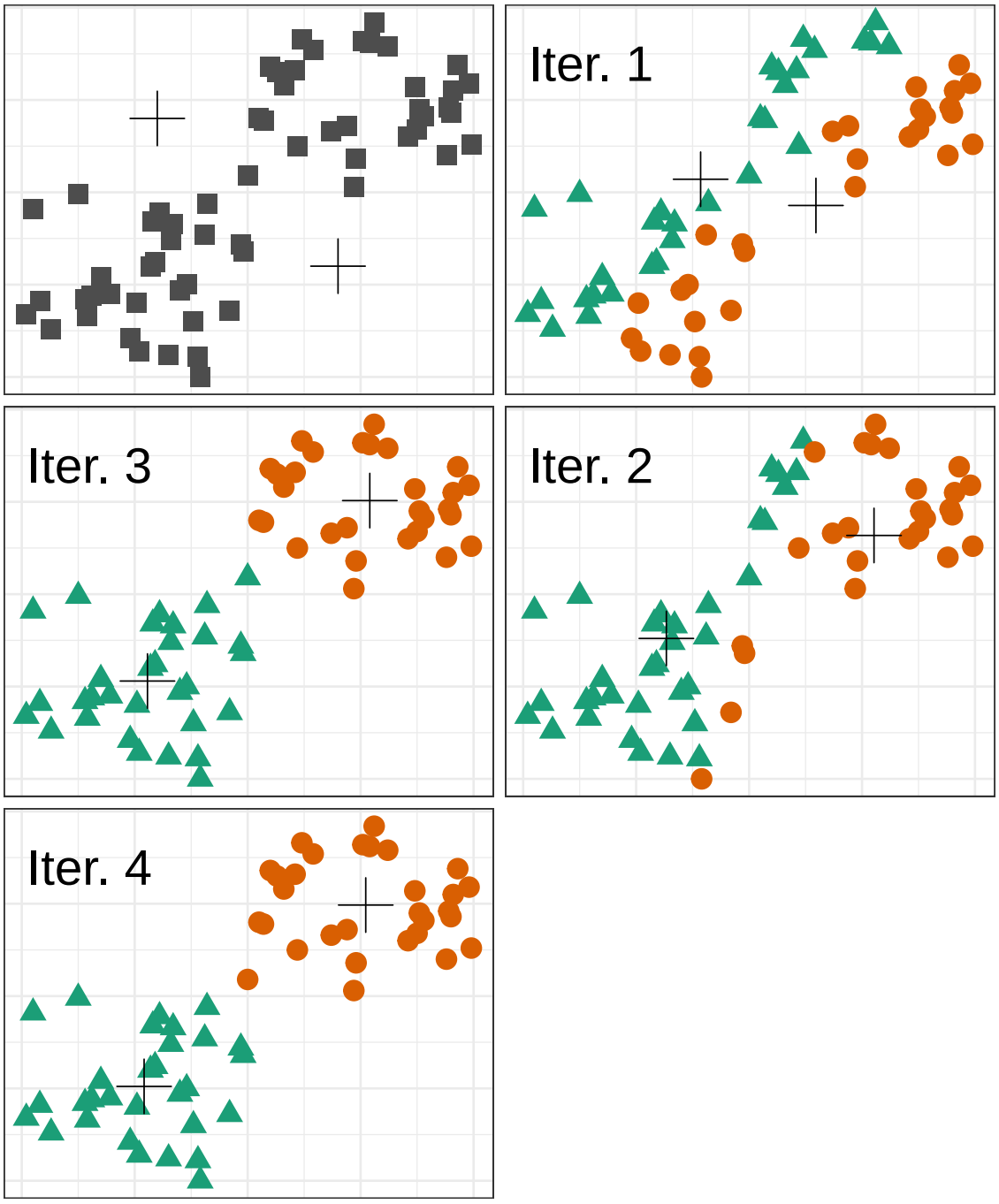

Figure 10.11: Iterations of the k-means algorithm

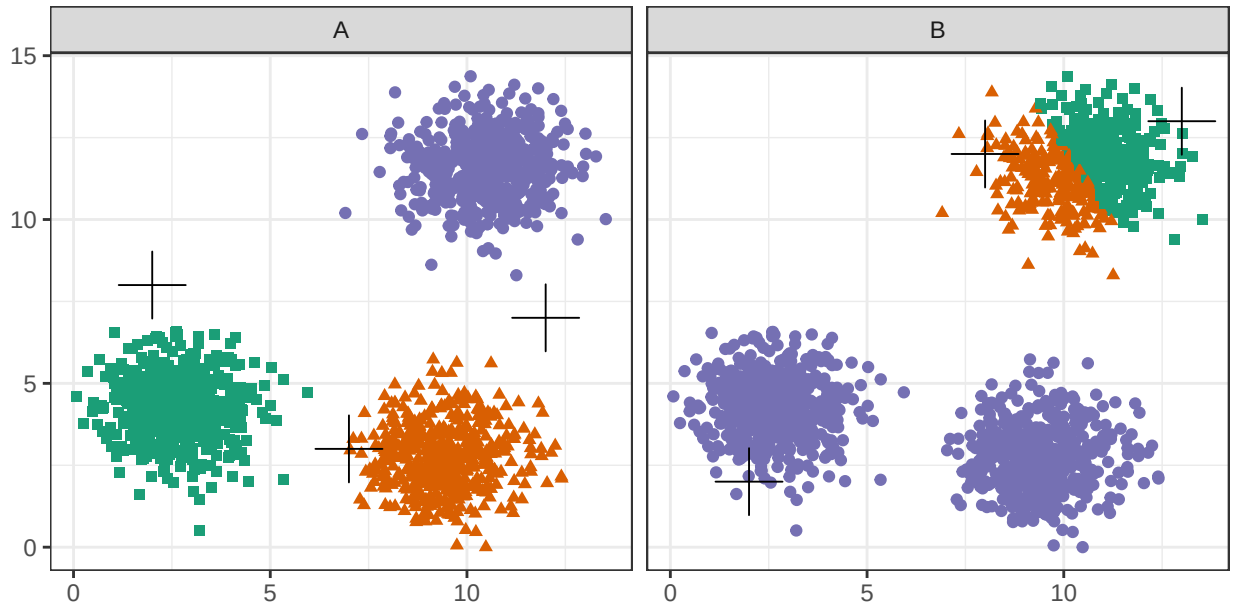

Figure 10.12: Initial centres determine clusters. The starting centres are shown as crosses. **A**, real clusters found; **B**, convergence to a local minimum.

```
center_point_size = 8

blobs <- as.data.frame(read.csv("data/example_clusters/blobs.csv", header=F))

good_centres <- as.data.frame(matrix(c(2,8,7,3,12,7), ncol=2, byrow=T))
bad_centres <- as.data.frame(matrix(c(13,13,8,12,2,2), ncol=2, byrow=T))

good_result <- kmeans(blobs[,1:2], centers=good_centres)
bad_result <- kmeans(blobs[,1:2], centers=bad_centres)

plotList <- list(
ggplot(blobs, aes(V1,V2)) +
  geom_point(col=point_colours[good_result$cluster], shape=point_shapes[good_result$cluster],
             size=point_size) +
  geom_point(data=good_centres, aes(V1,V2), shape=3, col="black", size=center_point_size) +
  theme_bw(),
ggplot(blobs, aes(V1,V2)) +
  geom_point(col=point_colours[bad_result$cluster], shape=point_shapes[bad_result$cluster],
             size=point_size) +
  geom_point(data=bad_centres, aes(V1,V2), shape=3, col="black", size=center_point_size) +
  theme_bw()
)

pm <- ggmatrix(
  plotList, nrow=1, ncol=2, showXAxisPlotLabels = T, showYAxisPlotLabels = T,
  xAxisLabels=c("A", "B")
) + theme_bw()

pm
```

Convergence to a local minimum can be avoided by starting the algorithm multiple times, with different random centres. The **nstart** argument to the **k-means** function can be used to specify the number of random sets and optimal solution will be selected automatically.

10.4.3 Choosing k

```
point_colours <- brewer.pal(9,"Set1")
