R and Data Mining: Examples and Case Studies [1]

Yanchang Zhao
yanchang@rdatamining.com
http://www.RDataMining.com

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Messages from the Author

Case studies: The case studies are not included in this online version. They are reserved exclusively for a book version published by Elsevier in December 2012.

Latest version: The latest online version is available at links below. See the websites also for an *R Reference Card for Data Mining*.

- `http://www.rdatamining.com`
- `http://www2.rdatamining.com` (for readers having no access to above website)

R code, data and FAQs: R code, data and FAQs are provided at links below.

- `http://www.rdatamining.com/books/rdm`
- `http://www2.rdatamining.com/r-and-data-mining-examples-and-case-studies.html`

Chapters/sections to add: topic modelling and stream graph; spatial data analysis; performance evaluation of classification/prediction models (with ROC and AUC); parallel computing and big data. Please let me know if some topics are interesting to you but not covered yet by this book.

Questions and feedback: If you have any questions or comments, or come across any problems with this document or its book version, please feel free to post them to *the RDataMining group* below or email them to me. Thanks.

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A sister book: See a new edited book titled *Data Mining Application with R* at links below, which features 15 real-world applications on data mining with R.

- `http://www.rdatamining.com/books/dmar`
- `http://www2.rdatamining.com/data-mining-applications-with-r.html`

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List of Abbreviations

ARIMA	Autoregressive integrated moving average
ARMA	Autoregressive moving average
AVF	Attribute value frequency
CLARA	Clustering for large applications
CRISP-DM	Cross industry standard process for data mining
DBSCAN	Density-based spatial clustering of applications with noise
DTW	Dynamic time warping
DWT	Discrete wavelet transform
GLM	Generalized linear model
IQR	Interquartile range, i.e., the range between the first and third quartiles
LOF	Local outlier factor
PAM	Partitioning around medoids
PCA	Principal component analysis
STL	Seasonal-trend decomposition based on Loess
TF-IDF	Term frequency-inverse document frequency

Chapter 1

Introduction

This book introduces into using R for data mining. It presents many examples of various data mining functionalities in R and three case studies of real world applications. The supposed audience of this book are postgraduate students, researchers, data miners and data scientists who are interested in using R to do their data mining research and projects. We assume that readers already have a basic idea of data mining and also have some basic experience with R. We hope that this book will encourage more and more people to use R to do data mining work in their research and applications.

This chapter introduces basic concepts and techniques for data mining, including a data mining process and popular data mining techniques. It also presents R and its packages, functions and task views for data mining. At last, some datasets used in this book are described.

1.1 Data Mining

Data mining is the process to discover interesting knowledge from large amounts of data [Han and Kamber, 2000]. It is an interdisciplinary field with contributions from many areas, such as statistics, machine learning, information retrieval, pattern recognition and bioinformatics. Data mining is widely used in many domains, such as retail, finance, telecommunication and social media.

The main techniques for data mining include classification and prediction, clustering, outlier detection, association rules, sequence analysis, time series analysis and text mining, and also some new techniques such as social network analysis and sentiment analysis. Detailed introduction of data mining techniques can be found in text books on data mining [Han and Kamber, 2000, Hand et al., 2001, Witten and Frank, 2005]. In real world applications, a data mining process can be broken into six major phases: business understanding, data understanding, data preparation, modeling, evaluation and deployment, as defined by the CRISP-DM (Cross Industry Standard Process for Data Mining)[1]. This book focuses on the modeling phase, with data exploration and model evaluation involved in some chapters. Readers who want more information on data mining are referred to online resources in Chapter 15.

1.2 R

R [2] [R Core Team, 2015b] is a free software environment for statistical computing and graphics. It provides a wide variety of statistical and graphical techniques. R can be easily extended with 7324 packages available on CRAN[3] (as of October 20, 2015). In addition, there are many packages

[1] http://www.crisp-dm.org/
[2] http://www.r-project.org/
[3] http://cran.r-project.org/

provided on other websites, such as Bioconductor[4], and also a lot of packages under development at R-Forge[5] and GitHub[6]. More details about R are available in *An Introduction to R* [7] [Venables et al., 2015] and *R Language Definition* [8] [R Core Team, 2015d] at the CRAN website. R is widely used in both academia and industry.

To help users to find our which R packages to use, the CRAN Task Views [9] are a good guidance. They provide collections of packages for different tasks. Some Task Views related to data mining are:

- Machine Learning & Statistical Learning,
- Cluster Analysis & Finite Mixture Models,
- Time Series Analysis,
- Natural Language Processing,
- Multivariate Statistics, and
- Analysis of Spatial Data.

Another guide to R for data mining is an *R Reference Card for Data Mining* (see page **??**), which provides a comprehensive indexing of R packages and functions for data mining, categorized by their functionalities. Its latest version is available at `http://www.rdatamining.com/docs` and `http://www2.rdatamining.com/`.

Readers who want more information on R are referred to online resources in Chapter 15.

1.2.1 R Basics

Please refer to *An Introduction to R* [Venables et al., 2015] for an introduction to basics of R.

1.2.2 RStudio

RStudio [10] is an integrated development environment (IDE) for R and can run on various operating systems like Windows, Mac OS X and Linux. It is a very useful and powerful tool for R programming, and therefore, readers are suggested to use RStudio when learning from this book or doing their projects, although all the provided code can run without it. What you normally need is RStudio Desktop open source edition, which is free of charge.

When RStudio is launched for the first time, you can see a window similar to Figure 1.1. There are four panels:

- Source panel (top left), which shows your R source code. If you cannot see the source panel, you can find it by clicking menu "File", "New File" and then "R Script". You can run a line or a selection of R code by clicking the "Run" bottom on top of source panel, or pressing "Ctrl + Enter".
- Console panel (bottom left), which shows outputs and system messages displayed in a normal R console;
- Environment/History/Presentation panel (top right), whose three tabs show respectively all objects and function loaded in R, a history of submitted R code, and Presentations generated with R;

[4] `http://www.bioconductor.org/`
[5] `http://r-forge.r-project.org/`
[6] `https://github.com/`
[7] `http://cran.r-project.org/doc/manuals/R-intro.pdf`
[8] `http://cran.r-project.org/doc/manuals/R-lang.pdf`
[9] `http://cran.r-project.org/web/views/`
[10] `http://www.rstudio.com/`

- Files/Plots/Packages/Help/Viewer panel (bottom right), whose tabs show respectively a list of files, plots, R packages installed, help documentation and local web content.

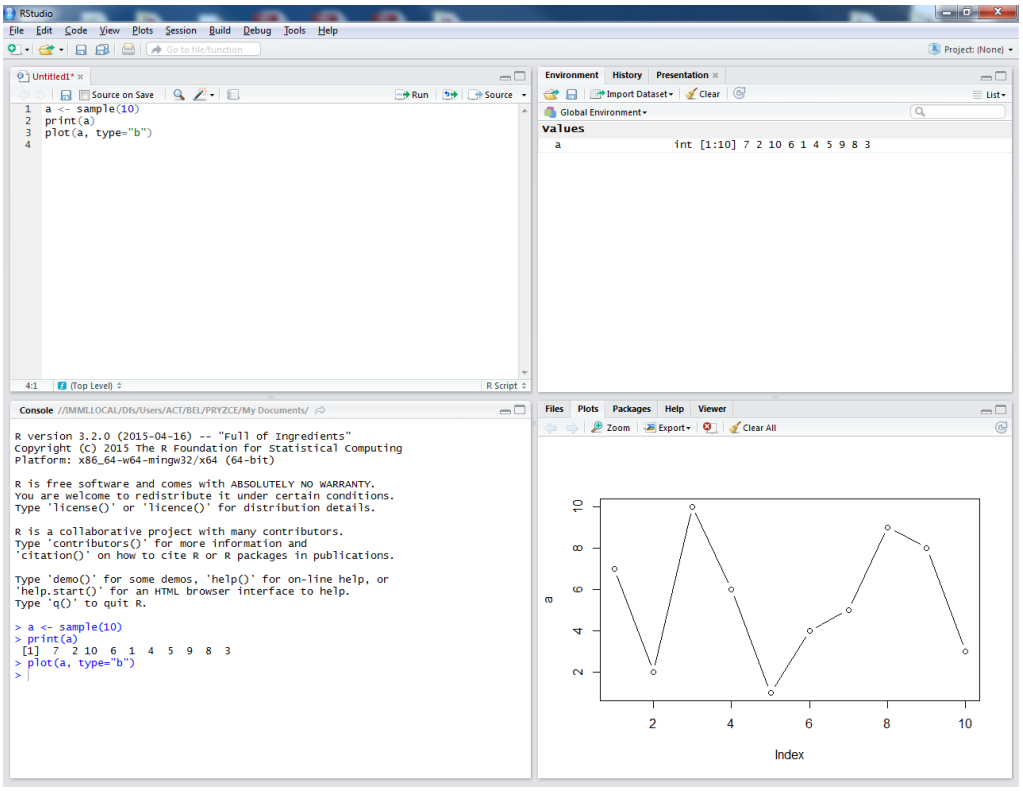

Figure 1.1: RStudio

It is always a good practice to begin R programming with an RStudio project, which is a folder where to put your R code, data files and figures. To create a new project, click the "Project" button at the top-right corner and then choose "New Project". After that, select "create project from new directory" and then "Empty Project". After typing a directory name, which will also be your project name, click "Create Project" to create your project folder and files. If you open an existing project, RStudio will automatically set the working directory to the project directory, which is very convenient. After that, create three folders as below:

- *code*, where to put your R souce code;
- *data*, where to put your datasets; and
- *figures*, where to put produced diagrams.

In addition to above three folders which are usesul to most projects, depending on your project and preference, you may create additional folders below:

- *rawdata*, where to put all raw data,
- *models*, where to put all produced analytics models, and
- *reports*, where to put your analysis reports.

1.3 Datasets

Some datasets used in this book are briefly described in this section.

1.3.1 The Iris Dataset

The `iris` dataset has been used for classification in many research publications. It consists of 50 samples from each of three classes of iris flowers [Frank and Asuncion, 2010]. One class is linearly separable from the other two, while the latter are not linearly separable from each other. There are five attributes in the dataset:

- sepal length in cm,
- sepal width in cm,
- petal length in cm,
- petal width in cm, and
- class: Iris Setosa, Iris Versicolour, and Iris Virginica.

Detailed desription of the dataset and research publications citing it can be found at the UCI Machine Learning Repository [11].

Below we have a look at the structure of the dataset with `str()`. Note that all variable names, package names and function names in R are case sensitive.

```
> str(iris)

data.frame:        150 obs. of  5 variables:
 $ Sepal.Length: num  5.1 4.9 4.7 4.6 5 5.4 4.6 5 4.4 4.9 ...
 $ Sepal.Width : num  3.5 3 3.2 3.1 3.6 3.9 3.4 3.4 2.9 3.1 ...
 $ Petal.Length: num  1.4 1.4 1.3 1.5 1.4 1.7 1.4 1.5 1.4 1.5 ...
 $ Petal.Width : num  0.2 0.2 0.2 0.2 0.2 0.4 0.3 0.2 0.2 0.1 ...
 $ Species     : Factor w/ 3 levels "setosa","versicolor",..: 1 1 1 1 1 1 1 1 1 1 ...
```

From the output, we can see that there are 150 observations (records, or rows) and 5 variables (or columns) in the dataset. The first four variables are numeric. The last one, `Species`, is categoric (called as "factor" in R) and has three levels of values.

1.3.2 The Bodyfat Dataset

`Bodyfat` is a dataset available in package *TH.data* [Hothorn, 2015]. It has 71 rows, and each row contains information of one person. It contains the following 10 numeric columns.

- `age`: age in years.
- `DEXfat`: body fat measured by DXA, response variable.
- `waistcirc`: waist circumference.
- `hipcirc`: hip circumference.
- `elbowbreadth`: breadth of the elbow.
- `kneebreadth`: breadth of the knee.
- `anthro3a`: sum of logarithm of three anthropometric measurements.
- `anthro3b`: sum of logarithm of three anthropometric measurements.
- `anthro3c`: sum of logarithm of three anthropometric measurements.
- `anthro4`: sum of logarithm of three anthropometric measurements.

[11] `https://archive.ics.uci.edu/ml/datasets/Iris`

The value of `DEXfat` is to be predicted by the other variables.

```
> data("bodyfat", package = "TH.data")
> str(bodyfat)

data.frame:        71 obs. of  10 variables:
 $ age         : num  57 65 59 58 60 61 56 60 58 62 ...
 $ DEXfat      : num  41.7 43.3 35.4 22.8 36.4 ...
 $ waistcirc   : num  100 99.5 96 72 89.5 83.5 81 89 80 79 ...
 $ hipcirc     : num  112 116.5 108.5 96.5 100.5 ...
 $ elbowbreadth: num  7.1 6.5 6.2 6.1 7.1 6.5 6.9 6.2 6.4 7 ...
 $ kneebreadth : num  9.4 8.9 8.9 9.2 10 8.8 8.9 8.5 8.8 8.8 ...
 $ anthro3a    : num  4.42 4.63 4.12 4.03 4.24 3.55 4.14 4.04 3.91 3.66 ...
 $ anthro3b    : num  4.95 5.01 4.74 4.48 4.68 4.06 4.52 4.7 4.32 4.21 ...
 $ anthro3c    : num  4.5 4.48 4.6 3.91 4.15 3.64 4.31 4.47 3.47 3.6 ...
 $ anthro4     : num  6.13 6.37 5.82 5.66 5.91 5.14 5.69 5.7 5.49 5.25 ...
```

Chapter 2

Data Import and Export

This chapter shows how to import foreign data into R and export R objects to other formats. At first, examples are given to demonstrate saving R objects to and loading them from `.Rdata` files. After that, it demonstrates importing data from and exporting data to `.CSV` files, SAS databases, ODBC databases and EXCEL files.

2.1 Save and Load R Data

Data in R can be saved as `.Rdata` files with function `save()` and `.Rdata` files can be reloaded into R with `load()`. With the code below, we first create a new object `a` as a numeric sequence (`1, 2, ..., 10`) and a second new object `b` as a vector of characters (`'a', 'b', 'c', 'd', 'e'`). Object `letters` is a built-in vector in R of 26 English letters, and `letters[1:5]` returns the first five letters. We then save them to a file and remove them from R with function `rm()`. After that, we reload both `a` and `b` from the file and print their values.

```
> a <- 1:10
> b <- letters[1:5]
> save(a, b, file="./data/mydatafile.Rdata")
> rm(a, b)
> load("./data/mydatafile.Rdata")
> print(a)
```

```
 [1]  1  2  3  4  5  6  7  8  9 10
```

```
> print(b)
```

```
[1] "a" "b" "c" "d" "e"
```

An alternative way to save and load R data objects is using functions `saveRDS()` and `readRDS()`. They work in a similar way as `save()` and `load()`. The differences are: 1) multiple R objects can be saved into one single file with `save()`, but only one object can be saved in a file with `saveRDS()`; and 2) `readRDS()` enables us to restore the data under a different object name, while `load()` restores the data under the same object name as when it was saved.

```
> a <- 1:10
> saveRDS(a, file="./data/mydatafile2.rds")
> a2 <- readRDS("./data/mydatafile2.rds")
> print(a2)
```

```
 [1]  1  2  3  4  5  6  7  8  9 10
```

R also provides function `save.image()` to save everything in current workspace into a single file, which is very convenient to save your current work and resume it later, if the data loaded into R are not very big.

2.2 Import from and Export to .CSV Files

Data frame is a data format that we mostly deal with in R. A data frame is similar to a table in databases, with each row being an observation (or record) and each column beding a variable (or feature).

The example below demonstrates saving a dataframe into file and then reloaded it into R. At first, we create three vectors, an integer vector, a numeric (real) vector and a character vector, use function `data.frame()` to build them into dataframe `df1` and save it into a `.CSV` file with `write.csv()`. Function `sample(5)` produces a random sample of five numbers out of 1 to 5. Column names in the data frame are then set with function `names()`. After that, we reload the data frame from the file to a new data frame `df2` with `read.csv()`. Note that the very first column printed below is the row names, created automatically by R.

```
> var1 <- sample(5)
> var2 <- var1 / 10
> var3 <- c("R", "and", "Data Mining", "Examples", "Case Studies")
> df1 <- data.frame(var1, var2, var3)
> names(df1) <- c("Var.Int", "Var.Num", "Var.Char")
> write.csv(df1, "./data/mydatafile3.csv", row.names = FALSE)
> df2 <- read.csv("./data/mydatafile3.csv")
> print(df2)

  Var.Int Var.Num     Var.Char
1       3     0.3            R
2       4     0.4          and
3       1     0.1  Data Mining
4       2     0.2     Examples
5       5     0.5 Case Studies
```

2.3 Import Data from SAS

Package *foreign* [R Core Team, 2015a] provides function `read.ssd()` for importing SAS datasets (`.sas7bdat` files) into R. However, the following points are essential to make importing successful.

- SAS must be available on your computer, and `read.ssd()` will call SAS to read SAS datasets and import them into R.
- The file name of a SAS dataset has to be no longer than eight characters. Otherwise, the importing would fail. There is no such a limit when importing from a `.CSV` file.
- During importing, variable names longer than eight characters are truncated to eight characters, which often makes it difficult to know the meanings of variables. One way to get around this issue is to import variable names separately from a `.CSV` file, which keeps full names of variables.

An empty `.CSV` file with variable names can be generated with the following method.

1. Create an empty SAS table `dumVariables` from `dumData` as follows.

```
data work.dumVariables;
   set work.dumData(obs=0);
run;
```

2. Export table `dumVariables` as a .CSV file.

The example below demonstrates importing data from a SAS dataset. Assume that there is a SAS data file `dumData.sas7bdat` and a .CSV file `dumVariables.csv` in folder "`Current working directory/data`".

```
> library(foreign) # for importing SAS data
> # the path of SAS on your computer
> sashome <- "C:/Program Files/SAS/SASFoundation/9.2"
> filepath <- "./data"
> # filename should be no more than 8 characters, without extension
> fileName <- "mySasDataFile"
> # read data from a SAS dataset
> a <- read.ssd(file.path(filepath), fileName, sascmd=file.path(sashome, "sas.exe"))
> print(a)
```

Note that the variable names above are truncated. The full names can be imported from a .CSV file with the following code.

```
> # read variable names from a .CSV file
> variableFileName <- "sasVariableNames.csv"
> myNames <- read.csv(file.path(filepath, variableFileName))
> names(a) <- names(myNames)
> print(a)
```

Although one can export a SAS dataset to a `.CSV` file and then import data from it, there are problems when there are special formats in the data, such as a value of "$100,000" for a numeric variable. In this case, it would be better to import from a `.sas7bdat` file. However, variable names may need to be imported into R separately as above.

Another way to import data from a SAS dataset is to use function `read.xport()` to read a file in SAS Transport (XPORT) format.

2.4 Import/Export via ODBC

Package *RODBC* provides connection to ODBC databases [Ripley and Lapsley, 2015].

2.4.1 Read from Databases

Below is an example of reading from an ODBC database. Function `odbcConnect()` sets up a connection to database, `sqlQuery()` sends an SQL query to the database, and `odbcClose()` closes the connection.

```
> library(RODBC)
> connection <- odbcConnect(dsn="servername",uid="userid",pwd="******")
> query <- "SELECT * FROM lib.table WHERE ..."
> # or read query from file
> # query <- readChar("data/myQuery.sql", nchars=99999)
> myData <- sqlQuery(connection, query, errors=TRUE)
> odbcClose(connection)
```

There are also `sqlSave()` and `sqlUpdate()` for writing or updating a table in an ODBC database.

2.4.2 Output to and Input from EXCEL Files

An example of writing data to and reading data from EXCEL files is shown below, where a sheet name needs to be provided in function `sqlFetch()`.

```
> library(RODBC)
> filename <- "data/myExcelFile.xls"
> xlsFile <- odbcConnectExcel(filename, readOnly = FALSE)
> sqlSave(xlsFile, a, rownames = FALSE)
> b <- sqlFetch(xlsFile, "sheetname")
> odbcClose(xlsFile)
```

Note that there might be a limit of 65,536 rows to write to an EXCEL file.

2.5 Read and Write EXCEL files with package *xlsx*

While package *RODBC* can read and write EXCEL files on Windows, but it does not work directly on Mac OS X, because an ODBC driver for EXCEL is not provided by default on Mac. However, package *xlsx* supports reading and writing Excel 2007 and Excel 97/2000/XP/2003 files [Dragulescu, 2014], with no additional drivers required. It works both on Windows and on Mac OS X.

The example below demonstrates creation of an EXCEL file `iris.xlsx` with three sheets. Function `library()` loads an R package (or library), and `table()` returns the frequencies of values in a vector. We can see that there are three species, with each having 50 observations. Observations of species "setosa" are extracted first with function `subset()` and then saved into sheet "setosa" in the EXCEl file with function `write.xlsx()`. Row names are excluded using `row.names=F`. Then data of the other two species are saved into the same file, but in different sheets. When writing the second and third sheets, we need to use `append=T` to add new sheets to the existing file, instead of overwriting it. Finally, we read from sheet "setosa" with function `read.xlsx()` and show the first six observations with function `head()`.

```
> library(xlsx)
> table(iris$Species)

    setosa versicolor  virginica
        50         50         50

> setosa <- subset(iris, Species == "setosa")
> write.xlsx(setosa, file="./data/iris.xlsx", sheetName="setosa", row.names=F)
> versicolor <- subset(iris, Species == "versicolor")
> write.xlsx(versicolor, file="./data/iris.xlsx", sheetName="versicolor",
+            row.names=F, append=T)
> virginica <- subset(iris, Species == "virginica")
> write.xlsx(virginica, file="./data/iris.xlsx", sheetName="virginica",
+            row.names=F, append=T)
> a <- read.xlsx("./data/iris.xlsx", sheetName="setosa")
> head(a)

  Sepal.Length Sepal.Width Petal.Length Petal.Width Species
1          5.1         3.5          1.4         0.2  setosa
2          4.9         3.0          1.4         0.2  setosa
3          4.7         3.2          1.3         0.2  setosa
4          4.6         3.1          1.5         0.2  setosa
5          5.0         3.6          1.4         0.2  setosa
6          5.4         3.9          1.7         0.4  setosa
```

2.6 Further Readings

For more details on data import and export, please refer to *R Data Import/Export* [1] [R Core Team, 2015c], which covers importing data from text files, XML files, spreadsheet-like data, various statistical systems, relational databases, binary files, image files, connections and network interfaces.

[1] `http://cran.r-project.org/doc/manuals/R-data.pdf`

Chapter 3

Data Exploration and Visualization

This chapter shows examples on data exploration with R. It starts with inspecting the dimensionality, structure and data of an R object, followed by basic statistics and various charts like pie charts and histograms. Exploration of multiple variables are then demonstrated, including grouped distribution, grouped boxplots, scattered plot and pairs plot. After that, examples are presented on level plot, contour plot and 3D plot. It also shows how to saving charts into files of various formats.

3.1 Have a Look at Data

The `iris` data is used in this chapter for demonstration of data exploration with R. See Section 1.3.1 for details of the `iris` data.

We first check the size and structure of data. In code below, function `dim()` returns the dimensionality of data, which shows that there are 150 observations (or rows or records) and 5 variables (or columns). The name of variables are returned by `names()`. Functions `str()` and `attributes()` return the structure and attributes of data.

```
> dim(iris)

[1] 150   5

> names(iris)

[1] "Sepal.Length" "Sepal.Width"  "Petal.Length" "Petal.Width"  "Species"

> str(iris)

data.frame:        150 obs. of  5 variables:
 $ Sepal.Length: num  5.1 4.9 4.7 4.6 5 5.4 4.6 5 4.4 4.9 ...
 $ Sepal.Width : num  3.5 3 3.2 3.1 3.6 3.9 3.4 3.4 2.9 3.1 ...
 $ Petal.Length: num  1.4 1.4 1.3 1.5 1.4 1.7 1.4 1.5 1.4 1.5 ...
 $ Petal.Width : num  0.2 0.2 0.2 0.2 0.2 0.4 0.3 0.2 0.2 0.1 ...
 $ Species     : Factor w/ 3 levels "setosa","versicolor",..: 1 1 1 1 1 1 1 1 1 1 ...

> attributes(iris)

$names
[1] "Sepal.Length" "Sepal.Width"  "Petal.Length" "Petal.Width"  "Species"
```

```
$row.names
  [1]   1   2   3   4   5   6   7   8   9  10  11  12  13  14  15  16  17  18  19
 [20]  20  21  22  23  24  25  26  27  28  29  30  31  32  33  34  35  36  37  38
 [39]  39  40  41  42  43  44  45  46  47  48  49  50  51  52  53  54  55  56  57
 [58]  58  59  60  61  62  63  64  65  66  67  68  69  70  71  72  73  74  75  76
 [77]  77  78  79  80  81  82  83  84  85  86  87  88  89  90  91  92  93  94  95
 [96]  96  97  98  99 100 101 102 103 104 105 106 107 108 109 110 111 112 113 114
[115] 115 116 117 118 119 120 121 122 123 124 125 126 127 128 129 130 131 132 133
[134] 134 135 136 137 138 139 140 141 142 143 144 145 146 147 148 149 150

$class
[1] "data.frame"
```

Next, we have a look at the first five rows of data.

```
> iris[1:5, ]

  Sepal.Length Sepal.Width Petal.Length Petal.Width Species
1          5.1         3.5          1.4         0.2  setosa
2          4.9         3.0          1.4         0.2  setosa
3          4.7         3.2          1.3         0.2  setosa
4          4.6         3.1          1.5         0.2  setosa
5          5.0         3.6          1.4         0.2  setosa
```

The first or last rows of data can be retrieved with `head()` or `tail()`, which by default return the first or last 6 rows. Alternatively, we can get a certain number of rows by setting the 2nd parameter to both functions. For example, the first 10 rows will be returned with `head(iris, 10)`.

```
> head(iris)

  Sepal.Length Sepal.Width Petal.Length Petal.Width Species
1          5.1         3.5          1.4         0.2  setosa
2          4.9         3.0          1.4         0.2  setosa
3          4.7         3.2          1.3         0.2  setosa
4          4.6         3.1          1.5         0.2  setosa
5          5.0         3.6          1.4         0.2  setosa
6          5.4         3.9          1.7         0.4  setosa

> tail(iris)

    Sepal.Length Sepal.Width Petal.Length Petal.Width   Species
145          6.7         3.3          5.7         2.5 virginica
146          6.7         3.0          5.2         2.3 virginica
147          6.3         2.5          5.0         1.9 virginica
148          6.5         3.0          5.2         2.0 virginica
149          6.2         3.4          5.4         2.3 virginica
150          5.9         3.0          5.1         1.8 virginica
```

A random sample of the data can be retrieved with function `sample()` in code below.

```
> ## draw a sample of 5 rows
> idx <- sample(1:nrow(iris), 5)
> idx

[1] 142 100 103 128 138
```

```
> iris[idx, ]
```

```
    Sepal.Length Sepal.Width Petal.Length Petal.Width    Species
142          6.9         3.1          5.1         2.3  virginica
100          5.7         2.8          4.1         1.3 versicolor
103          7.1         3.0          5.9         2.1  virginica
128          6.1         3.0          4.9         1.8  virginica
138          6.4         3.1          5.5         1.8  virginica
```

We can also retrieve the values of a single column. For example, the first 10 values of `Sepal.Length` can be obtained in three different ways below.

```
> iris[1:10, "Sepal.Length"]
```

```
 [1] 5.1 4.9 4.7 4.6 5.0 5.4 4.6 5.0 4.4 4.9
```

```
> iris[1:10, 1]
```

```
 [1] 5.1 4.9 4.7 4.6 5.0 5.4 4.6 5.0 4.4 4.9
```

```
> iris$Sepal.Length[1:10]
```

```
 [1] 5.1 4.9 4.7 4.6 5.0 5.4 4.6 5.0 4.4 4.9
```

3.2 Explore Individual Variables

Distribution of every numeric variable can be checked with function `summary()`, which returns the minimum, maximum, mean, median, and the first (25%) and third (75%) quartiles. Take `Sepal.Length` as an example, the result below shows that, its minimum value is 4.3 and the maximum 7.9. Its first quartile ("1st Qu.") is 5.1, which means that 25% out of all records have `Sepal.Length` below 5.1. Similarly, a value of 6.4 in the third quartile ("3rd Qu.") indidates that 75% out of all records have `Sepal.Length` below 6.4. It has a median of 5.8, which means that half of records have `Sepal.Length` below 5.8. The value of mean shows that the arithemetic mean (calculated by adding all values together and dividing by the number of values) of `Sepal.Length` is 5.843.

For factors (or categorical variables), it shows the frequency of every level. In the result below, we can see that each one of the three Species, "setosa", "versicolor" and "virginica", has 50 observations.

```
> summary(iris)
```

```
  Sepal.Length    Sepal.Width     Petal.Length    Petal.Width          Species
 Min.   :4.300   Min.   :2.000   Min.   :1.000   Min.   :0.100   setosa    :50
 1st Qu.:5.100   1st Qu.:2.800   1st Qu.:1.600   1st Qu.:0.300   versicolor:50
 Median :5.800   Median :3.000   Median :4.350   Median :1.300   virginica :50
 Mean   :5.843   Mean   :3.057   Mean   :3.758   Mean   :1.199
 3rd Qu.:6.400   3rd Qu.:3.300   3rd Qu.:5.100   3rd Qu.:1.800
 Max.   :7.900   Max.   :4.400   Max.   :6.900   Max.   :2.500
```

The mean, median and range can also be obtained respectively with functions with `mean()`, `median()` and `range()`. Quartiles and percentiles are supported by function `quantile()` as below,

```
> quantile(iris$Sepal.Length)
```

```
  0%  25%  50%  75% 100%
 4.3  5.1  5.8  6.4  7.9
```

```
> quantile(iris$Sepal.Length, c(0.1, 0.3, 0.65))
```

```
 10%  30%  65%
4.80 5.27 6.20
```

Then we check the variance of `Sepal.Length` with `var()`, and also check its distribution with histogram and density using functions `hist()` and `density()`.

```
> var(iris$Sepal.Length)
```

```
[1] 0.6856935
```

```
> hist(iris$Sepal.Length)
```

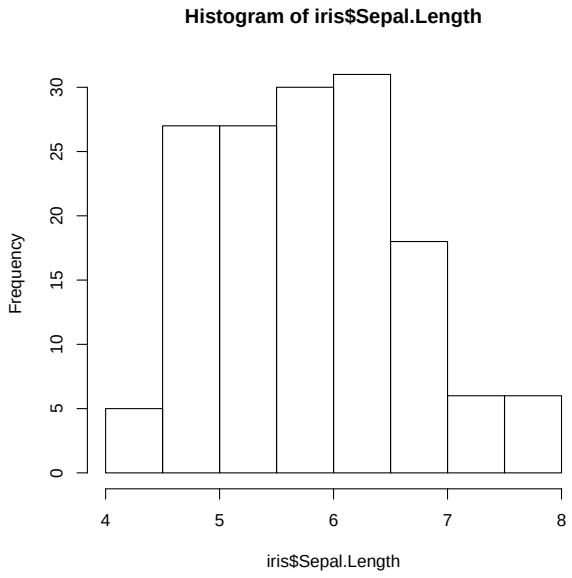

Figure 3.1: Histogram

```
> plot(density(iris$Sepal.Length))
```

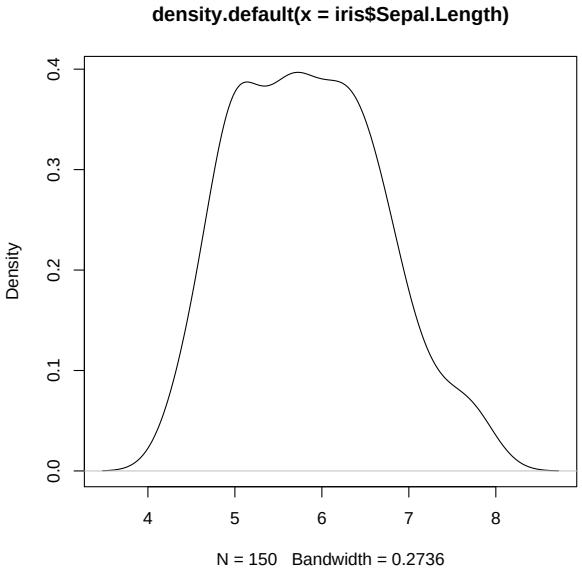

Figure 3.2: Density

The frequency of a factor variable can be calculated with function `table()`, and then plotted

as a pie chart with `pie()` or a bar chart with `barplot()`.

```
> table(iris$Species)

    setosa versicolor  virginica
        50         50         50

> pie(table(iris$Species))
```

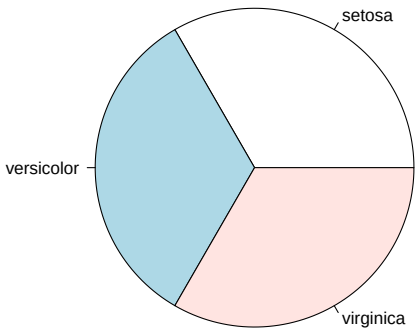

Figure 3.3: Pie Chart

```
> barplot(table(iris$Species))
```

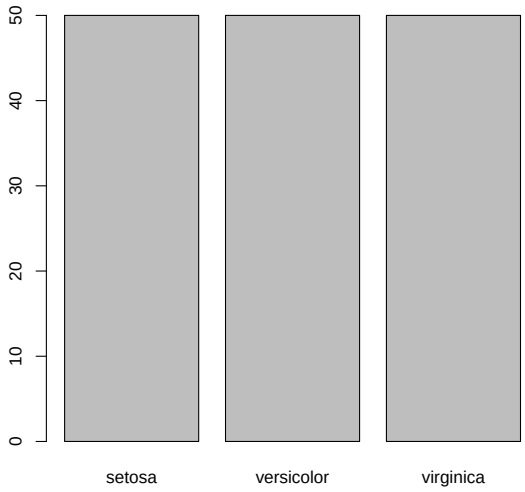

Figure 3.4: Bar Chart

3.3 Explore Multiple Variables

After checking the distributions of individual variables, we then investigate the relationships between two variables. Below we calculate covariance and correlation between variables with `cov()` and `cor()`.

```
> cov(iris$Sepal.Length, iris$Petal.Length)

[1] 1.274315

> cov(iris[,1:4])

             Sepal.Length Sepal.Width Petal.Length Petal.Width
Sepal.Length    0.6856935  -0.0424340    1.2743154   0.5162707
Sepal.Width    -0.0424340   0.1899794   -0.3296564  -0.1216394
Petal.Length    1.2743154  -0.3296564    3.1162779   1.2956094
Petal.Width     0.5162707  -0.1216394    1.2956094   0.5810063

> cor(iris$Sepal.Length, iris$Petal.Length)

[1] 0.8717538

> cor(iris[,1:4])

             Sepal.Length Sepal.Width Petal.Length Petal.Width
Sepal.Length    1.0000000  -0.1175698    0.8717538   0.8179411
Sepal.Width    -0.1175698   1.0000000   -0.4284401  -0.3661259
Petal.Length    0.8717538  -0.4284401    1.0000000   0.9628654
Petal.Width     0.8179411  -0.3661259    0.9628654   1.0000000
```

Correlation shows whether and how strongly a pair of variables are related to each other. It ranges from -1 to +1. The closer the correlation is to +1 (or -1), the more strongly the two variables are positively (or negatively) related. When it is close to zero, it means that there is no relationship between them. From above results, we can see that the correlation between `Sepal.Length` and `Petal.Length` is 0.87, which means that they are positively related to each other. Similarly, `Sepal.Length` and `Petal.Width` are highly related, as well as `Petal.Length` and `Petal.Width`. In contrast, `Sepal.Width` is weakly negatively related with the other three.

