

# R and Data Mining: Examples and Case Studies<sup>1 2</sup>

Yanchang Zhao  
yanchangzhao@gmail.com  
<http://www.RDataMining.com>

May 7, 2012

<sup>1</sup>©2012 Yanchang Zhao. To be published by Elsevier Inc. All rights reserved.

<sup>2</sup>The latest version is available at <http://www.rdatamining.com>. See the website also for an *R Reference Card for Data Mining*.

# Contents

<b>1</b>	<b>Introduction</b>	<b>1</b>
1.1	Data Mining . . . . .	1
1.2	R . . . . .	1
1.2.1	R Packages and Functions for Data Mining . . . . .	2
1.3	Datasets . . . . .	3
1.3.1	Iris Dataset . . . . .	4
1.3.2	Bodyfat Dataset . . . . .	4
<b>2</b>	<b>Data Import/Export</b>	<b>7</b>
2.1	Save/Load R Data . . . . .	7
2.2	Import from and Export to .CSV Files . . . . .	7
2.3	Import Data from SAS . . . . .	8
2.4	Import/Export via ODBC . . . . .	9
2.4.1	Read from Databases . . . . .	9
2.4.2	Output to and Input from EXCEL Files . . . . .	9
<b>3</b>	<b>Data Exploration</b>	<b>11</b>
3.1	Have a Look at Data . . . . .	11
3.2	Explore Individual Variables . . . . .	13
3.3	Explore Multiple Variables . . . . .	16
3.4	More Explorations . . . . .	21
3.5	Save Charts into Files . . . . .	26
<b>4</b>	<b>Decision Trees and Random Forest</b>	<b>27</b>
4.1	Building Decision Trees with Package <i>party</i> . . . . .	27
4.2	Building Decision Trees with Package <i>rpart</i> . . . . .	29
4.3	Random Forest . . . . .	33
<b>5</b>	<b>Regression</b>	<b>37</b>
5.1	Linear Regression . . . . .	37
5.2	Logistic Regression . . . . .	41
5.3	Generalized Linear Regression . . . . .	42
5.4	Non-linear Regression . . . . .	43
<b>6</b>	<b>Clustering</b>	<b>45</b>
6.1	k-Means Clustering . . . . .	45
6.2	k-Medoids Clustering . . . . .	46
6.3	Hierarchical Clustering . . . . .	48
6.4	Density-based Clustering . . . . .	49
6.5	Fuzzy Clustering . . . . .	52
6.6	Subspace Clustering . . . . .	52
<b>7</b>	<b>Outlier Detection</b>	<b>53</b>

<b>8</b>	<b>Time Series Analysis and Mining</b>	<b>55</b>
8.1	Time Series Data in R . . . . .	55
8.2	Time Series Decomposition . . . . .	56
8.3	Time Series Forecasting . . . . .	58
8.4	Time Series Clustering . . . . .	59
8.4.1	Dynamic Time Warping . . . . .	59
8.4.2	Synthetic Control Chart Time Series Data . . . . .	60
8.4.3	Hierarchical Clustering with Euclidean Distance . . . . .	61
8.4.4	Hierarchical Clustering with DTW Distance . . . . .	64
8.5	Time Series Classification . . . . .	65
8.5.1	Classification with Original Data . . . . .	65
8.5.2	Classification with Extracted Features . . . . .	66
8.5.3	$k$ -NN Classification . . . . .	68
8.6	Discussion . . . . .	68
8.7	Further Readings . . . . .	68
<b>9</b>	<b>Association Rules and Sequential Patterns</b>	<b>69</b>
<b>10</b>	<b>Text Mining</b>	<b>71</b>
10.1	Retrieving Text from Twitter . . . . .	71
10.2	Transforming Text . . . . .	72
10.3	Stemming Words . . . . .	73
10.4	Building a Term-Document Matrix . . . . .	74
10.5	Frequent Terms and Associations . . . . .	75
10.6	Word Cloud . . . . .	77
10.7	Clustering Words . . . . .	78
10.8	Clustering Tweets . . . . .	79
10.8.1	Clustering Tweets with the $k$ -means Algorithm . . . . .	80
10.8.2	Clustering Tweets with the $k$ -medoids Algorithm . . . . .	81
10.9	Packages, Further Readings and Discussions . . . . .	83
<b>11</b>	<b>Social Network Analysis</b>	<b>85</b>
11.1	Network of Terms . . . . .	85
11.2	Network of Tweets . . . . .	87
11.3	Two-Mode Network . . . . .	92
11.4	Further Readings . . . . .	95
<b>12</b>	<b>Case Study I: Analysis and Forecasting of House Price Indices</b>	<b>97</b>
<b>13</b>	<b>Case Study II: Customer Response Prediction</b>	<b>99</b>
<b>14</b>	<b>Case Study III: Risk Rating on Big Data with Limited Memory</b>	<b>101</b>
<b>15</b>	<b>Case Study IV: Customer Behavior Prediction and Intervention</b>	<b>103</b>
<b>16</b>	<b>Online Resources</b>	<b>105</b>
16.1	R Reference Cards . . . . .	105
16.2	R . . . . .	105
16.3	Data Mining . . . . .	106
16.4	Data Mining with R . . . . .	106
16.5	Decision Trees . . . . .	106
16.6	Time Series Analysis . . . . .	106
16.7	Spatial Data Analysis . . . . .	107
16.8	Text Mining . . . . .	107
16.9	Regression . . . . .	107

<i>CONTENTS</i>	iii
<b>Bibliography</b>	<b>108</b>
<b>Index</b>	<b>112</b>



# List of Figures

3.1	Pie Chart . . . . .	14
3.2	Histogram . . . . .	15
3.3	Density . . . . .	16
3.4	Boxplot . . . . .	17
3.5	Scatter Plot . . . . .	18
3.6	Scatter Plot with Jitter . . . . .	19
3.7	Pairs Plot . . . . .	20
3.8	3D Scatter plot . . . . .	21
3.9	Level Plot . . . . .	21
3.10	Contour . . . . .	22
3.11	3D Surface . . . . .	23
3.12	Parallel Coordinates . . . . .	24
3.13	Parallel Coordinates with <i>lattice</i> . . . . .	25
3.14	with <i>ggplot2</i> . . . . .	26
4.1	Decision Tree . . . . .	28
4.2	Decision Tree (Simple Style) . . . . .	29
4.3	Decision Tree with <i>rpart</i> . . . . .	32
4.4	Prediction Result . . . . .	33
4.5	Error Rate of Random Forest . . . . .	34
4.6	Variable Importance . . . . .	35
4.7	Margin of Predictions . . . . .	36
5.1	Australian CPIs in Year 2008 to 2010 . . . . .	38
5.2	Prediction with Linear Regression Model - 1 . . . . .	40
5.3	Prediction of CPIs in 2011 with Linear Regression Model . . . . .	41
5.4	Prediction with Generalized Linear Regression Model . . . . .	43
6.1	Results of k-Means Clustering . . . . .	46
6.2	Clustering with the <i>k</i> -medoids Algorithm - I . . . . .	47
6.3	Clustering with the <i>k</i> -medoids Algorithm - II . . . . .	48
6.4	Cluster Dendrogram . . . . .	49
6.5	Density-based Clustering - I . . . . .	50
6.6	Density-based Clustering - II . . . . .	51
6.7	Density-based Clustering - III . . . . .	51
6.8	Prediction with Clustering Model . . . . .	52
8.1	A Time Series of <code>AirPassengers</code> . . . . .	56
8.2	Seasonal Component . . . . .	57
8.3	Time Series Decomposition . . . . .	58
8.4	Time Series Forecast . . . . .	59
8.5	Alignment with Dynamic Time Warping . . . . .	60

8.6	Six Classes in Synthetic Control Chart Time Series . . . . .	61
8.7	Hierarchical Clustering with Euclidean Distance . . . . .	62
8.8	Hierarchical Clustering with DTW Distance . . . . .	64
8.9	Decision Tree . . . . .	66
8.10	Decision Tree with DWT . . . . .	67
10.1	Frequent Terms . . . . .	76
10.2	Word Cloud . . . . .	77
10.3	Clustering of Words . . . . .	79
10.4	Clusters of Tweets . . . . .	82
11.1	A Network of Terms - I . . . . .	86
11.2	A Network of Terms - II . . . . .	87
11.3	A Network of Tweets - I . . . . .	88
11.4	Density of Degree . . . . .	89
11.5	A Network of Tweets - II . . . . .	90
11.6	A Network of Tweets - III . . . . .	91
11.7	A Network of Tweets - IV . . . . .	92
11.8	A Two-Mode Network of Terms and Tweets - I . . . . .	93
11.9	A Two-Mode Network of Terms and Tweets - II . . . . .	94

# List of Tables



# Chapter 1

## Introduction

This book presents examples and case studies on how to use R for data mining applications.

This chapter introduces some basic concepts and techniques for data mining, including a data mining procedure and popular data mining techniques, such as clustering, classification and association rules. 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 main techniques for data mining are listed below. More detailed introduction can be found in text books on data mining [Han and Kamber, 2000, Hand et al., 2001, Witten and Frank, 2005].

- Clustering:
- Classification:
- Association Rules:
- Sequential Patterns:
- Time Series Analysis:
- Text Mining:

### 1.2 R

R<sup>1</sup> [R Development Core Team, 2010a] is a free software environment for statistical computing and graphics. It provides a wide variety of statistical and graphical techniques. R can be extended easily via packages. There are more than 3000 packages available in the CRAN package repository<sup>2</sup>, as on May 20, 2011. More details about R are available in *An Introduction to R*<sup>3</sup> [Venables et al., 2010] and *R Language Definition*<sup>4</sup> [R Development Core Team, 2010c].

R is widely used in academia and research, as well as industrial applications.

---

<sup>1</sup><http://www.r-project.org/>

<sup>2</sup><http://cran.r-project.org/>

<sup>3</sup><http://cran.r-project.org/doc/manuals/R-intro.pdf>

<sup>4</sup><http://cran.r-project.org/doc/manuals/R-lang.pdf>

### 1.2.1 R Packages and Functions for Data Mining

A collection of R packages and functions available for data mining are listed below. Some of them are not specially for data mining, but they are included here because they are useful in data mining applications.

#### 1. Clustering

- Packages:
  - *fpc*
  - *cluster*
  - *pvclust*
  - *mclust*
- Partitioning-based clustering: `kmeans`, `pam`, `pamk`, `clara`
- Hierarchical clustering: `hclust`, `pvclust`, `agnes`, `diana`
- Model-based clustering: `mclust`
- Density-based clustering: `dbscan`
- Plotting cluster solutions: `plotcluster`, `plot.hclust`
- Validating cluster solutions: `cluster.stats`

#### 2. Classification

- Packages:
  - *rpart*
  - *party*
  - *randomForest*
  - *rpartOrdinal*
  - *tree*
  - *marginTree*
  - *maptree*
  - *survival*
- Decision trees: `rpart`, `ctree`
- Random forest: `cforest`, `randomForest`
- Regression, Logistic regression, Poisson regression: `glm`, `predict`, `residuals`
- Survival analysis: `survfit`, `survdiff`, `coxph`

#### 3. Association Rules and Frequent Itemsets

- Packages:
  - *arules*: supports to mine frequent itemsets, maximal frequent itemsets, closed frequent itemsets and association rules
  - *drm*: regression and association models for repeated categorical data
- APRIORI algorithm, a level-wise, breadth-first algorithm which counts transactions: `apriori`, `drm`
- ECLAT algorithm: employs equivalence classes, depth-first search and set intersection instead of counting: `eclat`

#### 4. Sequential Patterns

- Package: *arulesSequences*

- SPADE algorithm: `cSPADE`

#### 5. Time Series

- Package: *timsac*
- Time series construction: `ts`
- Decomposition: `decomp`, `decompose`, `stl`, `tsr`

#### 6. Statistics

- Package: Base R, *nlme*
- Analysis of Variance: `aov`, `anova`
- Density analysis: `density`
- Statistical test: `t.test`, `prop.test`, `anova`, `aov`
- Linear mixed-effects model fit: `lme`
- Principal components and factor analysis: `princomp`

#### 7. Graphics

- Bar chart: `barplot`
- Pie chart: `pie`
- Scattered plot: `dotchart`
- Histogram: `hist`
- Density: `densityplot`
- Candlestick chart, box plot: `boxplot`
- QQ (quantile-quantile) plot: `qqnorm`, `qqplot`, `qqline`
- Bi-variate plot: `coplot`
- Tree: `rpart`
- Parallel coordinates: `parallel`, `paracoor`, `parcoord`
- Heatmap, contour: `contour`, `filled.contour`
- Other plots: `stripplot`, `sunflowerplot`, `interaction.plot`, `matplot`, `fourfoldplot`, `assocplot`, `mosaicplot`
- Saving graphs: `pdf`, `postscript`, `win.metafile`, `jpeg`, `bmp`, `png`

#### 8. Data Manipulation

- Missing values: `na.omit`
- Standardize variables: `scale`
- Transpose: `t`
- Sampling: `sample`
- Stack: `stack`, `unstack`
- Others: `aggregate`, `merge`, `reshape`

#### 9. Interface to Weka

- *RWeka*: an R/Weka interface enabling to use all Weka functions in R.