k <- 1:9
res <- lapply(k, function(i){kmeans(blobs[,1:2], i, nstart=50)})

plotList <- lapply(k, function(i){
  ggplot(blobs, aes(V1, V2)) +
    geom_point(col=point_colours[res[[i]]$cluster], size=1) +
    geom_point(data=as.data.frame(res[[i]]$centers), aes(V1,V2), shape=3, col="black", size=5) +
    annotate("text", x=2, y=13, label=paste("k=", i, sep=""), size=8, col="black") +
    theme_bw()
}
)

pm <- ggmatrix(
  plotList, nrow=3, ncol=3, showXAxisPlotLabels = T, showYAxisPlotLabels = T
) + theme_bw()

pm
```

```
tot_withinss <- sapply(k, function(i){res[[i]]$tot.withinss})
qplot(k, tot_withinss, geom=c("point", "line"),
      ylab="Total within-cluster sum of squares") + theme_bw()
```

N.B. we have set `nstart=50` to run the algorithm 50 times, starting from different, random sets of centroids.

10.4.4 Example: clustering synthetic data sets

Let's see how k-means performs on the other toy data sets. First we will define some variables and functions we will use in the analysis of all data sets.

```
k=1:9
point_shapes <- c(15,17,19,5,6,0,1)
point_colours <- brewer.pal(7,"Dark2")
point_size = 1.5
center_point_size = 8

plot_tot_withinss <- function(kmeans_output){
  tot_withinss <- sapply(k, function(i){kmeans_output[[i]]$tot.withinss})
  qplot(k, tot_withinss, geom=c("point", "line"),
        ylab="Total within-cluster sum of squares") + theme_bw()
}

plot_clusters <- function(data_set, kmeans_output, num_clusters){
    ggplot(data_set, aes(V1,V2)) +
    geom_point(col=point_colours[kmeans_output[[num_clusters]]$cluster],
               shape=point_shapes[kmeans_output[[num_clusters]]$cluster],
               size=point_size) +
```