Next, we compute the stats of `Sepal.Length` of every `Species` with `aggregate()`.

```
> aggregate(Sepal.Length ~ Species, summary, data=iris)

     Species Sepal.Length.Min. Sepal.Length.1st Qu. Sepal.Length.Median
1     setosa             4.300                4.800                5.000
2 versicolor             4.900                5.600                5.900
3  virginica             4.900                6.225                6.500
  Sepal.Length.Mean Sepal.Length.3rd Qu. Sepal.Length.Max.
1             5.006                5.200             5.800
2             5.936                6.300             7.000
3             6.588                6.900             7.900
```

We then use function `boxplot()` to plot a box plot, also known as box-and-whisker plot, to show the median, first and third quartile of a distribution (i.e., the 50%, 25% and 75% points in cumulative distribution), and outliers. The bar in the middle is the median. The box shows the interquartile range (IQR), which is the range between the 75% and 25% observation. The result shows that the three species are of different distributions in their `Sepal.Length`. "Virginica" tends to have large `Sepal.Length`, "setosa" has small `Sepal.Length` and "versicolor" sits in between. It suggests that the varialbe can be used to predict the species of flowers.

```
> boxplot(Sepal.Length ~ Species, data=iris, xlab="Species", ylab="Sepal.Length")
```

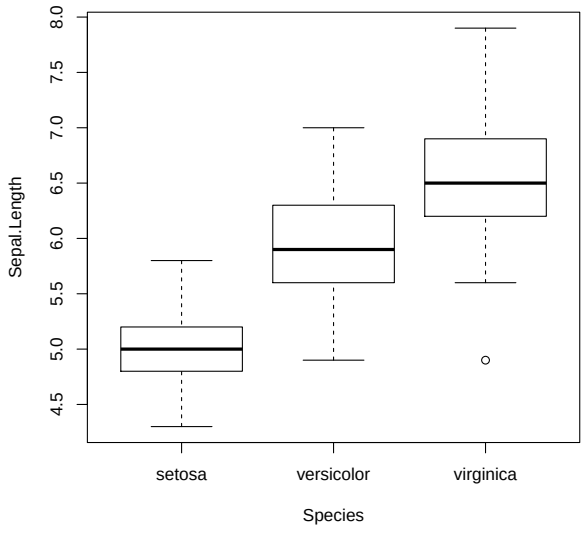

Figure 3.5: Boxplot

A scatter plot can be drawn for two numeric variables with `plot()` as below. Using function `with()`, we don't need to add "`iris$`" before variable names. In the code below, the colors (`col`)

and symbols (`pch`) of points are set to `Species`.

```
> with(iris, plot(Sepal.Length, Sepal.Width, col=Species, pch=as.numeric(Species)))
> ## same function as above
> # plot(iris$Sepal.Length, iris$Sepal.Width, col=iris$Species, pch=as.numeric(iris$Species))
```

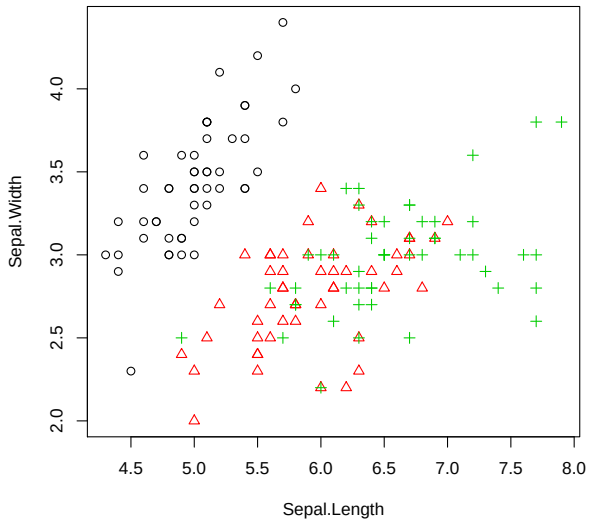

Figure 3.6: Scatter Plot

When there are many points, some of them may overlap. We can use `jitter()` to add a small amount of noise to the data before plotting.

```
> plot(jitter(iris$Sepal.Length), jitter(iris$Sepal.Width))
```

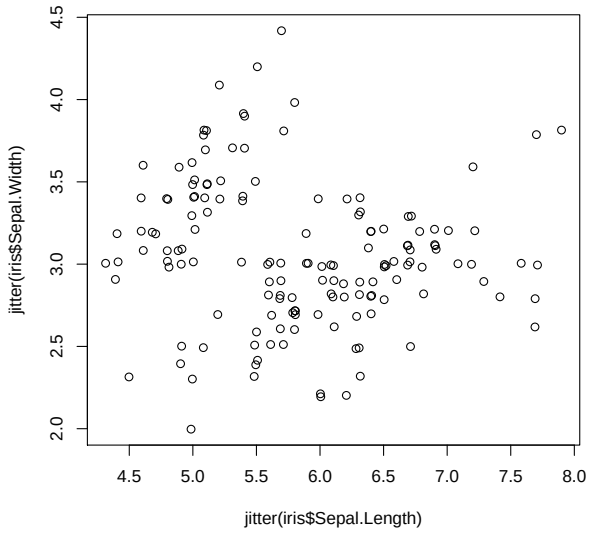

Figure 3.7: Scatter Plot with Jitter

A smooth scatter plot can be plotted with function `smoothScatter()`, which a smoothed color density representation of the scatterplot, obtained through a kernel density estimate.

```
> smoothScatter(iris$Sepal.Length, iris$Sepal.Width)
```

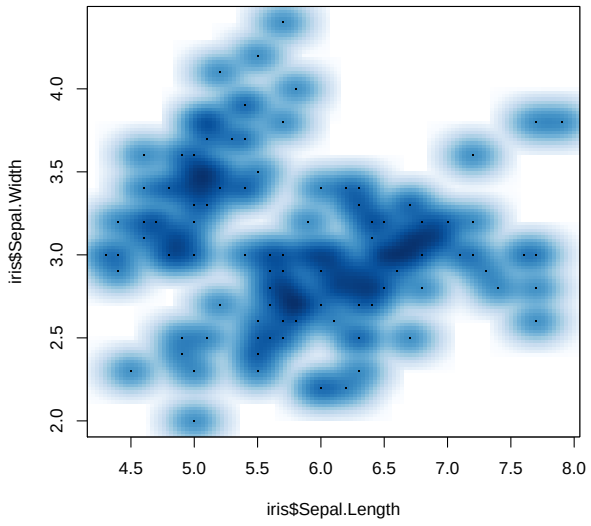

Figure 3.8: Smooth Scatter Plot

A matrix of scatter plots can be produced with function `pairs()`, where each sub figure is the scatter plot of a pair of variables.

```
> pairs(iris)
```

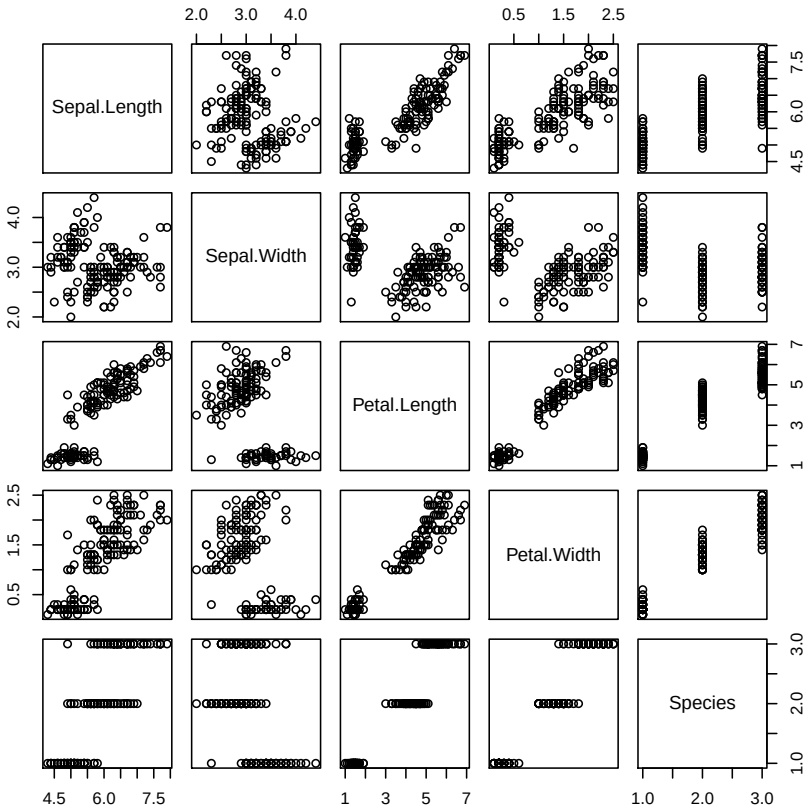

Figure 3.9: A Matrix of Scatter Plots

3.4 More Explorations

This section presents some fancy graphs, including 3D plots, level plots, contour plots, interactive plots and parallel coordinates.

A 3D scatter plot can be produced with package *scatterplot3d* [Ligges and Mächler, 2003].

```
> library(scatterplot3d)
> scatterplot3d(iris$Petal.Width, iris$Sepal.Length, iris$Sepal.Width)
```

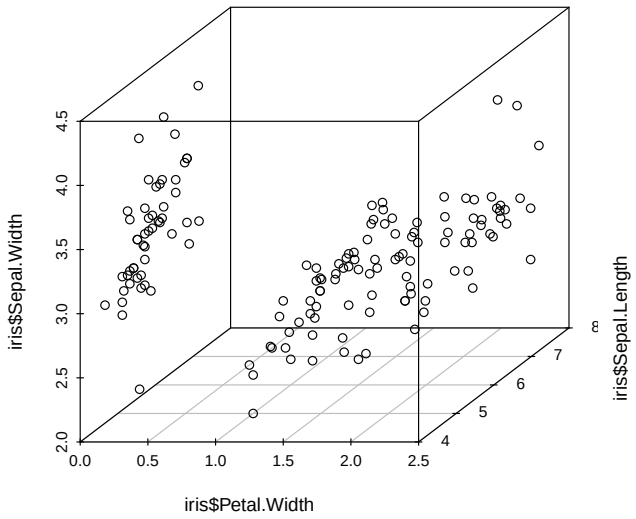

Figure 3.10: 3D Scatter plot

Package *rgl* [Adler et al., 2015] supports interactive 3D scatter plot with `plot3d()`.

```
> library(rgl)
> plot3d(iris$Petal.Width, iris$Sepal.Length, iris$Sepal.Width)
```

A heat map presents a 2D display of a data matrix, which can be generated with `heatmap()` in R. With the code below, we calculate the similarity between different flowers in the `iris` data

with `dist()` and then plot it with a heat map.

```
> distMatrix <- as.matrix(dist(iris[,1:4]))
> heatmap(distMatrix)
```

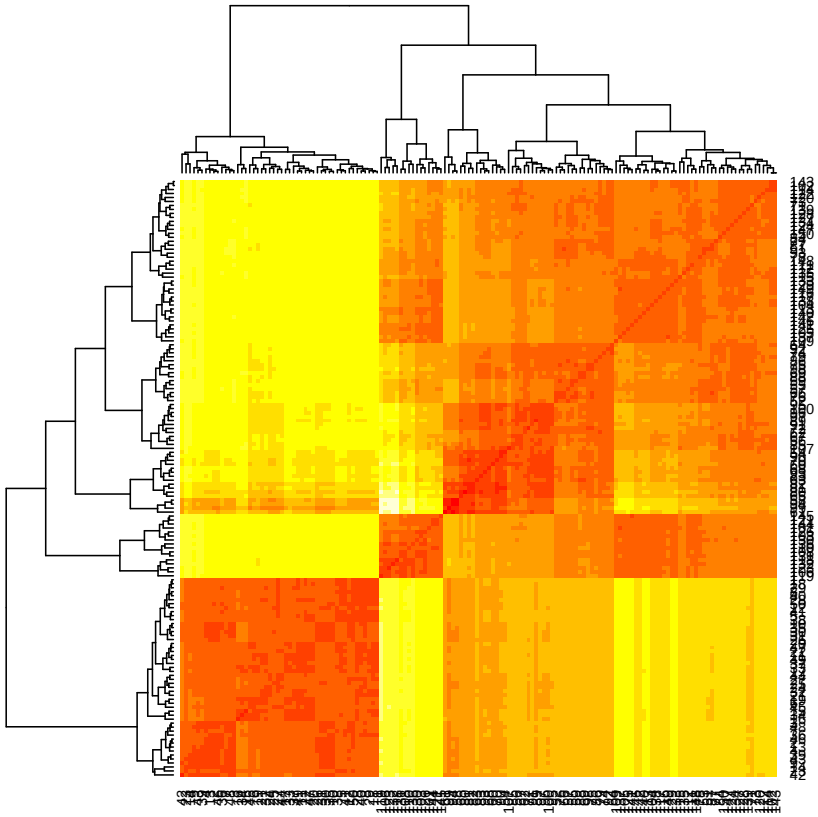

Figure 3.11: Heat Map

A level plot can be produced with function `levelplot()` in package *lattice* [Sarkar, 2008]. Function `grey.colors()` creates a vector of gamma-corrected gray colors. A similar function is

`rainbow()`, which creates a vector of contiguous colors.

```
> library(lattice)
> levelplot(Petal.Width~Sepal.Length*Sepal.Width, iris, cuts=9,
+           col.regions=grey.colors(10)[10:1])
```

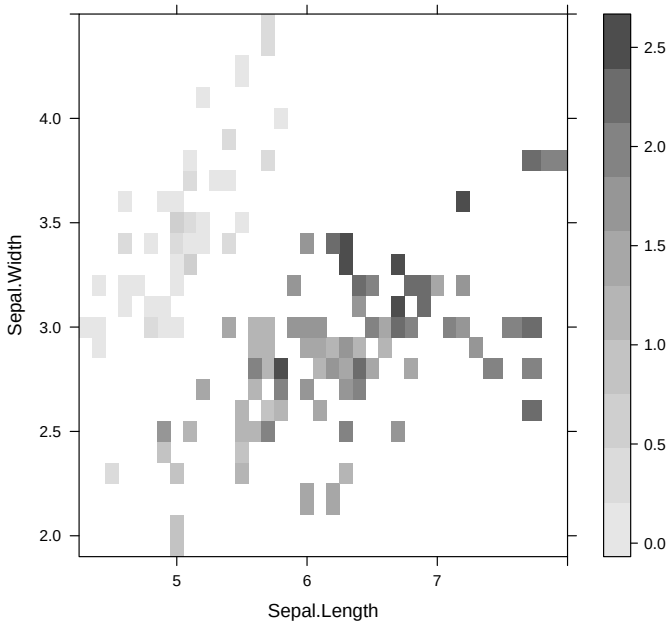

Figure 3.12: Level Plot

Contour plots can be plotted with `contour()` and `filled.contour()` in package *graphics*, and

with `contourplot()` in package *lattice*.

```
> filled.contour(volcano, color=terrain.colors, asp=1,
+                plot.axes=contour(volcano, add=T))
```

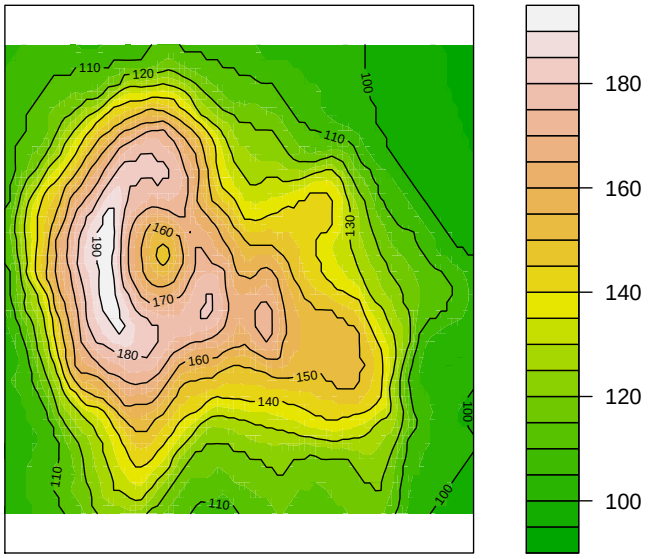

Figure 3.13: Contour

Another way to illustrate a numeric matrix is a 3D surface plot shown as below, which is

generated with function `persp()`.

```
> persp(volcano, theta=25, phi=30, expand=0.5, col="lightblue")
```

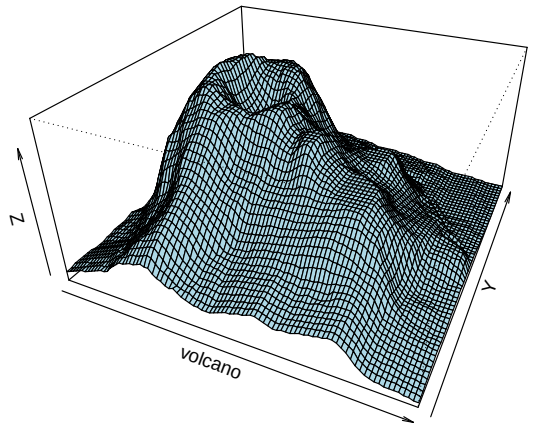

Figure 3.14: 3D Surface

Parallel coordinates provide nice visualization of multiple dimensional data. A parallel coordinates plot can be produced with `parcoord()` in package *MASS*, and with `parallelplot()` in

package *lattice*.

```
> library(MASS)
> parcoord(iris[1:4], col=iris$Species)
```

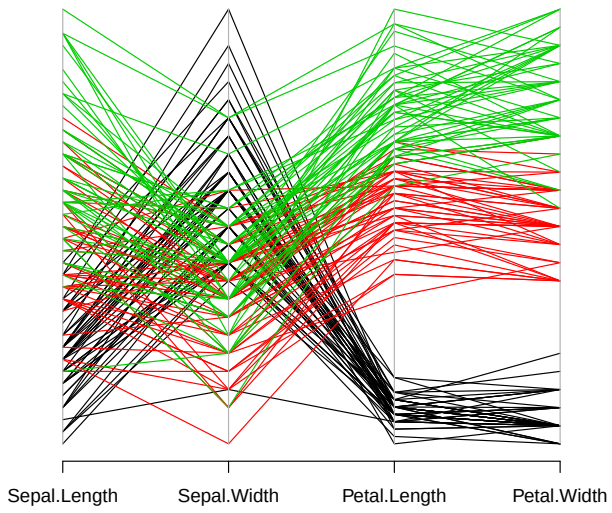

Figure 3.15: Parallel Coordinates

```
> library(lattice)
> parallelplot(~iris[1:4] | Species, data=iris)
```

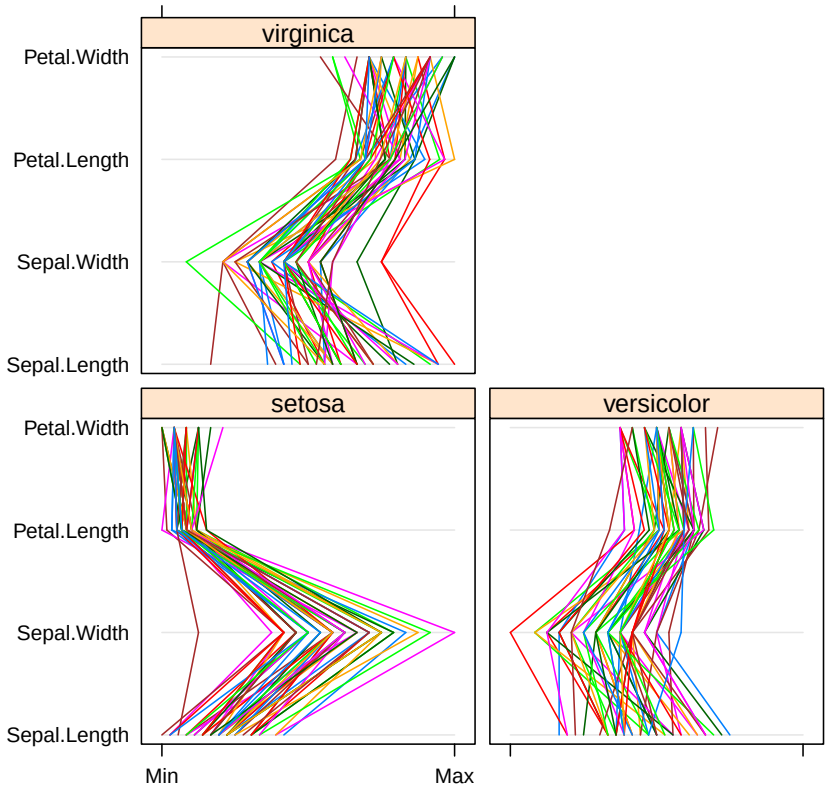

Figure 3.16: Parallel Coordinates with Package *lattice*

Package *ggplot2* [Wickham, 2009] supports complex graphics, which are very useful for exploring data. A simple example is given below. More examples on that package can be found at `http://had.co.nz/ggplot2/`.

```
> library(ggplot2)
> qplot(Sepal.Length, Sepal.Width, data=iris, facets=Species ~.)
```

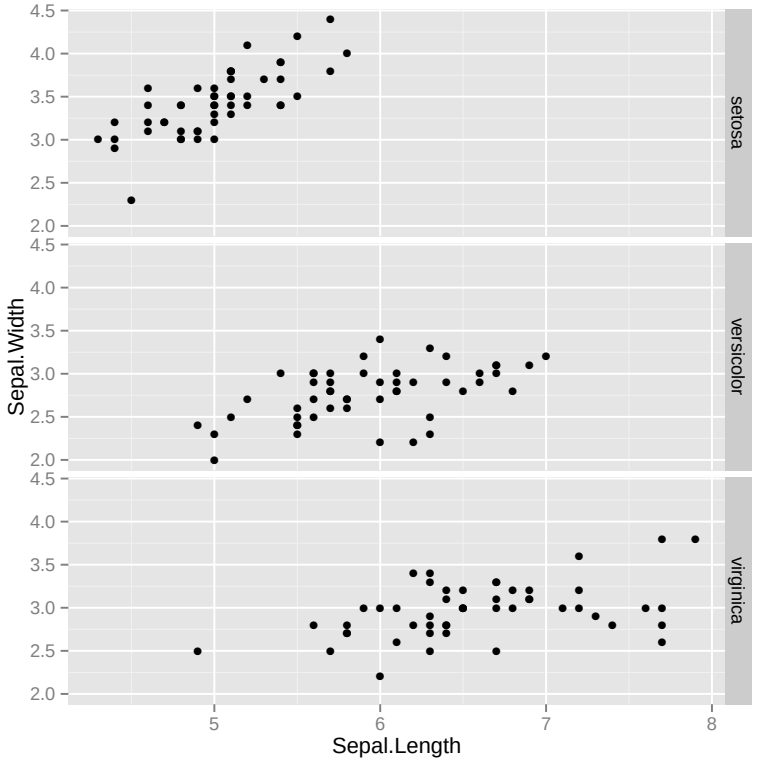

Figure 3.17: Scatter Plot with Package *ggplot2*

3.5 Save Charts into Files

If there are many graphs produced in data exploration, a good practice is to save them into files. R provides a variety of functions for that purpose. Below are examples of saving charts into PDF and PS files respectively with functions `pdf()` and `postscript()`. Picture files of BMP, JPEG, PNG and TIFF formats can be generated respectively with `bmp()`, `jpeg()`, `png()` and `tiff()`. Note that the files (or graphics devices) need be closed with `graphics.off()` or `dev.off()` after plotting.

```
> # save as a PDF file
> pdf("myPlot.pdf")
> x <- 1:50
> plot(x, log(x))
> graphics.off()
> #
> # Save as a postscript file
> postscript("myPlot2.ps")
> x <- -20:20
> plot(x, x^2)
> graphics.off()
```

3.6 Further Readings

Besides the basic plots presented in this chapter, R can produce complex and nice graphics with Package *ggplot2* [Wickham, 2009]. Moreover, R can also produce interactive graphs. Two widely used packages for that purpose are *ggvis* and *googleVis*. Package *ggvis* [1] [Chang and Wickham, 2015] is an implementation of an interactive grammar of graphics. Package *googleVis* [2] [Gesmann and de Castillo, 2011] provides an R interface to Google Charts API, allowing users to create interactive charts based on data frames.

[1] https://cran.r-project.org/web/packages/ggvis/index.html
[2] https://cran.r-project.org/web/packages/googleVis/index.html

Chapter 4

Decision Trees and Random Forest

This chapter shows how to build predictive models with packages *party*, *rpart* and *randomForest*. It starts with building decision trees with package *party* and using the built tree for classification, followed by another way to build decision trees with package *rpart*. After that, it presents an example on training a random forest model with package *randomForest*.

4.1 Decision Trees with Package *party*

This section shows how to build a decision tree for the `iris` data with function `ctree()` in package *party* [Hothorn et al., 2015]. Details of the data can be found in Section 1.3.1. `Sepal.Length`, `Sepal.Width`, `Petal.Length` and `Petal.Width` are used to predict the `Species` of flowers. In the package, function `ctree()` builds a decision tree, and `predict()` makes prediction for new data.

Before modeling, the `iris` data is split below into two subsets: training (70%) and test (30%). The random seed is set to a fixed value below to make the results reproducible.

```
> str(iris)

data.frame:        150 obs. of  5 variables:
 $ Sepal.Length: num  5.1 4.9 4.7 4.6 5 5.4 4.6 5 4.4 4.9 ...
 $ Sepal.Width : num  3.5 3 3.2 3.1 3.6 3.9 3.4 3.4 2.9 3.1 ...
 $ Petal.Length: num  1.4 1.4 1.3 1.5 1.4 1.7 1.4 1.5 1.4 1.5 ...
 $ Petal.Width : num  0.2 0.2 0.2 0.2 0.2 0.4 0.3 0.2 0.2 0.1 ...
 $ Species     : Factor w/ 3 levels "setosa","versicolor",..: 1 1 1 1 1 1 1 1 1 1 ...

> set.seed(1234)
> ind <- sample(2, nrow(iris), replace=TRUE, prob=c(0.7, 0.3))
> trainData <- iris[ind==1,]
> testData <- iris[ind==2,]
```

We then load package *party*, build a decision tree, and check the prediction result. Function `ctree()` provides some parameters, such as `MinSplit`, `MinBusket`, `MaxSurrogate` and `MaxDepth`, to control the training of decision trees. Below we use default settings to build a decision tree. Examples of setting the above parameters are available in Chapter 13. In the code below, `myFormula` specifies that `Species` is the target variable and all other variables are independent variables.

```
> library(party)
> myFormula <- Species ~ Sepal.Length + Sepal.Width + Petal.Length + Petal.Width
> iris_ctree <- ctree(myFormula, data=trainData)
> # check the prediction
> table(predict(iris_ctree), trainData$Species)
```

```
            setosa versicolor virginica
  setosa         40          0         0
  versicolor      0         37         3
  virginica       0          1        31
```

After that, we can have a look at the built tree by printing the rules and plotting the tree.

```
> print(iris_ctree)

         Conditional inference tree with 4 terminal nodes

Response:  Species
Inputs:  Sepal.Length, Sepal.Width, Petal.Length, Petal.Width
Number of observations:  112

1) Petal.Length <= 1.9; criterion = 1, statistic = 104.643
  2)*  weights = 40
1) Petal.Length > 1.9
  3) Petal.Width <= 1.7; criterion = 1, statistic = 48.939
    4) Petal.Length <= 4.4; criterion = 0.974, statistic = 7.397
      5)*  weights = 21
    4) Petal.Length > 4.4
      6)*  weights = 19
  3) Petal.Width > 1.7
    7)*  weights = 32


> plot(iris_ctree)
```

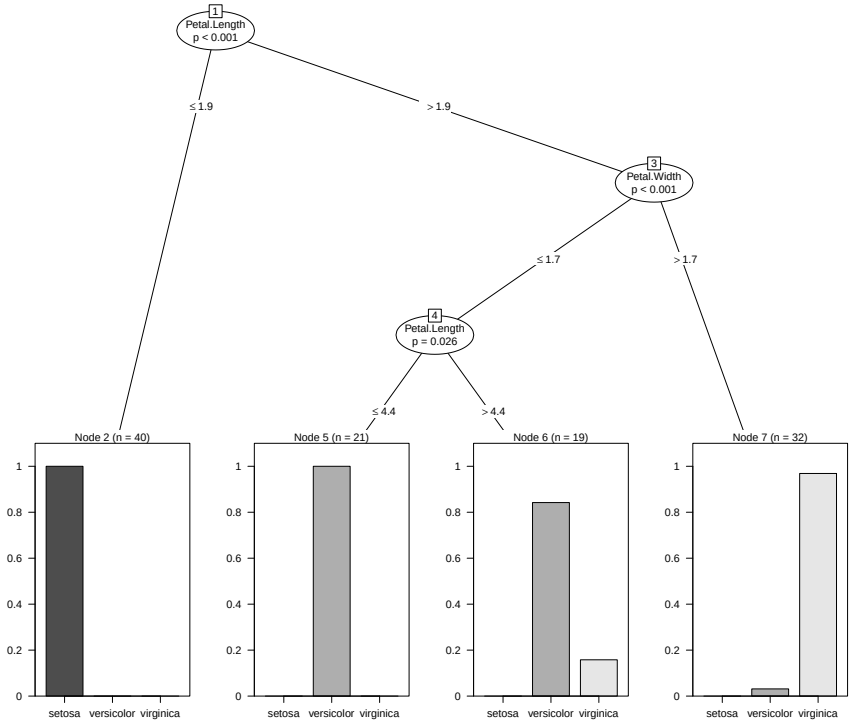

Figure 4.1: Decision Tree

```
> plot(iris_ctree, type="simple")
```

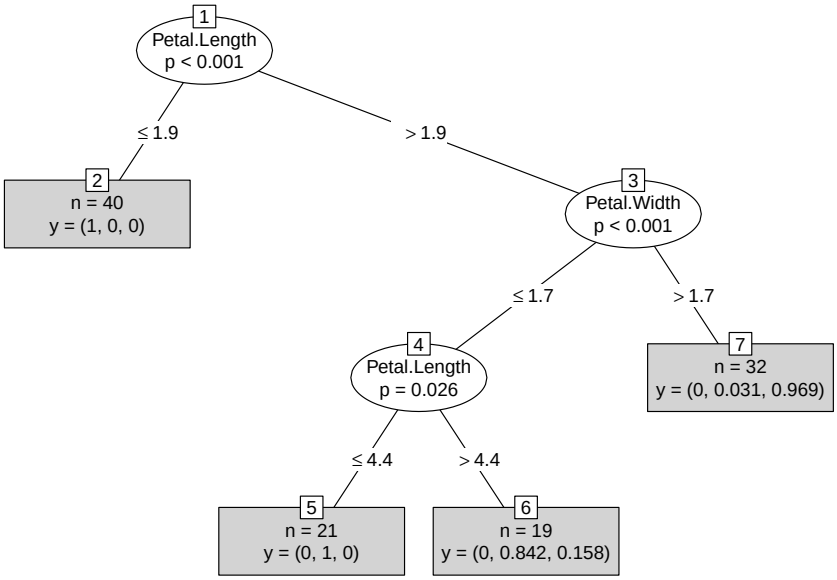

Figure 4.2: Decision Tree (Simple Style)

In the above Figure 4.1, the barplot for each leaf node shows the probabilities of an instance falling into the three species. In Figure 4.2, they are shown as "y" in leaf nodes. For example, node 2 is labeled with "n=40, y=(1, 0, 0)", which means that it contains 40 training instances and all of them belong to the first class "setosa".

After that, the built tree needs to be tested with test data.

```
> # predict on test data
> testPred <- predict(iris_ctree, newdata = testData)
> table(testPred, testData$Species)
```

```
testPred     setosa versicolor virginica
  setosa         10          0         0
  versicolor      0         12         2
  virginica       0          0        14
```

The current version of `ctree()` (i.e. version 0.9-9995) does not handle missing values well, in that an instance with a missing value may sometimes go to the left sub-tree and sometimes to the right. This might be caused by surrogate rules.

Another issue is that, when a variable exists in training data and is fed into `ctree()` but does not appear in the built decision tree, the test data must also have that variable to make prediction. Otherwise, a call to `predict()` would fail. Moreover, if the value levels of a categorical variable in test data are different from that in training data, it would also fail to make prediction on the test data. One way to get around the above issue is, after building a decision tree, to call `ctree()` to build a new decision tree with data containing only those variables existing in the first tree, and to explicitly set the levels of categorical variables in test data to the levels of the corresponding variables in training data. An example on that can be found in Chapter 13.

4.2 Decision Trees with Package *rpart*

Package *rpart* [Therneau et al., 2015] is used in this section to build a decision tree on the `bodyfat` data (see Section 1.3.2 for details of the data). Function `rpart()` is used to build a decision tree, and the tree with the minimum prediction error is selected. After that, it is applied to new data to make prediction with function `predict()`.

At first, we load the `bodyfat` data and have a look at it.

```
> data("bodyfat", package = "TH.data")
> dim(bodyfat)
```

```
[1] 71 10
```

```
> attributes(bodyfat)
```

```
$names
 [1] "age"          "DEXfat"       "waistcirc"    "hipcirc"      "elbowbreadth"
 [6] "kneebreadth"  "anthro3a"     "anthro3b"     "anthro3c"     "anthro4"

$row.names
 [1] "47"  "48"  "49"  "50"  "51"  "52"  "53"  "54"  "55"  "56"  "57"  "58"  "59"
[14] "60"  "61"  "62"  "63"  "64"  "65"  "66"  "67"  "68"  "69"  "70"  "71"  "72"
[27] "73"  "74"  "75"  "76"  "77"  "78"  "79"  "80"  "81"  "82"  "83"  "84"  "85"
[40] "86"  "87"  "88"  "89"  "90"  "91"  "92"  "93"  "94"  "95"  "96"  "97"  "98"
[53] "99"  "100" "101" "102" "103" "104" "105" "106" "107" "108" "109" "110" "111"
[66] "112" "113" "114" "115" "116" "117"

$class
[1] "data.frame"
```

```
> bodyfat[1:5,]
```

```
   age DEXfat waistcirc hipcirc elbowbreadth kneebreadth anthro3a anthro3b
47  57  41.68     100.0   112.0          7.1         9.4     4.42     4.95
48  65  43.29      99.5   116.5          6.5         8.9     4.63     5.01
49  59  35.41      96.0   108.5          6.2         8.9     4.12     4.74
50  58  22.79      72.0    96.5          6.1         9.2     4.03     4.48
51  60  36.42      89.5   100.5          7.1        10.0     4.24     4.68
   anthro3c anthro4
47     4.50    6.13
48     4.48    6.37
49     4.60    5.82
50     3.91    5.66
51     4.15    5.91
```

Next, the data is split into training and test subsets, and a decision tree is built on the training data.

```
> set.seed(1234)
> ind <- sample(2, nrow(bodyfat), replace=TRUE, prob=c(0.7, 0.3))
> bodyfat.train <- bodyfat[ind==1,]
> bodyfat.test <- bodyfat[ind==2,]
> # train a decision tree
> library(rpart)
> myFormula <- DEXfat ~ age + waistcirc + hipcirc + elbowbreadth + kneebreadth
> bodyfat_rpart <- rpart(myFormula, data = bodyfat.train,
+                        control = rpart.control(minsplit = 10))
> attributes(bodyfat_rpart)
```

```
$names
 [1] "frame"               "where"               "call"
 [4] "terms"               "cptable"             "method"
 [7] "parms"               "control"             "functions"
[10] "numresp"             "splits"              "variable.importance"
[13] "y"                   "ordered"

$xlevels
named list()

$class
[1] "rpart"
```

```
> print(bodyfat_rpart$cptable)
```

```
          CP nsplit  rel error    xerror       xstd
1 0.67272638      0 1.00000000 1.0194546 0.18724382
2 0.09390665      1 0.32727362 0.4415438 0.10853044
3 0.06037503      2 0.23336696 0.4271241 0.09362895
4 0.03420446      3 0.17299193 0.3842206 0.09030539
5 0.01708278      4 0.13878747 0.3038187 0.07295556
6 0.01695763      5 0.12170469 0.2739808 0.06599642
7 0.01007079      6 0.10474706 0.2693702 0.06613618
8 0.01000000      7 0.09467627 0.2695358 0.06620732
```

```
> print(bodyfat_rpart)
```

```
n= 56

node), split, n, deviance, yval
      * denotes terminal node

 1) root 56 7265.0290000 30.94589
   2) waistcirc< 88.4 31  960.5381000 22.55645
     4) hipcirc< 96.25 14  222.2648000 18.41143
       8) age< 60.5 9   66.8809600 16.19222 *
       9) age>=60.5 5   31.2769200 22.40600 *
     5) hipcirc>=96.25 17  299.6470000 25.97000
      10) waistcirc< 77.75 6   30.7345500 22.32500 *
      11) waistcirc>=77.75 11  145.7148000 27.95818
        22) hipcirc< 99.5 3    0.2568667 23.74667 *
        23) hipcirc>=99.5 8   72.2933500 29.53750 *
   3) waistcirc>=88.4 25 1417.1140000 41.34880
     6) waistcirc< 104.75 18  330.5792000 38.09111
      12) hipcirc< 109.9 9   68.9996200 34.37556 *
      13) hipcirc>=109.9 9   13.0832000 41.80667 *
     7) waistcirc>=104.75 7  404.3004000 49.72571 *
```

With the code below, the built tree is plotted (see Figure 4.3).

```
> plot(bodyfat_rpart)
> text(bodyfat_rpart, use.n=T)
```

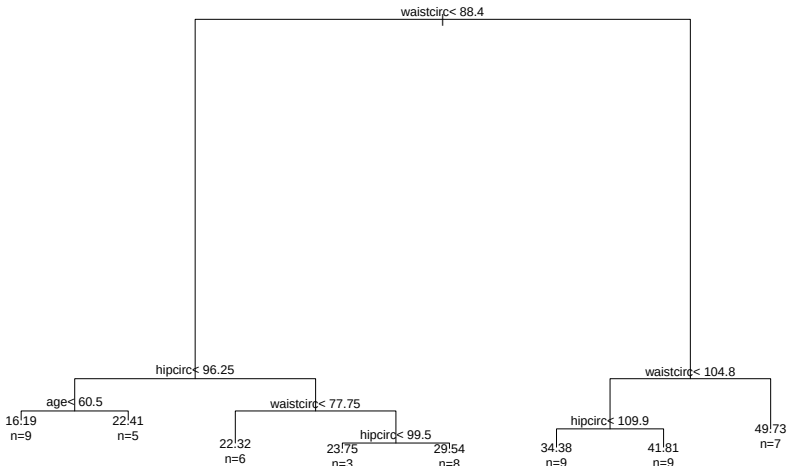

Figure 4.3: Decision Tree with Package *rpart*

Then we select the tree with the minimum prediction error (see Figure 4.4).

```
> opt <- which.min(bodyfat_rpart$cptable[,"xerror"])
> cp <- bodyfat_rpart$cptable[opt, "CP"]
> bodyfat_prune <- prune(bodyfat_rpart, cp = cp)
> print(bodyfat_prune)

n= 56

node), split, n, deviance, yval
      * denotes terminal node

 1) root 56 7265.02900 30.94589
   2) waistcirc< 88.4 31  960.53810 22.55645
     4) hipcirc< 96.25 14  222.26480 18.41143
       8) age< 60.5 9   66.88096 16.19222 *
       9) age>=60.5 5   31.27692 22.40600 *
     5) hipcirc>=96.25 17  299.64700 25.97000
      10) waistcirc< 77.75 6   30.73455 22.32500 *
      11) waistcirc>=77.75 11  145.71480 27.95818 *
   3) waistcirc>=88.4 25 1417.11400 41.34880
     6) waistcirc< 104.75 18  330.57920 38.09111
      12) hipcirc< 109.9 9   68.99962 34.37556 *
      13) hipcirc>=109.9 9   13.08320 41.80667 *
     7) waistcirc>=104.75 7  404.30040 49.72571 *

> plot(bodyfat_prune)
> text(bodyfat_prune, use.n=T)
```

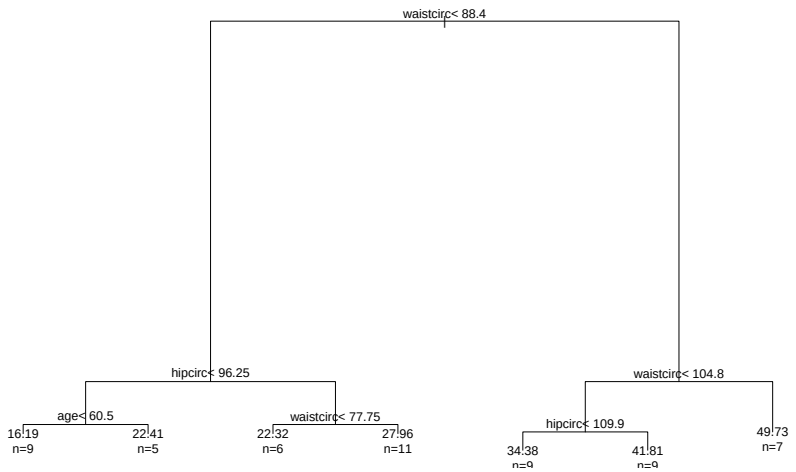

Figure 4.4: Selected Decision Tree

After that, the selected tree is used to make prediction and the predicted values are compared with actual labels. In the code below, function `abline()` draws a diagonal line. The predictions of a good model are expected to be equal or very close to their actual values, that is, most points should be on or close to the diagonal line.

```
> DEXfat_pred <- predict(bodyfat_prune, newdata=bodyfat.test)
> xlim <- range(bodyfat$DEXfat)
> plot(DEXfat_pred ~ DEXfat, data=bodyfat.test, xlab="Observed",
+      ylab="Predicted", ylim=xlim, xlim=xlim)
> abline(a=0, b=1)
```

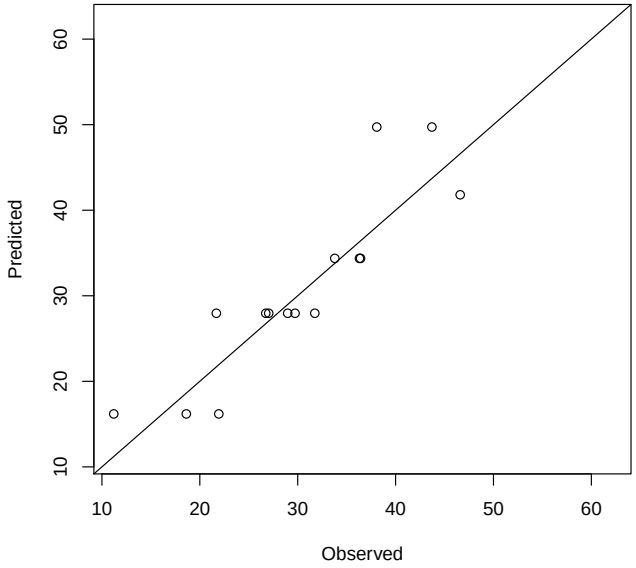

Figure 4.5: Prediction Result

4.3 Random Forest

Package *randomForest* [Liaw and Wiener, 2002] is used below to build a predictive model for the `iris` data (see Section 1.3.1 for details of the data). There are two limitations with function `randomForest()`. First, it cannot handle data with missing values, and users have to impute data before feeding them into the function. Second, there is a limit of 32 to the maximum number of levels of each categorical attribute. Attributes with more than 32 levels have to be transformed first before using `randomForest()`.