## 1.3 Datasets

The datasets used in this book.

### 1.3.1 Iris Dataset

Iris dataset 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.

```
> 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 ...
```

### 1.3.2 Bodyfat Dataset

Bodyfat is a dataset available in package *mboost*. It has 71 rows, which 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.

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

```
> data("bodyfat", package = "mboost")
> 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/Export

This chapter shows how to import data into R and how to export R data frames. For more details, please refer to *R Data Import/Export*<sup>1</sup> [R Development Core Team, 2010b].

### 2.1 Save/Load R Data

Data in R can be saved as `.Rdata` files with functions `save`. After that, they can then be loaded into R with `load`.

```
> a <- 1:10
> save(a, file = "data/dumData.Rdata")
> rm(a)
> load("data/dumData.Rdata")
> print(a)
```

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

### 2.2 Import from and Export to .CSV Files

The example below creates a dataframe `a` and save it as a `.CSV` file with `write.csv`. And then, the dataframe is loaded from file to variable `b` with `read.csv`.

```
> var1 <- 1:5
> var2 <- (1:5) / 10
> var3 <- c("R", "and", "Data Mining", "Examples", "Case Studies")
> a <- data.frame(var1, var2, var3)
> names(a) <- c("VariableInt", "VariableReal", "VariableChar")
> write.csv(a, "data/dummmmyData.csv", row.names = FALSE)
> #rm(a)
> b <- read.csv("data/dummmmyData.csv")
> print(b)
```

	VariableInt	VariableReal	VariableChar
1	1	0.1	R
2	2	0.2	and
3	3	0.3	Data Mining
4	4	0.4	Examples
5	5	0.5	Case Studies

---

<sup>1</sup><http://cran.r-project.org/doc/manuals/R-data.pdf>

## 2.3 Import Data from SAS

Package `foreign` 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
> sashome <- "C:/Program Files/SAS/SAS 9.1"
> filepath <- "data"
> # filename should be no more than 8 characters, without extension
> fileName <- "dumData"
> # read data from a SAS dataset
> a <- read.ssd(file.path(filepath), fileName, sascmd = file.path(sashome, "sas.exe"))
> print(a)
```

	VARIABLE	VARIABLE2	VARIABLE3
1	1	0.1	R
2	2	0.2	and
3	3	0.3	Data Mining
4	4	0.4	Examples
5	5	0.5	Case Studies

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

```
> variableFileName <- "dumVariables.csv"
> myNames <- read.csv(paste(filepath, variableFileName, sep="/"))
> names(a) <- names(myNames)
> print(a)
```

	VariableInt	VariableReal	VariableChar
1	1	0.1	R
2	2	0.2	and
3	3	0.3	Data Mining
4	4	0.4	Examples
5	5	0.5	Case Studies



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.

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.

### 2.4.1 Read from Databases

```
> 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)
> odbcCloseAll()
```

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

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

Note that there is a limit of the number of rows to write to an EXCEL file.



## Chapter 3

# Data Exploration

This chapter shows examples on data exploration in 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 given on level plot, contour plot and 3D plot. It also shows how to saving charts to files with various formats.

### 3.1 Have a Look at Data

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

Check the dimensionality

```
> dim(iris)
```

```
[1] 150    5
```

Variable names or column names

```
> names(iris)
```

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

Structure

```
> 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 0.2 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

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

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

Get the first 5 rows

```
> 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 parts of `iris` data can be retrieved with `head()` or `tail()`.

```
> 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
```

Get `Sepal.Length` of the first 10 rows

```
> 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
```

Same as above

```
> 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 quartile (75%). For factors, it shows the frequency of every level.

```
> summary(iris)
```

Sepal.Length	Sepal.Width	Petal.Length	Petal.Width
Min. :4.300	Min. :2.000	Min. :1.000	Min. :0.100
1st Qu.:5.100	1st Qu.:2.800	1st Qu.:1.600	1st Qu.:0.300
Median :5.800	Median :3.000	Median :4.350	Median :1.300
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

Species
setosa :50
versicolor:50
virginica :50

The mean, median and range can be obtained 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(.1, .3, .65))
```

10%	30%	65%
4.80	5.27	6.20

Frequency

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

setosa	versicolor	virginica
50	50	50

Pie chart

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

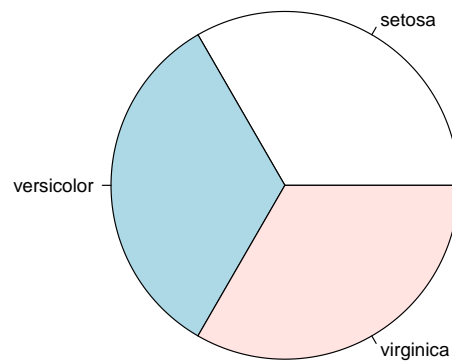


Figure 3.1: Pie Chart

Variance of Sepal.Length

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

```
[1] 0.6856935
```

Histogram

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

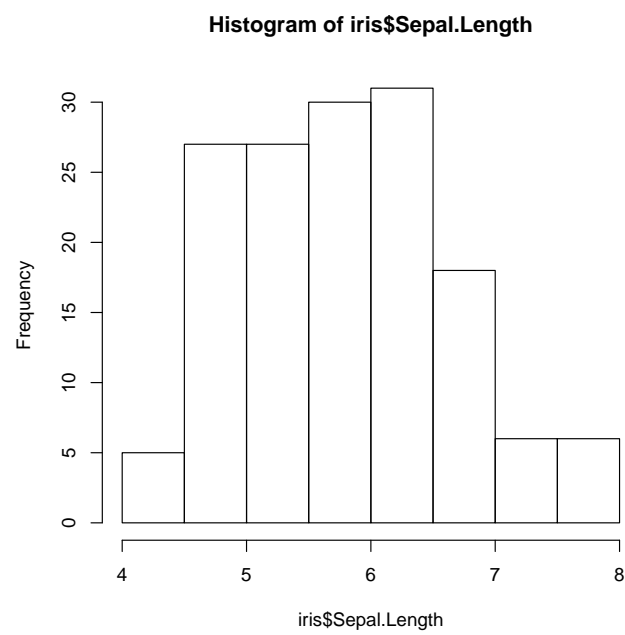


Figure 3.2: Histogram

```

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

```

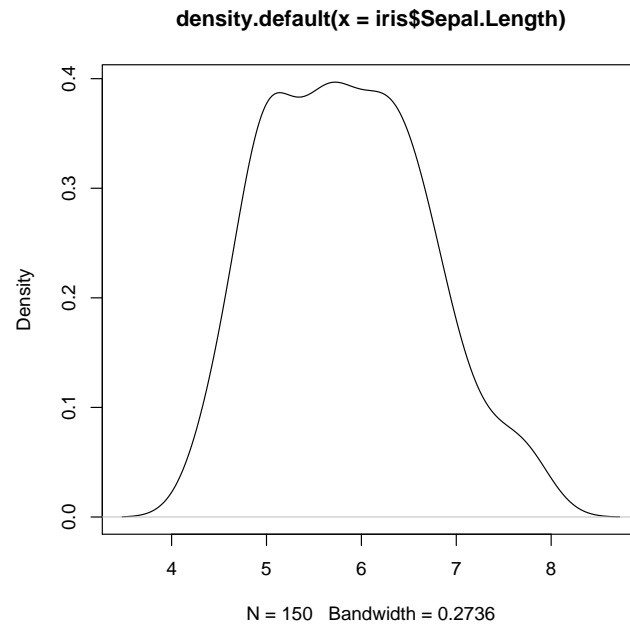


Figure 3.3: Density

### 3.3 Explore Multiple Variables

Covariance of two variables

```

> 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

```

Correlation of two variables

```

> 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

```



Distribution in subsets

```
> 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

Box plot, also known as box-and-whisker plot, shows 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.

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

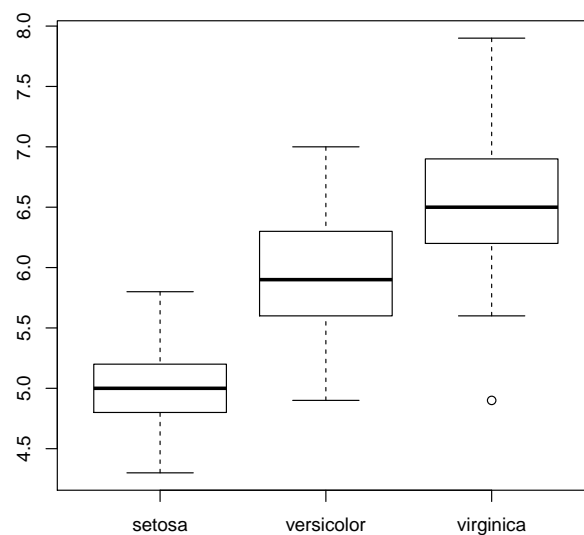


Figure 3.4: Boxplot

Scatter plot

```
> with(iris, plot(Sepal.Length, Sepal.Width, col=Species, pch=as.numeric(Species)))
```

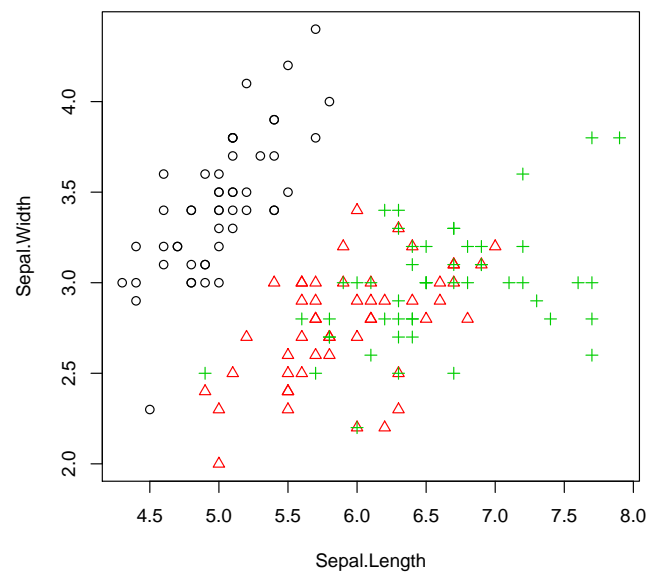


Figure 3.5: Scatter Plot

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

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

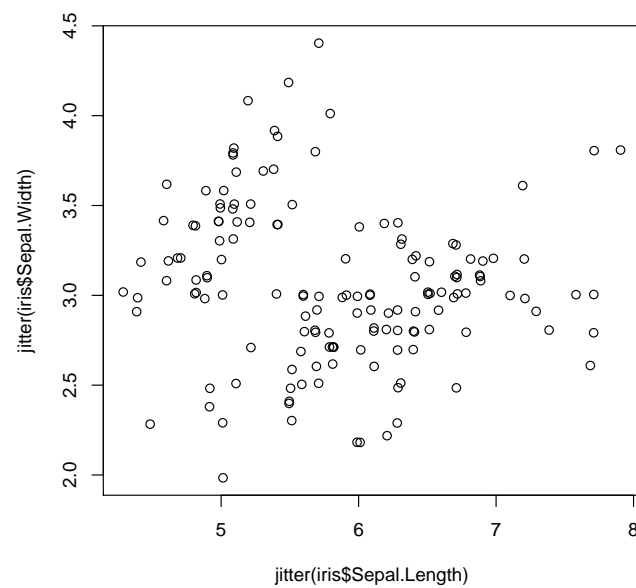


Figure 3.6: Scatter Plot with Jitter

Pairs plot