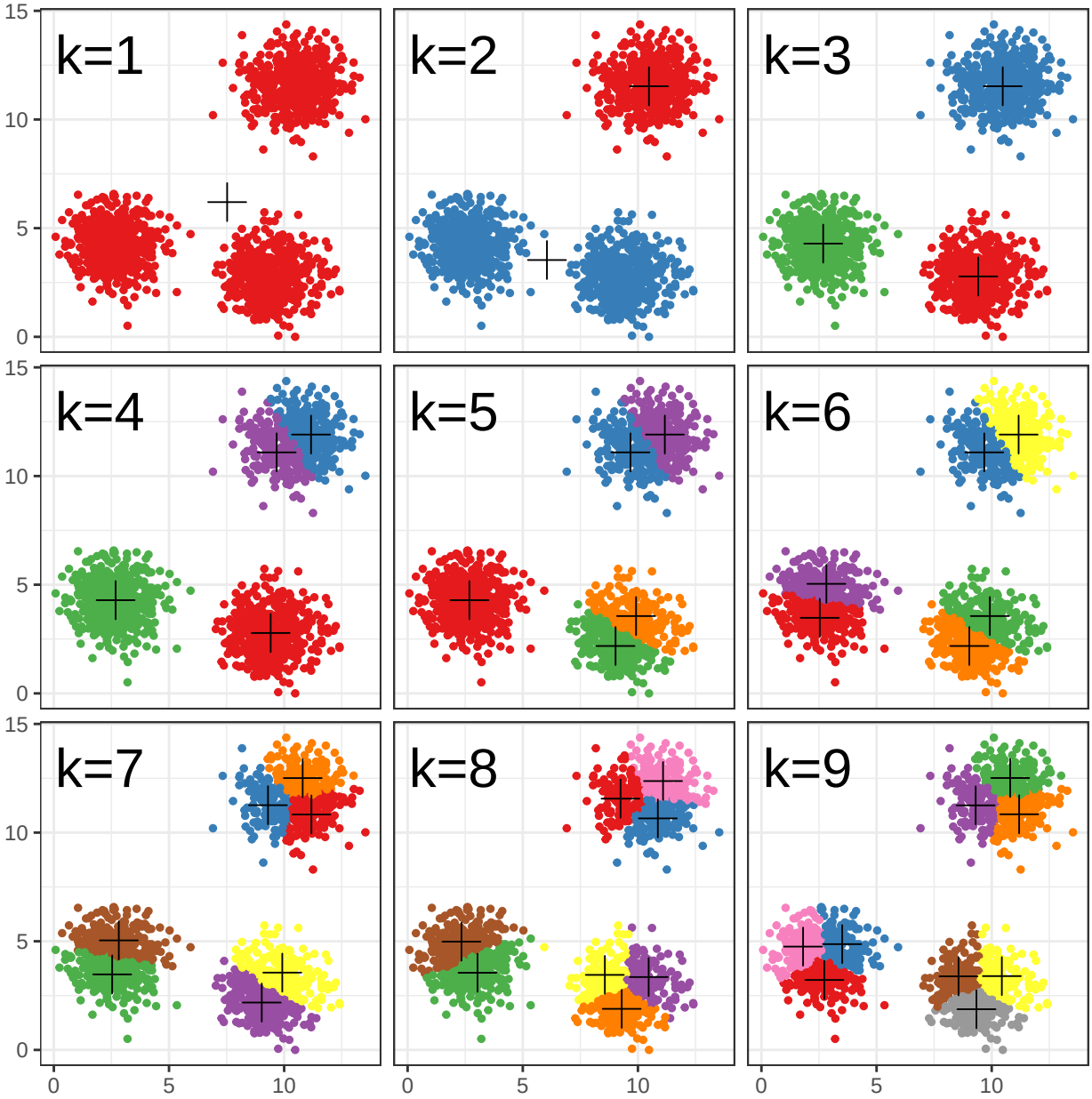

Figure 10.13: K-means clustering of the blobs data set using a range of values of k from 1-9. Cluster centres indicated with a cross.

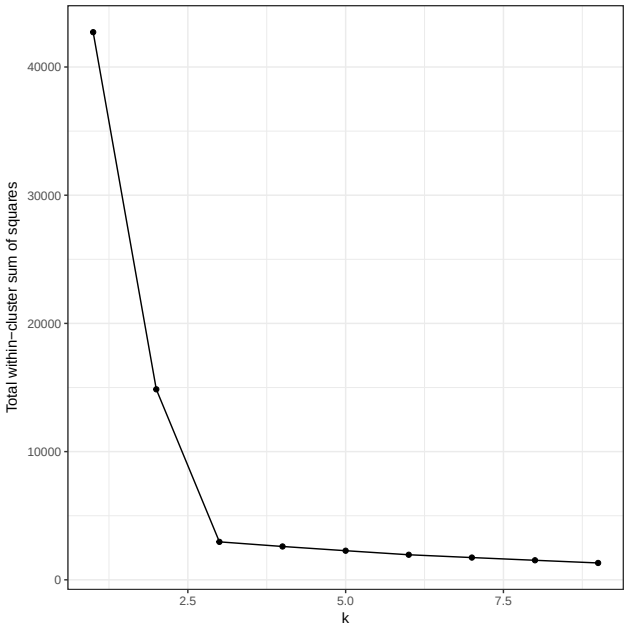

Figure 10.14: Variance within the clusters. Total within-cluster sum of squares plotted against k.

```
    geom_point(data=as.data.frame(kmeans_output[[num_clusters]]$centers), aes(V1,V2),
               shape=3,col="black",size=center_point_size) +
    theme_bw()
}
```

10.4.4.1 Aggregation

```
aggregation <- as.data.frame(read.table("data/example_clusters/aggregation.txt"))
res <- lapply(k, function(i){kmeans(aggregation[,1:2], i, nstart=50)})
plot_tot_withinss(res)
```

```
plotList <- list(
  plot_clusters(aggregation, res, 3),
  plot_clusters(aggregation, res, 7)
)
pm <- ggmatrix(
  plotList, nrow=1, ncol=2, showXAxisPlotLabels = T, showYAxisPlotLabels = T,
  xAxisLabels=c("k=3", "k=7")
) + theme_bw()
pm
```

10.4.4.2 Noisy moons

```
noisy_moons <- read.csv("data/example_clusters/noisy_moons.csv", header=F)
res <- lapply(k, function(i){kmeans(noisy_moons[,1:2], i, nstart=50)})
plot_tot_withinss(res)
```