An alternative way to build a random forest is to use function `cforest()` from package *party*, which is not limited to the above maximum levels. However, generally speaking, categorical variables with more levels will make it require more memory and take longer time to build a random forest.

Again, the `iris` data is first split into two subsets: training (70%) and test (30%).

```
> ind <- sample(2, nrow(iris), replace=TRUE, prob=c(0.7, 0.3))
> trainData <- iris[ind==1,]
> testData <- iris[ind==2,]
```

Then we load package *randomForest* and train a random forest. In the code below, the formula is set to "`Species` $\sim$.", which means to predict `Species` with all other variables in the data.

```
> library(randomForest)
> rf <- randomForest(Species ~ ., data=trainData, ntree=100, proximity=TRUE)
> table(predict(rf), trainData$Species)
```

```
            setosa versicolor virginica
  setosa         36          0         0
  versicolor      0         31         2
  virginica       0          1        34
```

```
> print(rf)
```

```
Call:
 randomForest(formula = Species ~ ., data = trainData, ntree = 100,      proximity = TRUE)
               Type of random forest: classification
                     Number of trees: 100
No. of variables tried at each split: 2

        OOB estimate of  error rate: 2.88%
Confusion matrix:
           setosa versicolor virginica class.error
setosa         36          0         0  0.00000000
versicolor      0         31         1  0.03125000
virginica       0          2        34  0.05555556
```

```
> attributes(rf)
```

```
$names
 [1] "call"            "type"            "predicted"       "err.rate"
 [5] "confusion"       "votes"           "oob.times"       "classes"
 [9] "importance"      "importanceSD"    "localImportance" "proximity"
[13] "ntree"           "mtry"            "forest"          "y"
[17] "test"            "inbag"           "terms"

$class
[1] "randomForest.formula" "randomForest"
```

After that, we plot the error rates with various number of trees.

```
> plot(rf)
```

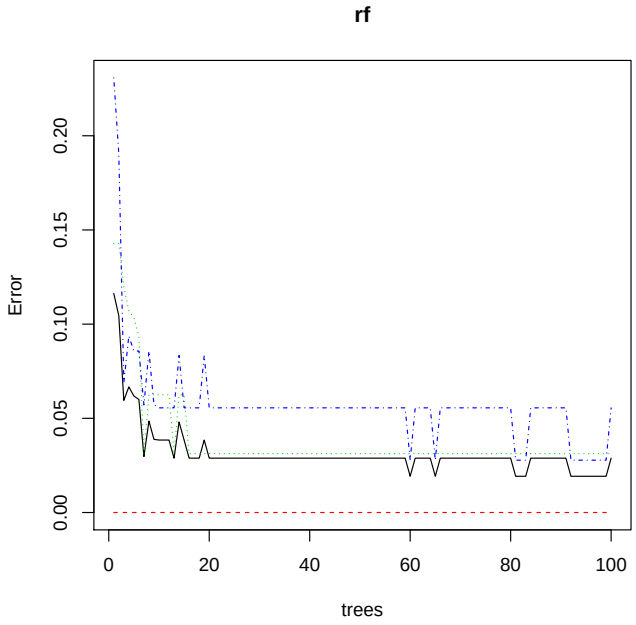

Figure 4.6: Error Rate of Random Forest

The importance of variables can be obtained with functions `importance()` and `varImpPlot()`.

```
> importance(rf)

             MeanDecreaseGini
Sepal.Length         6.913882
Sepal.Width          1.282567
Petal.Length        26.267151
Petal.Width         34.163836

> varImpPlot(rf)
```

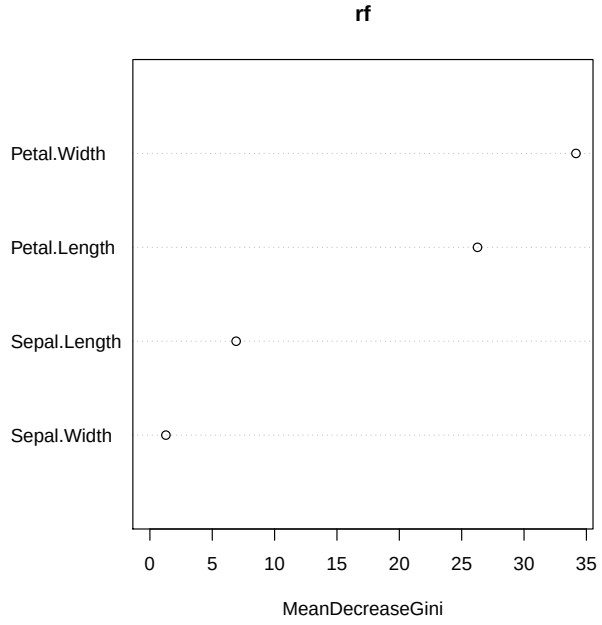

Figure 4.7: Variable Importance

Finally, the built random forest is tested on test data, and the result is checked with functions `table()` and `margin()`. The margin of a data point is as the proportion of votes for the correct class minus maximum proportion of votes for other classes. Generally speaking, positive margin

means correct classification.

```
> irisPred <- predict(rf, newdata=testData)
> table(irisPred, testData$Species)

irisPred     setosa versicolor virginica
  setosa         14          0         0
  versicolor      0         17         3
  virginica       0          1        11

> plot(margin(rf, testData$Species))
```

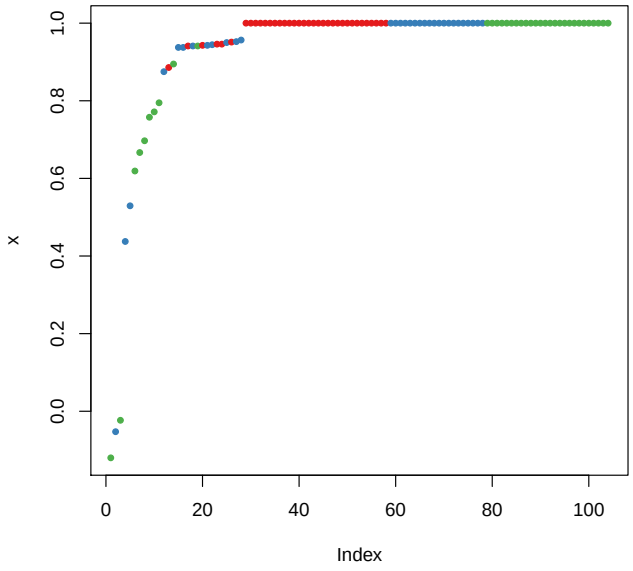

Figure 4.8: Margin of Predictions

Chapter 5

Regression

Regression is to build a function of *independent variables* (also known as *predictors*) to predict a *dependent variable* (also called *response*). For example, banks assess the risk of home-loan applicants based on their age, income, expenses, occupation, number of dependents, total credit limit, etc.

This chapter introduces basic concepts and presents examples of various regression techniques. At first, it shows an example on building a linear regression model to predict CPI data. After that, it introduces logistic regression. The generalized linear model (GLM) is then presented, followed by a brief introduction of non-linear regression.

A collection of some helpful R functions for regression analysis is available as a reference card on *R Functions for Regression Analysis* [1].

5.1 Linear Regression

Linear regression is to predict response with a linear function of predictors as follows:

$$y = c_0 + c_1 x_1 + c_2 x_2 + \cdots + c_k x_k,$$

where $x_1, x_2, \cdots, x_k$ are predictors and y is the response to predict.

Linear regression is demonstrated below with function `lm()` on the Australian CPI (Consumer Price Index) data, which are quarterly CPIs from 2008 to 2010 [2].

At first, the data is created and plotted. In the code below, an x-axis is added manually with function `axis()`, where `las=3` makes text vertical.

[1] `http://cran.r-project.org/doc/contrib/Ricci-refcard-regression.pdf`
[2] From Australian Bureau of Statistics <`http://www.abs.gov.au`>

```
> year <- rep(2008:2010, each=4)
> quarter <- rep(1:4, 3)
> cpi <- c(162.2, 164.6, 166.5, 166.0,
+          166.2, 167.0, 168.6, 169.5,
+          171.0, 172.1, 173.3, 174.0)
> plot(cpi, xaxt="n", ylab="CPI", xlab="")
> # draw x-axis
> axis(1, labels=paste(year,quarter,sep="Q"), at=1:12, las=3)
```

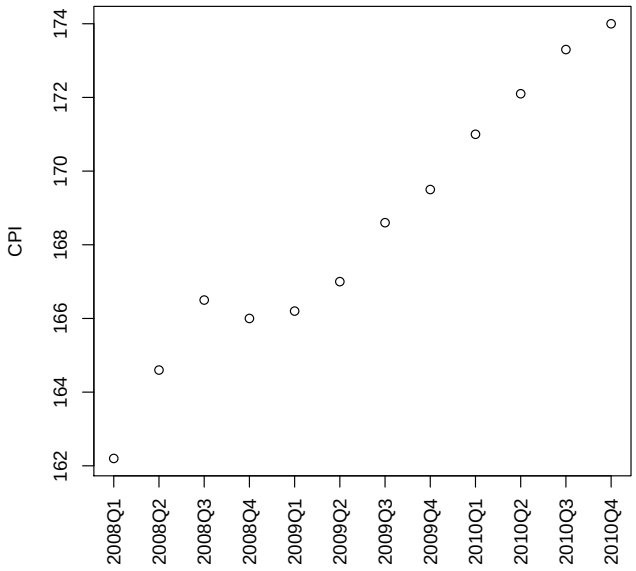

Figure 5.1: Australian CPIs in Year 2008 to 2010

We then check the correlation between `CPI` and the other variables, `year` and `quarter`.

```
> cor(year,cpi)

[1] 0.9096316

> cor(quarter,cpi)

[1] 0.3738028
```

Then a linear regression model is built with function `lm()` on the above data, using `year` and `quarter` as predictors and `CPI` as response.

```
> fit <- lm(cpi ~ year + quarter)
> fit

Call:
lm(formula = cpi ~ year + quarter)

Coefficients:
(Intercept)         year      quarter
  -7644.488        3.888        1.167
```

With the above linear model, CPI is calculated as

$$\text{cpi} = c_0 + c_1 * \text{year} + c_2 * \text{quarter},$$

where c_0, c_1 and c_2 are coefficients from model `fit`. Therefore, the CPIs in 2011 can be get as follows. An easier way for this is using function `predict()`, which will be demonstrated at the end of this subsection.

```
> (cpi2011 <- fit$coefficients[[1]] + fit$coefficients[[2]]*2011 +
+             fit$coefficients[[3]]*(1:4))

[1] 174.4417 175.6083 176.7750 177.9417
```

More details of the model can be obtained with the code below.

```
> attributes(fit)

$names
 [1] "coefficients"  "residuals"     "effects"       "rank"
 [5] "fitted.values" "assign"        "qr"            "df.residual"
 [9] "xlevels"       "call"          "terms"         "model"

$class
[1] "lm"

> fit$coefficients

 (Intercept)         year      quarter
-7644.487500     3.887500     1.166667
```

The differences between observed values and fitted values can be obtained with function `residuals()`.

```
> # differences between observed values and fitted values
> residuals(fit)

          1           2           3           4           5           6
-0.57916667  0.65416667  1.38750000 -0.27916667 -0.46666667 -0.83333333
          7           8           9          10          11          12
-0.40000000 -0.66666667  0.44583333  0.37916667  0.41250000 -0.05416667

> summary(fit)

Call:
lm(formula = cpi ~ year + quarter)

Residuals:
    Min      1Q  Median      3Q     Max
-0.8333 -0.4948 -0.1667  0.4208  1.3875

Coefficients:
             Estimate Std. Error t value Pr(>|t|)
(Intercept) -7644.4875   518.6543 -14.739 1.31e-07 ***
year            3.8875     0.2582  15.058 1.09e-07 ***
quarter         1.1667     0.1885   6.188 0.000161 ***
---
Signif. codes:  0 Ś***Š 0.001 Ś**Š 0.01 Ś*Š 0.05 Ś.Š 0.1 Ś Š 1

Residual standard error: 0.7302 on 9 degrees of freedom
Multiple R-squared:  0.9672,        Adjusted R-squared:  0.9599
F-statistic: 132.5 on 2 and 9 DF,  p-value: 2.108e-07
```

We then plot the fitted model as below.

```
> plot(fit)
```

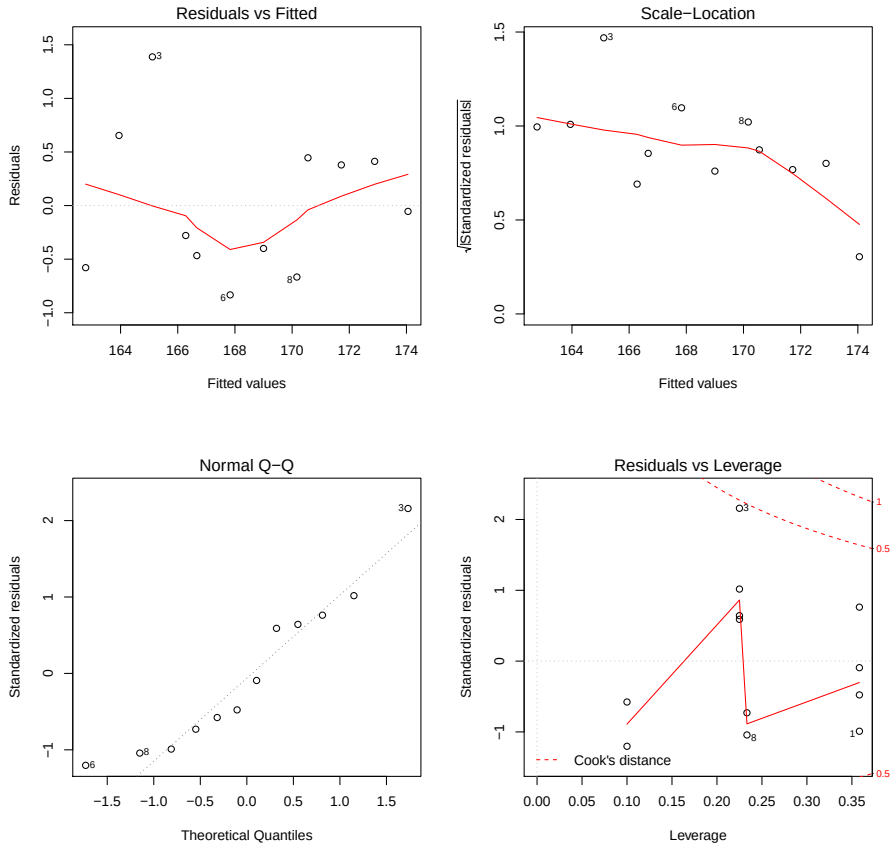

Figure 5.2: Prediction with Linear Regression Model - 1

We can also plot the model in a 3D plot as below, where function `scatterplot3d()` creates a 3D scatter plot and `plane3d()` draws the fitted plane. Parameter `lab` specifies the number of tickmarks on the x- and y-axes.

```
> library(scatterplot3d)
> s3d <- scatterplot3d(year, quarter, cpi, highlight.3d=T, type="h", lab=c(2,3))
> s3d$plane3d(fit)
```

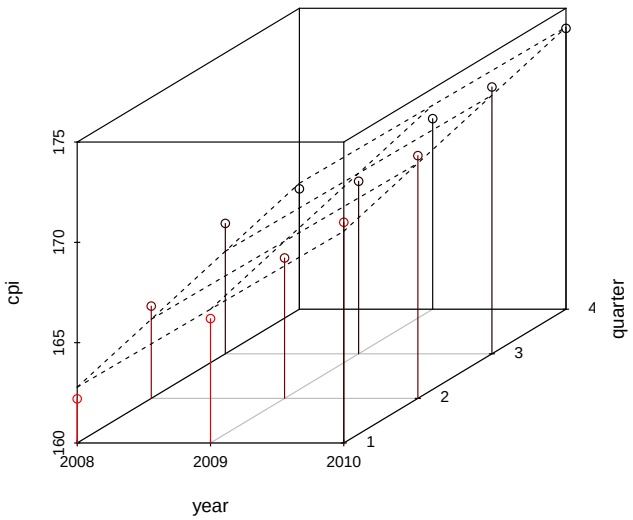

Figure 5.3: A 3D Plot of the Fitted Model

With the model, the CPIs in year 2011 can be predicted as follows, and the predicted values are shown as red triangles in Figure 5.4.

```
> data2011 <- data.frame(year=2011, quarter=1:4)
> cpi2011 <- predict(fit, newdata=data2011)
> style <- c(rep(1,12), rep(2,4))
> plot(c(cpi, cpi2011), xaxt="n", ylab="CPI", xlab="", pch=style, col=style)
> axis(1, at=1:16, las=3,
+      labels=c(paste(year,quarter,sep="Q"), "2011Q1", "2011Q2", "2011Q3", "2011Q4"))
```

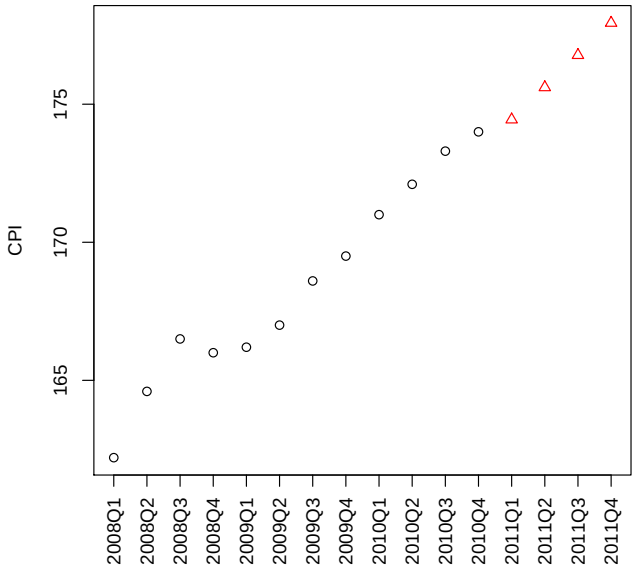

Figure 5.4: Prediction of CPIs in 2011 with Linear Regression Model

5.2 Logistic Regression

Logistic regression is used to predict the probability of occurrence of an event by fitting data to a logistic curve. A logistic regression model is built as the following equation:

$$logit(y) = c_0 + c_1 x_1 + c_2 x_2 + \cdots + c_k x_k,$$

where $x_1, x_2, \cdots, x_k$ are predictors, y is a response to predict, and $logit(y) = ln(\frac{y}{1-y})$. The above equation can also be written as

$$y = \frac{1}{1 + e^{-(c_0 + c_1 x_1 + c_2 x_2 + \cdots + c_k x_k)}}.$$

Logistic regression can be built with function `glm()` by setting `family` to `binomial(link="logit")`. Detailed introductions on logistic regression can be found at the following links.

- R Data Analysis Examples - Logit Regression
  `http://www.ats.ucla.edu/stat/r/dae/logit.htm`

- Logistic Regression (with R)
  `http://nlp.stanford.edu/~manning/courses/ling289/logistic.pdf`

5.3 Generalized Linear Regression

The generalized linear model (GLM) generalizes linear regression by allowing the linear model to be related to the response variable via a link function and allowing the magnitude of the variance of each measurement to be a function of its predicted value. It unifies various other statistical models, including linear regression, logistic regression and Poisson regression. Function `glm()` is used to fit generalized linear models, specified by giving a symbolic description of the linear predictor and a description of the error distribution.

A generalized linear model is built below with `glm()` on the `bodyfat` data (see Section 1.3.2 for details of the data).

```
> data("bodyfat", package="TH.data")
> myFormula <- DEXfat ~ age + waistcirc + hipcirc + elbowbreadth + kneebreadth
> bodyfat.glm <- glm(myFormula, family = gaussian("log"), data = bodyfat)
> summary(bodyfat.glm)

Call:
glm(formula = myFormula, family = gaussian("log"), data = bodyfat)

Deviance Residuals:
     Min        1Q    Median        3Q       Max
-11.5688   -3.0065    0.1266    2.8310   10.0966

Coefficients:
             Estimate Std. Error t value Pr(>|t|)
(Intercept)  0.734293   0.308949   2.377  0.02042 *
age          0.002129   0.001446   1.473  0.14560
waistcirc    0.010489   0.002479   4.231 7.44e-05 ***
hipcirc      0.009702   0.003231   3.003  0.00379 **
elbowbreadth 0.002355   0.045686   0.052  0.95905
kneebreadth  0.063188   0.028193   2.241  0.02843 *
---
Signif. codes:  0 Ś***Š 0.001 Ś**Š 0.01 Ś*Š 0.05 Ś.Š 0.1 Ś Š 1

(Dispersion parameter for gaussian family taken to be 20.31433)

    Null deviance: 8536.0  on 70  degrees of freedom
Residual deviance: 1320.4  on 65  degrees of freedom
AIC: 423.02

Number of Fisher Scoring iterations: 5

> pred <- predict(bodyfat.glm, type="response")
```

In the code above, `type` indicates the type of prediction required. The default is on the scale of the linear predictors, and the alternative `"response"` is on the scale of the response variable.

```
> plot(bodyfat$DEXfat, pred, xlab="Observed Values", ylab="Predicted Values")
> abline(a=0, b=1)
```

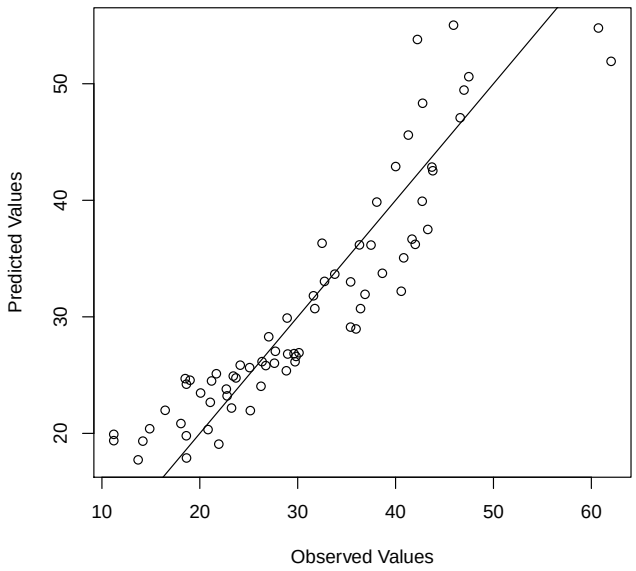

Figure 5.5: Prediction with Generalized Linear Regression Model

In the above code, if `family=gaussian("identity")` is used, the built model would be similar to linear regression. One can also make it a logistic regression by setting `family` to `binomial("logit")`.

5.4 Non-linear Regression

While linear regression is to find the line that comes closest to data, non-linear regression is to fit a curve through data. Function `nls()` provides nonlinear regression. Examples of nls() can be found by running "?nls" under R.

Chapter 6

Clustering

This chapter presents examples of various clustering techniques in R, including k-means clustering, k-medoids clustering, hierarchical clustering and density-based clustering. The first two sections demonstrate how to use the k-means and k-medoids algorithms to cluster the *iris* data. The third section shows an example on hierarchical clustering on the same data. The last section describes the idea of density-based clustering and the DBSCAN algorithm, and shows how to cluster with DBSCAN and then label new data with the clustering model. For readers who are not familiar with clustering, introductions of various clustering techniques can be found in [Zhao et al., 2009a] and [Jain et al., 1999].

6.1 The k-Means Clustering

This section shows k-means clustering of `iris` data (see Section 1.3.1 for details of the data). At first, we remove species from the data to cluster. After that, we apply function `kmeans()` to `iris2`, and store the clustering result in `kmeans.result`. The cluster number is set to 3 in the code below.

```
> iris2 <- iris
> iris2$Species <- NULL
> (kmeans.result <- kmeans(iris2, 3))

K-means clustering with 3 clusters of sizes 38, 50, 62

Cluster means:
  Sepal.Length Sepal.Width Petal.Length Petal.Width
1     6.850000    3.073684     5.742105    2.071053
2     5.006000    3.428000     1.462000    0.246000
3     5.901613    2.748387     4.393548    1.433871

Clustering vector:
  [1] 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2
 [39] 2 2 2 2 2 2 2 2 2 2 2 2 3 3 1 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3
 [77] 3 1 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 1 3 1 1 1 1 3 1 1 1 1 1 1 3
[115] 3 1 1 1 1 3 1 3 1 3 1 1 3 3 1 1 1 1 1 3 1 1 1 1 3 1 1 1 3 1 1 1 3 1 1 1 3

Within cluster sum of squares by cluster:
[1] 23.87947 15.15100 39.82097
 (between_SS / total_SS =  88.4 %)

Available components:
```

```
[1] "cluster"      "centers"      "totss"        "withinss"     "tot.withinss"
[6] "betweenss"    "size"         "iter"         "ifault"
```

The clustering result is then compared with the class label (`Species`) to check whether similar objects are grouped together.

```
> table(iris$Species, kmeans.result$cluster)

             1  2  3
  setosa     0 50  0
  versicolor  2  0 48
  virginica  36  0 14
```

The above result shows that cluster "setosa" can be easily separated from the other clusters, and that clusters "versicolor" and "virginica" are to a small degree overlapped with each other.

Next, the clusters and their centers are plotted (see Figure 6.1). Note that there are four dimensions in the data and that only the first two dimensions are used to draw the plot below. Some black points close to the green center (asterisk) are actually closer to the black center in the four dimensional space. We also need to be aware that the results of k-means clustering may vary from run to run, due to random selection of initial cluster centers.

```
> plot(iris2[c("Sepal.Length", "Sepal.Width")], col = kmeans.result$cluster)
> # plot cluster centers
> points(kmeans.result$centers[,c("Sepal.Length", "Sepal.Width")], col = 1:3,
+        pch = 8, cex=2)
```

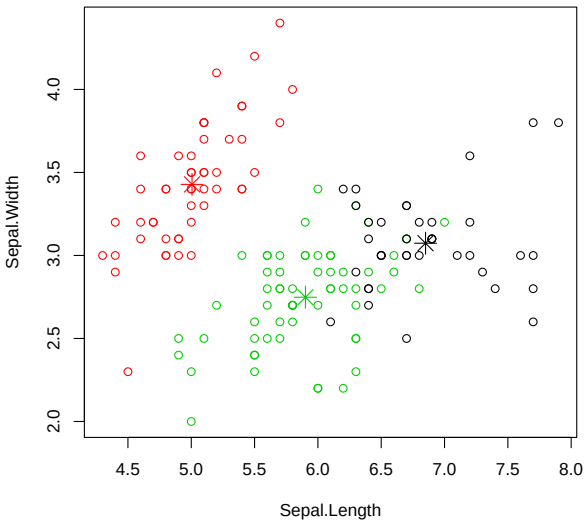

Figure 6.1: Results of k-Means Clustering

More examples of k-means clustering can be found in Section 7.3 and Section 10.8.1.

6.2 The k-Medoids Clustering

This sections shows k-medoids clustering with functions `pam()` and `pamk()`. The k-medoids clustering is very similar to k-means, and the major difference between them is that: while a cluster

is represented with its center in the k-means algorithm, it is represented with the object closest to the center of the cluster in the k-medoids clustering. The k-medoids clustering is more robust than k-means in presence of outliers. PAM (Partitioning Around Medoids) is a classic algorithm for k-medoids clustering. While the PAM algorithm is inefficient for clustering large data, the CLARA algorithm is an enhanced technique of PAM by drawing multiple samples of data, applying PAM on each sample and then returning the best clustering. It performs better than PAM on larger data. Functions `pam()` and `clara()` in package *cluster* [Maechler et al., 2015] are respectively implementations of PAM and CLARA in R. For both algorithms, a user has to specify k, the number of clusters to find. As an enhanced version of `pam()`, function `pamk()` in package *fpc* [Hennig, 2015] does not require a user to choose k. Instead, it calls the function `pam()` or `clara()` to perform a partitioning around medoids clustering with the number of clusters estimated by optimum average silhouette width.

With the code below, we demonstrate how to find clusters with `pam()` and `pamk()`.

```
> library(fpc)
> pamk.result <- pamk(iris2)
> # number of clusters
> pamk.result$nc
```

```
[1] 2
```

```
> # check clustering against actual species
> table(pamk.result$pamobject$clustering, iris$Species)
```

```
   setosa versicolor virginica
1      50          1         0
2       0         49        50
```

```
> layout(matrix(c(1,2),1,2)) # 2 graphs per page
> plot(pamk.result$pamobject)
> layout(matrix(1)) # change back to one graph per page
```

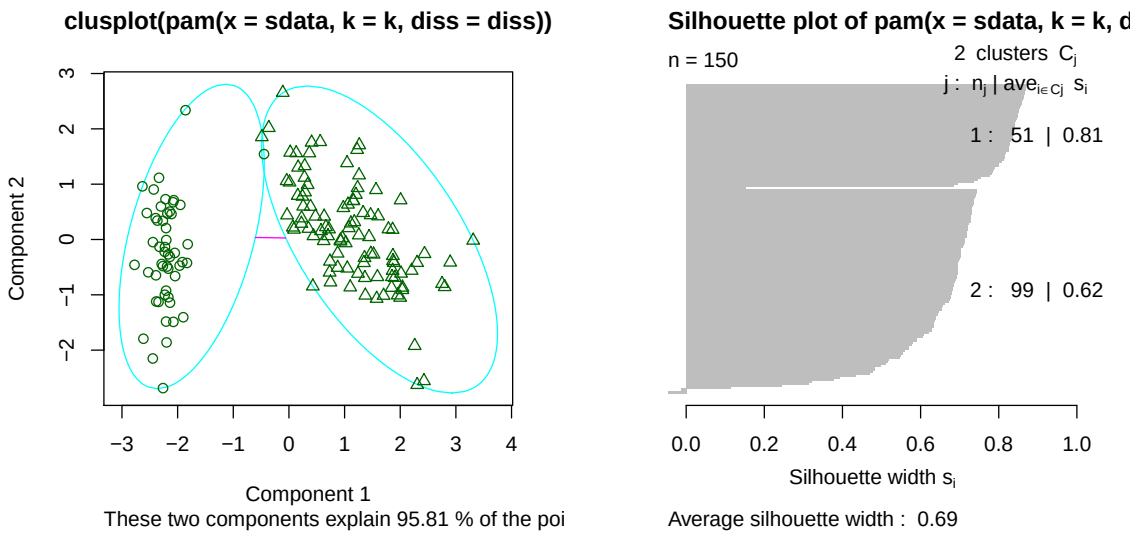

Figure 6.2: Clustering with the k-medoids Algorithm - I

In the above example, `pamk()` produces two clusters: one is "setosa", and the other is a mixture of "versicolor" and "virginica". In Figure 6.2, the left chart is a 2-dimensional "clusplot" (clustering

plot) of the two clusters and the lines show the distance between clusters. The right one shows their silhouettes. In the silhouette, a large s_i (almost 1) suggests that the corresponding observations are very well clustered, a small s_i (around 0) means that the observation lies between two clusters, and observations with a negative s_i are probably placed in the wrong cluster. Since the average S_i are respectively 0.81 and 0.62 in the above silhouette, the identified two clusters are well clustered.

Next, we try `pam()` with $k = 3$.

```
> library(cluster)
> pam.result <- pam(iris2, 3)
> table(pam.result$clustering, iris$Species)
```

```
   setosa versicolor virginica
1      50          0         0
2       0         48        14
3       0          2        36
```

```
> layout(matrix(c(1,2),1,2)) # 2 graphs per page
> plot(pam.result)
> layout(matrix(1)) # change back to one graph per page
```

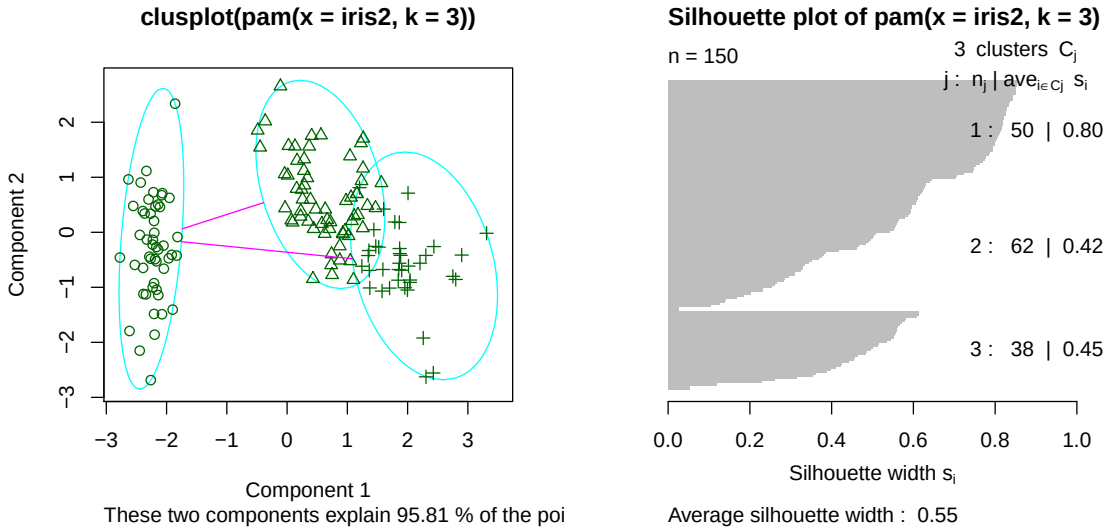

Figure 6.3: Clustering with the k-medoids Algorithm - II

With the above result produced with `pam()`, there are three clusters: 1) cluster 1 is species "setosa" and is well separated from the other two; 2) cluster 2 is mainly composed of "versicolor", plus some cases from "virginica"; and 3) the majority of cluster 3 are "virginica", with two cases from "versicolor".