```
> pairs(iris)
```

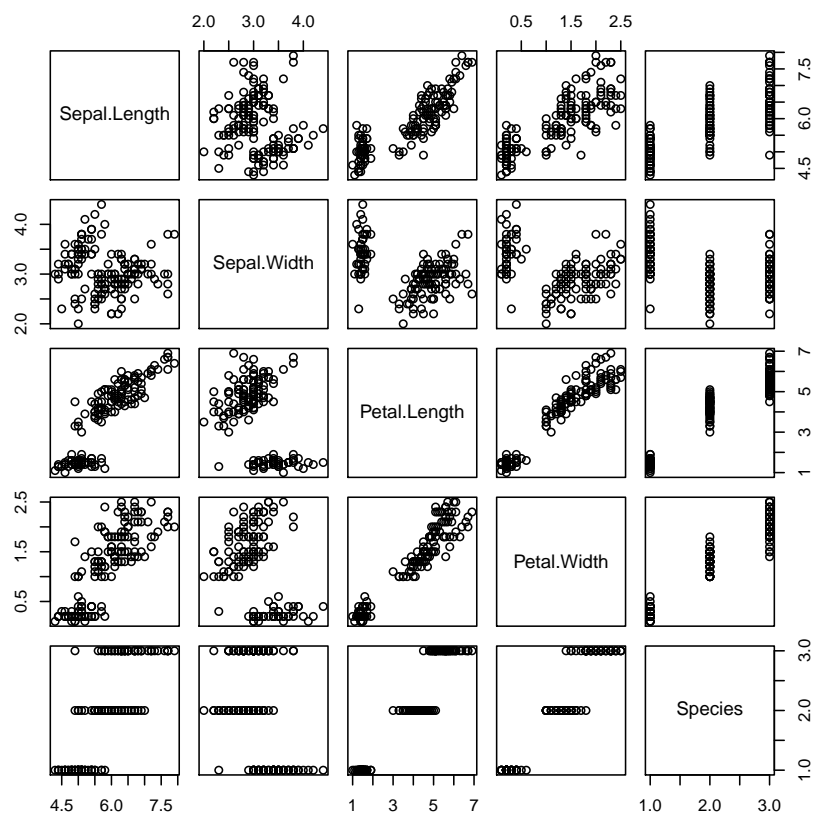


Figure 3.7: Pairs Plot

## 3.4 More Explorations

3D Scatter plot with package *scatterplot3d* [Ligges and Mächler, 2003]

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

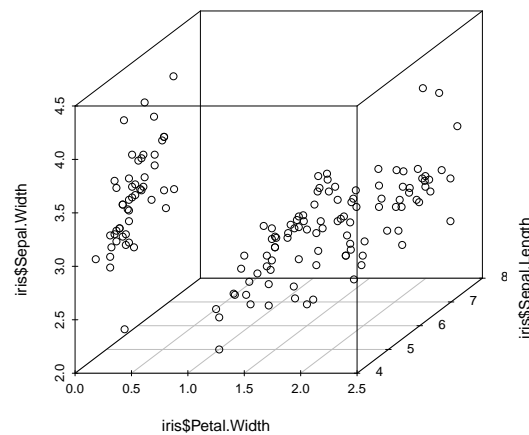


Figure 3.8: 3D Scatter plot

Level Plot with package *lattice* [Sarkar, 2008]

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

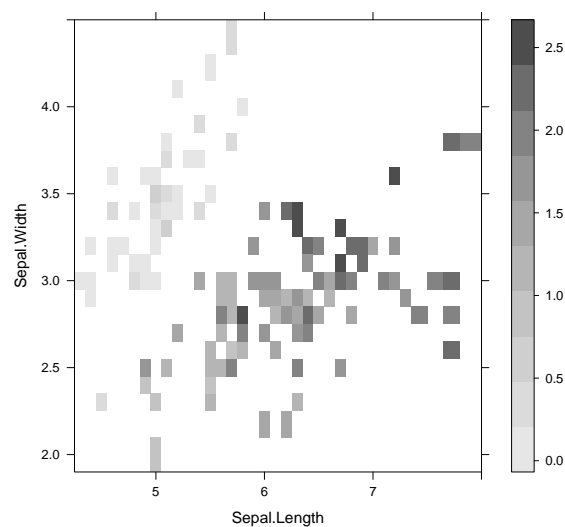


Figure 3.9: Level Plot

## Contour

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

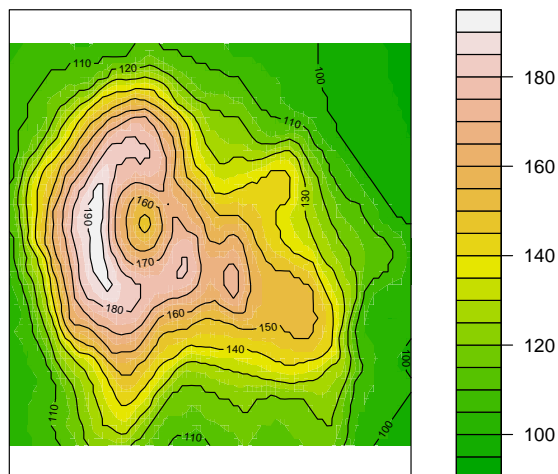


Figure 3.10: Contour

## 3D Surface

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

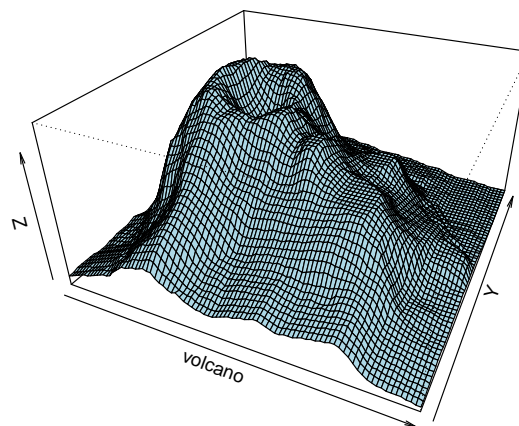


Figure 3.11: 3D Surface

Interactive 3D Scatter Plot with package *rgl* [Adler and Murdoch, 2012]

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

Parallel coordinates

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

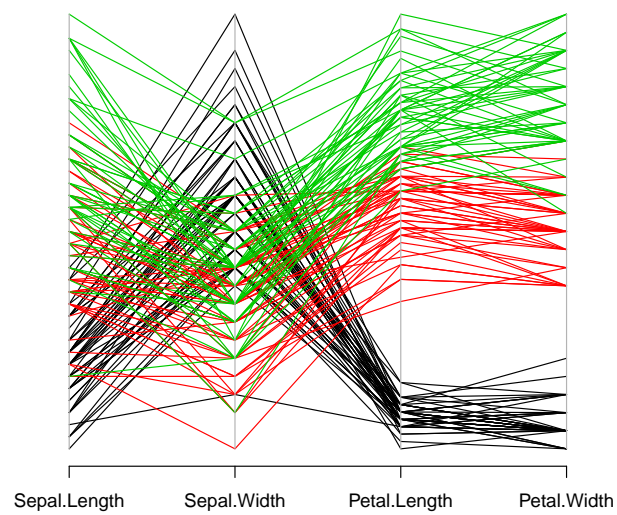


Figure 3.12: Parallel Coordinates



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

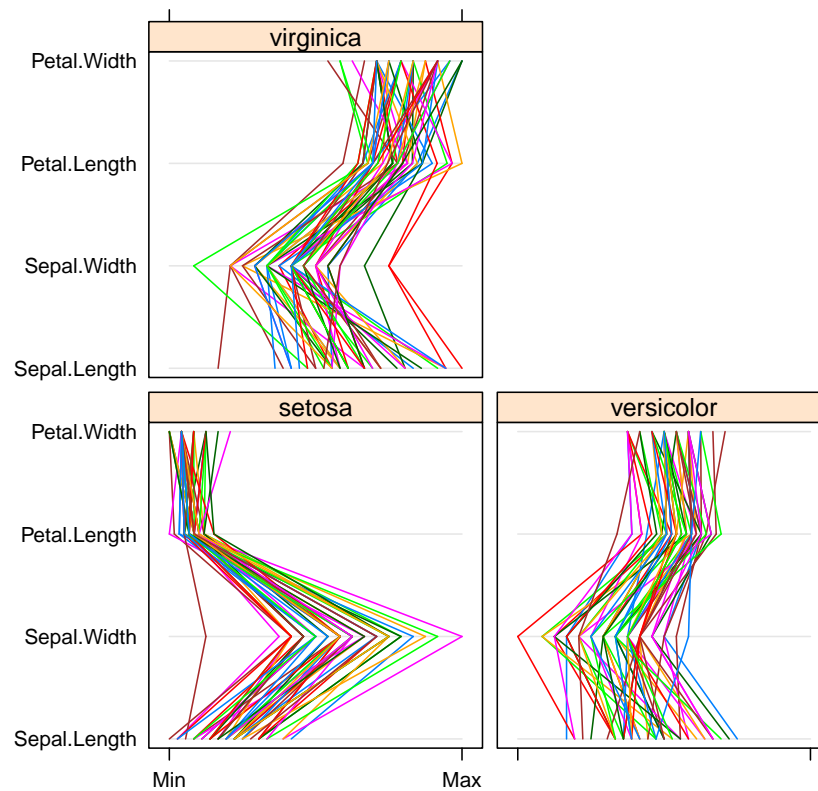


Figure 3.13: Parallel Coordinates with *lattice*

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 ~.)
```

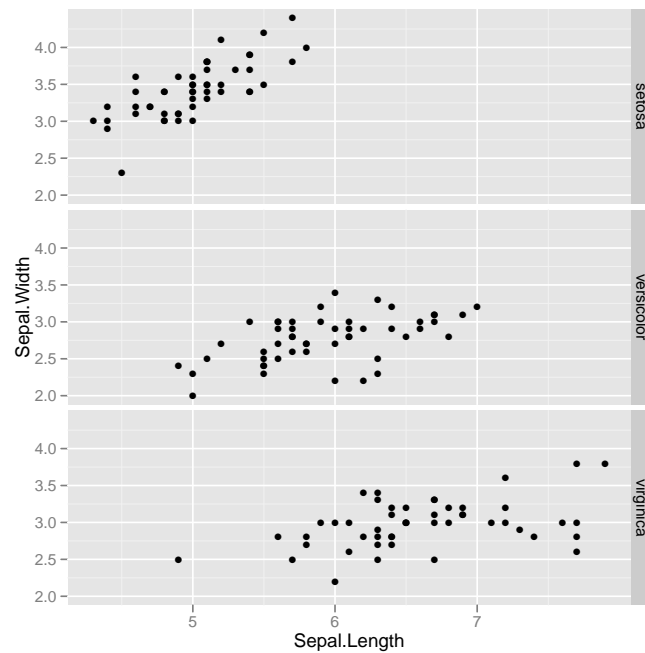


Figure 3.14: with *ggplot2*

### 3.5 Save Charts into Files

Save as a .PDF file

```
> pdf("myPlot.pdf")
> x <- 1:50
> plot(x, log(x))
> graphics.off()
```

Save as a postscript file

```
> postscript("myPlot.ps")
> x <- -20:20
> plot(x, x^2)
> graphics.off()
```

## Chapter 4

# Decision Trees and Random Forest

There are a couple of R packages on decision trees , regression trees and random forest, such as *rpart*, *rpartOrdinal*, *randomForest*, *party*, *tree*, *marginTree* and *maptree*.

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 Building Decision Trees with Package *party*

This section shows how to build a decision tree for *iris* data (see Section 1.3.1 for details of the data) with *ctree* in package *party* [Hothorn et al., 2010]. *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 unlabeled data.