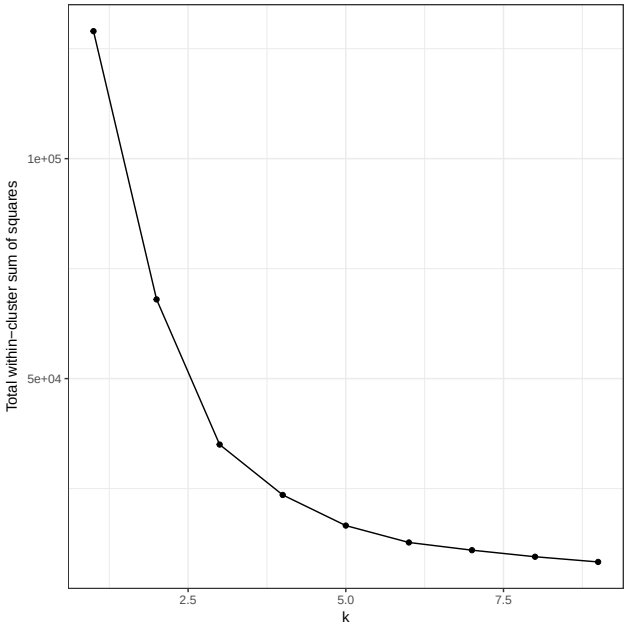

Figure 10.15: K-means clustering of the aggregation data set: variance within clusters.

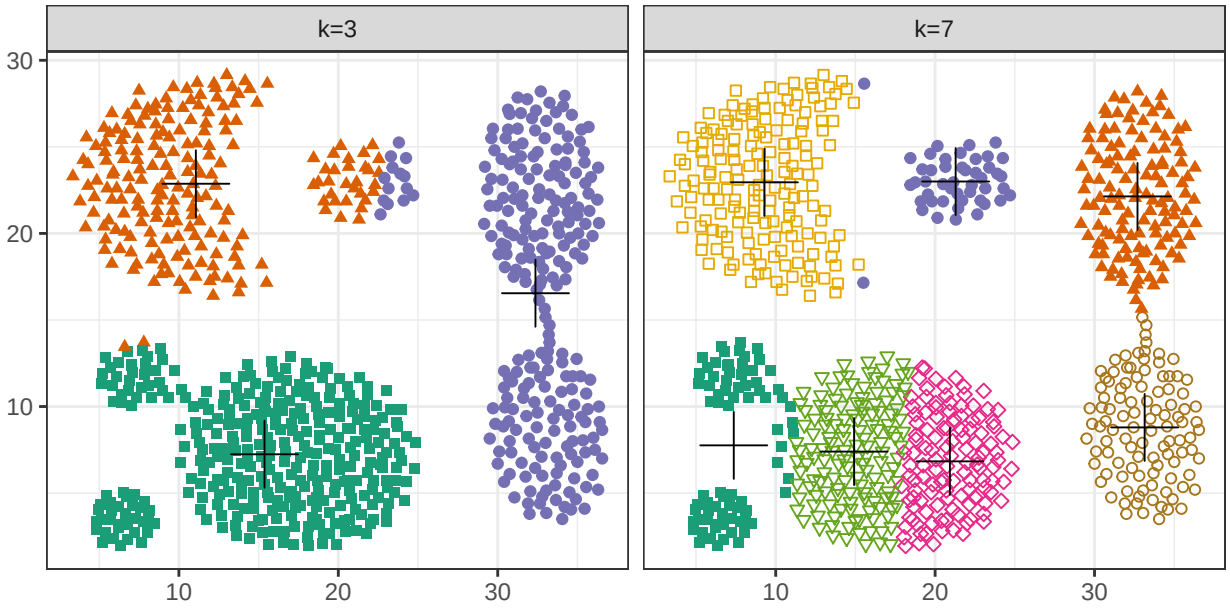

Figure 10.16: K-means clustering of the aggregation data set: scatterplots of clusters for k=3 and k=7. Cluster centres indicated with a cross.

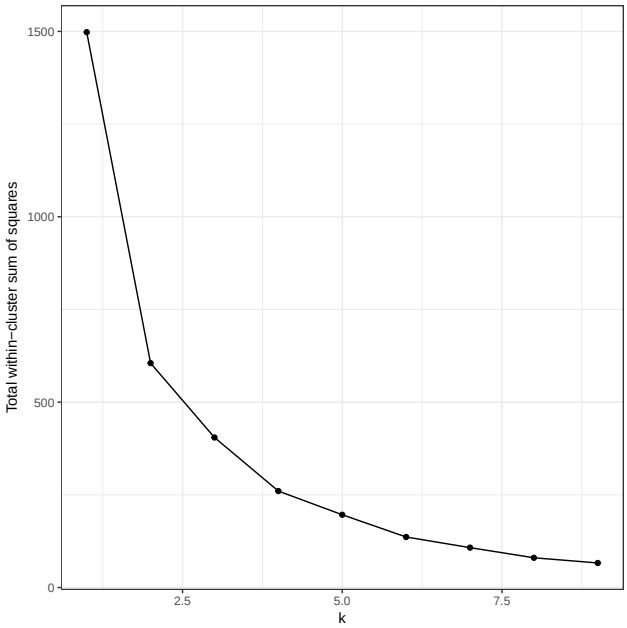

Figure 10.17: K-means clustering of the noisy moons data set: variance within clusters.

```
plot_clusters(noisy_moons, res, 2)
```