It's hard to say which one is better out of the above two clusterings produced respectively with `pamk()` and `pam()`. It depends on the target problem and domain knowledge and experience. In this example, the result of `pam()` seems better, because it identifies three clusters, corresponding to three species. Therefore, the heuristic way to identify the number of clusters in `pamk()` does not necessarily produce the best result. Note that we cheated by setting $k = 3$ when using `pam()`, which is already known to us as the number of species.

More examples of k-medoids clustering can be found in Section 10.8.2.

6.3 Hierarchical Clustering

This section demonstrates hierarchical clustering with `hclust()` on `iris` data (see Section 1.3.1 for details of the data).

We first draw a sample of 40 records from the iris data, so that the clustering plot will not be over crowded. Same as before, variable `Species` is removed from the data. After that, we apply hierarchical clustering to the data.

```
> idx <- sample(1:dim(iris)[1], 40)
> irisSample <- iris[idx,]
> irisSample$Species <- NULL
> hc <- hclust(dist(irisSample), method="ave")

> plot(hc, hang = -1, labels=iris$Species[idx])
> # cut tree into 3 clusters
> rect.hclust(hc, k=3)
> groups <- cutree(hc, k=3)
```

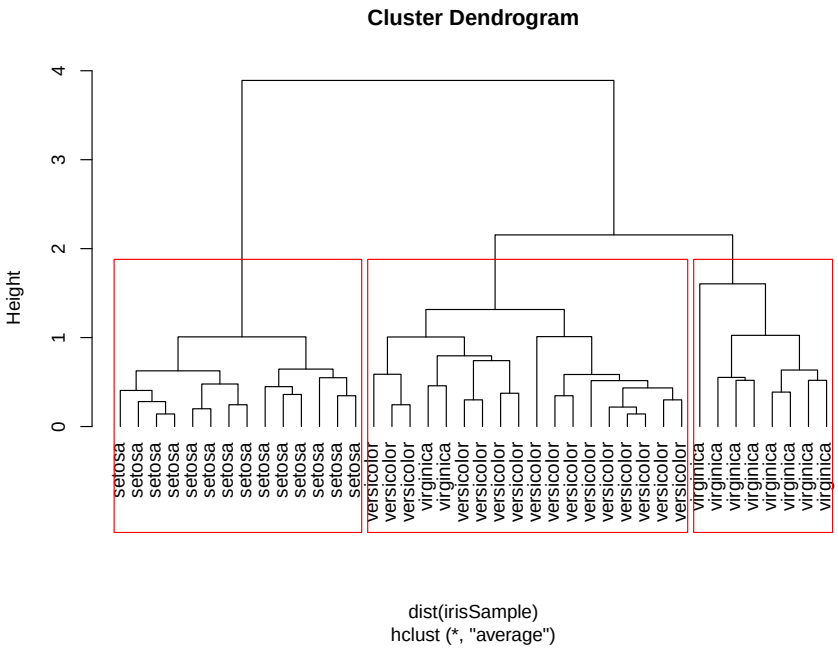

Figure 6.4: Cluster Dendrogram

Similar to the above clustering of k-means, Figure 6.4 also shows that cluster "setosa" can be easily separated from the other two clusters, and that clusters "versicolor" and "virginica" are to a small degree overlapped with each other.

More examples of hierarchical clustering can be found in Section 8.4 and Section 10.7.

6.4 Density-based Clustering

The DBSCAN algorithm [Ester et al., 1996] from package *fpc* [Hennig, 2015] provides a density-based clustering for numeric data. The idea of density-based clustering is to group objects into one cluster if they are connected to one another by densely populated area. There are two key parameters in DBSCAN :

- `eps:` reachability distance, which defines the size of neighborhood; and

- `MinPts:` minimum number of points.

If the number of points in the neighborhood of point α is no less than `MinPts`, then α is a *dense point*. All the points in its neighborhood are *density-reachable* from α and are put into the same cluster as α.

The strengths of density-based clustering are that it can discover clusters with various shapes and sizes and is insensitive to noise. As a comparison, the k-means algorithm tends to find clusters with sphere shape and with similar sizes.

Below is an example of density-based clustering of the `iris` data.

```
> library(fpc)
> iris2 <- iris[-5] # remove class tags
> ds <- dbscan(iris2, eps=0.42, MinPts=5)
> # compare clusters with original class labels
> table(ds$cluster, iris$Species)
```

```
   setosa versicolor virginica
0       2         10        17
1      48          0         0
2       0         37         0
3       0          3        33
```

In the above table, "1" to "3" in the first column are three identified clusters, while "0" stands for noises or outliers, i.e., objects that are not assigned to any clusters. The noises are shown as black circles in Figure 6.5.

```
> plot(ds, iris2)
```

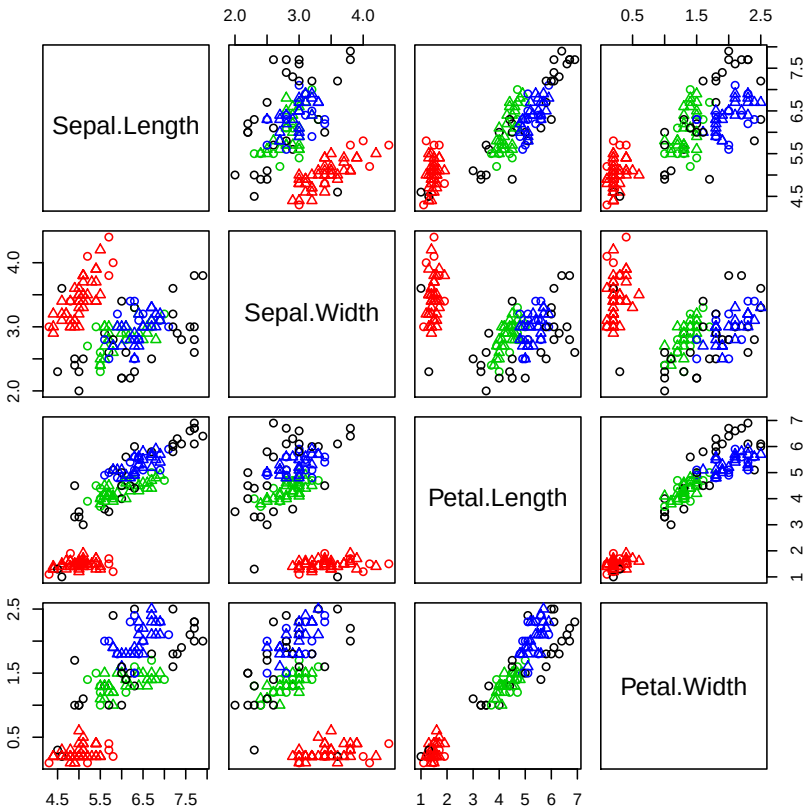

Figure 6.5: Density-based Clustering - I

The clusters are shown below in a scatter plot using the first and fourth columns of the data.

```
> plot(ds, iris2[c(1,4)])
```

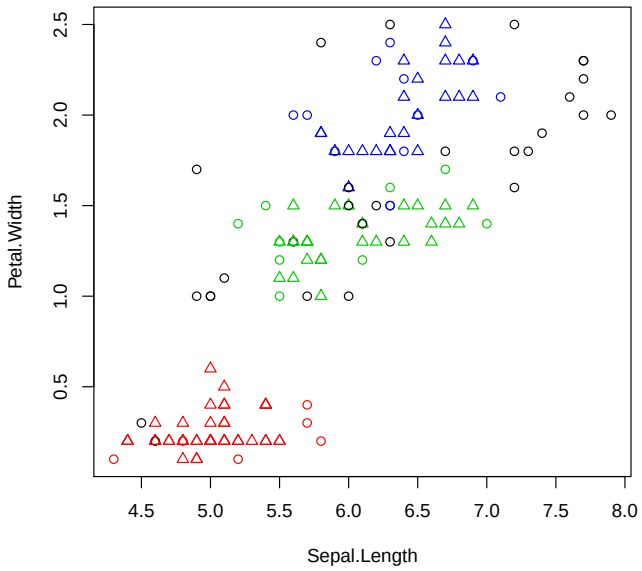

Figure 6.6: Density-based Clustering - II

Another way to show the clusters is using function `plotcluster()` in package *fpc*. Note that the data are projected to distinguish classes.

```
> plotcluster(iris2, ds$cluster)
```

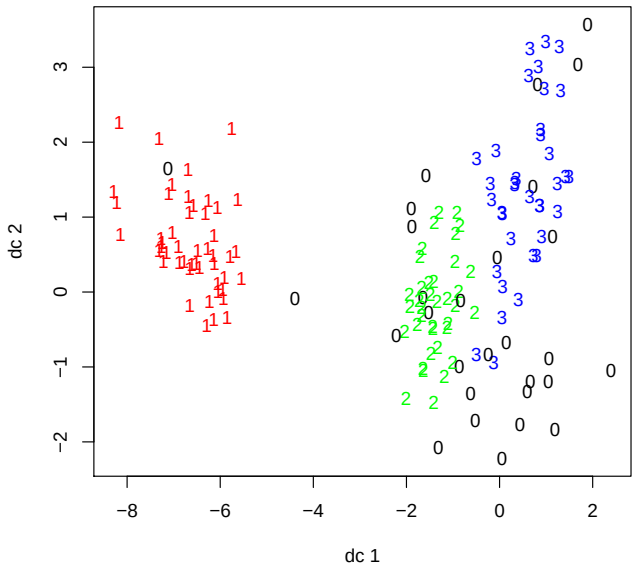

Figure 6.7: Density-based Clustering - III

The clustering model can be used to label new data, based on the similarity between new data and the clusters. The following example draws a sample of 10 objects from `iris` and adds small noises to them to make a new dataset for labeling. The random noises are generated with a uniform distribution using function `runif()`.

```
> # create a new dataset for labeling
> set.seed(435)
> idx <- sample(1:nrow(iris), 10)
> newData <- iris[idx,-5]
> newData <- newData + matrix(runif(10*4, min=0, max=0.2), nrow=10, ncol=4)
> # label new data
> myPred <- predict(ds, iris2, newData)
> # plot result
> plot(iris2[c(1,4)], col=1+ds$cluster)
> points(newData[c(1,4)], pch="*", col=1+myPred, cex=3)
> # check cluster labels
> table(myPred, iris$Species[idx])

myPred setosa versicolor virginica
     0      0          0         1
     1      3          0         0
     2      0          3         0
     3      0          1         2
```

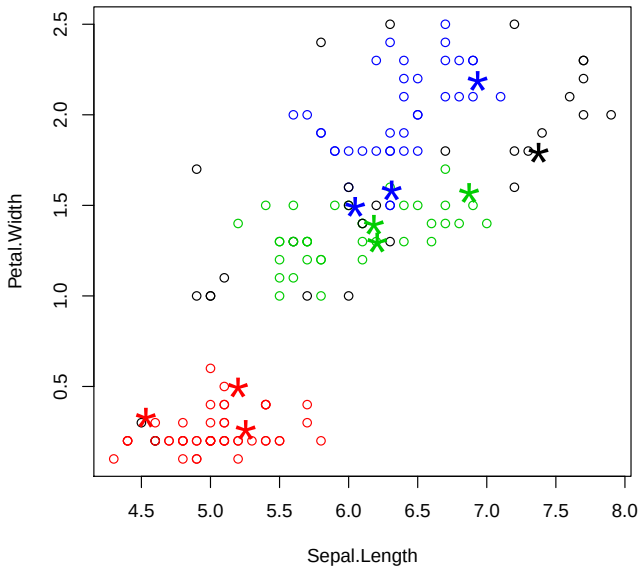

Figure 6.8: Prediction with Clustering Model

As we can see from the above result, out of the 10 new unlabeled data, 8(=3+3+2) are assigned with correct class labels. The new data are shown as asterisk("*") in the above figure and the colors stand for cluster labels in Figure 6.8.

Chapter 7

Outlier Detection

This chapter presents examples of outlier detection with R. At first, it demonstrates univariate outlier detection. After that, an example of outlier detection with LOF (Local Outlier Factor) is given, followed by examples on outlier detection by clustering. At last, it demonstrates outlier detection from time series data.

7.1 Univariate Outlier Detection

This section shows an example of univariate outlier detection, and demonstrates how to apply it to multivariate data. In the example, univariate outlier detection is done with function `boxplot.stats()`, which returns the statistics for producing boxplots. In the result returned by the above function, one component is `out`, which gives a list of outliers. More specifically, it lists data points lying beyond the extremes of the whiskers. An argument of `coef` can be used to control how far the whiskers extend out from the box of a boxplot. More details on that can be obtained by running `?boxplot.stats` in R. Figure 7.1 shows a boxplot, where the four circles are outliers.

```
> set.seed(3147)
> x <- rnorm(100)
> summary(x)

   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
-3.3150 -0.4837  0.1867  0.1098  0.7120  2.6860

> # outliers
> boxplot.stats(x)$out

[1] -3.315391  2.685922 -3.055717  2.571203

> boxplot(x)
```

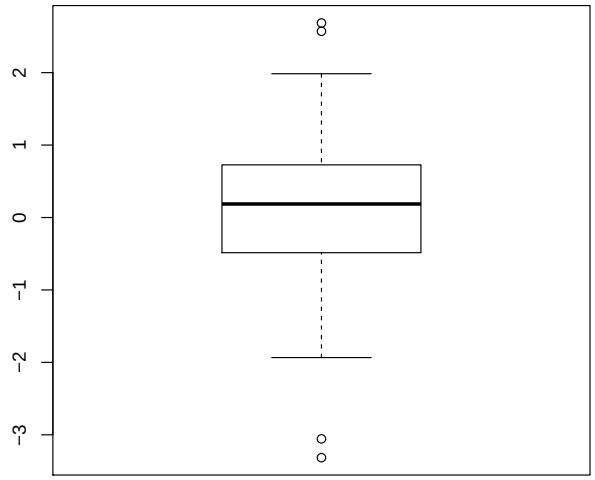

Figure 7.1: Univariate Outlier Detection with Boxplot

The above univariate outlier detection can be used to find outliers in multivariate data in a simple ensemble way. In the example below, we first generate a dataframe `df`, which has two columns, `x` and `y`. After that, outliers are detected separately from `x` and `y`. We then take outliers as those data which are outliers for both columns. In Figure 7.2, outliers are labeled with "+" in red.

```
> y <- rnorm(100)
> df <- data.frame(x, y)
> rm(x, y)
> head(df)

            x          y
1 -3.31539150  0.7619774
2 -0.04765067 -0.6404403
3  0.69720806  0.7645655
4  0.35979073  0.3131930
5  0.18644193  0.1709528
6  0.27493834 -0.8441813
```

```
> attach(df)
> # find the index of outliers from x
> (a <- which(x %in% boxplot.stats(x)$out))


[1]  1 33 64 74


> # find the index of outliers from y
> (b <- which(y %in% boxplot.stats(y)$out))


[1] 24 25 49 64 74


> detach(df)



> # outliers in both x and y
> (outlier.list1 <- intersect(a,b))

[1] 64 74

> plot(df)
> points(df[outlier.list1,], col="red", pch="+", cex=2.5)
```

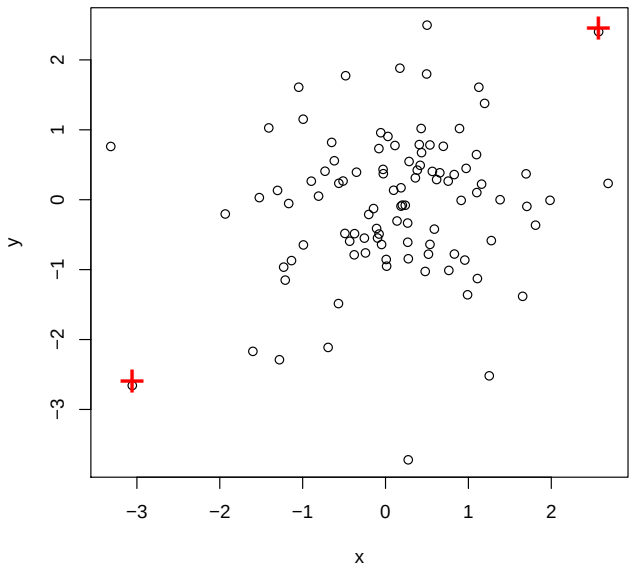

Figure 7.2: Outlier Detection - I

Similarly, we can also take outliers as those data which are outliers in either `x` or `y`. In Figure 7.3, outliers are labeled with "x" in blue.

```
> # outliers in either x or y
> (outlier.list2 <- union(a,b))

[1]  1 33 64 74 24 25 49

> plot(df)
> points(df[outlier.list2,], col="blue", pch="x", cex=2)
```

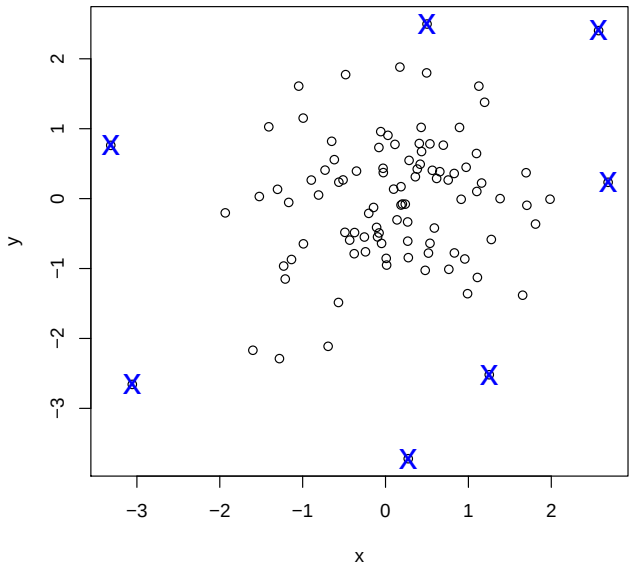

Figure 7.3: Outlier Detection - II

When there are three or more variables in an application, a final list of outliers might be produced with majority voting of outliers detected from individual variables. Domain knowledge should be involved when choosing the optimal way to ensemble in real-world applications.

7.2 Outlier Detection with LOF

LOF (Local Outlier Factor) is an algorithm for identifying density-based local outliers [Breunig et al., 2000]. With LOF, the local density of a point is compared with that of its neighbors. If the former is significantly lower than the latter (with an LOF value greater than one), the point is in a sparser region than its neighbors, which suggests it be an outlier. A shortcoming of LOF is that it works on numeric data only.

Function `lofactor()` calculates local outlier factors using the LOF algorithm, and it is available in packages *DMwR* [Torgo, 2010] and *dprep*. An example of outlier detection with LOF is given below, where k is the number of neighbors used for calculating local outlier factors. Figure 7.4 shows a density plot of outlier scores.

```
> library(DMwR)
> # remove "Species", which is a categorical column
> iris2 <- iris[,1:4]
> outlier.scores <- lofactor(iris2, k=5)
> plot(density(outlier.scores))
```

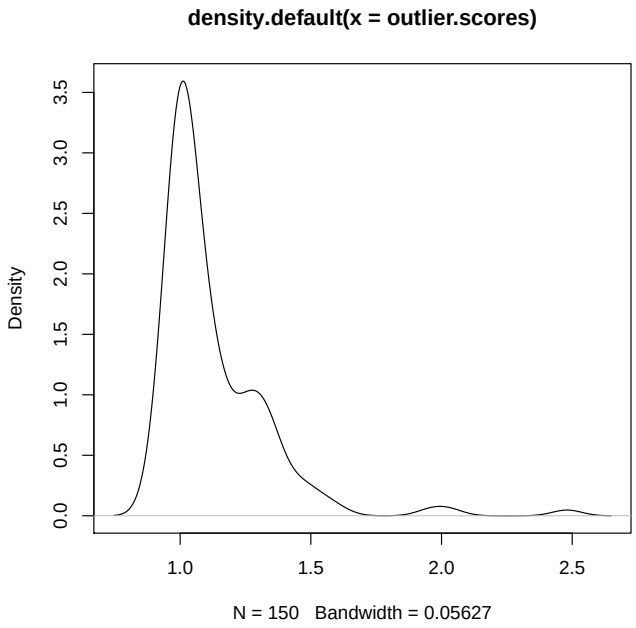

Figure 7.4: Density of outlier factors

```
> # pick top 5 as outliers
> outliers <- order(outlier.scores, decreasing=T)[1:5]
> # who are outliers
> print(outliers)
```

```
[1]  42 107  23 110  63
```

```
> print(iris2[outliers,])
```

```
    Sepal.Length Sepal.Width Petal.Length Petal.Width
42           4.5         2.3          1.3         0.3
107          4.9         2.5          4.5         1.7
23           4.6         3.6          1.0         0.2
110          7.2         3.6          6.1         2.5
63           6.0         2.2          4.0         1.0
```

Next, we show outliers with a biplot of the first two principal components (see Figure 7.5).

```
> n <- nrow(iris2)
> labels <- 1:n
> labels[-outliers] <- "."
> biplot(prcomp(iris2), cex=.8, xlabs=labels)
```

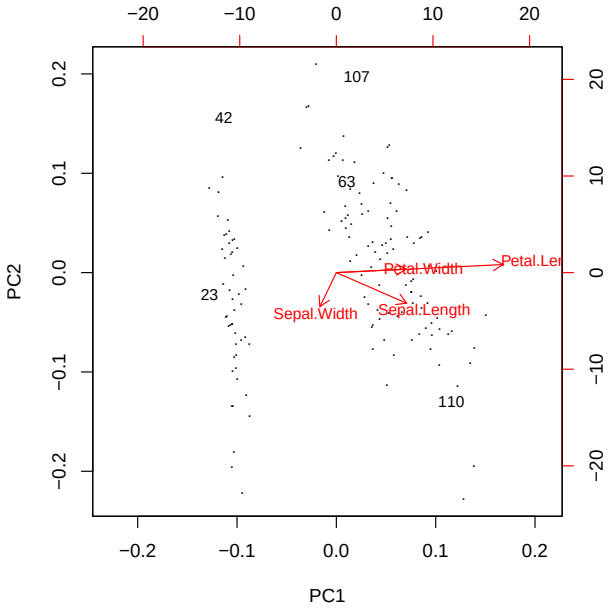

Figure 7.5: Outliers in a Biplot of First Two Principal Components

In the above code, `prcomp()` performs a principal component analysis, and `biplot()` plots the data with its first two principal components. In Figure 7.5, the x- and y-axis are respectively the first and second principal components, the arrows show the original columns (variables), and the five outliers are labeled with their row numbers.

We can also show outliers with a pairs plot as below, where outliers are labeled with "+" in red.

```
> pch <- rep(".", n)
> pch[outliers] <- "+"
> col <- rep("black", n)
> col[outliers] <- "red"
> pairs(iris2, pch=pch, col=col)
```

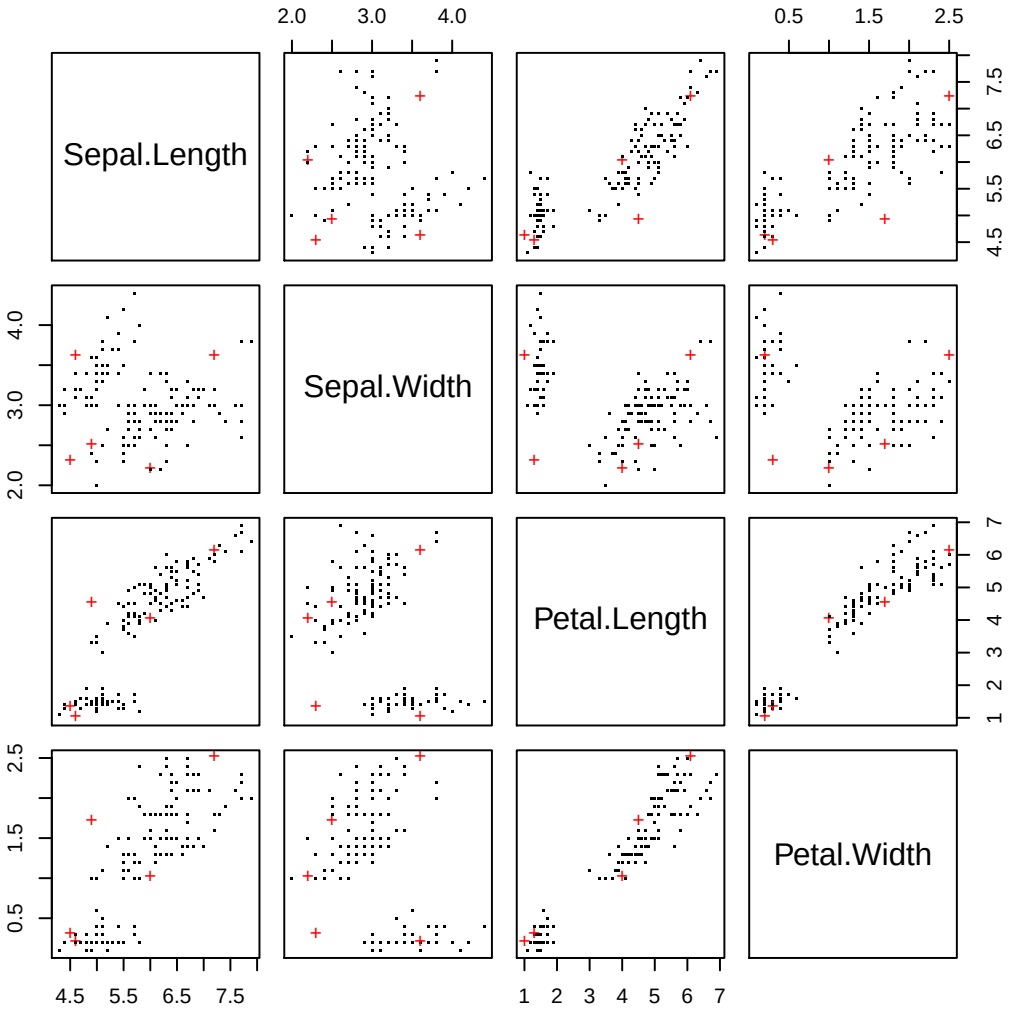

Figure 7.6: Outliers in a Matrix of Scatter Plots

Package *Rlof* [Hu et al., 2015] provides function `lof()`, a parallel implementation of the LOF algorithm. Its usage is similar to `lofactor()`, but `lof()` has two additional features of supporting multiple values of k and several choices of distance metrics. Below is an example of `lof()`. After computing outlier scores, outliers can be detected by selecting the top ones. Note that the current version of package *Rlof* (v1.0.0) works under MacOS X and Linux, but does not work under Windows, because it depends on package *multicore* for parallel computing.

```
> library(Rlof)
> outlier.scores <- lof(iris2, k=5)
```

```
> # try with different number of neighbors (k = 5,6,7,8,9 and 10)
> outlier.scores <- lof(iris2, k=c(5:10))
```

7.3 Outlier Detection by Clustering

Another way to detect outliers is clustering. By grouping data into clusters, those data not assigned to any clusters are taken as outliers. For example, with density-based clustering such as DBSCAN [Ester et al., 1996], objects are grouped into one cluster if they are connected to one another by densely populated area. Therefore, objects not assigned to any clusters are isolated from other objects and are taken as outliers. An example of DBSCAN be found in Section 6.4 Density-based Clustering.

We can also detect outliers with the k-means algorithm. With k-means, the data are partitioned into k groups by assigning them to the closest cluster centers. After that, we can calculate the distance (or dissimilarity) between each object and its cluster center, and pick those with largest distances as outliers. An example of outlier detection with k-means from the `iris` data (see Section 1.3.1 for details of the data) is given below.

```
> # remove species from the data to cluster
> iris2 <- iris[,1:4]
> kmeans.result <- kmeans(iris2, centers=3)
> # cluster centers
> kmeans.result$centers

  Sepal.Length Sepal.Width Petal.Length Petal.Width
1     5.006000    3.428000     1.462000    0.246000
2     6.850000    3.073684     5.742105    2.071053
3     5.901613    2.748387     4.393548    1.433871

> # cluster IDs
> kmeans.result$cluster

  [1] 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
 [39] 1 1 1 1 1 1 1 1 1 1 1 1 3 3 2 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3
 [77] 3 2 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 2 3 2 2 2 2 3 2 2 2 2 2 2 3
[115] 3 2 2 2 2 3 2 3 2 3 2 2 3 3 2 2 2 2 2 3 2 2 2 2 3 2 2 2 3 2 2 2 3 2 2 3

> # calculate distances between objects and cluster centers
> centers <- kmeans.result$centers[kmeans.result$cluster, ]
> distances <- sqrt(rowSums((iris2 - centers)^2))
> # pick top 5 largest distances
> outliers <- order(distances, decreasing=T)[1:5]
> # who are outliers
> print(outliers)

[1]  99  58  94  61 119

> print(iris2[outliers,])

    Sepal.Length Sepal.Width Petal.Length Petal.Width
99           5.1         2.5          3.0         1.1
58           4.9         2.4          3.3         1.0
94           5.0         2.3          3.3         1.0
61           5.0         2.0          3.5         1.0
119          7.7         2.6          6.9         2.3
```

```
> # plot clusters
> plot(iris2[,c("Sepal.Length", "Sepal.Width")], pch="o",
+      col=kmeans.result$cluster, cex=0.3)
> # plot cluster centers
> points(kmeans.result$centers[,c("Sepal.Length", "Sepal.Width")], col=1:3,
+        pch=8, cex=1.5)
> # plot outliers
> points(iris2[outliers, c("Sepal.Length", "Sepal.Width")], pch="+", col=4, cex=1.5)
```

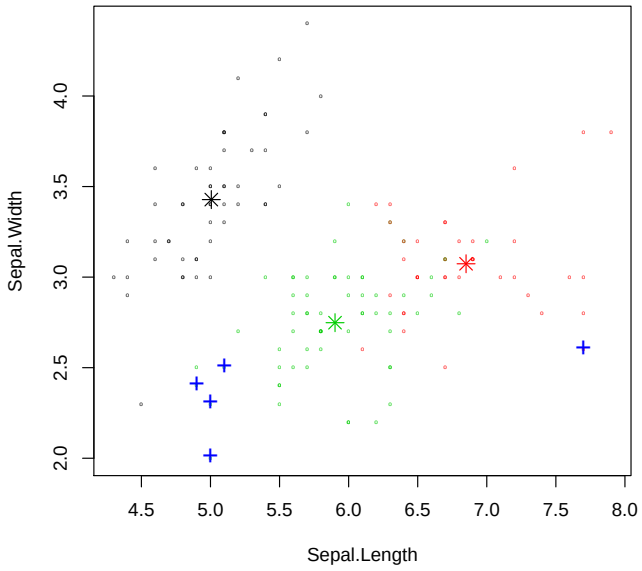

Figure 7.7: Outliers with k-Means Clustering

In the above figure, cluster centers are labeled with asterisks and outliers with "+".

7.4 Outlier Detection from Time Series

This section presents an example of outlier detection from time series data. In the example, the time series data are first decomposed with robust regression using function `stl()` and then outliers are identified. An introduction of STL (Seasonal-trend decomposition based on Loess) [Cleveland et al., 1990] is available at `http://cs.wellesley.edu/~cs315/Papers/stl%20statistical%20model.pdf`. More examples of time series decomposition can be found in Section 8.2.

```
> # use robust fitting
> f <- stl(AirPassengers, "periodic", robust=TRUE)
> (outliers <- which(f$weights<1e-8))

 [1]  79  91  92 102 103 104 114 115 116 126 127 128 138 139 140

> # set layout
> op <- par(mar=c(0, 4, 0, 3), oma=c(5, 0, 4, 0), mfcol=c(4, 1))
> plot(f, set.pars=NULL)
> sts <- f$time.series
> # plot outliers
> points(time(sts)[outliers], 0.8*sts[,"remainder"][outliers], pch="x", col="red")
> par(op) # reset layout
```

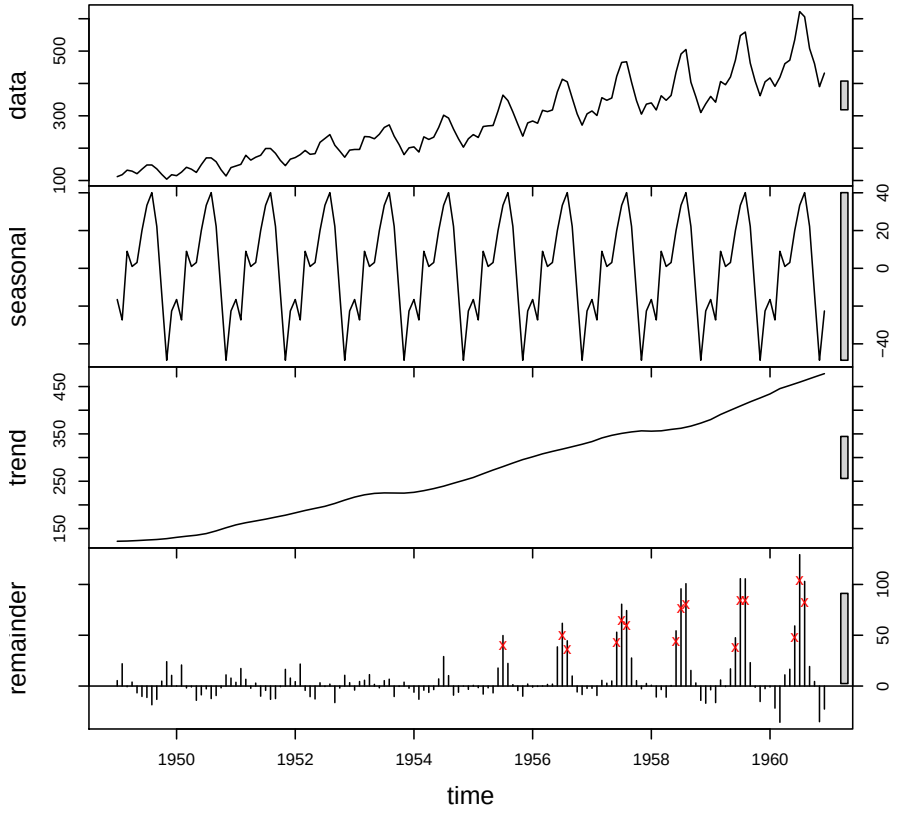

Figure 7.8: Outliers in Time Series Data

In above figure, outliers are labeled with "x" in red.

7.5 Discussions

The LOF algorithm is good at detecting local outliers, but it works on numeric data only. Package *Rlof* relies on the *multicore* package, which does not work under Windows. A fast and scalable outlier detection strategy for categorical data is the Attribute Value Frequency (AVF) algorithm [Koufakou et al., 2007].

Some other R packages for outlier detection are:

- Package *extremevalues* [van der Loo, 2010]: univariate outlier detection;
- Package *mvoutlier* [Filzmoser and Gschwandtner, 2015]: multivariate outlier detection based on robust methods; and
- Package *outliers* [Komsta, 2011]: tests for outliers.

Chapter 8

Time Series Analysis and Mining

This chapter presents examples on time series decomposition, forecasting, clustering and classification. The first section introduces briefly time series data in R. The second section shows an example on decomposing time series into trend, seasonal and random components. The third section presents how to build an autoregressive integrated moving average (ARIMA) model in R and use it to predict future values. The fourth section introduces Dynamic Time Warping (DTW) and hierarchical clustering of time series data with Euclidean distance and with DTW distance. The fifth section shows three examples on time series classification: one with original data, the other with DWT (Discrete Wavelet Transform) transformed data, and another with k-NN classification. The chapter ends with discussions and further readings.

8.1 Time Series Data in R

Class `ts` represents data which has been sampled at equispaced points in time. A frequency of 7 indicates that a time series is composed of weekly data, and 12 and 4 are used respectively for monthly and quarterly series. An example below shows the construction of a time series with 30 values (1 to 30). `Frequency=12` and `start=c(2011,3)` specify that it is a monthly series starting from March 2011.

```
> a <- ts(1:30, frequency=12, start=c(2011,3))
> print(a)

     Jan Feb Mar Apr May Jun Jul Aug Sep Oct Nov Dec
2011           1   2   3   4   5   6   7   8   9  10
2012  11  12  13  14  15  16  17  18  19  20  21  22
2013  23  24  25  26  27  28  29  30

> str(a)

 Time-Series [1:30] from 2011 to 2014: 1 2 3 4 5 6 7 8 9 10 ...

> attributes(a)

$tsp
[1] 2011.167 2013.583   12.000

$class
[1] "ts"
```

8.2 Time Series Decomposition

Time Series Decomposition is to decompose a time series into trend, seasonal, cyclical and irregular components. The trend component stands for long term trend, the seasonal component is seasonal variation, the cyclical component is repeated but non-periodic fluctuations, and the residuals are irregular component.