The *iris* data is split below into two subsets: training (70%) and testing (30%).

```
> 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,]
```

Load package *party*, build a decision tree, and check the prediction.

```
> 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

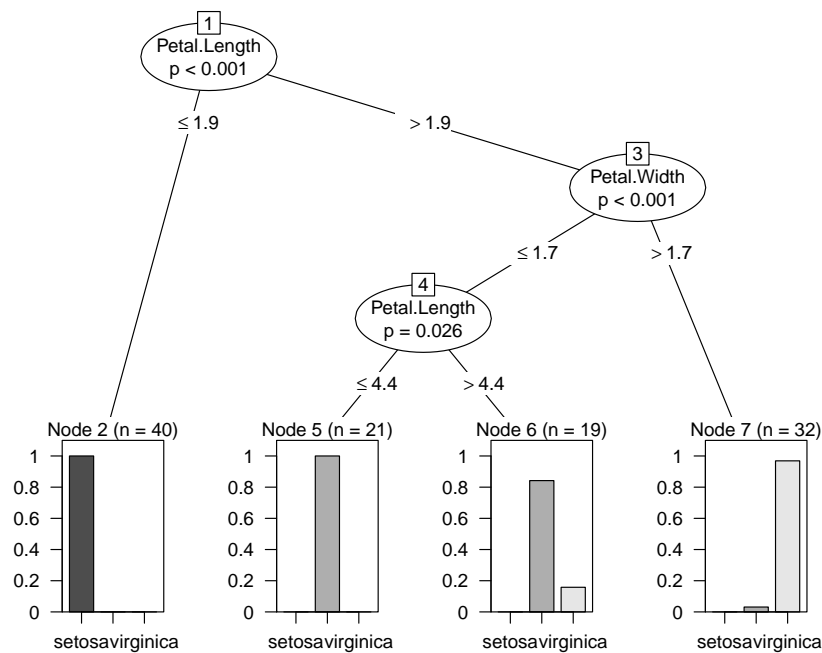
Response: Species

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)
```



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

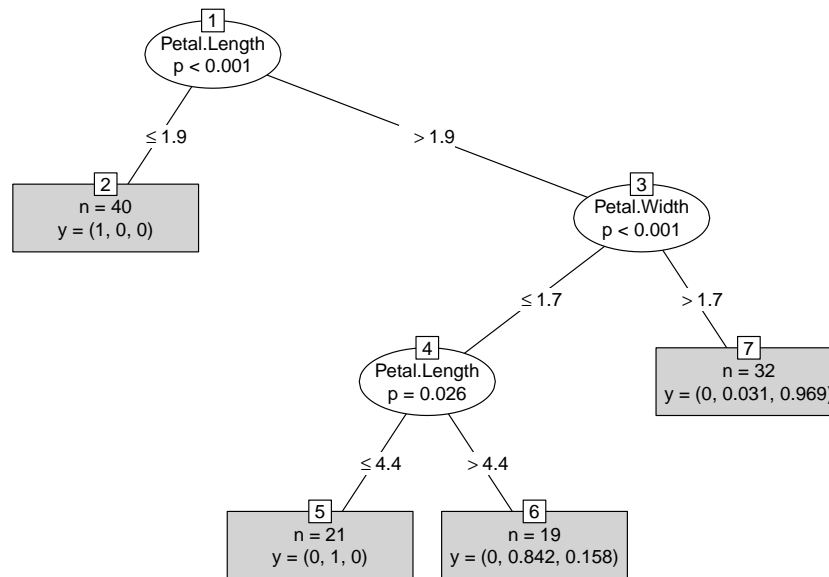


Figure 4.2: Decision Tree (Simple Style)

Test the built tree 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. An instance with a missing value may sometimes go to the left sub-tree and sometimes to the right. It might be because of 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 train 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 train data.

## 4.2 Building Decision Trees with Package *rpart*

Package *rpart* [Therneau et al., 2010] is used to build a decision tree on `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 select. After that, it is applied to makes prediction for unlabeled data with function `predict()`.

```

> data("bodyfat", package = "mboost")
> # have a look at the data
> dim(bodyfat)

[1] 71 10

> attributes(bodyfat)

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

$row.names
 [1] "47" "48" "49" "50" "51" "52" "53" "54" "55" "56" "57"
[12] "58" "59" "60" "61" "62" "63" "64" "65" "66" "67" "68"
[23] "69" "70" "71" "72" "73" "74" "75" "76" "77" "78" "79"
[34] "80" "81" "82" "83" "84" "85" "86" "87" "88" "89" "90"
[45] "91" "92" "93" "94" "95" "96" "97" "98" "99" "100" "101"
[56] "102" "103" "104" "105" "106" "107" "108" "109" "110" "111" "112"
[67] "113" "114" "115" "116" "117"

$class
[1] "data.frame"

> bodyfat[1:5,]

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

> # split into training and test subsets
> 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"       "terms"      "cptable"
 [6] "splits"     "method"     "parms"      "control"    "functions"

```

```
[11] "y"          "ordered"
```

```
$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

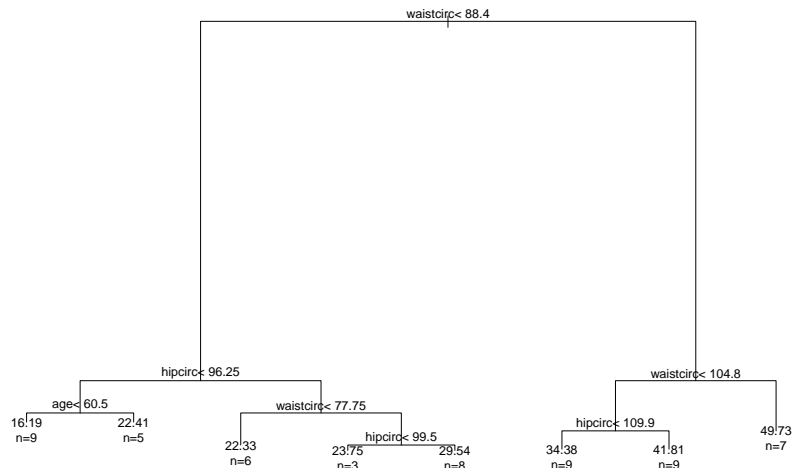
```
> print(bodyfat_rpart)
```

```
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 *
```

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

Figure 4.3: Decision Tree with *rpart*

```
> 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 *
```

```
> DEXfat_pred <- predict(bodyfat_prune, newdata = bodyfat.test)
```

The predicted values are compared with real labels.



```

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

```

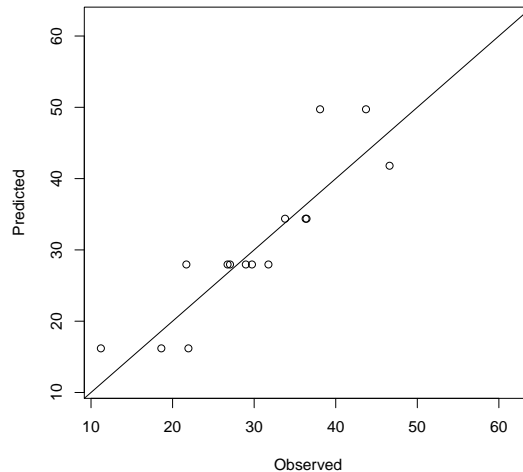


Figure 4.4: Prediction Result

### 4.3 Random Forest

Package *randomForest* [Liaw and Wiener, 2002] is used below to build a predictive model for *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 in 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.

The *iris* data is split below into two subsets: training (70%) and testing (30%).

```

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

```

Load *randomForest* and then train a random forest.

```

> 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"
[4] "err.rate"	"confusion"	"votes"
[7] "oob.times"	"classes"	"importance"
[10] "importanceSD"	"localImportance"	"proximity"
[13] "ntree"	"mtry"	"forest"
[16] "y"	"test"	"inbag"
[19] "terms"		

\$class

[1] "randomForest.formula" "randomForest"

Error rates with various number of trees

```
> plot(rf)
```

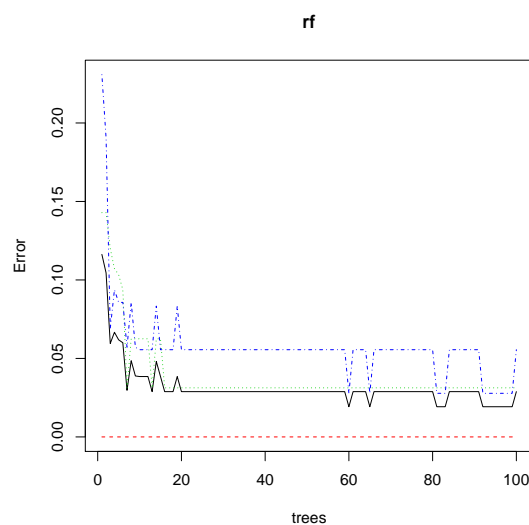


Figure 4.5: Error Rate of Random Forest

Variable importance.

```
> importance(rf)

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

> varImpPlot(rf)
```



Figure 4.6: Variable Importance

Test the built random forest on test data

```
> 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))
```

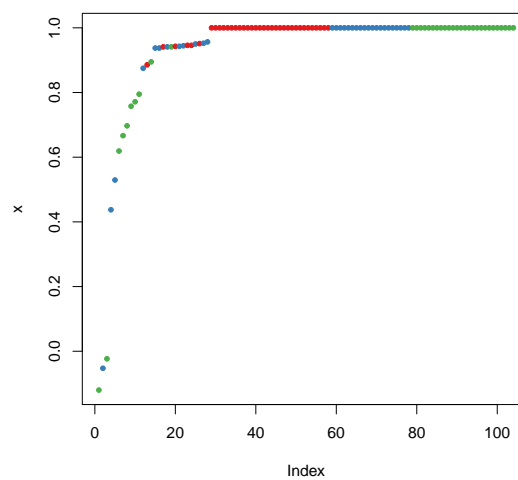


Figure 4.7: Margin of Predictions

The margin of a data point is as the proportion of votes for the correct class minus maximum proportion of votes for the other classes. Generally speaking, positive margin means correct classification.

## 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 customers 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*<sup>1</sup>.

### 5.1 Linear Regression

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

$$y = c_0 + c_1x_1 + c_2x_2 + \cdots + c_kx_k,$$

where  $x_1, x_2, \dots, x_k$  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 CPIs in four quarters in every year from 2008 to 2010<sup>2</sup>.

---

<sup>1</sup><http://cran.r-project.org/doc/contrib/Ricci-refcard-regression.pdf>

<sup>2</sup>From Australian Bureau of Statistics <<http://www.abs.gov.au>>

```

> ##cpi <- read.csv("CPI.csv")
> 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)

```

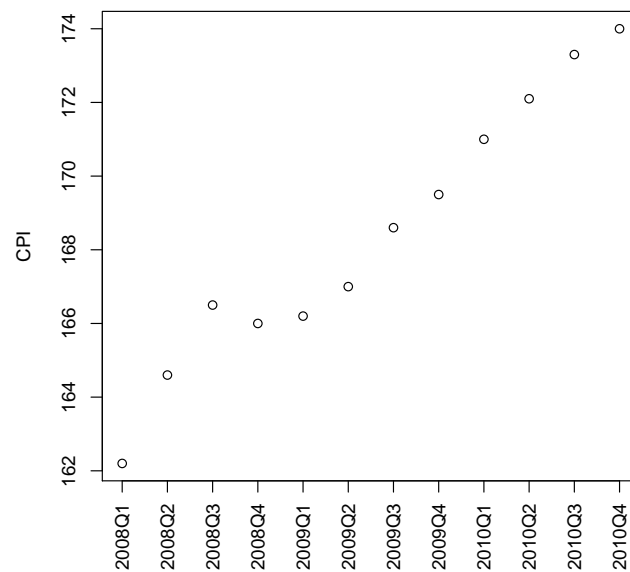


Figure 5.1: Australian CPIs in Year 2008 to 2010

We 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 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. A simpler 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)
```

More details of the model:

```
> 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 are

```
> #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 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 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