10.4.4.3 Different density

```
diff_density <- as.data.frame(read.csv("data/example_clusters/different_density.csv", header=F))
res <- lapply(k, function(i){kmeans(diff_density[,1:2], i, nstart=50)})
plot_tot_withinss(res)
```

```
plot_clusters(diff_density, res, 2)
```

10.4.4.4 Anisotropic distributions

```
aniso <- as.data.frame(read.csv("data/example_clusters/aniso.csv", header=F))
res <- lapply(k, function(i){kmeans(aniso[,1:2], i, nstart=50)})
plot_tot_withinss(res)
```

```
plotList <- list(
  plot_clusters(aniso, res, 2),
  plot_clusters(aniso, res, 3)
)
pm <- ggmatrix(
  plotList, nrow=1, ncol=2, showXAxisPlotLabels = T,
  showYAxisPlotLabels = T, xAxisLabels=c("k=2", "k=3")
) + theme_bw()
pm
```

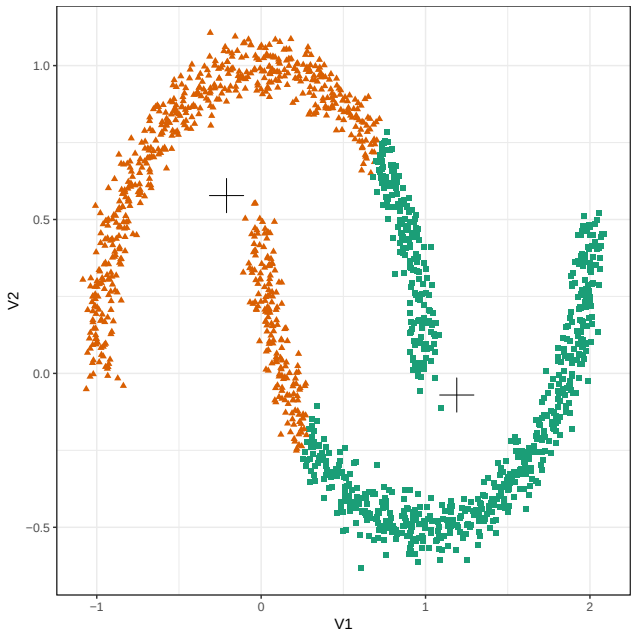

Figure 10.18: K-means clustering of the noisy moons data set: scatterplot of clusters for k=2. Cluster centres indicated with a cross.

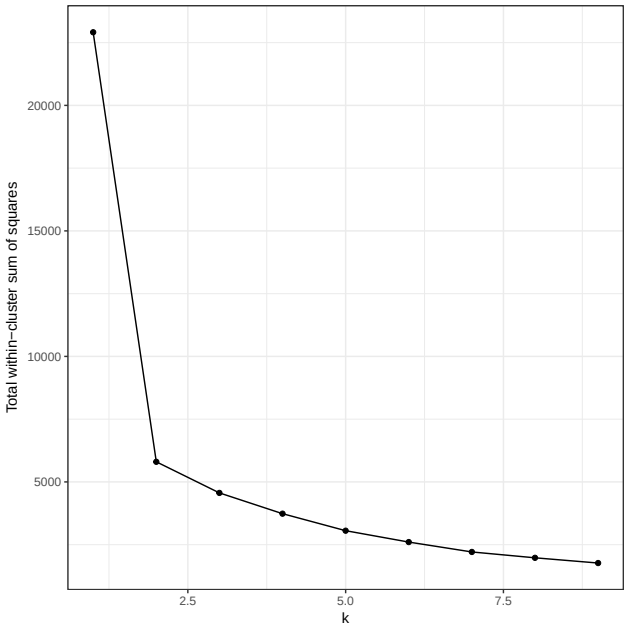

Figure 10.19: K-means clustering of the different density distributions data set: variance within clusters.

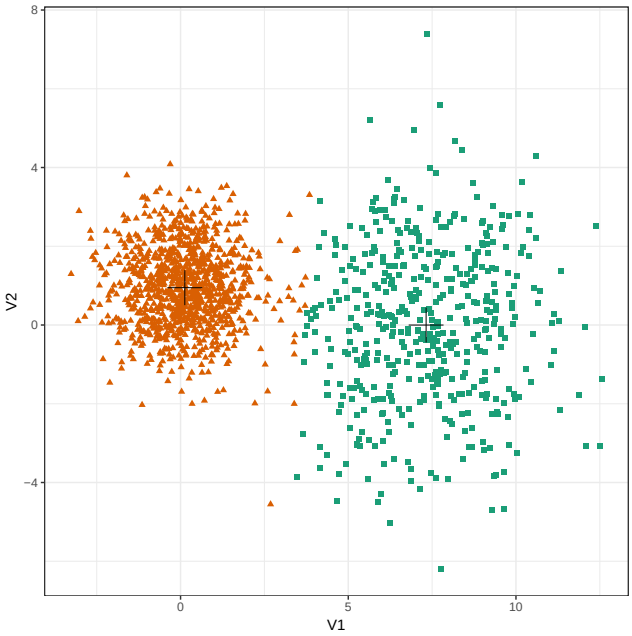

Figure 10.20: K-means clustering of the different density distributions data set: scatterplots of clusters for k=2 and k=3. Cluster centres indicated with a cross.