A time series of `AirPassengers` is used below as an example to demonstrate time series decomposition. It is composed of monthly totals of Box & Jenkins international airline passengers from 1949 to 1960. It has 144(=12*12) values.

```
> plot(AirPassengers)
```

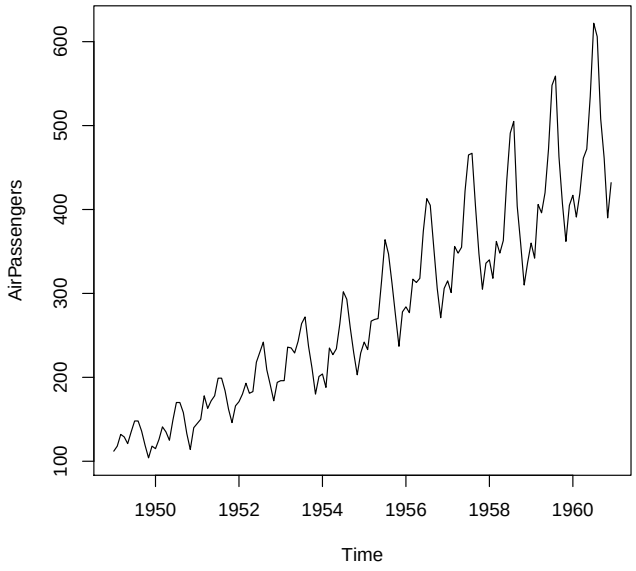

Figure 8.1: A Time Series of `AirPassengers`

Function `decompose()` is applied below to `AirPassengers` to break it into various components.

```
> # decompose time series
> apts <- ts(AirPassengers, frequency=12)
> f <- decompose(apts)
```

If package igraph has been loaded, you may get an error saying "Error in decompose(apts) : Not a graph object". The reason is that function `decomposed()` from package *stats* is maksed by a function with the same name from package *igraph*. To avoid above error, please run code instead, which tells R to run the `decomposed()` function from package *stats*.

```
> apts <- ts(AirPassengers, frequency=12)
> f <- stats::decompose(apts)

> # seasonal figures
> f$figure

 [1] -24.748737 -36.188131  -2.241162  -8.036616  -4.506313  35.402778  63.830808
 [8]  62.823232  16.520202 -20.642677 -53.593434 -28.619949

> plot(f$figure, type="b", xaxt="n", xlab="")
> # get names of 12 months in English words
> monthNames <- months(ISOdate(2011,1:12,1))
> # label x-axis with month names
> # las is set to 2 for vertical label orientation
> axis(1, at=1:12, labels=monthNames, las=2)
```

Figure 8.2: Seasonal Component

```
> plot(f)
```

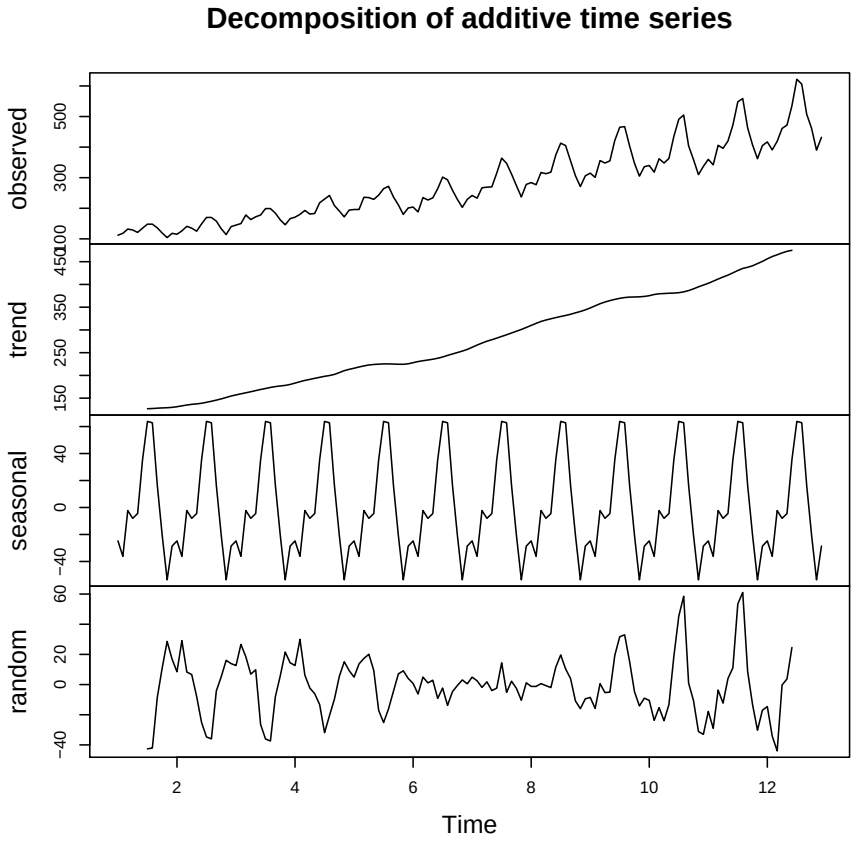

Figure 8.3: Time Series Decomposition

In Figure 8.3, the first chart is the original time series. The second is trend of the data, the third shows seasonal factors, and the last chart is the remaining components after removing trend and seasonal factors.

Some other functions for time series decomposition are `stl()` in package *stats* [R Core Team, 2015b], `decomp()` in package *timsac* [The Institute of Statistical Mathematics, 2012], and `tsr()` in package *ast*.

8.3 Time Series Forecasting

Time series forecasting is to forecast future events based on historical data. One example is to predict the opening price of a stock based on its past performance. Two popular models for time series forecasting are autoregressive moving average (ARMA) and autoregressive integrated moving average (ARIMA).

Here is an example to fit an ARIMA model to a univariate time series and then use it for forecasting.

```
> fit <- arima(AirPassengers, order=c(1,0,0), list(order=c(2,1,0), period=12))
> fore <- predict(fit, n.ahead=24)
> # error bounds at 95% confidence level
> U <- fore$pred + 2*fore$se
> L <- fore$pred - 2*fore$se
> ts.plot(AirPassengers, fore$pred, U, L, col=c(1,2,4,4), lty = c(1,1,2,2))
> legend("topleft", c("Actual", "Forecast", "Error Bounds (95% Confidence)"),
+        col=c(1,2,4), lty=c(1,1,2))
```

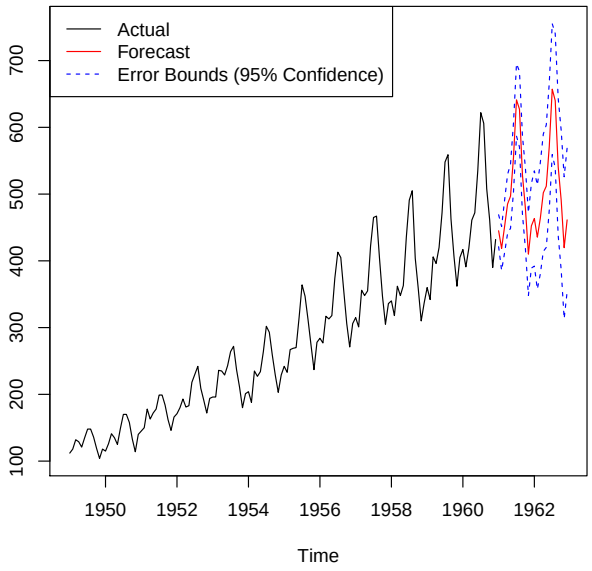

Figure 8.4: Time Series Forecast

In Figure 8.4, the red solid line shows the forecasted values, and the blue dotted lines are error bounds at a confidence level of 95%.

8.4 Time Series Clustering

Time series clustering is to partition time series data into groups based on similarity or distance, so that time series in the same cluster are similar to each other. There are various measures of distance or dissimilarity, such as Euclidean distance, Manhattan distance, Maximum norm, Hamming distance, the angle between two vectors (inner product), and Dynamic Time Warping (DTW) distance.

8.4.1 Dynamic Time Warping

Dynamic Time Warping (DTW) finds optimal alignment between two time series [Keogh and Pazzani, 2001] and an implement of it in R is package *dtw* [Giorgino, 2009]. In that package, function `dtw(x, y, ...)` computes dynamic time warp and finds optimal alignment between two time series `x` and `y`, and `dtwDist(mx, my=mx, ...)` or `dist(mx, my=mx, method="DTW", ...)` calculates the distances between time series `mx` and `my`.

```
> library(dtw)
> idx <- seq(0, 2*pi, len=100)
> a <- sin(idx) + runif(100)/10
> b <- cos(idx)
> align <- dtw(a, b, step=asymmetricP1, keep=T)
> dtwPlotTwoWay(align)
```

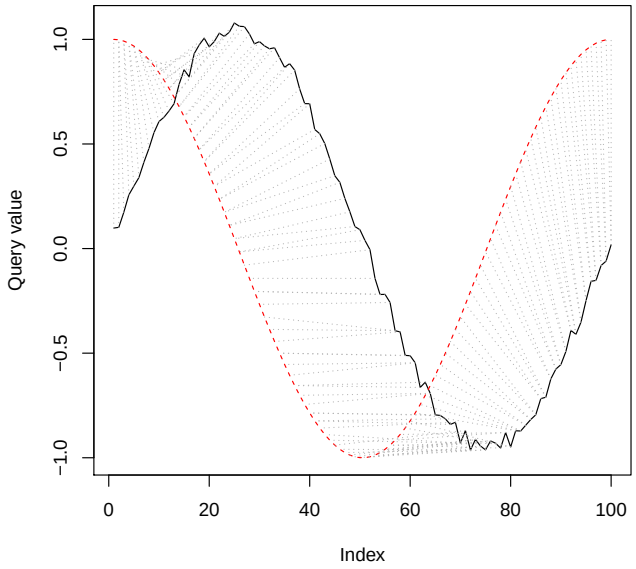

Figure 8.5: Alignment with Dynamic Time Warping

8.4.2 Synthetic Control Chart Time Series Data

The synthetic control chart time series [1] is used in the examples in the following sections. The dataset contains 600 examples of control charts synthetically generated by the process in Alcock and Manolopoulos (1999). Each control chart is a time series with 60 values, and there are six classes:

- 1-100: Normal;
- 101-200: Cyclic;
- 201-300: Increasing trend;
- 301-400: Decreasing trend;
- 401-500: Upward shift; and
- 501-600: Downward shift.

Firstly, the data is read into R with `read.table()`. Parameter `sep` is set to `""` (no space between double quotation marks), which is used when the separator is white space, i.e., one or more spaces, tabs, newlines or carriage returns.

[1] `http://kdd.ics.uci.edu/databases/synthetic_control/synthetic_control.html`

```
> sc <- read.table("./data/synthetic_control.data", header=F, sep="")
> # show one sample from each class
> idx <- c(1,101,201,301,401,501)
> sample1 <- t(sc[idx,])
> plot.ts(sample1, main="")
```

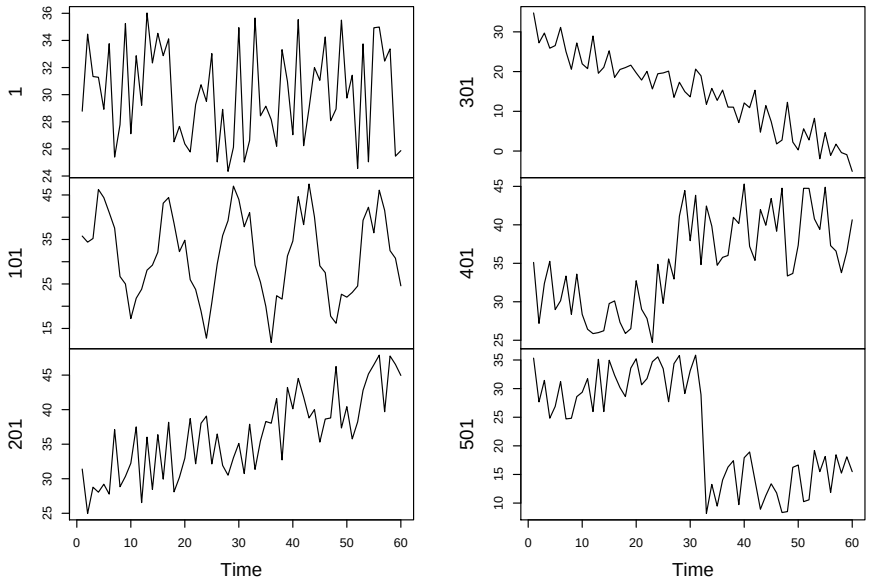

Figure 8.6: Six Classes in Synthetic Control Chart Time Series

8.4.3 Hierarchical Clustering with Euclidean Distance

At first, we select 10 cases randomly from each class. Otherwise, there will be too many cases and the plot of hierarchical clustering will be over crowded.

```
> set.seed(6218)

> n <- 10
> s <- sample(1:100, n)
> idx <- c(s, 100+s, 200+s, 300+s, 400+s, 500+s)
> sample2 <- sc[idx,]
> observedLabels <- rep(1:6, each=n)
> # hierarchical clustering with Euclidean distance
> hc <- hclust(dist(sample2), method="average")
> plot(hc, labels=observedLabels, main="")
> # cut tree to get 6 clusters
> rect.hclust(hc, k=6)
> memb <- cutree(hc, k=6)
> table(observedLabels, memb)

               memb
observedLabels  1  2  3  4  5  6
             1 10  0  0  0  0  0
             2  1  6  2  1  0  0
             3  0  0  0  0 10  0
             4  0  0  0  0  0 10
             5  0  0  0  0 10  0
             6  0  0  0  0  0 10
```

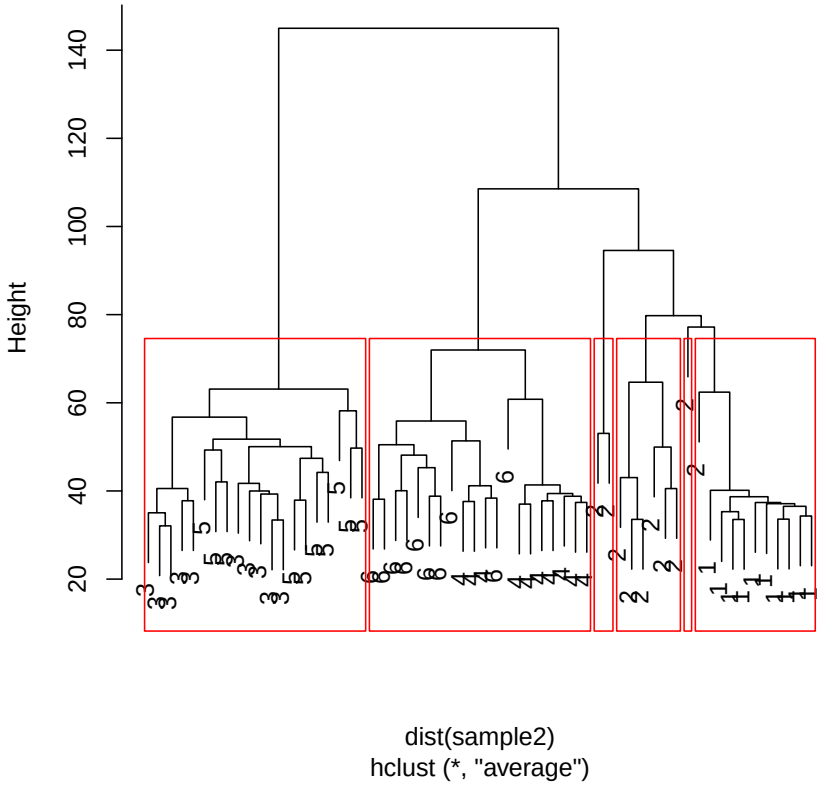

Figure 8.7: Hierarchical Clustering with Euclidean Distance

The clustering result in Figure 8.7 shows that, increasing trend (class 3) and upward shift (class 5) are not well separated, and decreasing trend (class 4) and downward shift (class 6) are also mixed.

8.4.4 Hierarchical Clustering with DTW Distance

Next, we try hierarchical clustering with the DTW distance.

```
> library(dtw)
> distMatrix <- dist(sample2, method="DTW")
> hc <- hclust(distMatrix, method="average")
> plot(hc, labels=observedLabels, main="")
> # cut tree to get 6 clusters
> rect.hclust(hc, k=6)
> memb <- cutree(hc, k=6)
> table(observedLabels, memb)
```

observedLabels	memb 1	2	3	4	5	6
1	10	0	0	0	0	0
2	0	7	3	0	0	0
3	0	0	0	10	0	0
4	0	0	0	0	7	3
5	2	0	0	8	0	0
6	0	0	0	0	0	10

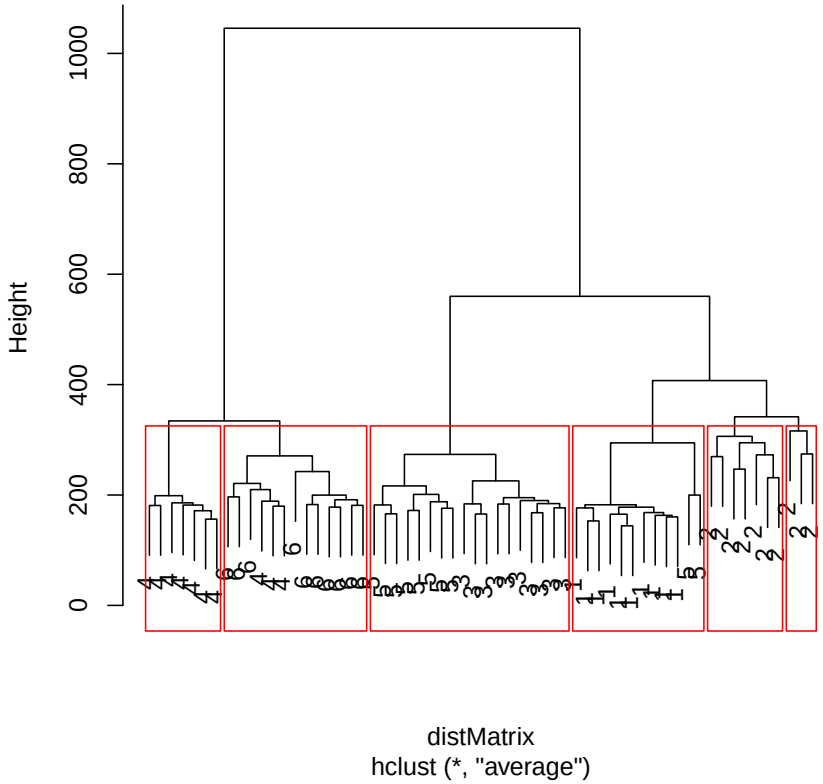

Figure 8.8: Hierarchical Clustering with DTW Distance

By comparing Figure 8.8 with Figure 8.7, we can see that the DTW distance are better than the Euclidean distance for measuring the similarity between time series.

8.5 Time Series Classification

Time series classification is to build a classification model based on labeled time series and then use the model to predict the label of unlabeled time series. New features extracted from time series may help to improve the performance of classification models. Techniques for feature extraction include Singular Value Decomposition (SVD), Discrete Fourier Transform (DFT), Discrete Wavelet Transform (DWT), Piecewise Aggregate Approximation (PAA), Perpetually Important Points (PIP), Piecewise Linear Representation, and Symbolic Representation.

8.5.1 Classification with Original Data

We use `ctree()` from package *party* [Hothorn et al., 2015] to demonstrate classification of time series with the original data. The class labels are changed into categorical values before feeding the data into `ctree()`, so that we won't get class labels as a real number like 1.35. The built decision tree is shown in Figure 8.9.

```
> classId <- rep(as.character(1:6), each=100)
> newSc <- data.frame(cbind(classId, sc))
> library(party)
> ct <- ctree(classId ~ ., data=newSc,
+             controls = ctree_control(minsplit=30, minbucket=10, maxdepth=5))
> pClassId <- predict(ct)
> table(classId, pClassId)

       pClassId
classId   1   2   3   4   5   6
      1  97   0   0   0   0   3
      2   1  93   2   0   0   4
      3   0   0  96   0   4   0
      4   0   0   0 100   0   0
      5   4   0  10   0  86   0
      6   0   0   0  87   0  13

> # accuracy
> (sum(classId==pClassId)) / nrow(sc)

[1] 0.8083333

> plot(ct, ip_args=list(pval=FALSE), ep_args=list(digits=0))
```

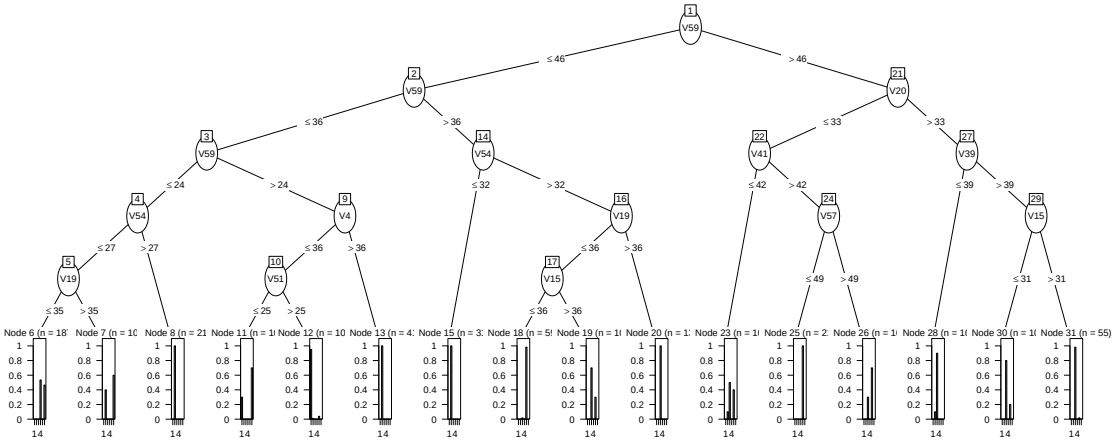

Figure 8.9: Decision Tree

8.5.2 Classification with Extracted Features

Next, we use DWT (Discrete Wavelet Transform) [Burrus et al., 1998] to extract features from time series and then build a classification model. Wavelet transform provides a multi-resolution representation using wavelets. An example of Haar Wavelet Transform, the simplest DWT, is available at `http://dmr.ath.cx/gfx/haar/`. Another popular feature extraction technique is Discrete Fourier Transform (DFT) [Agrawal et al., 1993].

An example on extracting DWT (with Haar filter) coefficients is shown below. Package *wavelets* [Aldrich, 2013] is used for discrete wavelet transform. In the package, function `dwt(X, filter, n.levels, ...)` computes the discrete wavelet transform coefficients, where `X` is a univariate or multi-variate time series, `filter` indicates which wavelet filter to use, and `n.levels` specifies the level of decomposition. It returns an object of class `dwt`, whose slot `W` contains wavelet coefficients

and `V` contains scaling coefficients. The original time series can be reconstructed via an inverse discrete wavelet transform with function `idwt()` in the same package. The produced model is shown in Figure 8.10.

```
> library(wavelets)
> wtData <- NULL
> for (i in 1:nrow(sc)) {
+   a <- t(sc[i,])
+   wt <- dwt(a, filter="haar", boundary="periodic")
+   wtData <- rbind(wtData, unlist(c(wt@W, wt@V[[wt@level]])))
+ }
> wtData <- as.data.frame(wtData)
> wtSc <- data.frame(cbind(classId, wtData))


> # build a decision tree with DWT coefficients
> ct <- ctree(classId ~ ., data=wtSc,
+             controls = ctree_control(minsplit=30, minbucket=10, maxdepth=5))
> pClassId <- predict(ct)
> table(classId, pClassId)

       pClassId
classId  1  2  3  4  5  6
      1 97  3  0  0  0  0
      2  1 99  0  0  0  0
      3  0  0 81  0 19  0
      4  0  0  0 63  0 37
      5  0  0 16  0 84  0
      6  0  0  0  1  0 99

> (sum(classId==pClassId)) / nrow(wtSc)

[1] 0.8716667

> plot(ct, ip_args=list(pval=FALSE), ep_args=list(digits=0))
```

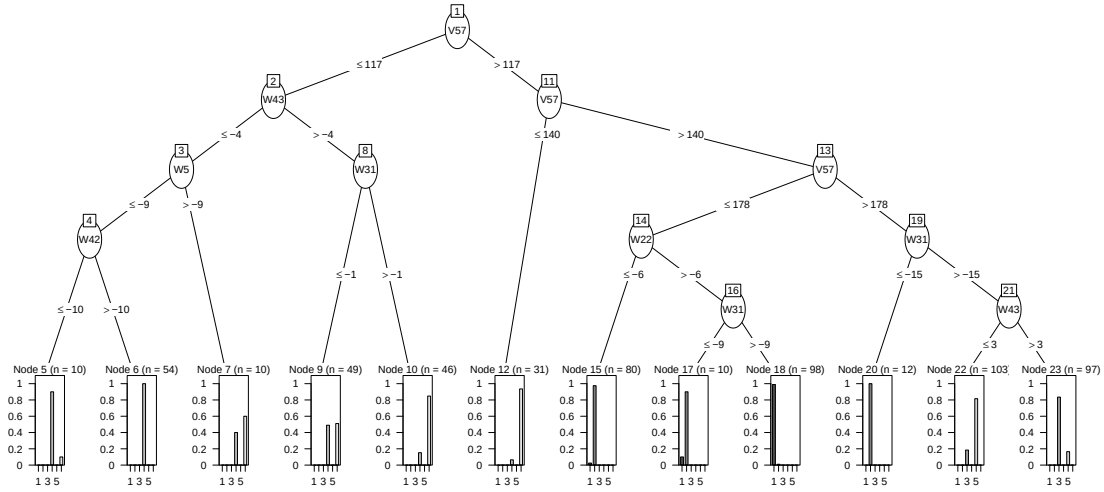

Figure 8.10: Decision Tree with DWT

8.5.3 k-NN Classification

The k-NN classification can also be used for time series classification. It finds out the k nearest neighbors of a new instance and then labels it by majority voting. However, the time complexity of a naive way to find k nearest neighbors is $O(n^2)$, where n is the size of data. Therefore, an efficient indexing structure is needed for large datasets. Package *RANN* supports fast nearest neighbor search with a time complexity of $O(n \log n)$ using Arya and Mount's ANN library (v1.1.1) [2]. Below is an example of k-NN classification of time series without indexing.

```
> k <- 20
> # create a new time series by adding noise to time series 501
> newTS <- sc[501,] + runif(100)*15
> distances <- dist(newTS, sc, method="DTW")
> s <- sort(as.vector(distances), index.return=TRUE)
> # class IDs of k nearest neighbors
> table(classId[s$ix[1:k]])

 4  6
 3 17
```

For the 20 nearest neighbors of the new time series, three of them are of class 4, and 17 are of class 6. With majority voting, that is, taking the more frequent label as winner, the label of the new time series is set to class 6.

8.6 Discussions

There are many R functions and packages available for time series decomposition and forecasting. However, there are no R functions or packages specially for time series classification and clustering. There are a lot of research publications on techniques specially for classifying/clustering time series data, but there are no R implementations for them (as far as I know).

To do time series classification, one is suggested to extract and build features first, and then apply existing classification techniques, such as SVM, k-NN, neural networks, regression and decision trees, to the feature set.

For time series clustering, one needs to work out his/her own distance or similarity metrics, and then use existing clustering techniques, such as k-means or hierarchical clustering, to find clusters.

8.7 Further Readings

An introduction of R functions and packages for time series is available as *CRAN Task View: Time Series Analysis* at `http://cran.r-project.org/web/views/TimeSeries.html`.

R code examples for time series can be found in slides *Time Series Analysis and Mining with R* at `http://www.rdatamining.com/docs`.

Some further readings on time series representation, similarity, clustering and classification are [Agrawal et al., 1993, Burrus et al., 1998, Chan and Fu, 1999, Chan et al., 2003, Keogh and Pazzani, 1998, Keogh et al., 2000, Keogh and Pazzani, 2000, Mörchen, 2003, Rafiei and Mendelzon, 1998, Vlachos et al., 2003, Wu et al., 2000, Zhao and Zhang, 2006].

[2] `http://www.cs.umd.edu/~mount/ANN/`

Chapter 9

Association Rules

This chapter presents examples of association rule mining with R. It starts with basic concepts of association rules, and then demonstrates association rules mining with R. After that, it presents examples of pruning redundant rules and interpreting and visualizing association rules. The chapter concludes with discussions and recommended readings.

9.1 Basics of Association Rules

Association rules are rules presenting association or correlation between itemsets. An association rule is in the form of $A \Rightarrow B$, where A and B are two disjoint itemsets, referred to respectively as the `lhs` (left-hand side) and `rhs` (right-hand side) of the rule. The three most widely-used measures for selecting interesting rules are *support*, *confidence* and *lift*. *Support* is the percentage of cases in the data that contains both A and B, *confidence* is the percentage of cases containing A that also contain B, and *lift* is the ratio of confidence to the percentage of cases containing B. The formulae to calculate them are:

$$\begin{aligned}
\text{support}(A \Rightarrow B) &= P(A \cup B) && (9.1)\\
\text{confidence}(A \Rightarrow B) &= P(B|A) && (9.2)\\
&= \frac{P(A \cup B)}{P(A)} && (9.3)\\
\text{lift}(A \Rightarrow B) &= \frac{\text{confidence}(A \Rightarrow B)}{P(B)} && (9.4)\\
&= \frac{P(A \cup B)}{P(A)P(B)} && (9.5)
\end{aligned}$$

where $P(A)$ is the percentage (or probability) of cases containing A.

In addition to support, confidence and lift, there are many other interestingness measures, such as chi-square, conviction, gini and leverage. An introduction to over 20 measures can be found in Tan et al.'s work [Tan et al., 2002].

9.2 The Titanic Dataset

The `Titanic` dataset in the *datasets* package is a 4-dimensional table with summarized information on the fate of passengers on the Titanic according to social class, sex, age and survival. To make it suitable for association rule mining, we reconstruct the raw data as `titanic.raw`, where each row represents a person. The reconstructed raw data can also be downloaded as file "titanic.raw.rdata" at `http://www.rdatamining.com/data`.

```
> str(Titanic)

 table [1:4, 1:2, 1:2, 1:2] 0 0 35 0 0 0 17 0 118 154 ...
 - attr(*, "dimnames")=List of 4
  ..$ Class   : chr [1:4] "1st" "2nd" "3rd" "Crew"
  ..$ Sex     : chr [1:2] "Male" "Female"
  ..$ Age     : chr [1:2] "Child" "Adult"
  ..$ Survived: chr [1:2] "No" "Yes"

> df <- as.data.frame(Titanic)
> head(df)

  Class    Sex   Age Survived Freq
1   1st   Male Child       No    0
2   2nd   Male Child       No    0
3   3rd   Male Child       No   35
4  Crew   Male Child       No    0
5   1st Female Child       No    0
6   2nd Female Child       No    0

> titanic.raw <- NULL
> for(i in 1:4) {
+    titanic.raw <- cbind(titanic.raw, rep(as.character(df[,i]), df$Freq))
+ }
> titanic.raw <- as.data.frame(titanic.raw)
> names(titanic.raw) <- names(df)[1:4]
> dim(titanic.raw)

[1] 2201    4

> str(titanic.raw)

data.frame:        2201 obs. of  4 variables:
 $ Class   : Factor w/ 4 levels "1st","2nd","3rd",..: 3 3 3 3 3 3 3 3 3 3 ...
 $ Sex     : Factor w/ 2 levels "Female","Male": 2 2 2 2 2 2 2 2 2 2 ...
 $ Age     : Factor w/ 2 levels "Adult","Child": 2 2 2 2 2 2 2 2 2 2 ...
 $ Survived: Factor w/ 2 levels "No","Yes": 1 1 1 1 1 1 1 1 1 1 ...

> head(titanic.raw)

  Class  Sex   Age Survived
1   3rd Male Child       No
2   3rd Male Child       No
3   3rd Male Child       No
4   3rd Male Child       No
5   3rd Male Child       No
6   3rd Male Child       No

> summary(titanic.raw)

  Class         Sex          Age       Survived
 1st :325   Female: 470   Adult:2092   No :1490
 2nd :285   Male  :1731   Child: 109   Yes: 711
 3rd :706
 Crew:885
```

Now we have a dataset where each row stands for a person, and it can be used for association rule mining.

The raw Titanic dataset can also be downloaded from `http://www.cs.toronto.edu/~delve/data/titanic/desc.html`. The data is file "Dataset.data" in the compressed archive "titanic.tar.gz". It can be read into R with the code below.

```
> # have a look at the 1st 5 lines
> readLines("./data/Dataset.data", n=5)

[1] "1st  adult male   yes" "1st  adult male   yes" "1st  adult male   yes"
[4] "1st  adult male   yes" "1st  adult male   yes"

> # read it into R
> titanic <- read.table("./data/Dataset.data", header=F)
> names(titanic) <- c("Class", "Sex", "Age", "Survived")
```

9.3 Association Rule Mining

A classic algorithm for association rule mining is APRIORI [Agrawal and Srikant, 1994]. It is a level-wise, breadth-first algorithm which counts transactions to find frequent itemsets and then derive association rules from them. An implementation of it is function `apriori()` in package *arules* [Hahsler et al., 2014]. Another algorithm for association rule mining is the ECLAT algorithm [Zaki, 2000], which finds frequent itemsets with equivalence classes, depth-first search and set intersection instead of counting. It is implemented as function `eclat()` in the same package.

Below we demonstrate association rule mining with `apriori()`. With the function, the default settings are: 1) `supp=0.1`, which is the minimum support of rules; 2) `conf=0.8`, which is the minimum confidence of rules; and 3) `maxlen=10`, which is the maximum length of rules.

```
> library(arules)
> # find association rules with default settings
> rules.all <- apriori(titanic.raw)

Parameter specification:
 confidence minval smax arem  aval originalSupport support minlen maxlen target
        0.8    0.1    1 none FALSE            TRUE     0.1      1     10  rules
   ext
 FALSE

Algorithmic control:
 filter tree heap memopt load sort verbose
    0.1 TRUE TRUE  FALSE TRUE    2    TRUE

apriori - find association rules with the apriori algorithm
version 4.21 (2004.05.09)        (c) 1996-2004   Christian Borgelt
set item appearances ...[0 item(s)] done [0.00s].
set transactions ...[10 item(s), 2201 transaction(s)] done [0.00s].
sorting and recoding items ... [9 item(s)] done [0.00s].
creating transaction tree ... done [0.00s].
checking subsets of size 1 2 3 4 done [0.00s].
writing ... [27 rule(s)] done [0.00s].
creating S4 object  ... done [0.00s].

> quality(rules.all) <- round(quality(rules.all), digits=3)
> rules.all
```

```
set of 27 rules
```

If package *tm* has been loaded, function `inspect()` would be masked from package *arules*. If there is an error saying *Error in UseMethod("inspect", x) : no applicable method for 'inspect' applied to an object of class "c('rules', 'associations')"*, readers are suggested to use `arules::inspect()` to explicitly tell R to use the function from package *arules*. Same applies to other calls to function `inspect()` in the rest of this chapter.

```
> inspect(rules.all)
> ## use code below if above code does not work
> arules::inspect(rules.all)
```

```
   lhs                                rhs           support confidence lift
1  {}                              => {Age=Adult}   0.950   0.950      1.000
2  {Class=2nd}                     => {Age=Adult}   0.119   0.916      0.964
3  {Class=1st}                     => {Age=Adult}   0.145   0.982      1.033
4  {Sex=Female}                    => {Age=Adult}   0.193   0.904      0.951
5  {Class=3rd}                     => {Age=Adult}   0.285   0.888      0.934
6  {Survived=Yes}                  => {Age=Adult}   0.297   0.920      0.968
7  {Class=Crew}                    => {Sex=Male}    0.392   0.974      1.238
8  {Class=Crew}                    => {Age=Adult}   0.402   1.000      1.052
9  {Survived=No}                   => {Sex=Male}    0.620   0.915      1.164
10 {Survived=No}                   => {Age=Adult}   0.653   0.965      1.015
11 {Sex=Male}                      => {Age=Adult}   0.757   0.963      1.013
12 {Sex=Female,Survived=Yes}       => {Age=Adult}   0.144   0.919      0.966
13 {Class=3rd,Sex=Male}            => {Survived=No} 0.192   0.827      1.222
14 {Class=3rd,Survived=No}         => {Age=Adult}   0.216   0.902      0.948
15 {Class=3rd,Sex=Male}            => {Age=Adult}   0.210   0.906      0.953
16 {Sex=Male,Survived=Yes}         => {Age=Adult}   0.154   0.921      0.969
17 {Class=Crew,Survived=No}        => {Sex=Male}    0.304   0.996      1.266
18 {Class=Crew,Survived=No}        => {Age=Adult}   0.306   1.000      1.052
19 {Class=Crew,Sex=Male}           => {Age=Adult}   0.392   1.000      1.052
20 {Class=Crew,Age=Adult}          => {Sex=Male}    0.392   0.974      1.238
21 {Sex=Male,Survived=No}          => {Age=Adult}   0.604   0.974      1.025
22 {Age=Adult,Survived=No}         => {Sex=Male}    0.604   0.924      1.175
23 {Class=3rd,Sex=Male,Survived=No}  => {Age=Adult}  0.176   0.917      0.965
24 {Class=3rd,Age=Adult,Survived=No} => {Sex=Male}   0.176   0.813      1.034
25 {Class=3rd,Sex=Male,Age=Adult}    => {Survived=No} 0.176  0.838      1.237
26 {Class=Crew,Sex=Male,Survived=No} => {Age=Adult}  0.304   1.000      1.052
27 {Class=Crew,Age=Adult,Survived=No} => {Sex=Male}  0.304   0.996      1.266
```

As a common phenomenon for association rule mining, many rules generated above are uninteresting. Suppose that we are interested in only rules with `rhs` indicating survival, so we set `rhs=c("Survived=No", "Survived=Yes")` in `appearance` to make sure that only "Survived=No" and "Survived=Yes" will appear in the `rhs` of rules. All other items can appear in the `lhs`, as set with `default="lhs"`. In the above result `rules.all`, we can also see that the left-hand side (`lhs`) of the first rule is empty. To exclude such rules, we set `minlen` to 2 in the code below. Moreover, the details of progress are suppressed with `verbose=F`. After association rule mining, rules are sorted by lift to make high-lift rules appear first.

```
> # rules with rhs containing "Survived" only
> rules <- apriori(titanic.raw, control = list(verbose=F),
+                  parameter = list(minlen=2, supp=0.005, conf=0.8),
+                  appearance = list(rhs=c("Survived=No", "Survived=Yes"),
+                                    default="lhs"))
```

```
> quality(rules) <- round(quality(rules), digits=3)
> rules.sorted <- sort(rules, by="lift")

> inspect(rules.sorted)

   lhs                                  rhs            support confidence lift
1  {Class=2nd,Age=Child}             => {Survived=Yes} 0.011   1.000      3.096
7  {Class=2nd,Sex=Female,Age=Child}  => {Survived=Yes} 0.006   1.000      3.096
4  {Class=1st,Sex=Female}            => {Survived=Yes} 0.064   0.972      3.010
10 {Class=1st,Sex=Female,Age=Adult}  => {Survived=Yes} 0.064   0.972      3.010
2  {Class=2nd,Sex=Female}            => {Survived=Yes} 0.042   0.877      2.716
5  {Class=Crew,Sex=Female}           => {Survived=Yes} 0.009   0.870      2.692
11 {Class=Crew,Sex=Female,Age=Adult} => {Survived=Yes} 0.009   0.870      2.692
8  {Class=2nd,Sex=Female,Age=Adult}  => {Survived=Yes} 0.036   0.860      2.663
9  {Class=2nd,Sex=Male,Age=Adult}    => {Survived=No}  0.070   0.917      1.354
3  {Class=2nd,Sex=Male}              => {Survived=No}  0.070   0.860      1.271
12 {Class=3rd,Sex=Male,Age=Adult}    => {Survived=No}  0.176   0.838      1.237
6  {Class=3rd,Sex=Male}              => {Survived=No}  0.192   0.827      1.222
```

When other settings are unchanged, with a lower minimum support, more rules will be produced, and the associations between itemsets shown in the rules will be more likely to be by chance. In the above code, the minimum support is set to 0.005, so each rule is supported at least by 12 (=`ceiling(0.005 * 2201)`) cases, which is acceptable for a population of 2201.