```
> plot(fit)
```

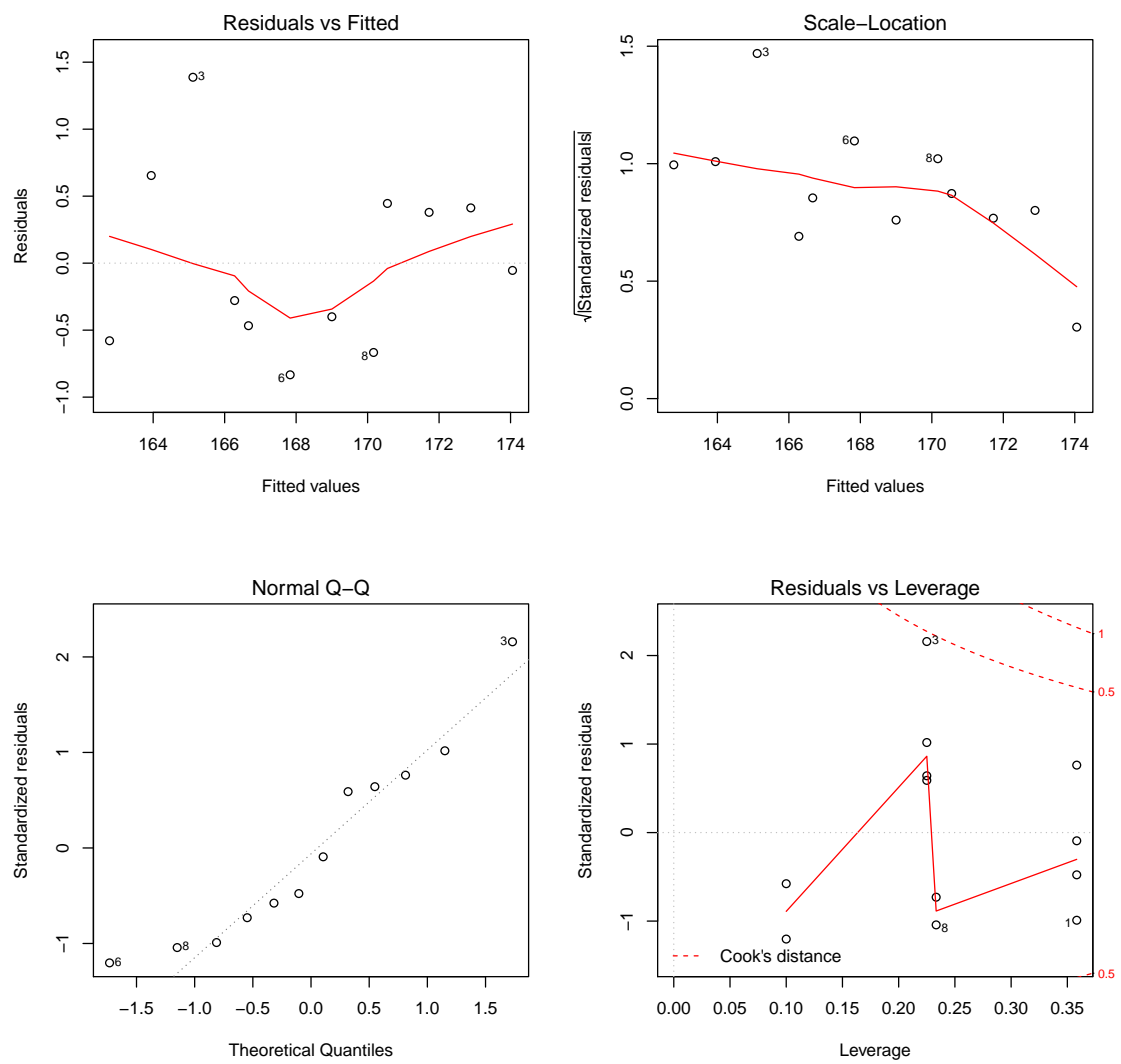


Figure 5.2: Prediction with Linear Regression Model - 1

With the model, the CPIs in year 2011 can be predicted as follows, and the predicted values are shown as red triangles in Figure 5.3.



```

> 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"))

```

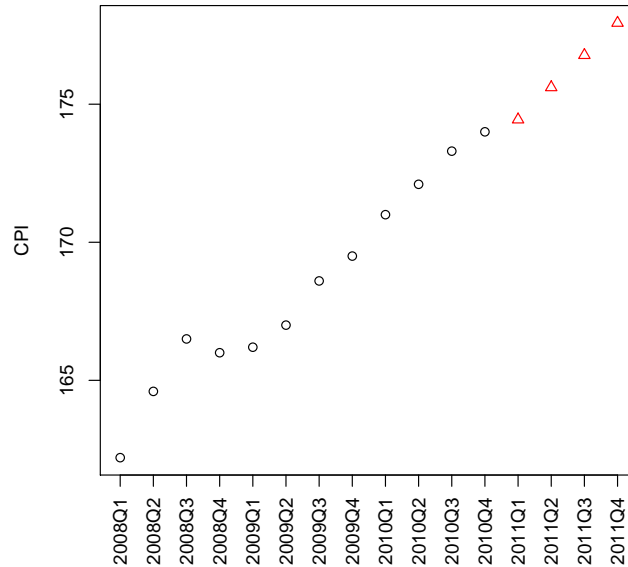


Figure 5.3: Prediction of CPIs in 2011 with Linear Regression Model

## 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:

$$\text{logit}(y) = c_0 + c_1x_1 + c_2x_2 + \cdots + c_kx_k,$$

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

$$y = \frac{1}{1 + e^{-(c_0 + c_1x_1 + c_2x_2 + \cdots + c_kx_k)}}.$$

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 by 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 `bodyfat` data (see Section 1.3.2 for details of the data).

```
> data("bodyfat", package = "mboost")
> 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 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 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")
```

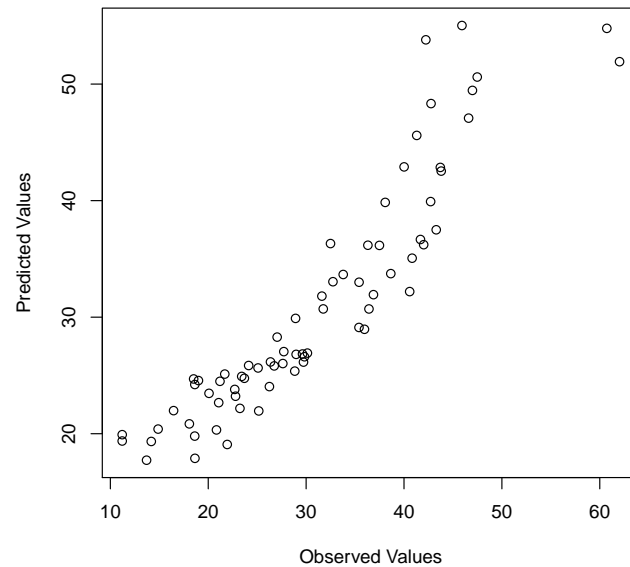


Figure 5.4: Prediction with Generalized Linear Regression Model

In the above code, if `family = gaussian("identity")` is used, the resulted 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. More details on non-linear regression can be found at

- A Complete Guide to Nonlinear Regression  
<http://www.curvefit.com/>.



# Clustering

This chapter presents examples of various clustering techniques, including  $k$ -means clustering, hierarchical clustering and density-based clustering. The first section demonstrates how to use  $k$ -means algorithm to cluster the *iris* data. The second section shows an example on hierarchical clustering on the same data. The third section describes the basic 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.

## 6.1 k-Means Clustering

This section shows k-means clustering of `iris` data (see Section 1.3.1 for details of the data).

```
> iris2 <- iris
> # remove species from the data to cluster
> iris2$Species <- NULL
```

3. Apply `kmeans()` to `iris2`, and store the clustering result in `kc`. The cluster number is set to

```
> (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:

[illegible]

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"
```

Compare the `Species` label with the clustering result

```
> 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.

Plot the clusters and their centers. 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. Note 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$cluster)
> points(kmeans.result$centers[,c("Sepal.Length", "Sepal.Width")], col = 1:3, pch = 8, cex=2)
```

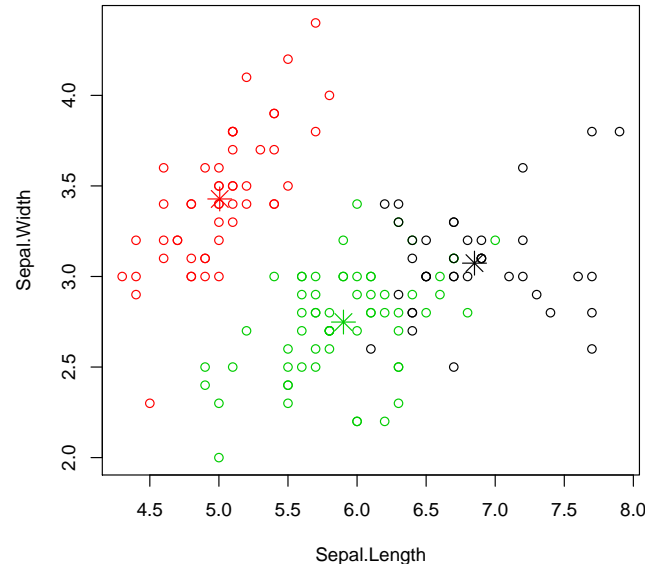


Figure 6.1: Results of k-Means Clustering

## 6.2 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* 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, 2010] 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 real 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
```

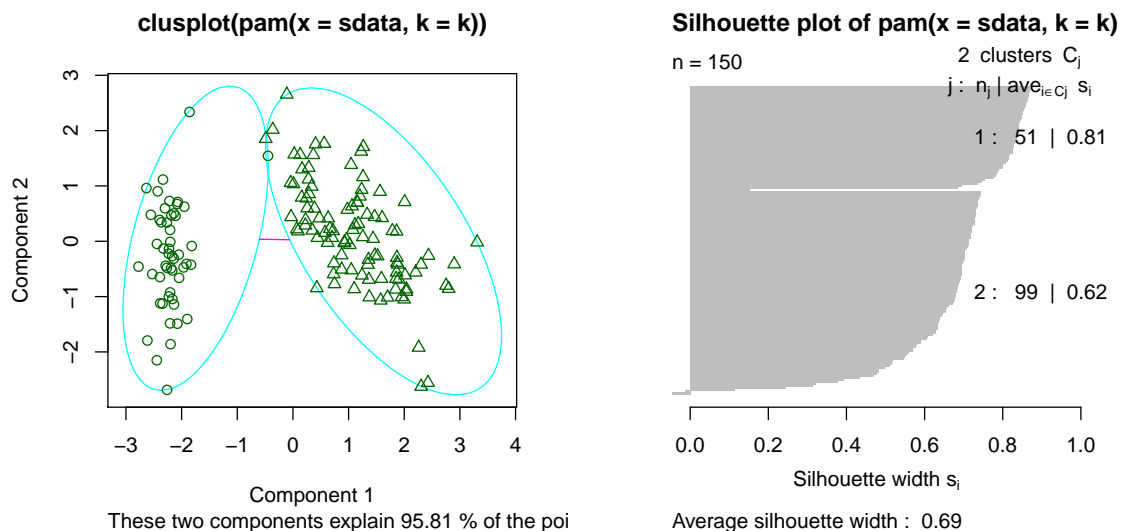


Figure 6.2: Clustering with the  $k$ -medoids Algorithm - I

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  $k = 3$ .

```
> 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
```

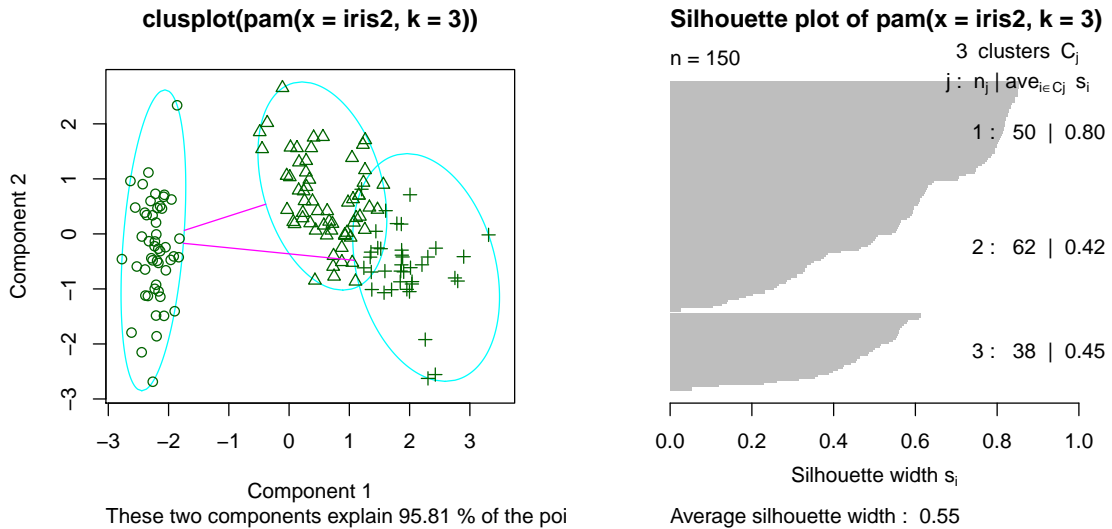


Figure 6.3: Clustering with the  $k$ -medoids Algorithm - II

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()` is 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 give the best result. Note that we cheat by setting  $k = 3$  when using `pam()`, which is already known to us as the number of species.