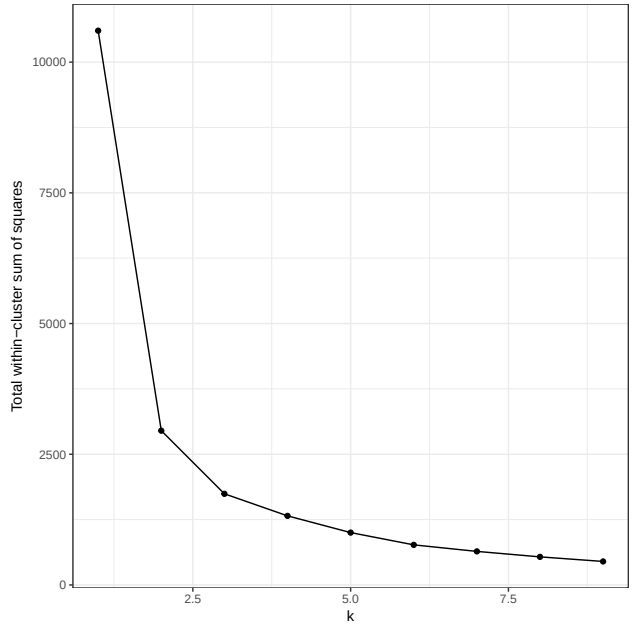

Figure 10.21: K-means clustering of the anisotropic distributions data set: variance within clusters.

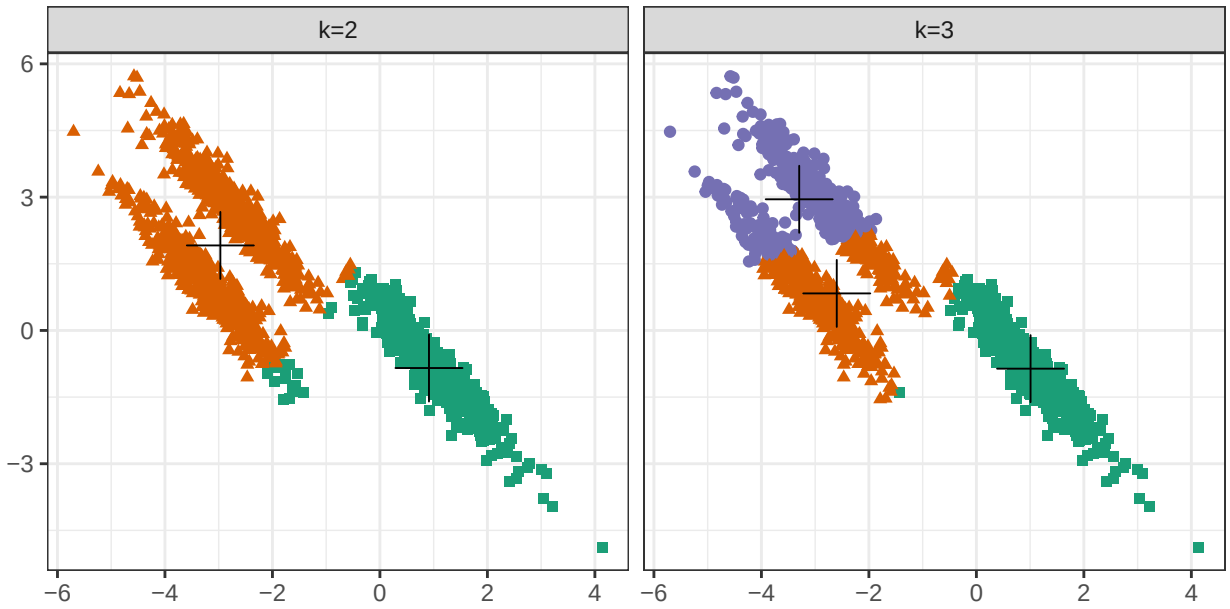

Figure 10.22: K-means clustering of the anisotropic distributions data set: scatterplots of clusters for k=2 and k=3. Cluster centres indicated with a cross.

10.4.4.5 No structure

```
no_structure <- as.data.frame(read.csv("data/example_clusters/no_structure.csv", header=F))
res <- lapply(k, function(i){kmeans(no_structure[,1:2], i, nstart=50)})
plot_tot_withinss(res)
```

```
plot_clusters(no_structure, res, 4)
```

10.4.5 Example: gene expression profiling of human tissues

Let's return to the data on gene expression of human tissues. Load data

```
load("data/tissues_gene_expression/tissuesGeneExpression.rda")
```

As we saw earlier, the data set contains expression levels for over 22,000 transcripts in seven tissues.

```
table(tissue)
```

```
## tissue
##  cerebellum       colon endometrium hippocampus      kidney       liver
##          38          34          15          31          39          26
##    placenta
##           6
```

```
dim(e)
```

```
## [1] 22215   189
```

First we will examine the total intra-cluster variance with different values of k. In practice we would set **nstart** to a large value (e.g. 50), but in the interests of speed for this demonstration we will set it to one. We use **set.seed** to make this example reproducible, but in practice you would allow **R** to generate a random seed.

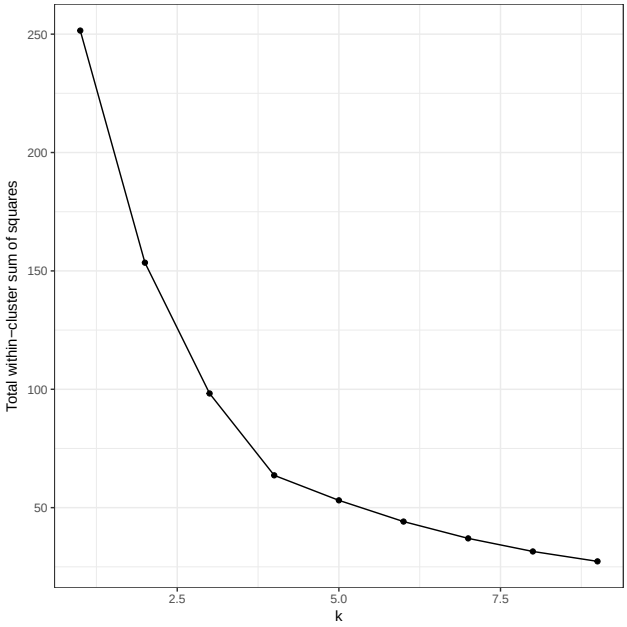

Figure 10.23: K-means clustering of the data set with no structure: variance within clusters.