Support, confidence and lift are three common measures for selecting interesting association rules. Besides them, there are many other interestingness measures, such as chi-square, conviction, gini and leverage [Tan et al., 2002]. More than twenty measures can be calculated with function `interestMeasure()` in the *arules* package.

9.4 Removing Redundancy

Some rules generated in the previous section (see `rules.sorted`, page 93) provide little or no extra information when some other rules are in the result. For example, the above rule 2 provides no extra knowledge in addition to rule 1, since rules 1 tells us that all 2nd-class children survived. Generally speaking, when a rule (such as rule 2) is a super rule of another rule (such as rule 1) and the former has the same or a lower lift, the former rule (rule 2) is considered to be redundant. Other redundant rules in the above result are rules 4, 7 and 8, compared respectively with rules 3, 6 and 5.

We prune redundant rules with code below. Note that the rules (in `rules.sorted`) have already been sorted descendingly by lift.

```
> # find redundant rules
> subset.matrix <- is.subset(rules.sorted, rules.sorted)
> subset.matrix[lower.tri(subset.matrix, diag=T)] <- NA
> redundant <- colSums(subset.matrix, na.rm=T) >= 1
> which(redundant)

 {Class=2nd,Sex=Female,Age=Child,Survived=Yes}
                                            2
 {Class=1st,Sex=Female,Age=Adult,Survived=Yes}
                                            4
{Class=Crew,Sex=Female,Age=Adult,Survived=Yes}
                                            7
 {Class=2nd,Sex=Female,Age=Adult,Survived=Yes}
                                            8
```

```
> # remove redundant rules
> rules.pruned <- rules.sorted[!redundant]

> inspect(rules.pruned)

   lhs                               rhs            support confidence lift
1  {Class=2nd,Age=Child}          => {Survived=Yes} 0.011   1.000      3.096
4  {Class=1st,Sex=Female}         => {Survived=Yes} 0.064   0.972      3.010
2  {Class=2nd,Sex=Female}         => {Survived=Yes} 0.042   0.877      2.716
5  {Class=Crew,Sex=Female}        => {Survived=Yes} 0.009   0.870      2.692
9  {Class=2nd,Sex=Male,Age=Adult} => {Survived=No}  0.070   0.917      1.354
3  {Class=2nd,Sex=Male}           => {Survived=No}  0.070   0.860      1.271
12 {Class=3rd,Sex=Male,Age=Adult} => {Survived=No}  0.176   0.838      1.237
6  {Class=3rd,Sex=Male}           => {Survived=No}  0.192   0.827      1.222
```

In the code above, function `is.subset(r1, r2)` checks whether `r1` is a subset of `r2` (i.e., whether r2 is a superset of `r1`). Function `lower.tri()` returns a logical matrix with `TURE` in lower triangle. From the above results, we can see that rules 2, 4, 7 and 8 (before redundancy removal) are successfully pruned.

9.5 Interpreting Rules

While it is easy to find high-lift rules from data, it is not an easy job to understand the identified rules. It is not uncommon that the association rules are misinterpreted to find their business meanings. For instance, in the above rule list `rules.pruned`, the first rule `"{Class=2nd, Age=Child} => {Survived=Yes}"` has a confidence of one and a lift of three and there are no rules on children of the 1st or 3rd classes. Therefore, it might be interpreted by users as *children of the 2nd class had a higher survival rate than other children*. This is wrong! The rule states only that all children of class 2 survived, but provides no information at all to compare the survival rates of different classes. To investigate the above issue, we run the code below to find rules whose `rhs` is `"Survived=Yes"` and `lhs` contains `"Class=1st"`, `"Class=2nd"`, `"Class=3rd"`, `"Age=Child"` and `"Age=Adult"` only, and which contains no other items (`default="none"`). We use lower thresholds for both support and confidence than before to find all rules for children of different classes.

```
> rules <- apriori(titanic.raw,
+                  parameter = list(minlen=3, supp=0.002, conf=0.2),
+                  appearance = list(rhs=c("Survived=Yes"),
+                                    lhs=c("Class=1st", "Class=2nd", "Class=3rd",
+                                          "Age=Child", "Age=Adult"),
+                                    default="none"),
+                  control = list(verbose=F))
> rules.sorted <- sort(rules, by="confidence")

> inspect(rules.sorted)

  lhs                       rhs            support     confidence lift
1 {Class=2nd,Age=Child}  => {Survived=Yes} 0.010904134 1.0000000  3.0956399
2 {Class=1st,Age=Child}  => {Survived=Yes} 0.002726034 1.0000000  3.0956399
5 {Class=1st,Age=Adult}  => {Survived=Yes} 0.089504771 0.6175549  1.9117275
4 {Class=2nd,Age=Adult}  => {Survived=Yes} 0.042707860 0.3601533  1.1149048
3 {Class=3rd,Age=Child}  => {Survived=Yes} 0.012267151 0.3417722  1.0580035
6 {Class=3rd,Age=Adult}  => {Survived=Yes} 0.068605179 0.2408293  0.7455209
```

In the above result, the first two rules show that children of the 1st class are of the same survival rate as children of the 2nd class and that all of them survived. The rule of 1st-class children didn't

appear before, simply because of its support was below the threshold specified in Section 9.3. Rule 5 presents a sad fact that children of class 3 had a low survival rate of 34%, which is comparable with that of 2nd-class adults (see rule 4) and much lower than 1st-class adults (see rule 3).

9.6 Visualizing Association Rules

Next we show some ways to visualize association rules, including scatter plot, balloon plot, graph and parallel coordinates plot. More examples on visualizing association rules can be found in the vignettes of package *arulesViz* [Hahsler and Chelluboina, 2014] on CRAN at `http://cran.r-project.org/web/packages/arulesViz/vignettes/arulesViz.pdf`.

```
> library(arulesViz)
> plot(rules.all)
```

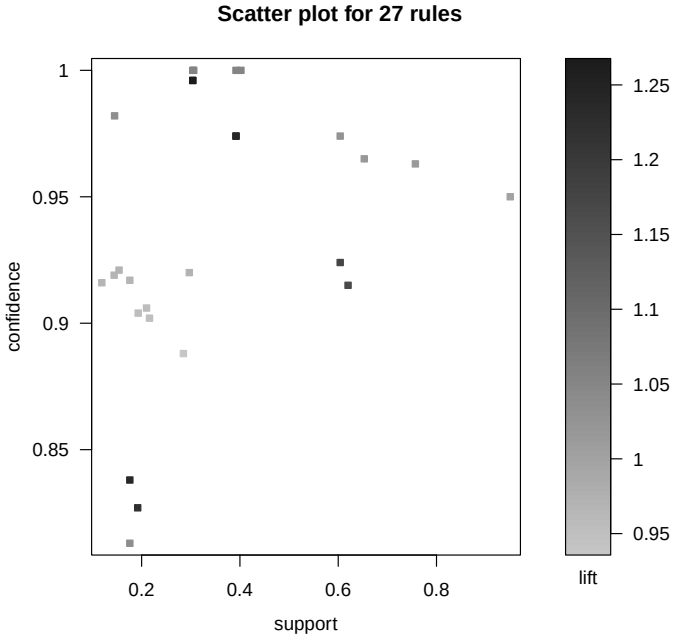

Figure 9.1: A Scatter Plot of Association Rules

```
> plot(rules.all, method="grouped")
```

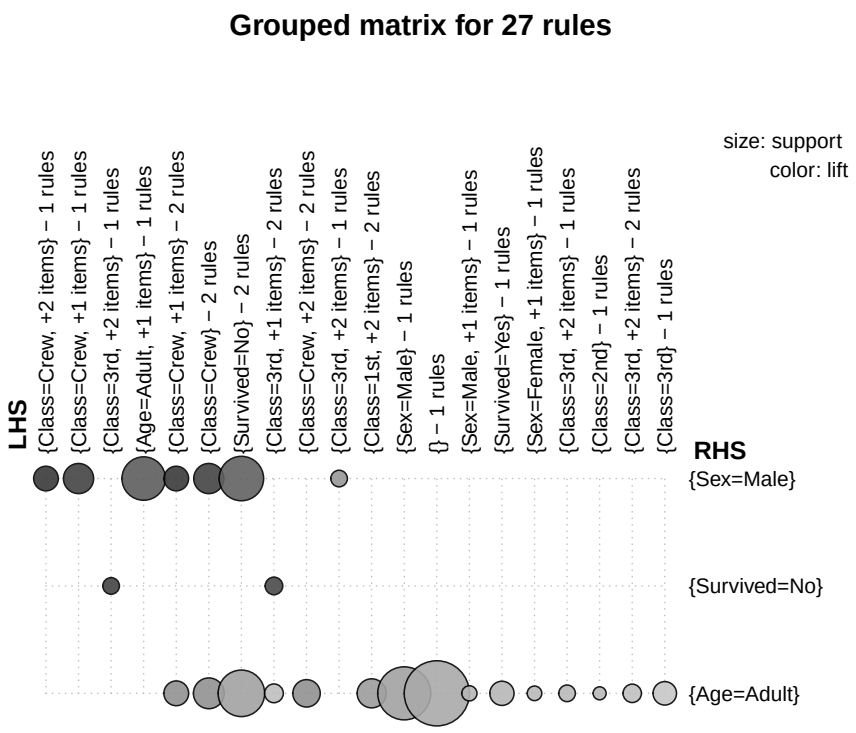

Figure 9.2: A Balloon Plot of Association Rules

```
> plot(rules.all, method="graph")
```

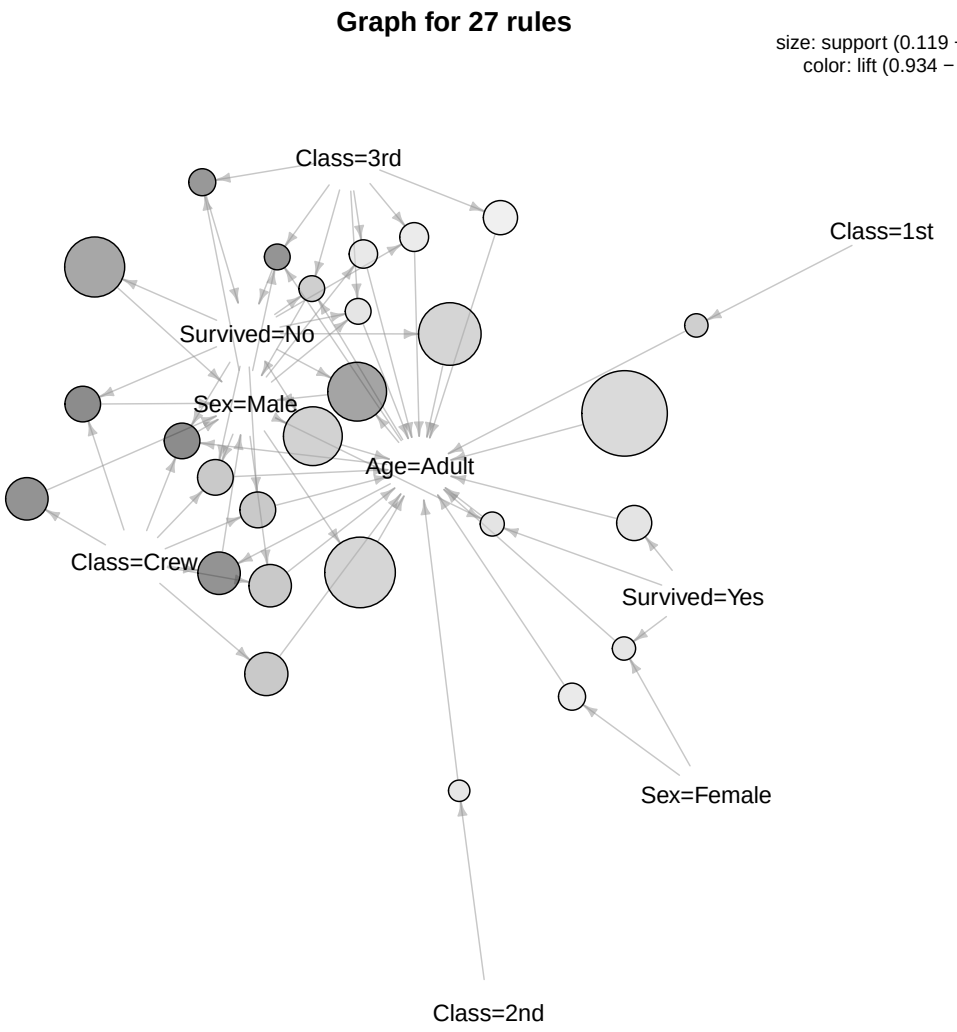

Figure 9.3: A Graph of Association Rules

```
> plot(rules.all, method="graph", control=list(type="items"))
```

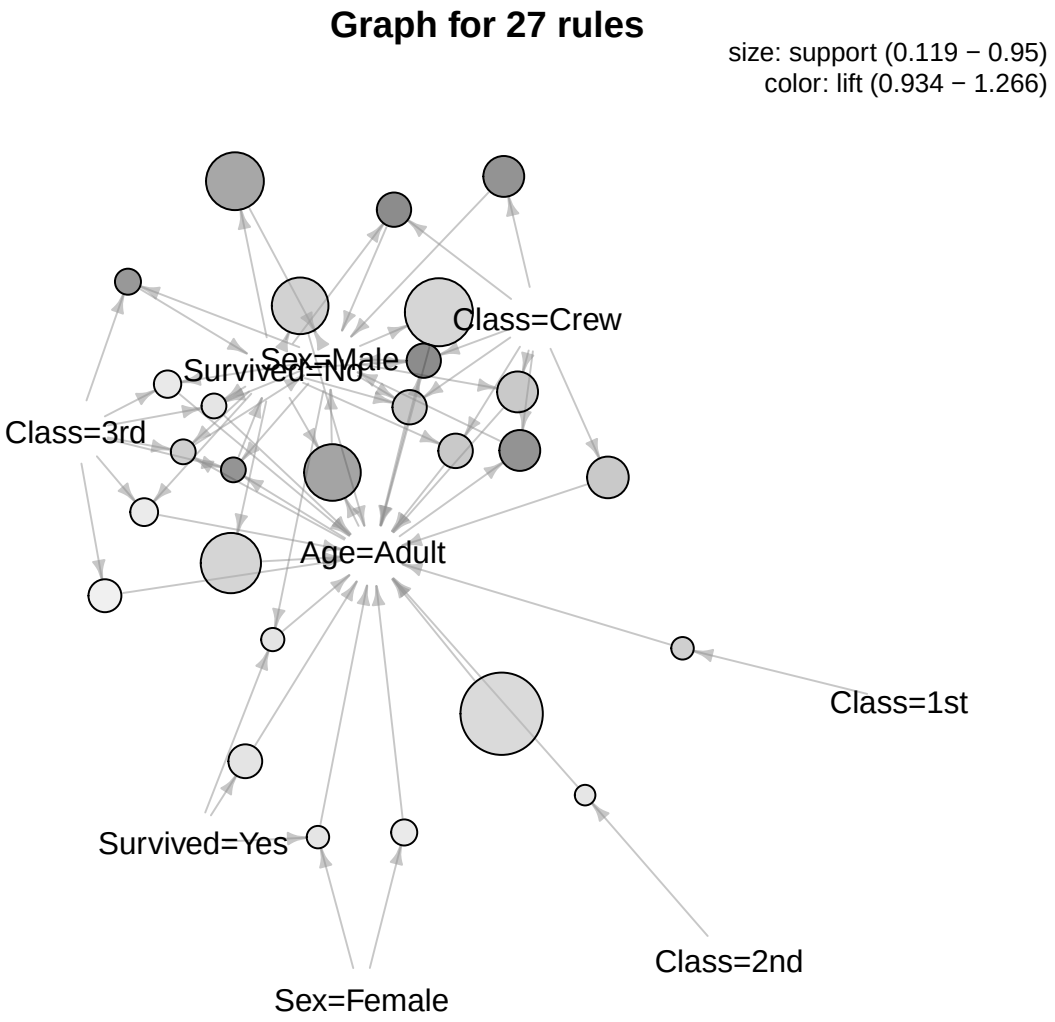

Figure 9.4: A Graph of Items

```
> plot(rules.all, method="paracoord", control=list(reorder=TRUE))
```

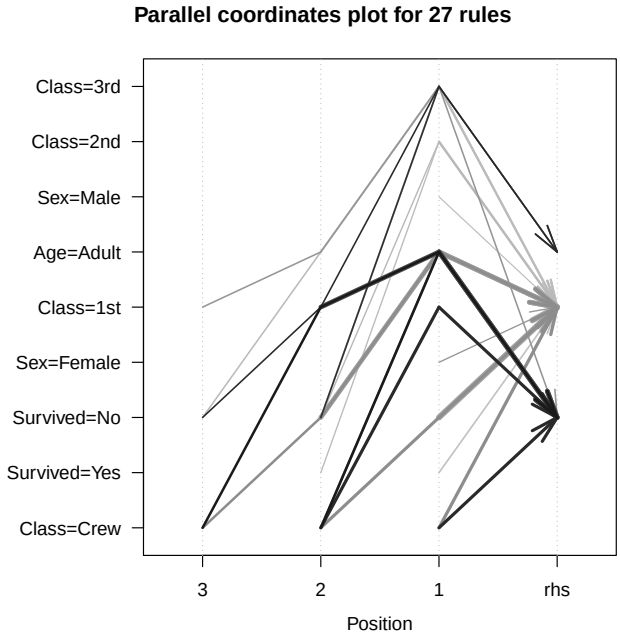

Figure 9.5: A Parallel Coordinates Plot of Association Rules

9.7 Further Readings

In this chapter, we have demonstrated association rule mining with package *arules* [Hahsler et al., 2014]. More examples on that package can be found in Hahsler et al.'s work [Hahsler et al., 2005]. Two other packages related to association rules are *arulesSequences* and *arulesNBMiner* [Hahsler, 2015]. Package *arulesSequences* provides functions for mining sequential patterns [Buchta et al., 2012]. Package *arulesNBMiner* implements an algorithm for mining negative binomial (NB) frequent itemsets and NB-precise rules [Hahsler, 2015].

More techniques on post mining of association rules, such as selecting interesting association rules, visualization of association rules and using association rules for classification, can be found in Zhao et al's work [Zhao et al., 2009b].

Chapter 10

Text Mining

This chapter presents examples of text mining with R. Twitter[1] text of @RDataMining is used as the data to analyze. It starts with extracting text from Twitter. The extracted text is then transformed to build a document-term matrix. After that, frequent words and associations are found from the matrix. A word cloud is used to present important words in documents. In the end, words and tweets are clustered to find groups of words and also groups of tweets. In this chapter, "tweet" and "document" will be used interchangeably, so are "word" and "term".

There are three important packages used in the examples: *twitteR*, *tm* and *wordcloud*. Package *twitteR* [Gentry, 2015] provides access to Twitter data, *tm* [Feinerer and Hornik, 2015] provides functions for text mining, and *wordcloud* [Fellows, 2014] visualizes the result with a word cloud [2].

10.1 Retrieving Text from Twitter

Twitter text is used in this chapter to demonstrate text mining. Tweets are extracted from Twitter with the code below using `userTimeline()` in package *twitteR* [Gentry, 2015]. Package *twitteR* depends on package *RCurl* [Lang and the CRAN team, 2015], which is available at `http://www.stats.ox.ac.uk/pub/RWin/bin/windows/contrib/`. Another way to retrieve text from Twitter is using package *XML* [Lang and the CRAN Team, 2015], and an example on that is given at `http://heuristically.wordpress.com/2011/04/08/text-data-mining-twitter-r/`.

For readers who have no access to Twitter, the tweets data "rdmTweets.RData" can be downloaded at `http://www.rdatamining.com/data`. Then readers can skip this section and proceed directly to Section 10.2.

Note that the Twitter API requires authentication since March 2013. Before running the code below, please complete authentication by following instructions in "Section 3: Authentication with OAuth" in the twitteR vignettes (`http://cran.r-project.org/web/packages/twitteR/vignettes/twitteR.pdf`).

```
> library(twitteR)
> # retrieve the first 200 tweets (or all tweets if fewer than 200) from the
> # user timeline of @rdatammining
> rdmTweets <- userTimeline("rdatamining", n=200)
> (nDocs <- length(rdmTweets))
```

```
> ## Option 2: download @RDataMining tweets from RDataMining.com
> url <- "http://www.rdatamining.com/data/rdmTweets-201306.RData"
> download.file(url, destfile = "./data/rdmTweets.RData")
```

```
[1] 154
```

[1] `http://www.twitter.com`
[2] `http://en.wikipedia.org/wiki/Word_cloud`

Next, we have a look at the five tweets numbered 11 to 15.

```
> rdmTweets[11:15]
```

With the above code, each tweet is printed in one single line, which may exceed the boundary of paper. Therefore, the following code is used in this book to print the five tweets by wrapping the text to fit the width of paper. The same method is used to print tweets in other codes in this chapter.

```
> for (i in 11:15) {
+   cat(paste0("[[", i, "]] ", sep=""))
+   writeLines(strwrap(rdmTweets[[i]]$getText(), width=73))
+ }
```

```
[[11]] Slides on massive data, shared and distributed memory,and concurrent
programming: bigmemory and foreach http://t.co/a6bQzxj5
[[12]] The R Reference Card for Data Mining is updated with functions &
packages for handling big data & parallel computing.
http://t.co/FHoVZCyk
[[13]] Post-doc on Optimizing a Cloud for Data Mining primitives, INRIA, France
http://t.co/cA28STPO
[[14]] Chief Scientist - Data Intensive Analytics, Pacific Northwest National
Laboratory (PNNL), US http://t.co/0Gdzq1Nt
[[15]] Top 10 in Data Mining http://t.co/7kAuNvuf
```

10.2 Transforming Text

The tweets are first converted to a data frame and then to a corpus, which is a collection of text documents. After that, the corpus can be processed with functions provided in package *tm* [Feinerer and Hornik, 2015].

```
> # convert tweets to a data frame
> #df <- do.call("rbind", lapply(rdmTweets, as.data.frame))
> #dim(df)
>
> # convert tweets to a data frame
> df <- twListToDF(rdmTweets)
> dim(df)
```

```
[1] 154  10
```

```
> library(tm)
> # build a corpus, and specify the source to be character vectors
> myCorpus <- Corpus(VectorSource(df$text))
```

After that, the corpus needs a couple of transformations, including changing letters to lower case, and removing punctuations, numbers and stop words. The general English stop-word list is tailored here by adding "available" and "via" and removing "r" and "big" (for big data). Hyperlinks are also removed in the example below.

```
> # convert to lower case
> # tm v0.6
> myCorpus <- tm_map(myCorpus, content_transformer(tolower))
> # tm v0.5-10
> # myCorpus <- tm_map(myCorpus, tolower)
>
```

```
> # remove URLs
> removeURL <- function(x) gsub("http[^[:space:]]*", "", x)
> # tm v0.6
> myCorpus <- tm_map(myCorpus, content_transformer(removeURL))
> # tm v0.5-10
> # myCorpus <- tm_map(myCorpus, removeURL)
>
> # remove anything other than English letters or space
> removeNumPunct <- function(x) gsub("[^[:alpha:][:space:]]*", "", x)
> myCorpus <- tm_map(myCorpus, content_transformer(removeNumPunct))
> # remove punctuation
> #myCorpus <- tm_map(myCorpus, removePunctuation)
> # remove numbers
> #myCorpus <- tm_map(myCorpus, removeNumbers)
>
> # add two extra stop words: "available" and "via"
> myStopwords <- c(stopwords(english), "available", "via")
> # remove "r" and "big" from stopwords
> myStopwords <- setdiff(myStopwords, c("r", "big"))
> # remove stopwords from corpus
> myCorpus <- tm_map(myCorpus, removeWords, myStopwords)
> # remove extra whitespace
> myCorpus <- tm_map(myCorpus, stripWhitespace)
```

In the above code, `tm_map()` is an interface to apply transformations (mappings) to corpora. A list of available transformations can be obtained with `getTransformations()`, and the mostly used ones are `as.PlainTextDocument()`, `removeNumbers()`, `removePunctuation()`, `removeWords()`, `stemDocument()` and `stripWhitespace()`. A function `removeURL()` is defined above to remove hypelinks, where pattern `"http[[:alnum:]]*"` matches strings starting with "http" and then followed by any number of alphabetic characters and digits. Strings matching this pattern are removed with `gsub()`. The above pattern is specified as an regular expression, and detail about that can be found by running `?regex` in R.

10.3 Stemming Words

In many applications, words need to be stemmed to retrieve their radicals, so that various forms derived from a stem would be taken as the same when counting word frequency. For instance, words "update", "updated" and "updating" would all be stemmed to "updat". Word stemming can be done with the snowball stemmer, which requires packages *Snowball*, *RWeka*, *rJava* and *RWekajars*. After that, we can complete the stems to their original forms, i.e., "update" for the above example, so that the words would look normal. This can be achieved with function `stemCompletion()`.

```
> # keep a copy of corpus to use later as a dictionary for stem completion
> myCorpusCopy <- myCorpus
> # stem words
> myCorpus <- tm_map(myCorpus, stemDocument)
```

```
> # inspect documents (tweets) numbered 11 to 15
> # inspect(myCorpus[11:15])
> # The code below is used for to make text fit for paper width
> for (i in 11:15) {
+   cat(paste("[[", i, "]] ", sep=""))
+   writeLines(strwrap(myCorpus[[i]], width=73))
+ }
```

```
[[11]] slide massiv data share distribut memoryand concurr program bigmemori
foreach
[[12]] r refer card data mine updat function packag handl big data parallel
comput
[[13]] postdoc optim cloud data mine primit inria franc
[[14]] chief scientist data intens analyt pacif northwest nation laboratori
pnnl us
[[15]] top data mine
```

```
> # inspect the first 5 documents (tweets)
> # inspect(myCorpus[1:5])
> # The code below is used for to make text fit for paper width
> for (i in 11:15) {
+   cat(paste0("[", i, "] "))
+   writeLines(strwrap(as.character(myCorpus[[i]]), 60))
+ }
```

```
[11] slide massiv data share distribut memoryand concurr program
bigmemori foreach
[12] r refer card data mine updat function packag handl big data
parallel comput
[13] postdoc optim cloud data mine primit inria franc
[14] chief scientist data intens analyt pacif northwest nation
laboratori pnnl us
[15] top data mine
```

After that, we use `stemCompletion()` to complete the stems with the unstemmed corpus `myCorpusCopy` as a dictionary. With the default setting, it takes the most frequent match in dictionary as completion.

```
> # tm v0.5-10
> # myCorpus <- tm_map(myCorpus, stemCompletion)
> # tm v0.6
> stemCompletion2 <- function(x, dictionary) {
+   x <- unlist(strsplit(as.character(x), " "))
+   # Unexpectedly, stemCompletion completes an empty string to
+   # a word in dictionary. Remove empty string to avoid above issue.
+   x <- x[x != ""]
+   x <- stemCompletion(x, dictionary=dictionary)
+   x <- paste(x, sep="", collapse=" ")
+   PlainTextDocument(stripWhitespace(x))
+ }
> myCorpus <- lapply(myCorpus, stemCompletion2, dictionary=myCorpusCopy)
> myCorpus <- Corpus(VectorSource(myCorpus))
```

Then we have a look at the documents numbered 11 to 15 in the built corpus.

```
> inspect(myCorpus[11:15])
```

```
[11] slides massive data share distributed memoryand concurrent
programming foreach
[12] r reference card data miners updated function package
handling big data parallel computer
[13] postdoc optimizing cloud data miners primitives inria
france
[14] chief scientist data intensive analytics pacific northwest
```

```
national pnnl us
[15] top data miners

[[11]] slides massive data share distributed memoryand concurrent programming
foreach
[[12]] r reference card data miners updated function package handling big data
parallel computer
[[13]] postdoc optimizing cloud data miners primitives inria france
[[14]] chief scientist data intensive analytics pacific northwest national pnnl
us
[[15]] top data miners
```

As we can see from the above results, there are something unexpected in the above stemming and completion.

1. In both the stemmed corpus and the completed one, "memoryand" is derived from "... memory,and ..." in the original tweet 11.
2. In tweet 11, word "bigmemory" is stemmed to "bigmemori", and then is removed during stem completion.
3. Word "mining" in tweets 12, 13 & 15 is first stemmed to "mine" and then completed to "miners".
4. "Laboratory" in tweet 14 is stemmed to "laboratori" and then also disappears after completion.

In the above issues, point 1 is caused by the missing of a space after the comma. It can be easily fixed by replacing comma with space before removing punctuation marks in Section 10.2. For points 2 & 4, we haven't figured out why it happened like that. Fortunately, the words involved in points 1, 2 & 4 are not important in @RDataMining tweets and ignoring them would not bring any harm to this demonstration of text mining.

Below we focus on point 3, where word "mining" is first stemmed to "mine" and then completed to "miners", instead of "mining", although there are many instances of "mining" in the tweets, compared to only two instances of "miners". There might be a solution for the above problem by changing the parameters and/or dictionaries for stemming and completion, but we failed to find one due to limitation of time and efforts. Instead, we chose a simple way to get around of that by replacing "miners" with "mining", since the latter has many more cases than the former in the corpus. The code for the replacement is given below.

```
> # count frequency of "mining"
> miningCases <- lapply(myCorpusCopy,
+       function(x) { grep(as.character(x), pattern = "\\<mining")} )
> sum(unlist(miningCases))

[1] 47

> # count frequency of "miner"
> minerCases <- lapply(myCorpusCopy,
+      function(x) {grep(as.character(x), pattern = "\\<miner")} )
> sum(unlist(minerCases))

[1] 2

> # replace "miner" with "mining"
> myCorpus <- tm_map(myCorpus, content_transformer(gsub),
+                    pattern = "miners", replacement = "mining")
```

In the first call of function `tm_map()` in the above code, `grep()` is applied to every document (tweet) with argument "`pattern="\\<mining"`". The pattern matches words starting with "mining", where "`\<`" matches the empty string at the beginning of a word. This ensures that text "rdatamining" would not contribute to the above counting of "mining".

10.4 Building a Term-Document Matrix

A term-document matrix represents the relationship between terms and documents, where each row stands for a term and each column for a document, and an entry is the number of occurrences of the term in the document. Alternatively, one can also build a document-term matrix by swapping row and column. In this section, we build a term-document matrix from the above processed corpus with function `TermDocumentMatrix()`. With its default setting, terms with less than three characters are discarded. To keep "r" in the matrix, we set the range of `wordLengths` in the example below.

```
> tdm <- TermDocumentMatrix(myCorpus, control=list(wordLengths=c(1,Inf)))
> tdm

<<TermDocumentMatrix (terms: 491, documents: 154)>>
Non-/sparse entries: 1163/74451
Sparsity           : 98%
Maximal term length: 27
Weighting          : term frequency (tf)
```

As we can see from the above result, the term-document matrix is composed of 491 terms and 154 documents. It is very sparse, with 98% of the entries being zero. We then have a look at the first six terms starting with "r" and tweets numbered 101 to 110.

```
> idx <- which(dimnames(tdm)$Terms == "r")
> inspect(tdm[idx+(0:5),101:110])

<<TermDocumentMatrix (terms: 6, documents: 10)>>
Non-/sparse entries: 9/51
Sparsity           : 85%
Maximal term length: 12
Weighting          : term frequency (tf)

              Docs
Terms          101 102 103 104 105 106 107 108 109 110
  r              1   1   0   0   2   0   0   1   1   1
  ramachandran   0   0   0   0   0   0   0   0   0   0
  random         0   0   0   0   0   0   0   0   0   0
  ranked         0   0   0   0   0   0   0   0   1   0
  rapidminer     1   0   0   0   0   0   0   0   0   0
  rdatamining    0   0   0   0   0   0   0   1   0   0
```

Note that the parameter to control word length used to be `minWordLength` prior to version 0.5-7 of package *tm*. The code to set the minimum word length for old versions of *tm* is below.

```
> tdm <- TermDocumentMatrix(myCorpus, control=list(minWordLength=1))
```

The list of terms can be retrieved with `rownames(tdm)`. Based on the above matrix, many data mining tasks can be done, for example, clustering, classification and association analysis.

When there are too many terms, the size of a term-document matrix can be reduced by selecting terms that appear in a minimum number of documents, or filtering terms with TF-IDF (term frequency-inverse document frequency) [Wu et al., 2008].

10.5 Frequent Terms and Associations

We have a look at the popular words and the association between words. Note that there are 154 tweets in total.

```
> # inspect frequent words
> findFreqTerms(tdm, lowfreq=10)

 [1] "analysis"     "computer"     "data"         "example"      "group"
 [6] "introduction" "mining"       "network"      "package"      "position"
[11] "r"            "research"     "slides"       "social"       "tutorial"
[16] "use"
```

In the code above, `findFreqTerms()` finds frequent terms with frequency no less than ten. Note that they are ordered alphabetically, instead of by frequency or popularity.