## 6.3 Hierarchical Clustering

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



Draw a sample of 40 records from iris data, and remove variable **Species**

```
> idx <- sample(1:dim(iris)[1], 40)
> irisSample <- iris[idx,]
> irisSample$Species <- NULL
```

Hierarchical clustering

```
> hc <- hclust(dist(irisSample), method="ave")
> plot(hc, hang = -1, labels=iris$Species[idx])
```

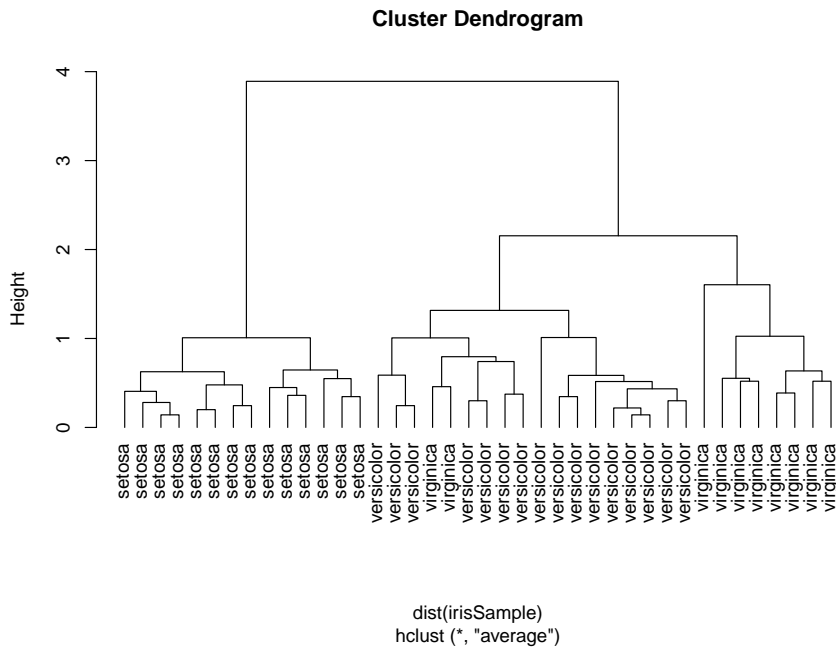


Figure 6.4: Cluster Dendrogram

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.

## 6.4 Density-based Clustering

DBSCAN from package *fpc* [Hennig, 2010] provides a density-based clustering for numeric data [Ester et al., 1996]. 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;
- **MinPts**: Reachability minimum no. of points.

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

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, k-means tends to find clusters with sphere shape and with similar sizes.

```
> 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 discovered clusters, while “0” stands for noises, i.e., objects that are not assigned to any clusters. The noises are shown as black circles in figures below.

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

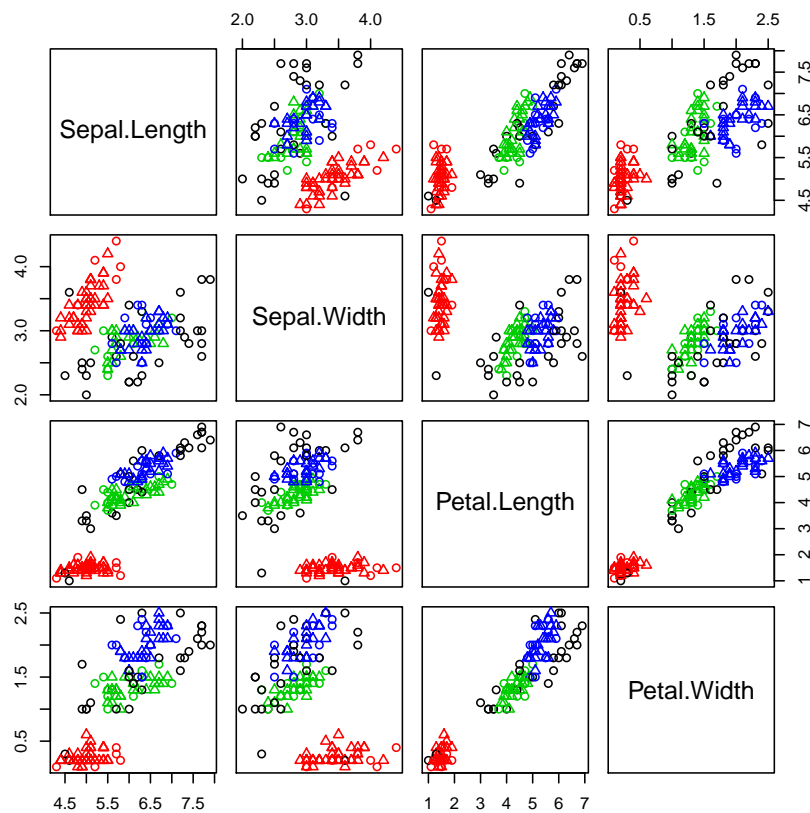


Figure 6.5: Density-based Clustering - I

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

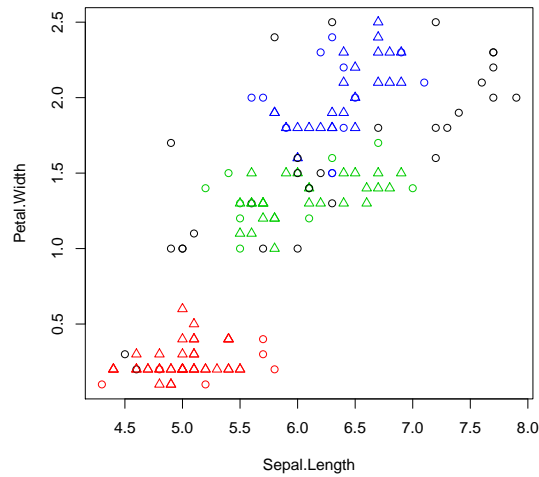


Figure 6.6: Density-based Clustering - II

Another way to show the clusters. Note that the data are projected to distinguish classes.

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

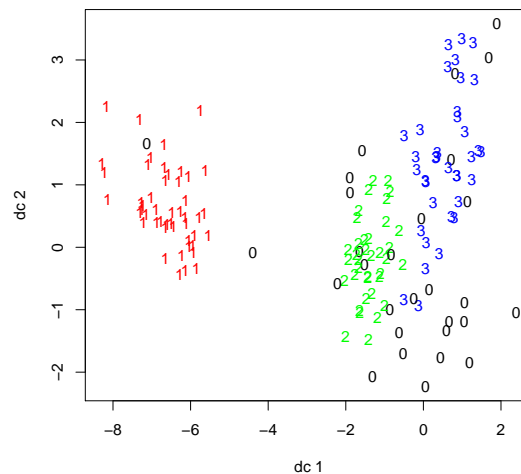


Figure 6.7: Density-based Clustering - III

Label new data

The clustering model can then be used to label new data, based on the similarity between a new object and the clusters. The following example draws a sample of 10 objects from iris and adds small noise to them to make a new dataset for labeling.

```

> # 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)
> # check the labels assigned to new data
> 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

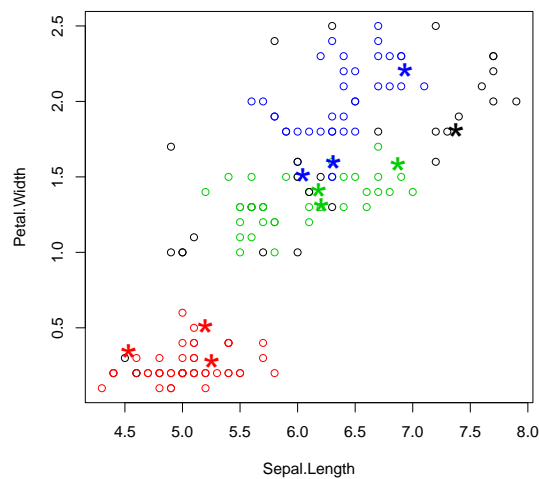


Figure 6.8: Prediction with Clustering Model

As we can see from the above result, in 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.

## 6.5 Fuzzy Clustering

This section is not available yet in this version.

## 6.6 Subspace Clustering

This section is not available yet in this version.

## Chapter 7

# Outlier Detection

This chapter presents examples of outlier detection with R.

This chapter is not available yet in this version.



## Chapter 8

# Time Series Analysis and Mining

This chapter presents examples on time series decomposition, forecast, 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 a 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 for respectively a monthly series and a 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)` suggest 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)

$ts
[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.

using moving averages

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)
```

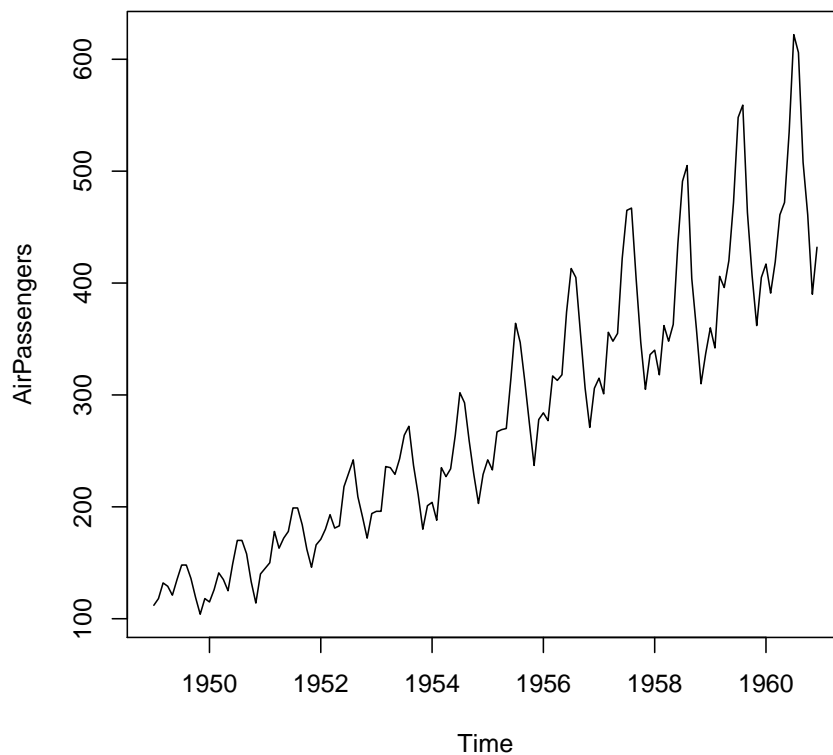


Figure 8.1: A Time Series of **AirPassengers**

Function `decompose` is called to **AirPassengers** to break it into various components.