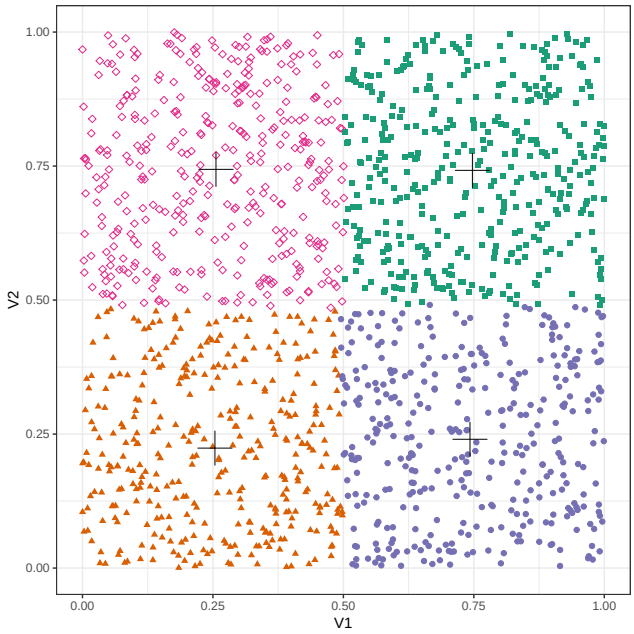

Figure 10.24: K-means clustering of the data set with no structure: scatterplot of clusters for k=4. Cluster centres indicated with a cross.

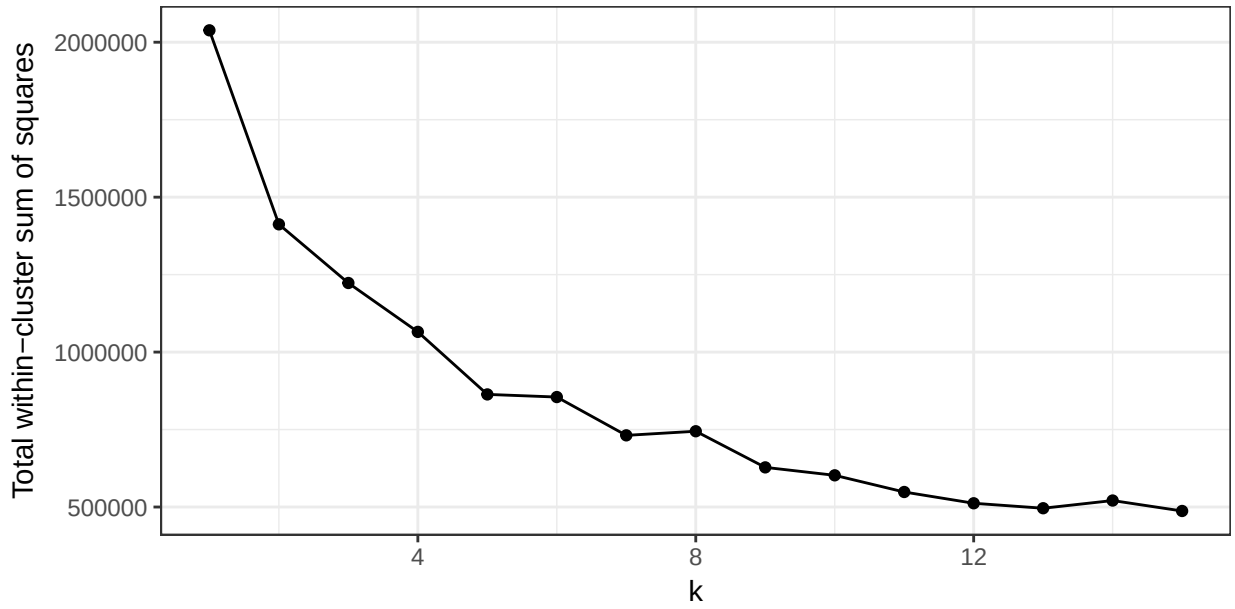

Figure 10.25: K-means clustering of human tissue gene expression: variance within clusters.

```
k<-1:15
set.seed(42)
res_k_15 <- lapply(k, function(i){kmeans(t(e), i, nstart=1)})
plot_tot_withinss(res_k_15)
```

If we had set **nstart** to a higher value we would have obtained a smoother curve in figure 10.25. There is no obvious elbow, but the rate of decrease in the total-within sum of squares appears to slow after k=5. Since we know that there are seven tissues in the data set we will try k=7.

```
set.seed(42)
res <- kmeans(t(e), 7, nstart=10)
table(tissue, res$cluster)
```

```
##
## tissue         1  2  3  4  5  6  7
##   cerebellum   0  0  0 33  0  0  5
##   colon        0  0  0  0  0 34  0
##   endometrium  0  0  0  0 15  0  0
##   hippocampus  0  0  0  0  0  0 31
##   kidney       0  0 39  0  0  0  0
##   liver       26  0  0  0  0  0  0
##   placenta     0  6  0  0  0  0  0
```

The analysis has found a distinct cluster for each tissue and therefore performed slightly better than the earlier hierarchical clustering analysis, which placed endometrium and kidney observations in the same cluster.