To show the top frequent words visually, we next make a barplot for them. From the term-document matrix, we can derive the frequency of terms with `rowSums()`. Then we select terms that appears in ten or more documents and shown them with a barplot using package *ggplot2* [Wickham, 2009]. In the code below, `geom="bar"` specifies a barplot and `coord_flip()` swaps x- and y-axis. The barplot in Figure 10.1 clearly shows that the three most frequent words are "r", "data" and "mining".

```
> termFrequency <- rowSums(as.matrix(tdm))
> termFrequency <- subset(termFrequency, termFrequency>=10)
> library(ggplot2)
> df <- data.frame(term=names(termFrequency), freq=termFrequency)
> ggplot(df, aes(x=term, y=freq)) + geom_bar(stat="identity") +
+    xlab("Terms") + ylab("Count") + coord_flip()
```

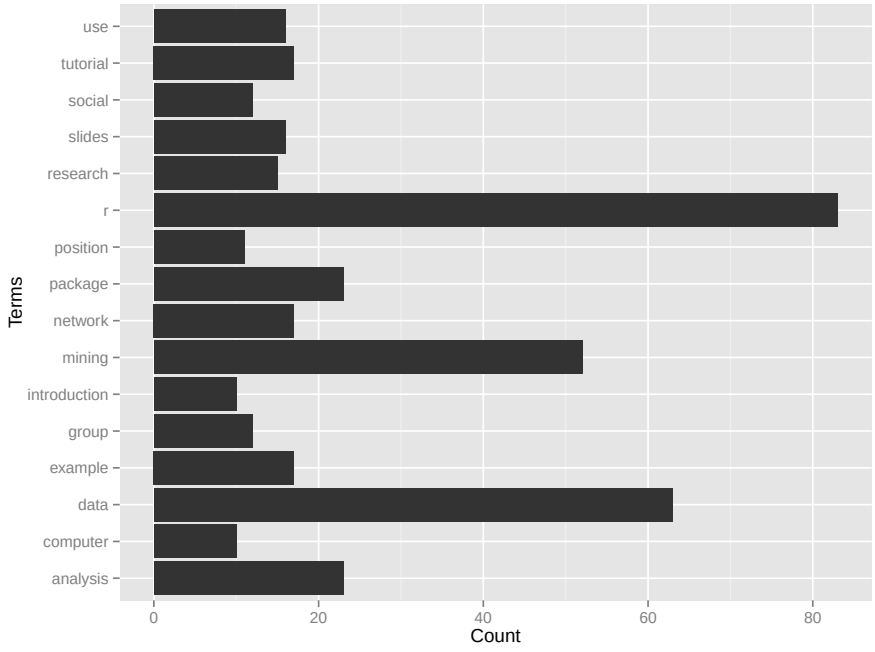

Figure 10.1: Frequent Terms

Alternatively, the above plot can also be drawn with `barplot()` as below, where `las` sets the direction of x-axis labels to be vertical.

```
> barplot(termFrequency, las=2)
```

We can also find what are highly associated with a word with function `findAssocs()`. Below we try to find terms associated with "r" (or "mining") with correlation no less than 0.25, and the words are ordered by their correlation with "r" (or "mining").

```
> # which words are associated with "r"?
> findAssocs(tdm, r, 0.25)


$r
canberra     cran     list  example     user
    0.26     0.26     0.26     0.25     0.25


> # which words are associated with "mining"?
> findAssocs(tdm, mining, 0.25)


$mining
          data         mahout recommendation           sets       supports
          0.55           0.39           0.39           0.39           0.39
      frequent        itemset           card       function      reference
          0.35           0.34           0.29           0.29           0.29
          text
          0.26
```

10.6 Word Cloud

After building a term-document matrix, we can show the importance of words with a word cloud (also known as a tag cloud), which can be easily produced with package *wordcloud* [Fellows, 2014]. In the code below, we first convert the term-document matrix to a normal matrix, and then calculate word frequencies. After that, we set gray levels based on word frequency and use `wordcloud()` to make a plot for it. With `wordcloud()`, the first two parameters give a list of words and their frequencies. Words with frequency below three are not plotted, as specified by `min.freq=3`. By setting `random.order=F`, frequent words are plotted first, which makes them appear in the center of cloud. We also set the colors to gray levels based on frequency. A colorful cloud can be generated by setting colors with `rainbow()`.

```
> library(wordcloud)
> m <- as.matrix(tdm)
> # calculate the frequency of words and sort it descendingly by frequency
> wordFreq <- sort(rowSums(m), decreasing=TRUE)
> # colors
> pal <- brewer.pal(9, "BuGn")
> pal <- pal[-(1:4)]
> # word cloud
> set.seed(375) # to make it reproducible
> grayLevels <- gray( (wordFreq+10) / (max(wordFreq)+10) )
> wordcloud(words=names(wordFreq), freq=wordFreq, min.freq=3, random.order=F,
+           colors=pal)
```

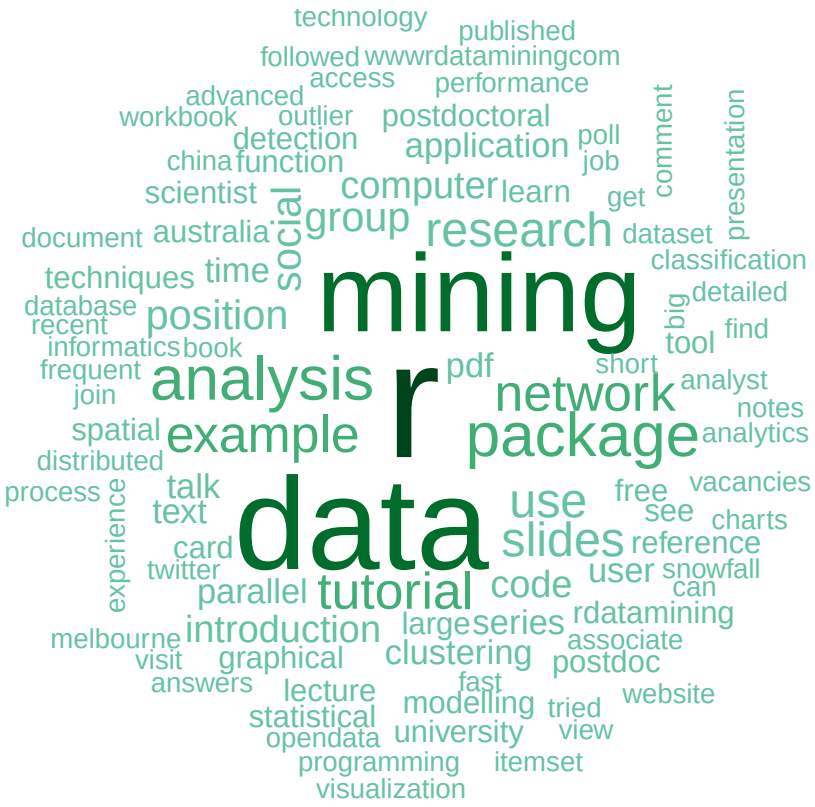

Figure 10.2: Word Cloud

The above word cloud clearly shows again that "r", "data" and "mining" are the top three words, which validates that the @RDataMining tweets present information on R and data mining. Some other important words are "analysis", "examples", "slides", "tutorial" and "package", which shows that it focuses on documents and examples on analysis and R packages. Another set of frequent words, "research", "postdoctoral" and "positions", are from tweets about vacancies on post-doctoral and research positions. There are also some tweets on the topic of social network analysis, as indicated by words "network" and "social" in the cloud.

10.7 Clustering Words

We then try to find clusters of words with hierarchical clustering. Sparse terms are removed, so that the plot of clustering will not be crowded with words. Then the distances between terms are calculated with `dist()` after scaling. After that, the terms are clustered with `hclust()` and the dendrogram is cut into 10 clusters. The agglomeration method is set to `ward`, which denotes the increase in variance when two clusters are merged. Some other options are single linkage, complete linkage, average linkage, median and centroid. Details about different agglomeration methods can be found in data mining textbooks [Han and Kamber, 2000, Hand et al., 2001, Witten and Frank, 2005].

```
> # remove sparse terms
> tdm2 <- removeSparseTerms(tdm, sparse=0.95)
> m2 <- as.matrix(tdm2)
> # cluster terms
```

```
> distMatrix <- dist(scale(m2))
> fit <- hclust(distMatrix, method="ward.D")


> plot(fit)
> # cut tree into 10 clusters
> rect.hclust(fit, k=10)
> (groups <- cutree(fit, k=10))
```

```
    analysis         code     computer         data      example        group
           1            2            3            4            2            5
introduction       mining      network      package     parallel     position
           5            6            1            7            3            8
           r     research       series       slides       social         time
           9            8           10            5            1           10
    tutorial          use
           5            5
```

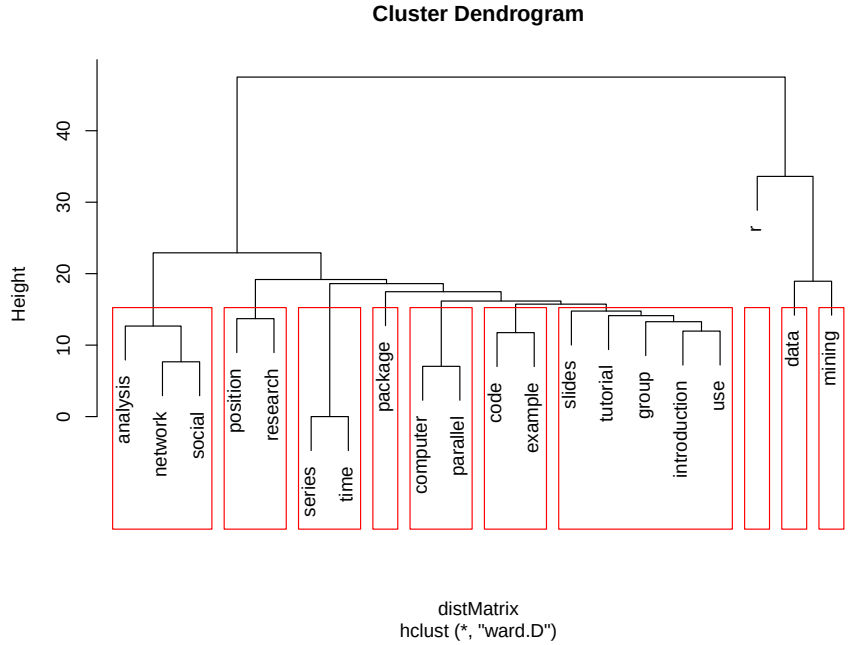

Figure 10.3: Clustering of Words

In the above dendrogram, we can see the topics in the tweets. Words "analysis", "network" and "social" are clustered into one group, because there are a couple of tweets on social network analysis. The second cluster from left comprises "positions", "postdoctoral" and "research", and they are clustered into one group because of tweets on vacancies of research and postdoctoral positions. We can also see cluster on time series, R packages, parallel computing, R codes and examples, and tutorial and slides. The rightmost three clusters consists of "r", "data" and "mining", which are the keywords of @RDataMining tweets.

10.8 Clustering Tweets

Tweets are clustered below with the k-means and the k-medoids algorithms.

10.8.1 Clustering Tweets with the k-means Algorithm

We first try k-means clustering, which takes the values in the matrix as numeric. We transpose the term-document matrix to a document-term one. The tweets are then clustered with `kmeans()` with the number of clusters set to eight. After that, we check the popular words in every cluster and also the cluster centers. Note that a fixed random seed is set with `set.seed()` before running `kmeans()`, so that the clustering result can be reproduced. It is for the convenience of book writing, and it is unnecessary for readers to set a random seed in their code.

```
> # transpose the matrix to cluster documents (tweets)
> m3 <- t(m2)
> # set a fixed random seed
> set.seed(122)
> # k-means clustering of tweets
> k <- 8
> kmeansResult <- kmeans(m3, k)
> # cluster centers
> round(kmeansResult$centers, digits=3)
```

```
  analysis  code computer  data example group introduction mining network package
1    0.122 0.195    0.000 0.317   0.293 0.049        0.049  0.268   0.073   0.000
2    0.000 0.000    0.091 1.909   0.000 0.091        0.091  1.273   0.000   0.545
3    0.857 0.000    0.000 0.000   0.071 0.000        0.143  0.071   1.000   0.071
4    0.000 0.000    1.000 0.000   0.000 0.000        0.000  0.000   0.000   0.125
5    0.052 0.017    0.017 0.397   0.052 0.034        0.086  0.379   0.000   0.052
6    0.111 0.000    0.000 0.111   0.111 0.111        0.000  0.111   0.000   1.222
7    0.667 0.000    0.000 0.000   0.000 2.000        0.000  0.667   0.000   0.000
8    0.000 0.000    0.000 0.500   0.000 0.000        0.000  0.100   0.000   0.100
  parallel position     r research series slides social  time tutorial   use
1    0.000    0.000 1.146    0.000  0.073  0.146  0.000 0.073    0.098 0.098
2    0.091    0.000 0.818    0.091  0.000  0.091  0.000 0.000    0.000 0.455
3    0.000    0.143 0.214    0.071  0.000  0.071  0.786 0.000    0.286 0.071
4    0.750    0.000 1.000    0.000  0.000  0.125  0.000 0.000    0.125 0.250
5    0.000    0.086 0.000    0.000  0.052  0.103  0.000 0.052    0.103 0.017
6    0.111    0.000 1.333    0.000  0.000  0.000  0.000 0.000    0.222 0.222
7    0.000    0.000 1.333    0.000  0.667  0.333  0.000 0.667    0.000 0.333
8    0.000    0.400 0.000    1.300  0.000  0.000  0.100 0.000    0.000 0.000
```

To make it easy to find what the clusters are about, we then check the top three words in every cluster.

```
> for (i in 1:k) {
+   cat(paste("cluster ", i, ":  ", sep=""))
+   s <- sort(kmeansResult$centers[i,], decreasing=T)
+   cat(names(s)[1:3], "\n")
+   # print the tweets of every cluster
+   # print(rdmTweets[which(kmeansResult$cluster==i)])
+ }
```

```
cluster 1:  r data example
cluster 2:  data mining r
cluster 3:  network analysis social
cluster 4:  computer r parallel
cluster 5:  data mining slides
cluster 6:  r package tutorial
cluster 7:  group r analysis
cluster 8:  research data position
```

From the above top words and centers of clusters, we can see that the clusters are of different topics. For instance, cluster 1 focuses on R codes and examples, cluster 2 on data mining with R, cluster 4 on parallel computing in R, cluster 6 on R packages and cluster 7 on slides of time series analysis with R. We can also see that, all clusters, except for cluster 3, 5 & 8, focus on R. Cluster 3, 5 & 8 are about general information on data mining and are not limited to R. Cluster 3 is on social network analysis, cluster 5 on data mining tutorials, and cluster 8 on positions for data mining research.

10.8.2 Clustering Tweets with the k-medoids Algorithm

We then try k-medoids clustering with the Partitioning Around Medoids (PAM) algorithm, which uses medoids (representative objects) instead of means to represent clusters. It is more robust to noise and outliers than k-means clustering, and provides a display of the silhouette plot to show the quality of clustering. In the example below, we use function `pamk()` from package *fpc* [Hennig, 2015], which calls the function `pam()` with the number of clusters estimated by optimum average silhouette.

```
> library(fpc)
> # partitioning around medoids with estimation of number of clusters
> pamResult <- pamk(m3, metric="manhattan")
> # number of clusters identified
> (k <- pamResult$nc)
```

```
[1] 9
```

```
> pamResult <- pamResult$pamobject
> # print cluster medoids
> for (i in 1:k) {
+   cat(paste("cluster", i, ":  "))
+   cat(colnames(pamResult$medoids)[which(pamResult$medoids[i,]==1)], "\n")
+   # print tweets in cluster i
+   # print(rdmTweets[pamResult$clustering==i])
+ }
```

```
cluster 1 :  data position research
cluster 2 :  computer parallel r
cluster 3 :  mining package r
cluster 4 :  data mining
cluster 5 :  analysis network social tutorial
cluster 6 :  r
cluster 7 :
cluster 8 :  example r
cluster 9 :  analysis group mining series time
```

```
> # plot clustering result
> layout(matrix(c(1,2),2,1)) # set to two graphs per page
> plot(pamResult, color=F, labels=4, lines=0, cex=.8, col.clus=1,
+      col.p=pamResult$clustering)
> layout(matrix(1)) # change back to one graph per page
```

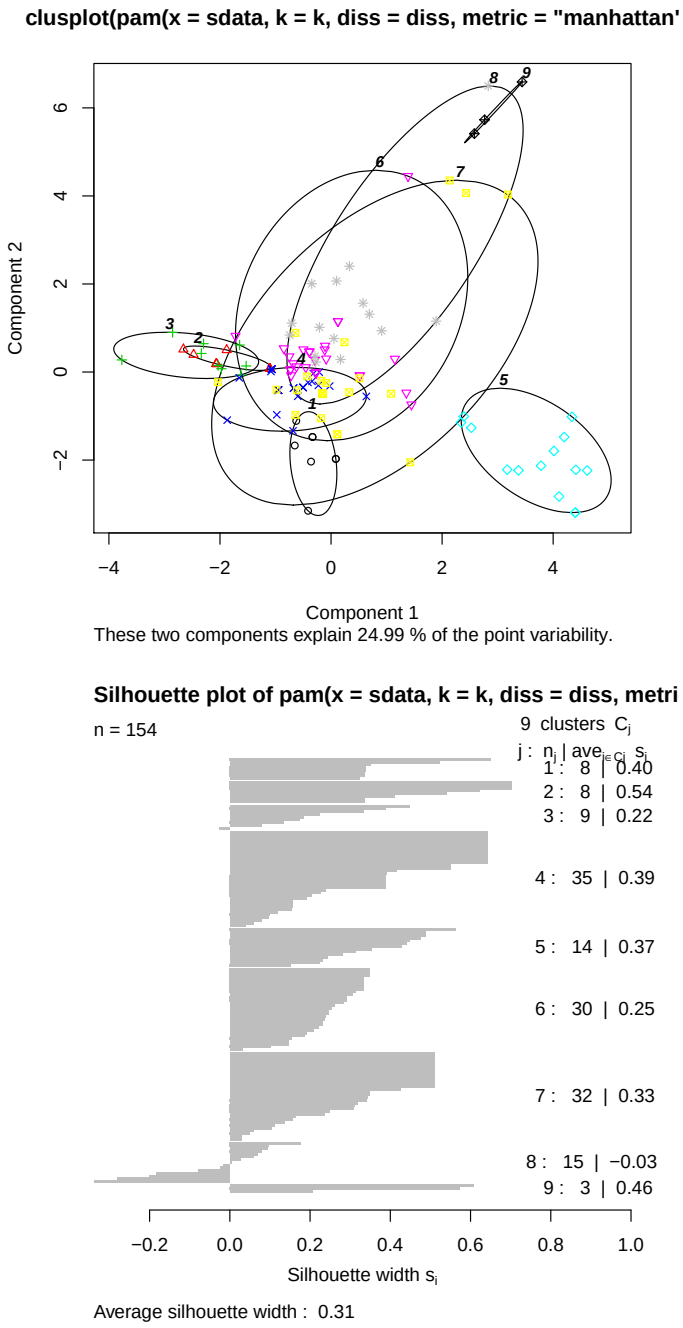

Figure 10.4: Clusters of Tweets

In Figure 10.4, the first chart is a 2D "clusplot" (clustering plot) of the k clusters, and the second one shows their silhouettes. With the silhouette, a large s_i (almost 1) suggests that

the corresponding observations are very well clustered, a small s_i (around 0) means that the observation lies between two clusters, and observations with a negative s_i are probably placed in the wrong cluster. The average silhouette width is 0.29, which suggests that the clusters are not well separated from one another.

The above results and Figure 10.4 show that there are nine clusters of tweets. Clusters 1, 2, 3, 5 and 9 are well separated groups, with each of them focusing on a specific topic. Cluster 7 is composed of tweets not fitted well into other clusters, and it overlaps all other clusters. There is also a big overlap between cluster 6 and 8, which is understandable from their medoids. Some observations in cluster 8 are of negative silhouette width, which means that they may fit better in other clusters than cluster 8.

To improve the clustering quality, we have also tried to set the range of cluster numbers `krange=2:8` when calling `pamk()`, and in the new clustering result, there are eight clusters, with the observations in the above cluster 8 assigned to other clusters, mostly to cluster 6. The results are not shown in this book, and readers can try it with the code below.

```
> pamResult2 <- pamk(m3, krange=2:8, metric="manhattan")
```

10.9 Packages, Further Readings and Discussions

In addition to frequent terms, associations and clustering demonstrated in this chapter, some other possible analysis on the above Twitter text is graph mining and social network analysis. For example, a graph of words can be derived from a document-term matrix, and then we can use techniques for graph mining to find links between words and groups of words. A graph of tweets (documents) can also be generated and analyzed in a similar way. It can also be presented and analyzed as a bipartite graph with two disjoint sets of vertices, that is, words and tweets. We will demonstrate social network analysis on the Twitter data in Chapter 11: Social Network Analysis.

Some R packages for text mining are listed below.

- Package *tm* [Feinerer and Hornik, 2015]: A framework for text mining applications within R.
- Package *tm.plugin.mail* [Feinerer and Mauerer, 2014]: Text Mining E-Mail Plug-In. A plug-in for the tm text mining framework providing mail handling functionality.
- package *textcat* [Hornik et al., 2013] provides n-Gram Based Text Categorization.
- *lda* [Chang, 2012] fit topic models with LDA (latent Dirichlet allocation)
- *topicmodels* [Grün and Hornik, 2011] fit topic models with LDA and CTM (correlated topics model)

For more information and examples on text mining with R, some online resources are:

- *Introduction to the tm Package – Text Mining in R*
  `http://cran.r-project.org/web/packages/tm/vignettes/tm.pdf`
- *Text Mining Infrastructure in R* [Feinerer et al., 2008]
  `http://www.jstatsoft.org/v25/i05`
- Text Mining Handbook
  `http://www.casact.org/pubs/forum/10spforum/Francis_Flynn.pdf`
- Distributed Text Mining in R
  `http://epub.wu.ac.at/3034/`
- Text mining with Twitter and R
  `http://heuristically.wordpress.com/2011/04/08/text-data-mining-twitter-r/`

Chapter 11

Social Network Analysis

This chapter presents examples of social network analysis with R, specifically, with package *igraph* [Csardi and Nepusz, 2006]. The data to analyze is Twitter text data used in Chapter 10 Text Mining. Putting it in a general scenario of social networks, the terms can be taken as people and the tweets as groups on LinkedIn[1], and the term-document matrix can then be taken as the group membership of people.

In this chapter, we first build a network of terms based on their co-occurrence in the same tweets, and then build a network of tweets based on the terms shared by them. At last, we build a two-mode network composed of both terms and tweets. We also demonstrate some tricks to plot nice network graphs. Some codes in this chapter are based on the examples at `http://www.stanford.edu/~messing/Affiliation%20Data.html`.

11.1 Network of Terms

In this section, we will build a network of terms based on their co-occurrence in tweets. At first, a matrix, `termDocMatrix`, is loaded into R, which is actually a copy of `m2`, an R object from Chapter 10 Text Mining (see page 110). After that, it is transformed into a term-term adjacency matrix, based on which a graph is built. Then we plot the graph to show the relationship between frequent terms, and also make the graph more readable by setting colors, font sizes and transparency of vertices and edges.

Note that `termDocMatrix` is a normal matrix, not of class `TermDocumentMatrix`. To run the code below with your own term-document matrix created with package *tm* [Feinerer and Hornik, 2015], you need to convert it first with `as.matrix()`.

```
> termDocMatrix <- as.matrix(yourTermDocMatrixCreatedWithTM)
```

```
> # load termDocMatrix
> load("./data/termDocMatrix.rdata")
> # inspect part of the matrix
> termDocMatrix[5:10,1:20]
```

```
             Docs
Terms         1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20
  example     0 0 0 0 0 0 0 0 0  0  0  0  0  0  0  0  0  0  0  0
  group       0 0 0 0 0 0 0 0 0  0  0  0  0  0  0  0  0  0  0  0
  introduction 0 0 0 0 0 0 0 0 0  0  0  0  0  0  0  0  0  0  0  1
  mining      0 0 0 0 0 0 0 0 0  0  0  1  1  0  1  0  0  0  0  0
  network     0 0 0 0 0 0 0 0 0  0  0  0  0  0  0  1  0  1  1  1
  package     0 0 0 1 1 0 0 0 0  0  0  1  0  0  0  0  0  0  0  0
```

[1] `http://www.linkedin.com`

```
> # change it to a Boolean matrix
> termDocMatrix[termDocMatrix>=1] <- 1
> # transform into a term-term adjacency matrix
> termMatrix <- termDocMatrix %*% t(termDocMatrix)
> # inspect terms numbered 5 to 10
> termMatrix[5:10,5:10]
```

```
             Terms
Terms         example group introduction mining network package
  example          17     0            2      5       2       2
  group             0     9            0      3       0       1
  introduction      2     0           10      2       2       0
  mining            5     3            2     47       1       5
  network           2     0            2      1      17       1
  package           2     1            0      5       1      21
```

In the above code, `%*%` is an operator for the product of two matrices, and `t()` transposes a matrix. Now we have built a term-term adjacency matrix, where the rows and columns represent terms, and every entry is the number of concurrences of two terms. Next we can build a graph with `graph.adjacency()` from package *igraph*.

```
> library(igraph)
> # build a graph from the above matrix
> g <- graph.adjacency(termMatrix, weighted=T, mode="undirected")
> # remove loops
> g <- simplify(g)
> # set labels and degrees of vertices
> V(g)$label <- V(g)$name
> V(g)$degree <- degree(g)
```

After that, we plot the network with `layout.fruchterman.reingold` (see Figure 11.1).

```
> # set seed to make the layout reproducible
> set.seed(3952)
> layout1 <- layout.fruchterman.reingold(g)
> plot(g, layout=layout1)
```

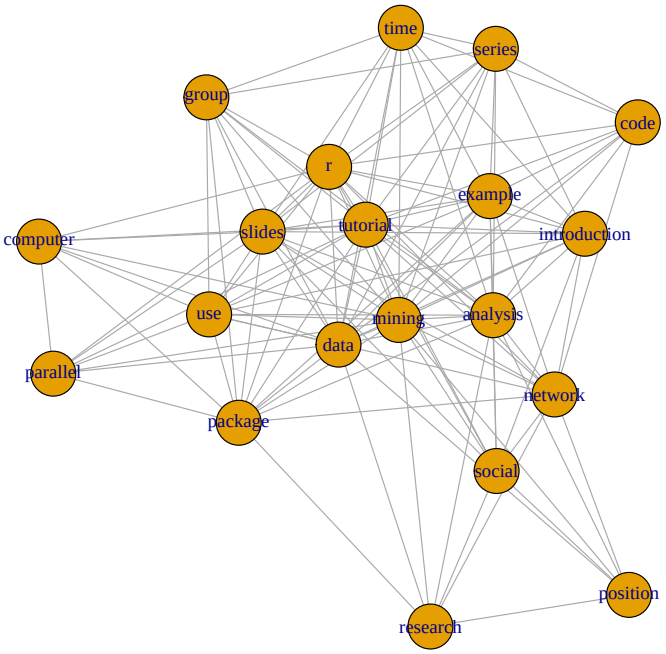

Figure 11.1: A Network of Terms - I

In the above code, the layout is kept as `layout1`, so that we can plot the graph in the same layout later.

A different layout can be generated with the first line of code below. The second line produces an interactive plot, which allows us to manually rearrange the layout. Details about other layout options can be obtained by running `?igraph::layout` in R.

```
> plot(g, layout=layout.kamada.kawai)
> tkplot(g, layout=layout.kamada.kawai)
```

A 3D plot of the graph can be shown `rglplot()` below.

```
> library(rgl)
> coords <- layout.kamada.kawai(g, dim=3)
> open3d()
> rglplot(g, vertex.size=3, vertex.label=NA, edge.arrow.size=0.6, layout=coords)
```

We can also save the network graph into a .PDF file with the code below.

```
> pdf("term-network.pdf")
> plot(g, layout=layout.fruchterman.reingold)
> dev.off()
```

The graph data object can be saved in various file formats, such as GraphML, GML and Pajek formats, with `write.graph()`, which can be loaded later into other software. Foreigh graph files can also be imported into R with `read.graph()`.

Next, we set the label size of vertices based on their degrees, to make important terms stand out. Similarly, we also set the width and transparency of edges based on their weights. This is useful in applications where graphs are crowded with many vertices and edges. In the code below, the vertices and edges are accessed with `V()` and `E()`. Function `rgb(red, green, blue, alpha)` defines a color, with an `alpha` transparency. With the same layout as Figure 11.1, we plot the graph again (see Figure 11.2).

```
> V(g)$label.cex <- 2.2 * V(g)$degree / max(V(g)$degree)+ .2
> V(g)$label.color <- rgb(0, 0, .2, .8)
> V(g)$frame.color <- NA
> egam <- (log(E(g)$weight)+.4) / max(log(E(g)$weight)+.4)
> E(g)$color <- rgb(.5, .5, 0, egam)
> E(g)$width <- egam
> # plot the graph in layout1
> plot(g, layout=layout1)
```

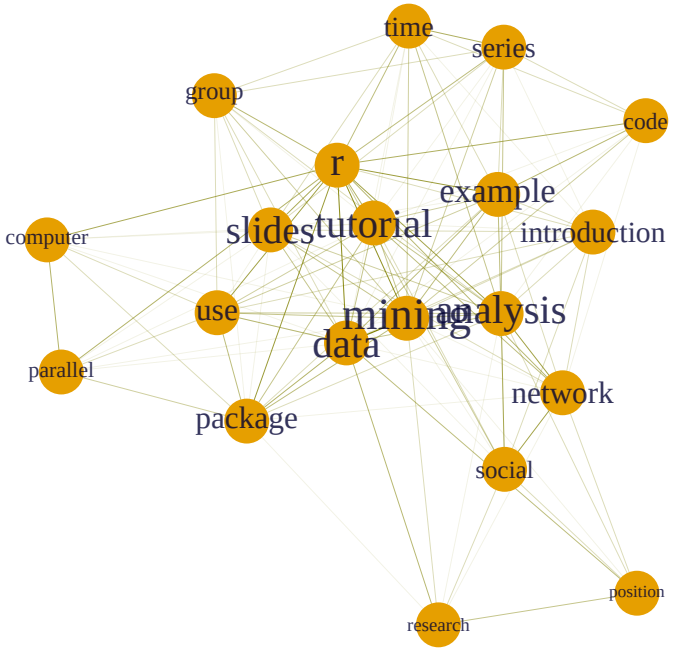

Figure 11.2: A Network of Terms - II

Next, we try to detection communities from the graph.

cohesive blocks

```
> blocks <- cohesive.blocks(g)
> blocks

Cohesive block structure:
B-1            c 6, n 20
- B-2         c 7, n 18   oooooooooo o.o.oooooo
   - B-3      c 8, n 16   oo.ooooooo ..o.oooooo
      - B-5   c 9, n 15   oo.ooooooo ..o.oo.ooo
   - B-4      c 8, n  9   ..oo...o.o o.o..o..oo

> plot(blocks, g, vertex.size=.3, vertex.label.cex=1.5, edge.color=rgb(.4,.4,0,.3))
```

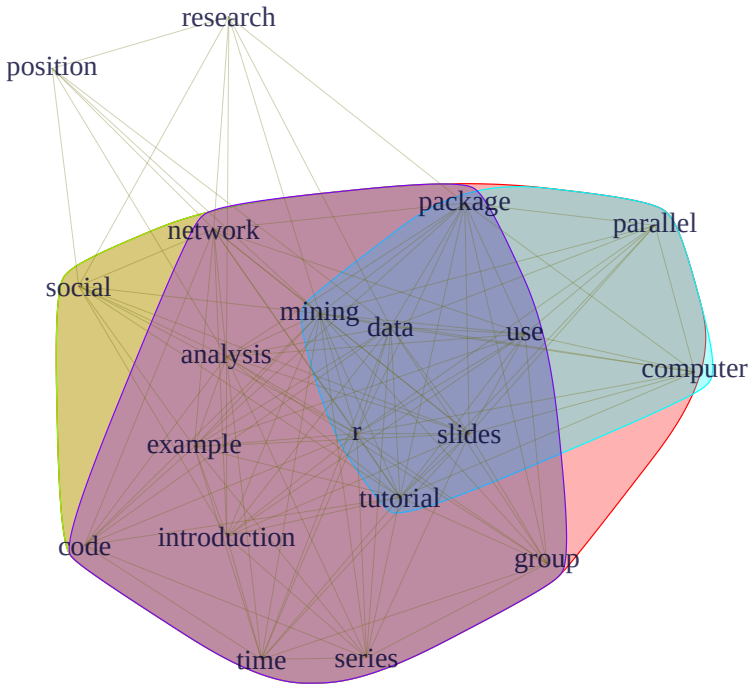

Figure 11.3: Cohesive Blocks

maximal cliques

```
> cl <- maximal.cliques(g)
> length(cl)

[1] 15

> colbar <- rainbow(length(cl) + 1)
> for (i in 1:length(cl)) {
+   V(g)[cl[[i]]]$color <- colbar[i+1]
+ }
> plot(g, mark.groups=cl,
+      vertex.size=.3, vertex.label.cex=1.5, edge.color=rgb(.4,.4,0,.3))
```

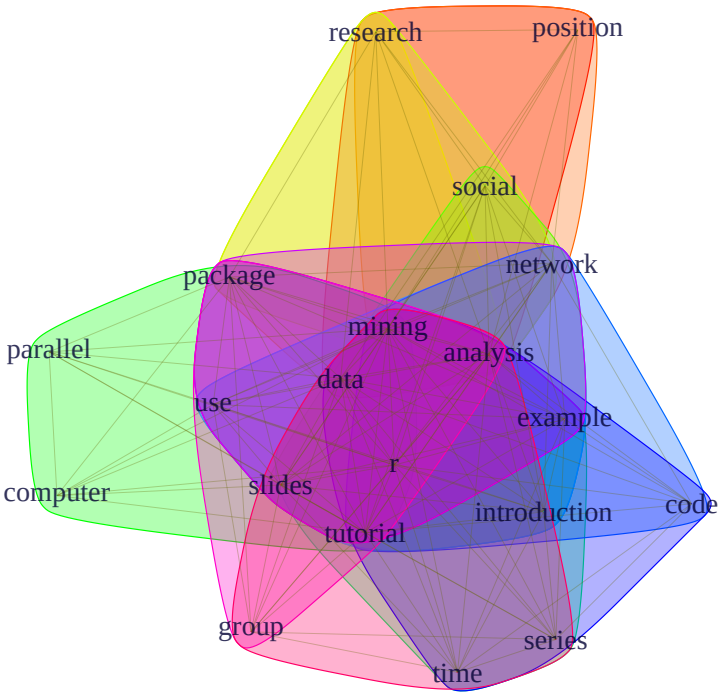

Figure 11.4: Cliques

largest cliques

```
> cl <- largest.cliques(g)
> length(cl)

[1] 1

> colbar <- rainbow(length(cl) + 1)
> for (i in 1:length(cl)) {
+   V(g)[cl[[i]]]$color <- colbar[i+1]
+ }
> plot(g, mark.groups=cl,
+      vertex.size=.3, vertex.label.cex=1.5, edge.color=rgb(.4,.4,0,.3))
```

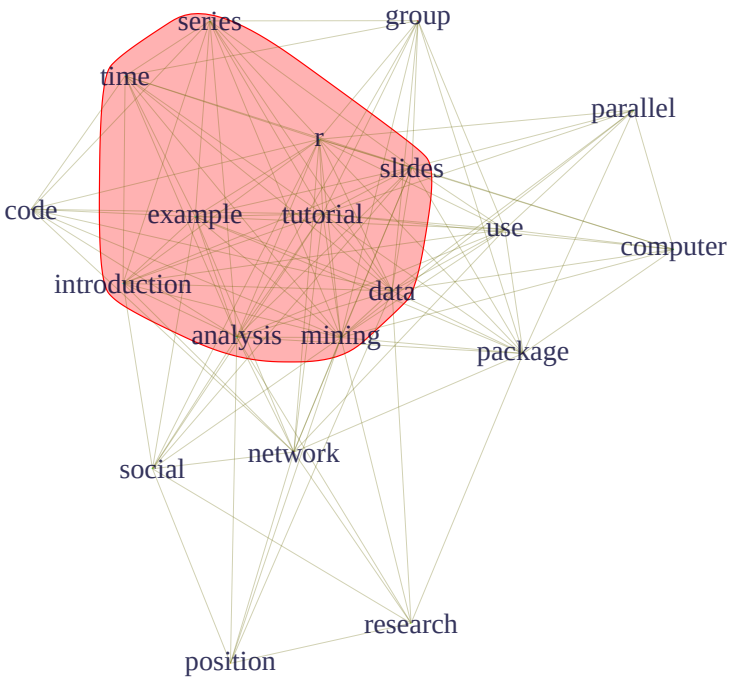

Figure 11.5: Cliques

11.2 Network of Tweets

Similar to the previous section, we can also build a graph of tweets base on the number of terms that they have in common. Because most tweets contain one or more words from "r", "data" and "mining", most tweets are connected with others and the graph of tweets is very crowded. To simplify the graph and find relationship between tweets beyond the above three keywords, we remove the three words before building a graph.

```
> # remove "r", "data" and "mining"
> idx <- which(dimnames(termDocMatrix)$Terms %in% c("r", "data", "mining"))
> M <- termDocMatrix[-idx,]
```

```
> # build a tweet-tweet adjacency matrix
> tweetMatrix <- t(M) %*% M
> library(igraph)
> g <- graph.adjacency(tweetMatrix, weighted=T, mode = "undirected")
> V(g)$degree <- degree(g)
> g <- simplify(g)
> # set labels of vertices to tweet IDs
> V(g)$label <- V(g)$name
> V(g)$label.cex <- 1
> V(g)$label.color <- rgb(.4, 0, 0, .7)
> V(g)$size <- 2
> V(g)$frame.color <- NA
```

Next, we have a look at the distribution of degree of vertices and the result is shown in Figure 11.6. We can see that there are around 40 isolated vertices (with a degree of zero). Note that most of them are caused by the removal of the three keywords, "r", "data" and "mining".

```
> barplot(table(V(g)$degree))
```

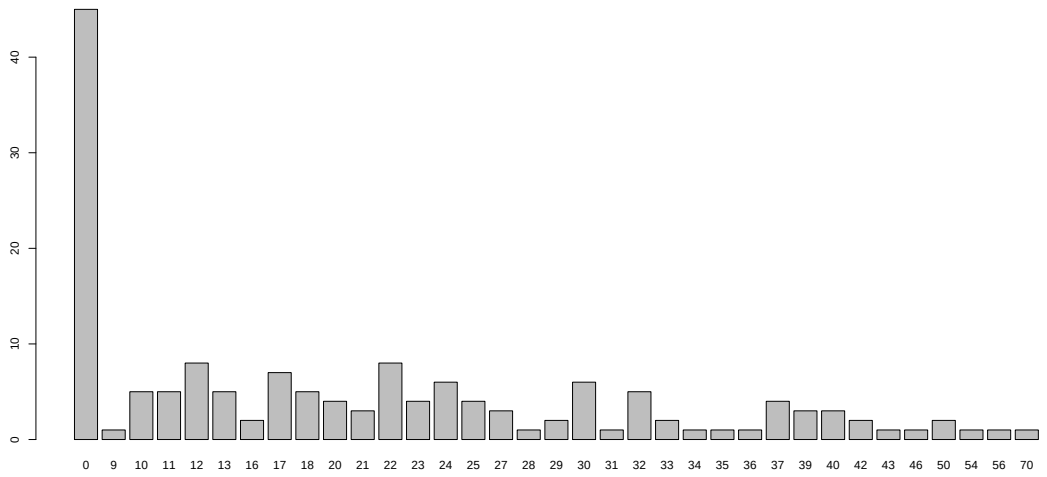

Figure 11.6: Distribution of Degree

With the code below, we set vertex colors based on degree, and set labels of isolated vertices to tweet IDs and the first 20 characters of every tweet. The labels of other vertices are set to tweet IDs only, so that the graph will not be overcrowded with labels. We also set the color and width of edges based on their weights. The produced graph is shown in Figure 11.7.

```
> idx <- V(g)$degree == 0
> V(g)$label.color[idx] <- rgb(0, 0, .3, .7)
> # load twitter text
> library(twitteR)
> load(file = "data/rdmTweets.RData")
> # convert tweets to a data frame
> df <- do.call("rbind", lapply(rdmTweets, as.data.frame))
> # set labels to the IDs and the first 20 characters of tweets
> V(g)$label[idx] <- paste(V(g)$name[idx], substr(df$text[idx], 1, 20), sep=": ")
```

```
> egam <- (log(E(g)$weight)+.2) / max(log(E(g)$weight)+.2)
> E(g)$color <- rgb(.5, .5, 0, egam)
> E(g)$width <- egam
```

```
> set.seed(3152)
> layout2 <- layout.fruchterman.reingold(g)
> plot(g, layout=layout2)
```