```

> # decompose time series
> apts <- ts(AirPassengers, frequency = 12)
> f <- decompose(apts)
> # seasonal figures
> f$figure

[1] -24.748737 -36.188131 -2.241162 -8.036616 -4.506313 35.402778
[7] 63.830808 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)

```

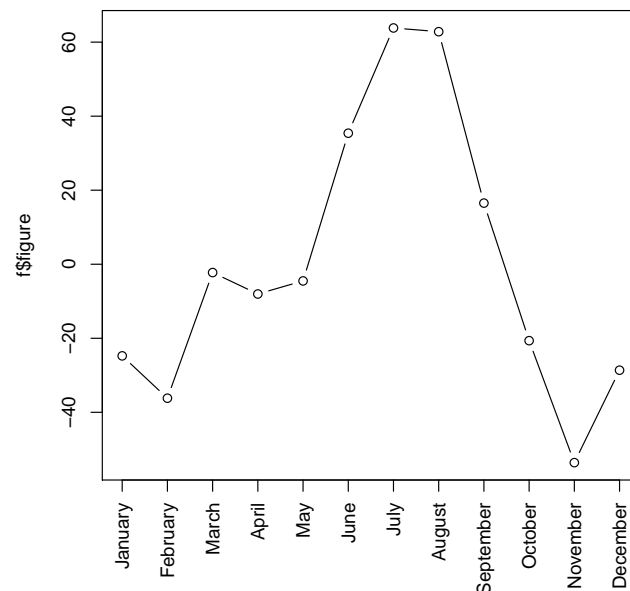


Figure 8.2: Seasonal Component

```
> plot(f)
```

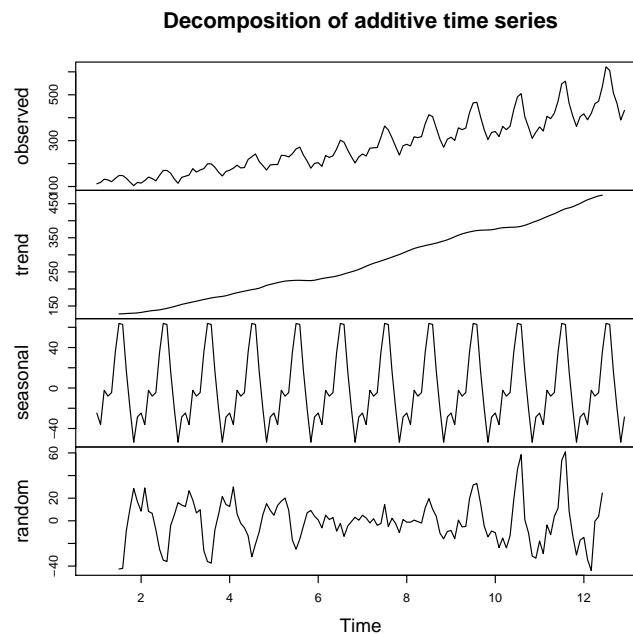


Figure 8.3: Time Series Decomposition

The first chart is the original time series. The second is trend in 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*, `decomp()` in package *timsac*, and `tsr()` in package *ast*.

### 8.3 Time Series Forecasting

Time series forecasting is to forecast future events based on known past data. One example is to predict the opening price of a stock based on its past performance. Some popular models 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))

```

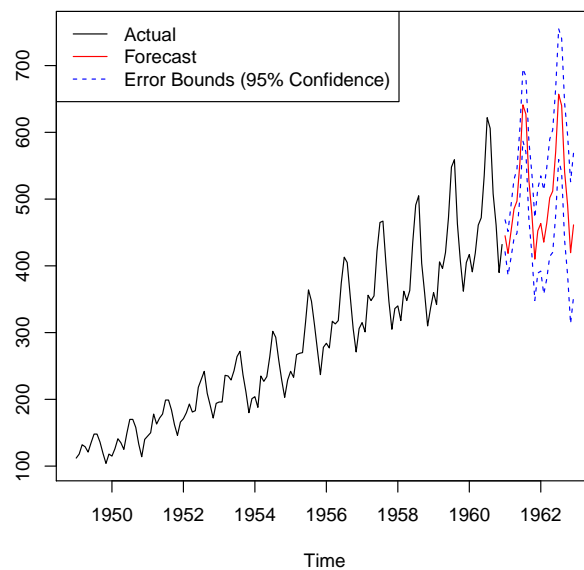


Figure 8.4: Time Series Forecast

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.

Measure of distance/dissimilarity: Euclidean distance, Manhattan distance, Maximum norm, Hamming distance, the angle between two vectors (inner product), Dynamic Time Warping (DTW) distance, etc.

### 8.4.1 Dynamic Time Warping

Dynamic Time Warping (DTW) [Keogh and Pazzani, 2001] finds optimal alignment between two time series. Package *dtw* [Giorgino, 2009] is used in the example below. In this 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)

```

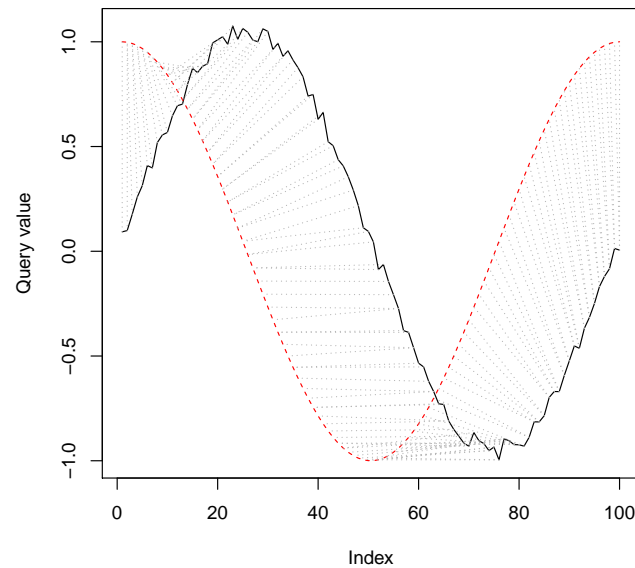


Figure 8.5: Alignment with Dynamic Time Warping

### 8.4.2 Synthetic Control Chart Time Series Data

Synthetic Control Chart Time Series <sup>1</sup> 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. There are six classes:

- 1-100 Normal
- 101-200 Cyclic
- 201-300 Increasing trend
- 301-400 Decreasing trend
- 401-500 Upward shift
- 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.

<sup>1</sup>[http://kdd.ics.uci.edu/databases/synthetic\\_control/synthetic\\_control.html](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="")

```

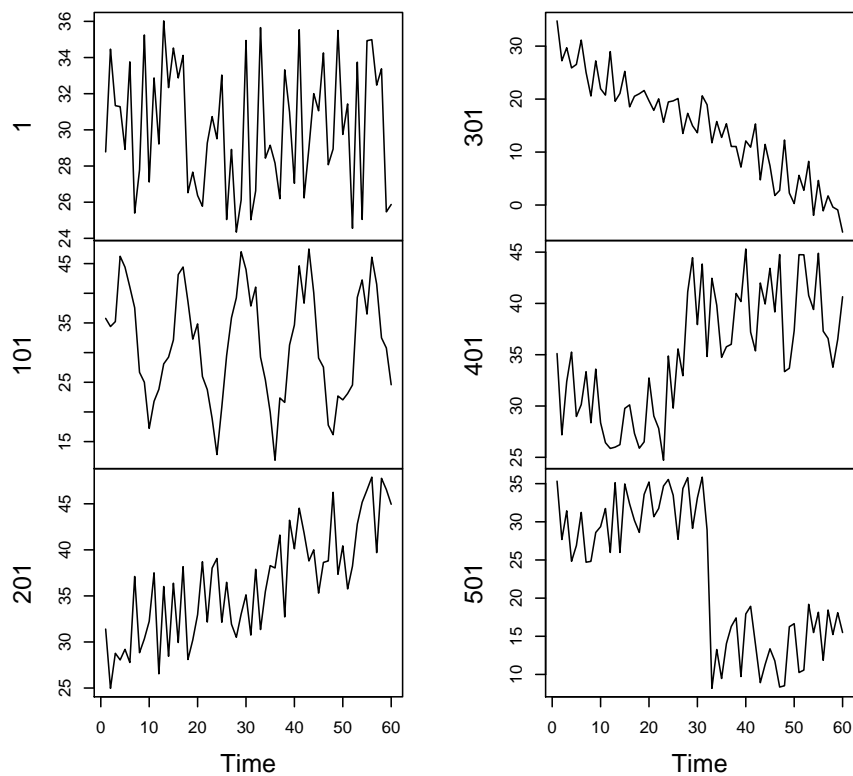


Figure 8.6: Six Classes in Synthetic Control Chart Time Series

### 8.4.3 Hierarchical Clustering with Euclidean Distance

$n$  cases were randomly sampled from each class.



5	0	0	0	0	10	0	0	0
6	1	0	0	0	0	0	6	3

### 8.4.4 Hierarchical Clustering with DTW Distance

```
> distMatrix <- dist(sample2, method="DTW")
> hc <- hclust(distMatrix, method="average")
> plot(hc, labels=observedLabels, main="")
> # cut tree to get 8 clusters
> memb <- cutree(hc, k=8)
> table(observedLabels, memb)
```

	memb							
observedLabels	1	2	3	4	5	6	7	8
1	10	0	0	0	0	0	0	0
2	0	2	2	3	2	1	0	0
3	0	0	0	0	0	0	10	0
4	0	0	0	0	0	0	0	10
5	0	0	0	0	0	0	10	0
6	1	0	0	0	0	0	0	9

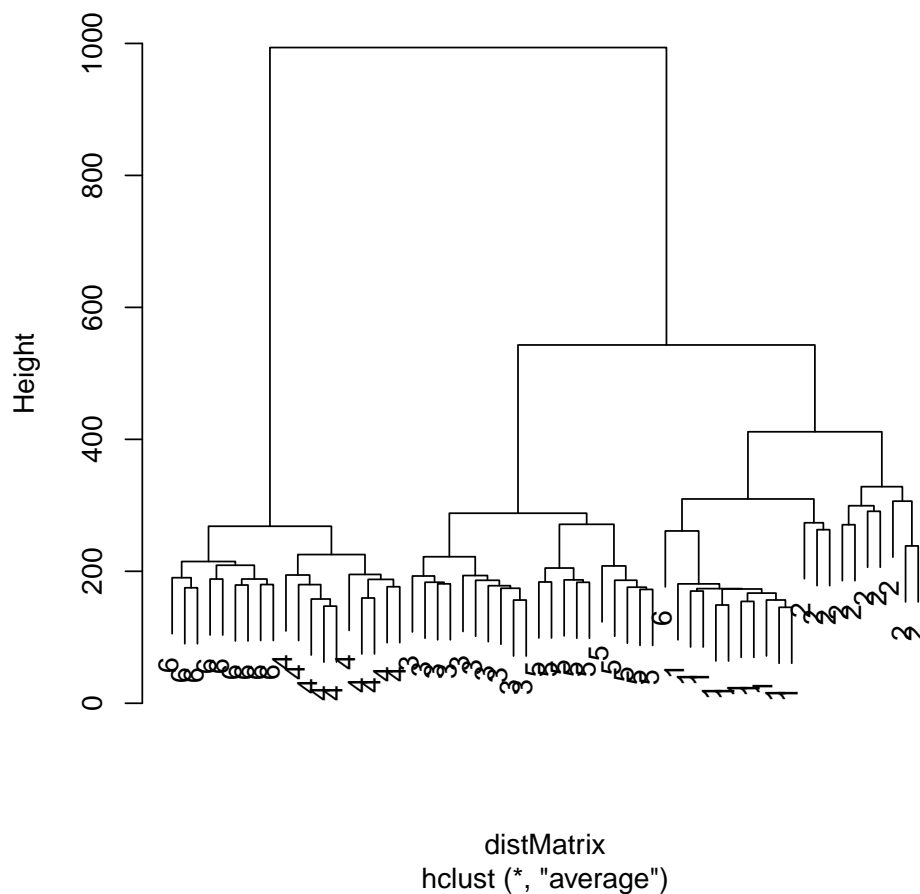


Figure 8.8: Hierarchical Clustering with DTW Distance



## 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.

Some techniques for feature extraction are 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., 2010] to demonstrate classification of time series with 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.

```

> classId <- c(rep("1",100), rep("2",100), rep("3",100),
+             rep("4",100), rep("5",100), rep("6",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))

```

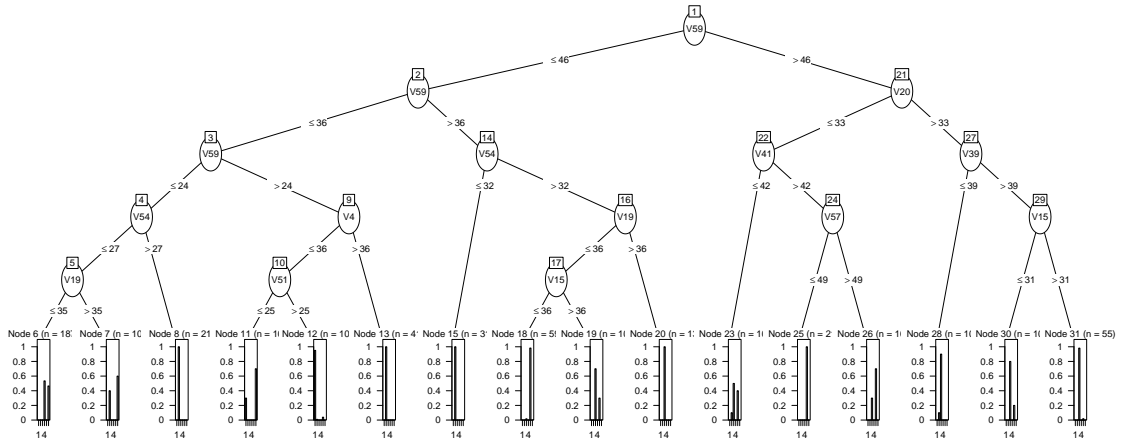


Figure 8.9: Decision Tree

### 8.5.2 Classification with Extracted Features

DWT (Discrete Wavelet Transform) [Burrus et al., 1998]

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/>. DFT (Discrete Fourier Transform) is another popular feature extraction technique [Agrawal et al., 1993].