To visualize the result in a 2D scatter plot we first need to apply dimensionality reduction. We will use principal component analysis (PCA), which was described in chapter 9.

```
pca <- prcomp(t(e))
ggplot(data=as.data.frame(pca$x), aes(PC1,PC2)) +
  geom_point(col=brewer.pal(7,"Dark2")[res$cluster],
```

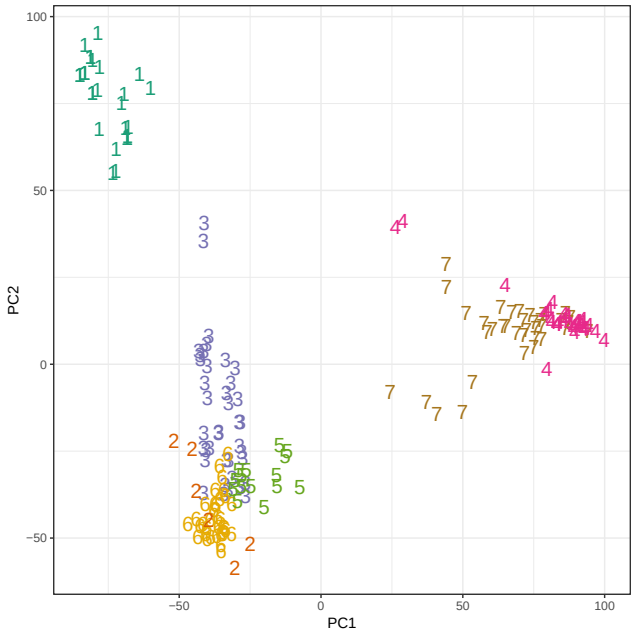

Figure 10.26: K-means clustering of human gene expression (k=7): scatterplot of first two principal components.

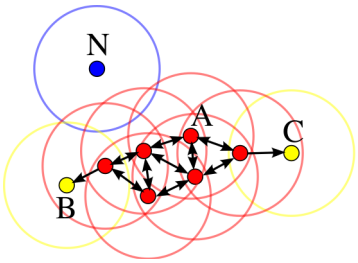

Figure 10.27: Illustration of the DBSCAN algorithm.

```
            shape=c(49:55)[res$cluster], size=5) +
  theme_bw()
```

10.5 DBSCAN

Density-based spatial clustering of applications with noise

10.5.1 Algorithm

Abstract DBSCAN algorithm in pseudocode (Schubert et al., 2017)

```
1 Compute neighbours of each point and identify core points   // Identify core points
2 Join neighbouring core points into clusters                 // Assign core points
3 foreach non-core point do
      Add to a neighbouring core point if possible            // Assign border points
      Otherwise, add to noise                                 // Assign noise points
```

10.5.2 Choosing parameters

The algorithm only needs parameteres **eps** and **minPts**.

```
library(dbscan)
```

```
blobs <- read.csv("data/example_clusters/blobs.csv", header=F)
dist2knn <- kNNdist(blobs, 3)
```

10.5.3 Example: clustering synthetic data sets

10.5.4 Gene expression

tissue types?

10.6 Summary

10.6.1 Applications

10.6.2 Strengths

10.6.3 Limitations

10.7 Exercises

Exercise solutions: I

Solutions to exercises can be found in appendix I.

Appendix A

Resources

A.1 Python

scikit-learn

A.2 Machine learning data set repository

mldata.org

This repository manages the following types of objects:

- Data Sets - Raw data as a collection of similarily structured objects.
- Material and Methods - Descriptions of the computational pipeline.
- Learning Tasks - Learning tasks defined on raw data.
- Challenges - Collections of tasks which have a particular theme.

Appendix B

Solutions ch. 3 - Linear models and matrix algebra

Solutions to exercises of chapter 3.

B.1 Exercise 1

B.2 Exercise 2

Appendix C

Solutions ch. 4 - Linear and non-linear logistic regression

Solutions to exercises of chapter 4.

C.1 Exercise 1

C.2 Exercise 2

Appendix D

Solutions ch. 5 - Nearest neighbours

Solutions to exercises of chapter 5.

D.1 Exercise 1

D.2 Exercise 2

Appendix E

Solutions ch. 6 - Decision trees and random forests

Solutions to exercises of chapter 6.

E.1 Exercise 1

E.2 Exercise 2

Appendix F

Solutions ch. 7 - Support vector machines

Solutions to exercises of chapter 7.

F.1 Exercise 1

F.2 Exercise 2

Appendix G

Solutions ch. 8 - Artificial neural networks

Solutions to exercises of chapter 8.

G.1 Exercise 1

G.2 Exercise 2

Appendix H

Solutions ch. 9 - Dimensionality reduction

Solutions to exercises of chapter 9.

H.1 Exercise 1

H.2 Exercise 2

Appendix I

Solutions ch. 10 - Clustering

Solutions to exercises of chapter 10.

I.1 Exercise 1

I.2 Exercise 2

Bibliography

Schubert, E., Sander, J., Ester, M., Kriegel, H. P., and Xu, X. (2017). Dbscan revisited, revisited: Why and how you should (still) use dbscan. *ACM Trans. Database Syst.*, 42(3):19:1–19:21.

Xie, Y. (2015). *Dynamic Documents with R and knitr*. Chapman and Hall/CRC, Boca Raton, Florida, 2nd edition. ISBN 978-1498716963.

Xie, Y. (2017). *bookdown: Authoring Books and Technical Documents with R Markdown*. R package version 0.4.