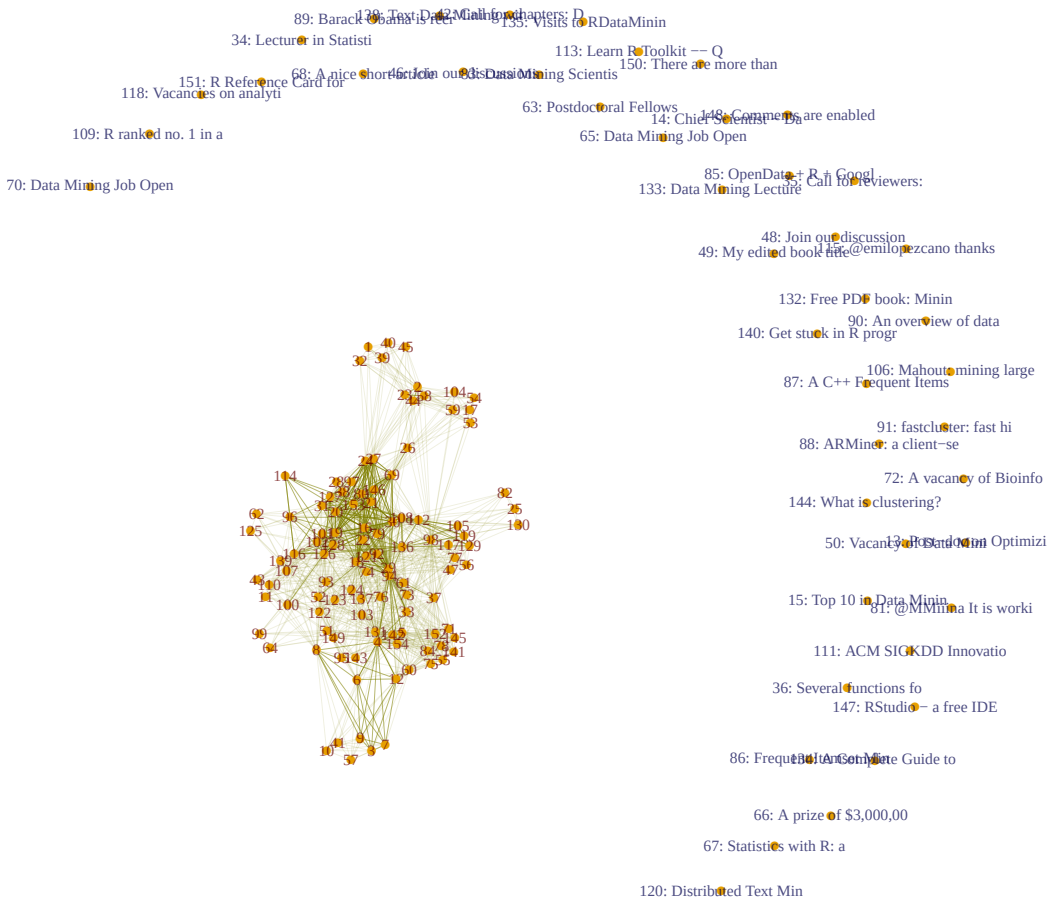

Figure 11.7: A Network of Tweets - I

The vertices in crescent are isolated from all others, and next we remove them from graph with function `delete.vertices()` and re-plot the graph (see Figure 11.8).

```
> g2 <- delete.vertices(g, V(g)[degree(g)==0])
```

```
> plot(g2, layout=layout.fruchterman.reingold)
```

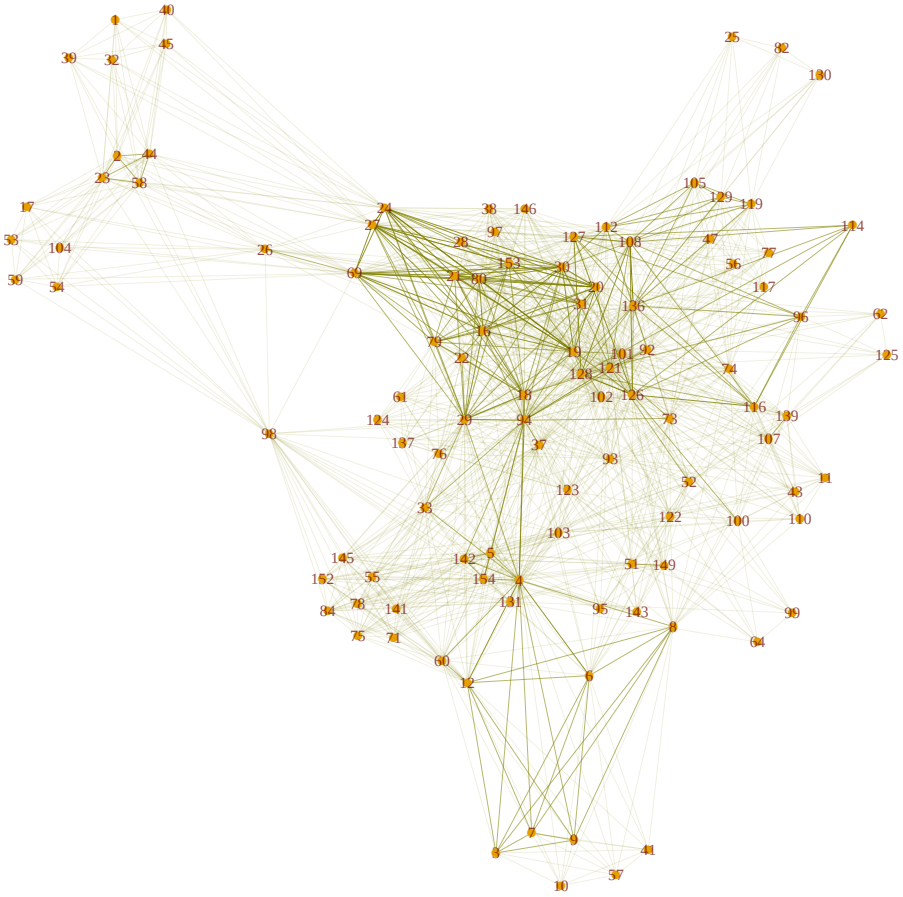

Figure 11.8: A Network of Tweets - II

Similarly, we can also remove edges with low degrees to simplify the graph. Below with function `delete.edges()`, we remove edges which have weight of one. After removing edges, some vertices become isolated and are also removed. The produced graph is shown in Figure 11.9.

```
> g3 <- delete.edges(g, E(g)[E(g)$weight <= 1])
> g3 <- delete.vertices(g3, V(g3)[degree(g3) == 0])
```

```
> plot(g3, layout=layout.fruchterman.reingold)
```

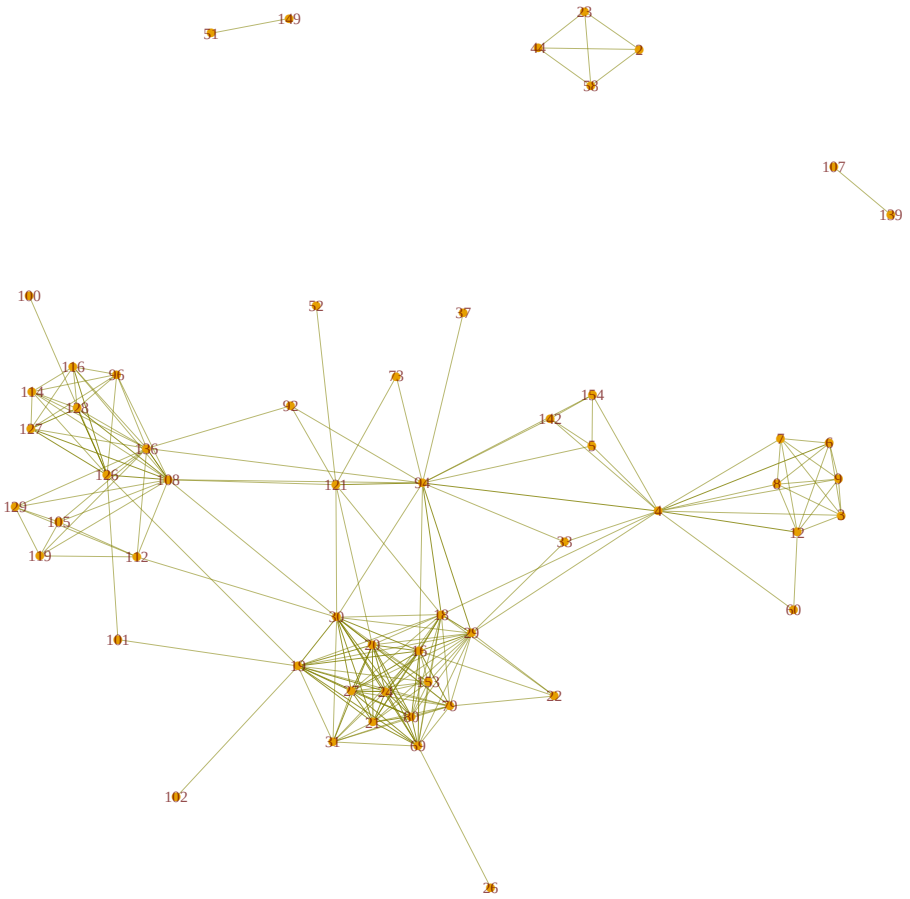

Figure 11.9: A Network of Tweets - III

In Figure 11.9, there are some groups (or cliques) of tweets. Let's have a look at the group in the middle left of the figure.

```
> df$text[c(7,12,6,9,8,3,4)]
```

```
[7] State of the Art in Parallel Computing with R http://t.co/zmClglqi
[12] The R Reference Card for Data Mining is updated with functions & packages
for handling big data & parallel computing. http://t.co/FHoVZCyk
[6] Parallel Computing with R using snow and snowfall http://t.co/nxp8EZpv
[9] R with High Performance Computing: Parallel processing and large memory
http://t.co/XZ3ZZBRF
[8] Slides on Parallel Computing in R http://t.co/AdDVxbOY
[3] Easier Parallel Computing in R with snowfall and sfCluster
```

```
http://t.co/BPcinvzK
[4] Tutorial: Parallel computing using R package snowfall http://t.co/CHBCyr76
```

We can see that tweets 7, 12, 6, 9, 8, 3, 4 are on parallel Computing with R. We can also see some other groups below:

- Tweets 4, 33, 94, 29, 18 and 92: tutorials for R;
- Tweets 4, 5, 154 and 71: R packages;
- Tweets 126, 128, 108, 136, 127, 116, 114 and 96: time series analysis;
- Tweets 112, 129, 119, 105, 108 and 136: R code examples; and
- Tweets 27, 24, 22,153, 79, 69, 31, 80, 21, 29, 16, 20, 18, 19 and 30: social network analysis.

Tweet 4 lies between multiple groups, because it contains keywords "parallel computing", "tutorial" and "package".

11.3 Two-Mode Network

In this section, we will build a two-mode network, which is composed of two types of vertices: tweets and terms. At first, we generate a graph `g` directly from `termDocMatrix`. After that, different colors and sizes are assigned to term vertices and tweet vertices. We also set the width and color of edges. The graph is then plotted with `layout.fruchterman.reingold` (see Figure 11.10).

```
> # create a graph
> g <- graph.incidence(termDocMatrix, mode=c("all"))
> # get index for term vertices and tweet vertices
> nTerms <- nrow(M)
> nDocs <- ncol(M)
> idx.terms <- 1:nTerms
> idx.docs <- (nTerms+1):(nTerms+nDocs)
> # set colors and sizes for vertices
> V(g)$degree <- degree(g)
> V(g)$color[idx.terms] <- rgb(0, 1, 0, .5)
> V(g)$size[idx.terms] <- 6
> V(g)$color[idx.docs] <- rgb(1, 0, 0, .4)
> V(g)$size[idx.docs] <- 4
> V(g)$frame.color <- NA
> # set vertex labels and their colors and sizes
> V(g)$label <- V(g)$name
> V(g)$label.color <- rgb(0, 0, 0, 0.5)
> V(g)$label.cex <- 1.4*V(g)$degree/max(V(g)$degree) + 1
> # set edge width and color
> E(g)$width <- .3
> E(g)$color <- rgb(.5, .5, 0, .3)
```

```
> set.seed(958)
> plot(g, layout=layout.fruchterman.reingold)
```

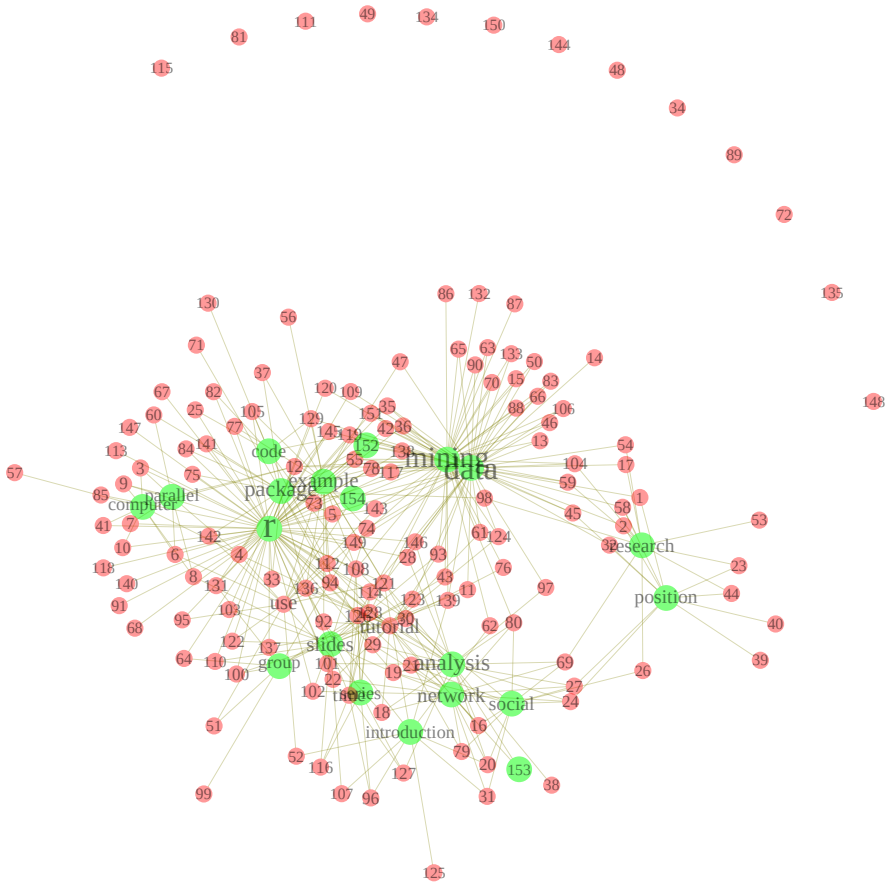

Figure 11.10: A Two-Mode Network of Terms and Tweets - I

Figure 11.10 shows that most tweets are around two centers, "r" and "data mining". Next, let's have a look at which tweets are about "r". In the code below, `nei("r")` returns all vertices which are neighbors of vertex "r".

```
> V(g)[nei("r")]
```

```
+ 70/174 vertices, named:
 [1] 3   4   5   6   7   8   9   10  12  19  21  22  25  28  30  33  35  36  41
[20] 42  55  64  67  68  73  74  75  77  78  82  84  85  91  92  94  95  100 101
[39] 102 105 108 109 110 112 113 114 117 118 119 120 121 122 126 128 129 131 136
[58] 137 138 140 141 142 143 145 146 147 149 151 152 154
```

An alternative way is using function `neighborhood()` as below.

```
> V(g)[neighborhood(g, order=1, "r")[[1]]]
```

We can also have a further look at which tweets contain all three terms: "r", "data" and "mining".

```
> (rdmVertices <- V(g)[nei("r") & nei("data") & nei("mining")])
```

```
+ 14/174 vertices, named:
 [1] 12  35  36  42  55  78  117 119 138 143 149 151 152 154
```

```
> df$text[as.numeric(rdmVertices$label)]
```

```
[12] The R Reference Card for Data Mining is updated with functions & packages
for handling big data & parallel computing. http://t.co/FHoVZCyk
[35] Call for reviewers: Data Mining Applications with R. Pls contact me if you
have experience on the topic. See details at http://t.co/rcYIXfnp
[36] Several functions for evaluating performance of classification models added
to R Reference Card for Data Mining: http://t.co/FHoVZCyk
[42] Call for chapters: Data Mining Applications with R, an edited book to be
published by Elsevier. Proposal due 30 April. http://t.co/HPaBSbRa
[55] Some R functions and packages for outlier detection have been added to R
Reference Card for Data Mining at http://t.co/FHoVZCyk.
[78] Access large amounts of Twitter data for data mining and other tasks within
R via the twitteR package. http://t.co/ApbAbnxs
[117] My document, R and Data Mining - Examples and Case Studies, is scheduled to
be published by Elsevier in mid 2012. http://t.co/BcqwQ1n
[119] Lecture Notes on data mining course at CMU, some of which contain R code
examples. http://t.co/7YY73OW
[138] Text Data Mining with Twitter and R.  http://t.co/a50ySNq
[143] A recent poll shows that R is the 2nd popular tool used for data mining.
See Poll: Data Mining/Analytic Tools Used http://t.co/ghpbQXq
```

To make it short, only the first 10 tweets are displayed in the above result. In the above code, `df` is a data frame which keeps tweets of RDataMining, and details of it can be found in Section 10.2.

Next, we remove "r", "data" and "mining" to show the relationship between tweets with other words. Isolated vertices are also deleted from graph.

```
> idx <- which(V(g)$name %in% c("r", "data", "mining"))
> g2 <- delete.vertices(g, V(g)[idx-1])
> g2 <- delete.vertices(g2, V(g2)[degree(g2)==0])
> set.seed(209)
> plot(g2, layout=layout.fruchterman.reingold)
```

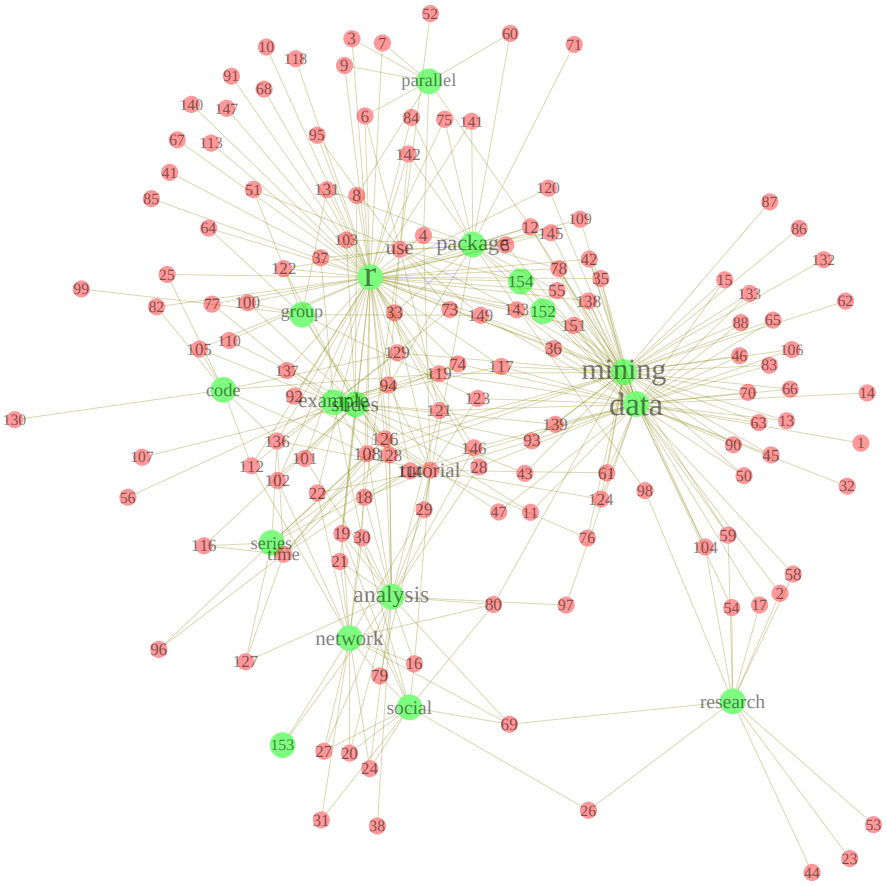

Figure 11.11: A Two-Mode Network of Terms and Tweets - II

From Figure 11.11, we can clearly see groups of tweets and their keywords, such as time series, social network analysis, parallel computing and postdoctoral and research positions, which are similar to the result presented at the end of Section 11.2.

11.4 Discussions and Further Readings

In this chapter, we have demonstrated how to find groups of tweets and some topics in the tweets with package *igraph*. Similar analysis can also be achieved with package *sna* [Butts, 2014]. There

are also packages designed for topic modeling, such as packages *lda* [Chang, 2012] and *topicmodels* [Grün and Hornik, 2011].

For readers interested in social network analysis with R, there are some further readings. Some examples on social network analysis with the *igraph* package [Csardi and Nepusz, 2006] are available as tutorial on *Network Analysis with Package igraph* at `http://igraph.sourceforge.net/igraphbook/` and R for Social Network Analysis at `http://www.stanford.edu/~messing/RforSNA.html`. There is a detailed introduction to Social Network Analysis with package *sna* [Butts, 2014] at `http://www.jstatsoft.org/v24/i06/paper`. A *statnet* Tutorial is available at `http://www.jstatsoft.org/v24/i09/paper` and more resources on using *statnet* [Handcock et al., 2015] for network analysis can be found at `http://csde.washington.edu/statnet/resources.shtml`. There is a short tutorial on package *network* [Butts, 2015] at `http://sites.stat.psu.edu/~dhunter/Rnetworks/`. Slides on Social network analysis with R *sna* package can be found at `http://user2010.org/slides/Zhang.pdf`. slides on Social Network Analysis in R can be found at `http://files.meetup.com/1406240/sna_in_R.pdf`. Some R codes for community detection are available at `http://igraph.wikidot.com/community-detection-in-r`.

Chapter 12

Case Study I: Analysis and Forecasting of House Price Indices

This chapter and the other case studies are not available in this online version. They are reserved exclusively for a book version published by Elsevier in December 2012. Below is abstract of this chapter.

Abstract: This chapter presents a case study on analyzing and forecasting of House Price Indices (HPI). It demonstrates data import from a .CSVfile, descriptive analysis of HPI time series data, and decomposition and forecasting of the data.

Keywords: Time series, decomposition, forecasting, seasonal component

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Chapter 13

Case Study II: Customer Response Prediction and Profit Optimization

This chapter and the other case studies are not available in this online version. They are reserved exclusively for a book version published by Elsevier in December 2012. Below is abstract of this chapter.

Abstract: This chapter presents a case study on using decision trees to predict customer response and optimize profit. To improve customer contact process and maximize the amount of profit, decision trees were built with R to model customer contact history and predict the response of customers. And then the customers can be prioritized to contact based on the prediction, so that profit can be maximized, given a limited amount of time, cost and human resources.

Keywords: Decision tree, prediction, profit optimization

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Chapter 14

Case Study III: Predictive Modeling of Big Data with Limited Memory

This chapter and the other case studies are not available in this online version. They are reserved exclusively for a book version published by Elsevier in December 2012. Below is abstract of this chapter.

Abstract: This chapter shows a case study on building a predictive model with limited memory. Because the training dataset was large and not easy to build decision trees within R, multiple subsets were drawn from it by random sampling, and a decision tree was built for each subset. After that, the variables appearing in any one of the built trees were used for variable selection from the original training dataset to reduce data size. In the scoring process, the scoring dataset was also split into subsets, so that the scoring could be done with limited memory. R codes for printing rules in plain English and in SAS format are also presented in this chapter.

Keywords: Predictive model, limited memory, large data, training, scoring

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Chapter 15

Online Resources

This chapter presents links to online resources on R and data mining, includes books, documents, tutorials and slides. A list of links is also available at `http://www.rdatamining.com/resources/onlinedocs`.

15.1 R Reference Cards

- *R Reference Card*, by Tom Short
  `http://cran.r-project.org/doc/contrib/Short-refcard.pdf`
- *R Reference Card for Data Mining*, by Yanchang Zhao
  `http://www.rdatamining.com/docs`
- *R Reference Card*, by Jonathan Baron
  `http://cran.r-project.org/doc/contrib/refcard.pdf`
- *R Functions for Regression Analysis*, by Vito Ricci
  `http://cran.r-project.org/doc/contrib/Ricci-refcard-regression.pdf`
- *R Functions for Time Series Analysis*, by Vito Ricci
  `http://cran.r-project.org/doc/contrib/Ricci-refcard-ts.pdf`

15.2 R

- *Quick-R*
  `http://www.statmethods.net/`
- *R Tips*: lots of tips for R programming
  `http://pj.freefaculty.org/R/Rtips.html`
- *R Tutorial*
  `http://www.cyclismo.org/tutorial/R/index.html`
- *The R Manuals*, including *an Introduction to R*, *R Language Definition*, *R Data Import/Export*, and other R manuals
  `http://cran.r-project.org/manuals.html`
- *R You Ready?*
  `http://pj.freefaculty.org/R/RUReady.pdf`
- *R for Beginners*
  `http://cran.r-project.org/doc/contrib/Paradis-rdebuts_en.pdf`

- *Econometrics in R*
  http://cran.r-project.org/doc/contrib/Farnsworth-EconometricsInR.pdf
- *Using R for Data Analysis and Graphics - Introduction, Examples and Commentary*
  http://www.cran.r-project.org/doc/contrib/usingR.pdf
- Lots of R Contributed Documents, including non-English ones
  http://cran.r-project.org/other-docs.html
- *The R Journal*
  http://journal.r-project.org/current.html
- *Learn R Toolkit*
  http://processtrends.com/Learn_R_Toolkit.htm
- *Resources to help you learn and use R* at UCLA
  http://www.ats.ucla.edu/stat/r/
- *R Tutorial - An R Introduction to Statistics*
  http://www.r-tutor.com/
- *Cookbook for R*
  http://wiki.stdout.org/rcookbook/
- *Slides for a couple of R short courses*
  http://courses.had.co.nz/
- *Tips on memory in R*
  http://www.matthewckeller.com/html/memory.html

15.3 Data Mining

- *Introduction to Data Mining*, by Pang-Ning Tan, Michael Steinbach and Vipin Kumar
  Lecture slides (in both PPT and PDF formats) and three sample chapters on classification, association and clustering available at the link below.
  http://www-users.cs.umn.edu/%7Ekumar/dmbook
- *Tutorial on Data Mining Algorithms* by Ian Witten
  http://www.cs.waikato.ac.nz/~ihw/DataMiningTalk/
- *Mining of Massive Datasets*, by Anand Rajaraman and Jeff Ullman
  The whole book and lecture slides are free and downloadable in PDF format.
  http://infolab.stanford.edu/%7Eullman/mmds.html
- *Lecture notes of data mining course*, by Cosma Shalizi at CMU
  R code examples are provided in some lecture notes, and also in solutions to home works.
  http://www.stat.cmu.edu/%7Ecshalizi/350/
- *Introduction to Information Retrieval*, by Christopher D. Manning, Prabhakar Raghavan and Hinrich Schütze at Stanford University
  It covers text classification, clustering, web search, link analysis, etc. The book and lecture slides are free and downloadable in PDF format.
  http://nlp.stanford.edu/IR-book/
- *Statistical Data Mining Tutorials*, by Andrew Moore
  http://www.autonlab.org/tutorials/
- *Tutorial on Spatial and Spatio-Temporal Data Mining*
  http://www.inf.ufsc.br/%7Evania/tutorial_icdm.html

- *Tutorial on Discovering Multiple Clustering Solutions*
  http://dme.rwth-aachen.de/en/DMCS

- *Time-Critical Decision Making for Business Administration*
  http://home.ubalt.edu/ntsbarsh/stat-data/Forecast.htm

- A paper on *Open-Source Tools for Data Mining*, published in 2008
  http://eprints.fri.uni-lj.si/893/1/2008-OpenSourceDataMining.pdf

- *An overview of data mining tools*
  http://onlinelibrary.wiley.com/doi/10.1002/widm.24/pdf

- *Textbook on Introduction to social network methods*
  http://www.faculty.ucr.edu/~hanneman/nettext/

- *Information Diffusion In Social Networks: Observing and Influencing Societal Interests*, a tutorial at VLDB'11
  http://www.cs.ucsb.edu/~cbudak/vldb_tutorial.pdf

- *Tools for large graph mining: structure and diffusion*, a tutorial at WWW2008
  http://cs.stanford.edu/people/jure/talks/www08tutorial/

- *Graph Mining: Laws, Generators and Tools*
  http://www.stanford.edu/group/mmds/slides2008/faloutsos.pdf

- *A tutorial on outlier detection techniques* at ACM SIGKDD'10
  http://www.dbs.ifi.lmu.de/~zimek/publications/KDD2010/kdd10-outlier-tutorial.pdf

- *A Taste of Sentiment Analysis* - 105-page slides in PDF format
  http://statmath.wu.ac.at/research/talks/resources/sentimentanalysis.pdf

15.4 Data Mining with R

- *Data Mining with R - Learning by Case Studies*
  http://www.liaad.up.pt/~ltorgo/DataMiningWithR/

- *Data Mining Algorithms In R*
  http://en.wikibooks.org/wiki/Data_Mining_Algorithms_In_R

- *Statistics with R*
  http://zoonek2.free.fr/UNIX/48_R/all.html

- *Data Mining Desktop Survival Guide*
  http://www.togaware.com/datamining/survivor/

15.5 Classification/Prediction with R

- *An Introduction to Recursive Partitioning Using the RPART Routines*
  http://www.mayo.edu/hsr/techrpt/61.pdf

- *Visualizing classifier performance with package ROCR*
  http://rocr.bioinf.mpi-sb.mpg.de/ROCR_Talk_Tobias_Sing.ppt

15.6 Time Series Analysis with R

- *An R Time Series Tutorial*
  http://www.stat.pitt.edu/stoffer/tsa2/R_time_series_quick_fix.htm
- *Time Series Analysis with R*
  http://www.statoek.wiso.uni-goettingen.de/veranstaltungen/zeitreihen/sommer03/ts_r_intro.pdf
- *Using R (with applications in Time Series Analysis)*
  http://people.bath.ac.uk/masgs/time%20series/TimeSeriesR2004.pdf
- *CRAN Task View: Time Series Analysis*
  http://cran.r-project.org/web/views/TimeSeries.html

15.7 Association Rule Mining with R

- *Introduction to arules: A computational environment for mining association rules and frequent item sets*
  http://cran.csiro.au/web/packages/arules/vignettes/arules.pdf
- *Visualizing Association Rules: Introduction to arulesViz*
  http://cran.csiro.au/web/packages/arulesViz/vignettes/arulesViz.pdf
- *Association Rule Algorithms In R*
  http://en.wikibooks.org/wiki/Data_Mining_Algorithms_In_R/Frequent_Pattern_Mining

15.8 Spatial Data Analysis with R

- *Applied Spatio-temporal Data Analysis with FOSS: R+OSGeo*
  http://www.geostat-course.org/GeoSciences_AU_2011
- *Spatial Regression Analysis in R - A Workbook*
  http://geodacenter.asu.edu/system/files/rex1.pdf

15.9 Text Mining with R

- *Text Mining Infrastructure in R*
  http://www.jstatsoft.org/v25/i05
- *Introduction to the tm Package Text Mining in R*
  http://cran.r-project.org/web/packages/tm/vignettes/tm.pdf
- *Text Mining Handbook* with R code examples
  http://www.casact.org/pubs/forum/10spforum/Francis_Flynn.pdf
- *Distributed Text Mining in R*
  http://epub.wu.ac.at/3034/

15.10 Social Network Analysis with R

- *R for networks: a short tutorial*
  http://sites.stat.psu.edu/~dhunter/Rnetworks/

- *Social Network Analysis in R*
  http://files.meetup.com/1406240/sna_in_R.pdf
- *A detailed introduction to Social Network Analysis with package sna*
  http://www.jstatsoft.org/v24/i06/paper
- *A statnet Tutorial*
  http://www.jstatsoft.org/v24/i09/paper
- *Slides on Social network analysis with R*
  http://user2010.org/slides/Zhang.pdf
- *Tutorials on using statnet for network analysis*
  http://csde.washington.edu/statnet/resources.shtml

15.11 Data Cleansing and Transformation with R

- *Tidy Data and Tidy Tools*
  http://vita.had.co.nz/papers/tidy-data-pres.pdf
- *The data.table package in R*
  http://files.meetup.com/1677477/R_Group_June_2011.pdf

15.12 Big Data and Parallel Computing with R

- *State of the Art in Parallel Computing with R*
  http://www.jstatsoft.org/v31/i01/paper
- *Taking R to the Limit, Part I - Parallelization in R*
  http://www.bytemining.com/2010/07/taking-r-to-the-limit-part-i-parallelization-in-r/
- *Taking R to the Limit, Part II - Large Datasets in R*
  http://www.bytemining.com/2010/08/taking-r-to-the-limit-part-ii-large-datasets-in-r/
- *Tutorial on MapReduce programming in R with package rmr*
  https://github.com/RevolutionAnalytics/RHadoop/wiki/Tutorial
- *Distributed Data Analysis with Hadoop and R*
  http://www.infoq.com/presentations/Distributed-Data-Analysis-with-Hadoop-and-R
- *Massive data, shared and distributed memory, and concurrent programming: bigmemory and foreach*
  http://sites.google.com/site/bigmemoryorg/research/documentation/bigmemorypresentation.pdf
- *High Performance Computing with R*
  http://igmcs.utk.edu/sites/igmcs/files/Patel-High-Performance-Computing-with-R-2011-10-20.pdf
- *R with High Performance Computing: Parallel processing and large memory*
  http://files.meetup.com/1781511/HighPerformanceComputingR-Szczepanski.pdf
- *Parallel Computing in R*
  http://blog.revolutionanalytics.com/downloads/BioC2009%20ParallelR.pdf
- *Parallel Computing with R using snow and snowfall*
  http://www.ics.uci.edu/~vqnguyen/talks/ParallelComputingSeminaR.pdf

- *Interacting with Data using the filehash Package for R*
  `http://cran.r-project.org/web/packages/filehash/vignettes/filehash.pdf`
- *Tutorial: Parallel computing using R package snowfall*
  `http://www.imbi.uni-freiburg.de/parallel/docs/Reisensburg2009_TutParallelComputing_Knaus_Porzelius.pdf`
- *Easier Parallel Computing in R with snowfall and sfCluster*
  `http://journal.r-project.org/2009-1/RJournal_2009-1_Knaus+et+al.pdf`

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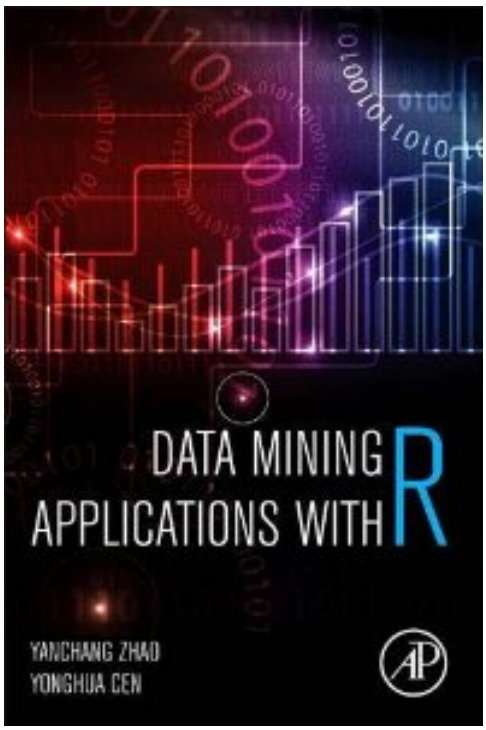
Appendix: Book Promotion - Data Mining Applications with R

Book title: Data Mining Applications with R
Editors: Yanchang Zhao, Yonghua Cen
Publisher: Elsevier
Publish date: December 2013
ISBN: 978-0-12-411511-8
Length: 514 pages
URL: http://www.rdatamining.com/books/dmar

Abstract: This book presents 15 real-world applications on data mining with R. Each application is presented as one chapter, covering business background and problems, data extraction and exploration, data preprocessing, modeling, model evaluation, findings and model deployment.

R code and data for the book are provided at http://www.rdatamining.com/books/dmar/code, so that readers can easily learn the techniques by running the code themselves.



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http://www.amazon.com/Data-Mining-Applications-Yanchang-Zhao/dp/012411511X

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