An example on extracting DWT (with Haar filter) coefficients is shown below. Package *wavelets* [Aldrich, 2010] 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.

```
> 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))
```

Decision Tree with DWT

```
> 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))
```

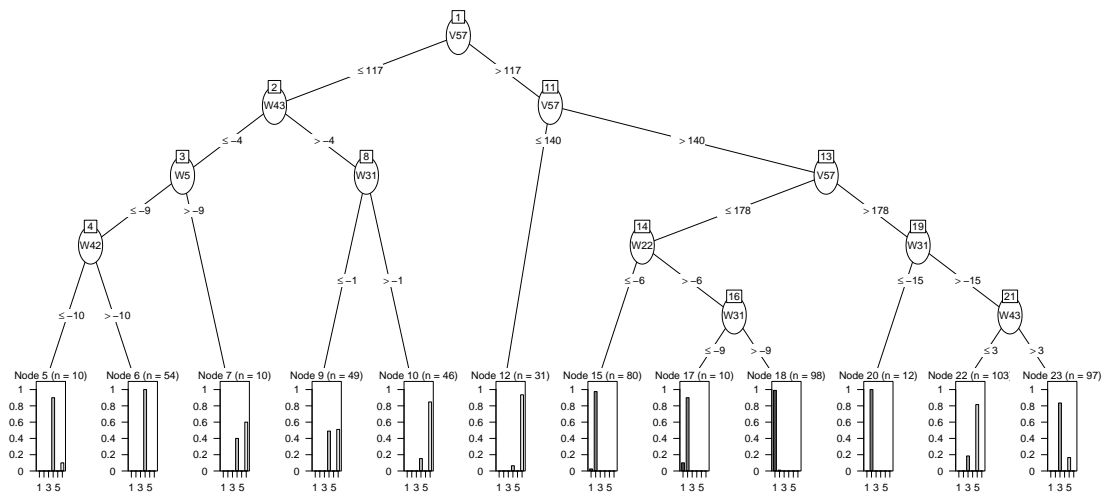


Figure 8.10: Decision Tree with DWT

### 8.5.3 $k$ -NN Classification

$k$ -NN Classification find the  $k$  nearest neighbors of a new instance; label it by majority voting; needs an efficient indexing structure for large datasets

```
> k <- 20
> 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 Discussion

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

## 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].

## Chapter 9

# Association Rules and Sequential Patterns

This chapter presents examples of association rule mining and sequential pattern analysis with R. It demonstrates mining frequent itemsets, generating association rules, selecting interesting rules, visualizing association rules and using association rules for classification.

This chapter is not available yet in this version.



## Chapter 10

# Text Mining

This chapter presents examples of text mining with R. Twitter<sup>1</sup> 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 section, “tweet” and “document” will be used interchangeably, so are “word” and “term”.

There are three packages used in the examples: *twitteR*, *tm* and *wordcloud*. Package *twitteR* [Gentry, 2012] provides access to Twitter data, *tm* [Feinerer, 2012] provides functions for text mining, and *wordcloud* [Fellows, 2012] visualizes the result with a word cloud <sup>2</sup>.

### 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, 2012].

If you have no access to Twitter, the tweets data can be downloaded as file “rdmTweets.RData” at <http://www.rdatamining.com/data>, and then you can skip this section and proceed directly to Section 10.2.

Package *twitteR* can be found at <http://cran.r-project.org/bin/windows/contrib/>. Package *twitteR* depends on package *RCurl*, which is available at <http://www.stats.ox.ac.uk/pub/RWin/bin/windows/contrib/2.14/>. Another way to retrieve text from Twitter is using package *XML*, and an example on that is given at <http://heuristically.wordpress.com/2011/04/08/text-data-mining-twitter-r/>.

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

[1] 154
```

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.

---

<sup>1</sup><http://www.twitter.com>

<sup>2</sup>[http://en.wikipedia.org/wiki/Word\\_cloud](http://en.wikipedia.org/wiki/Word_cloud)

```

> for (i in 11:15) {
+   cat(paste("[", 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/cA28STP0
[[14]] Chief Scientist - Data Intensive Analytics, Pacific Northwest National
Laboratory (PNNL), US http://t.co/OGdzq1Nt
[[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, 2012].

```

> # convert tweets to a data frame
> df <- do.call("rbind", lapply(rdmTweets, as.data.frame))
> 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, 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). Hyerlinks are also removed in the example below.

```

> # convert to lower case
> myCorpus <- tm_map(myCorpus, tolower)
> # remove punctuation
> myCorpus <- tm_map(myCorpus, removePunctuation)
> # remove numbers
> myCorpus <- tm_map(myCorpus, removeNumbers)
> # remove URLs
> removeURL <- function(x) gsub("http[[:alnum:]]*", "", x)
> myCorpus <- tm_map(myCorpus, removeURL)
> # add two extra stop words: "available" and "via"
> myStopwords <- c(stopwords('english'), "available", "via")
> # remove "r" and "big" from stopwords
> idx <- which(myStopwords %in% c("r", "big"))
> myStopwords <- myStopwords[-idx]
> # remove stopwords from corpus
> myCorpus <- tm_map(myCorpus, removeWords, myStopwords)

```



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 to remove hypelinks. Within the function, 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 it can be found by runing ?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 done 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
[[15]] top data mine
```

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

```
> # stem completion
> myCorpus <- tm_map(myCorpus, stemCompletion, dictionary=myCorpusCopy)
```

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 functions package handling big data
parallel computing
[[13]] postdoctoral optimizing cloud data miners primitives inria france
[[14]] chief scientist data intensive analytics pacific northwest national pnnl
[[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 ingoring 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 <- tm_map(myCorpusCopy, grep, pattern="\\<mining")
> sum(unlist(miningCases))

[1] 47

> # count frequency of "miners"
> minerCases <- tm_map(myCorpusCopy, grep, pattern="\\<miners")
> sum(unlist(minerCases))

[1] 2

> # replace "miners" with "mining"
> myCorpus <- tm_map(myCorpus, 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.

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

A term-document matrix (444 terms, 154 documents)

```
Non-/sparse entries: 1085/67291
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 444 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(myTdm)$Terms == "r")
> inspect(myTdm[idx+(0:5),101:110])
```

A term-document matrix (6 terms, 10 documents)

```
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.

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

The list of terms can be retrieved with `rownames(myTdm)`. 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(myTdm, lowfreq=10)
```

[1] "analysis"	"computing"	"data"	"examples"
[5] "introduction"	"mining"	"network"	"package"
[9] "positions"	"postdoctoral"	"r"	"research"
[13] "slides"	"social"	"tutorial"	"users"

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 of 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(myTdm))
> termFrequency <- subset(termFrequency, termFrequency>=10)
> library(ggplot2)
> qplot(names(termFrequency), termFrequency, geom="bar") + coord_flip()
```

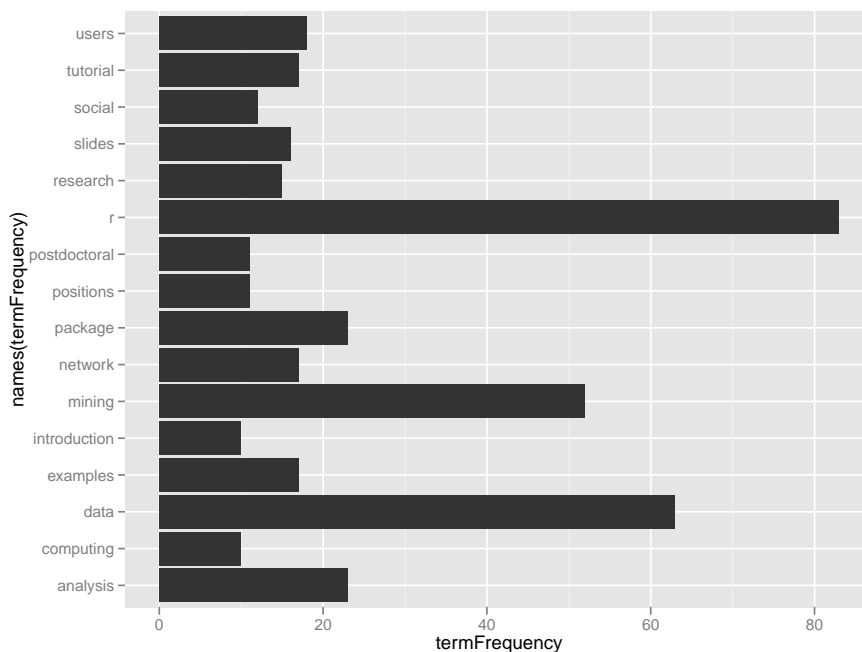


Figure 10.1: Frequent Terms

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(myTdm, 'r', 0.25)
```

r	users	canberra	cran	list	examples
1.00	0.32	0.26	0.26	0.26	0.25

```
> # which words are associated with "mining"?
> findAssocs(myTdm, 'mining', 0.25)
```



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 text books [Han and Kamber, 2000, Hand et al., 2001, Witten and Frank, 2005].

```
> # remove sparse terms
> myTdm2 <- removeSparseTerms(myTdm, sparse=0.95)
> m2 <- as.matrix(myTdm2)
> # cluster terms
> distMatrix <- dist(scale(m2))
> fit <- hclust(distMatrix, method="ward")
```

```

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

```

analysis	applications	code	computing	data
1	2	3	4	5
examples	introduction	mining	network	package
3	2	6	1	7
parallel	positions	postdoctoral	r	research
4	8	8	9	8
series	slides	social	time	tutorial
10	2	1	10	2
users				
2				

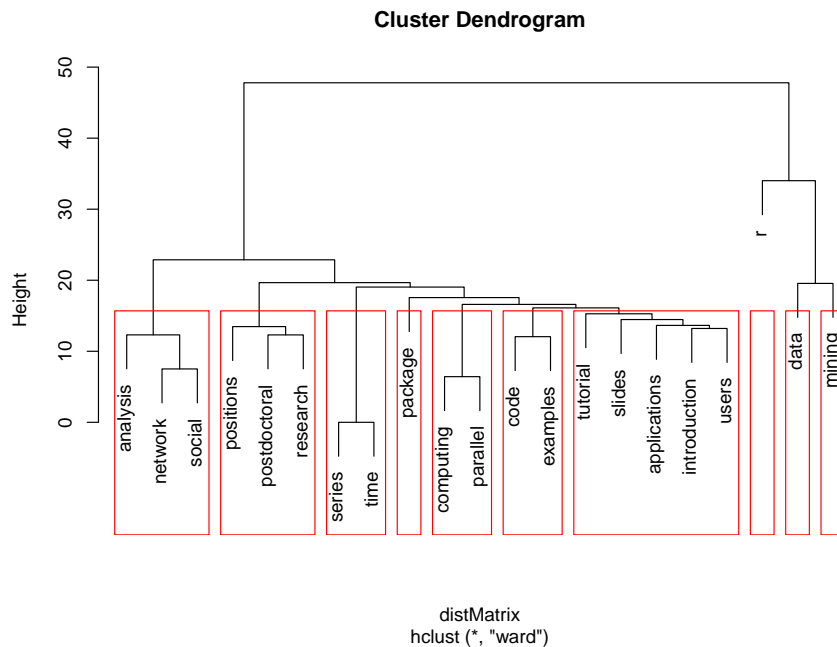


Figure 10.3: Clustering of Words

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.

```
> # 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	applications	code	computing	data	examples	introduction
1	0.040	0.040	0.240	0.000	0.040	0.320	0.040
2	0.000	0.158	0.053	0.053	1.526	0.105	0.053
3	0.857	0.000	0.000	0.000	0.000	0.071	0.143
4	0.000	0.000	0.000	1.000	0.000	0.000	0.000
5	0.037	0.074	0.019	0.019	0.426	0.037	0.093
6	0.000	0.000	0.000	0.000	0.000	0.100	0.000
7	0.533	0.000	0.067	0.000	0.333	0.200	0.067
8	0.000	0.111	0.000	0.000	0.556	0.000	0.000

	mining	network	package	parallel	positions	postdoctoral	r
1	0.120	0.080	0.080	0.000	0.000	0.000	1.320
2	1.158	0.000	0.368	0.053	0.000	0.000	0.947
3	0.071	1.000	0.071	0.000	0.143	0.143	0.214
4	0.000	0.000	0.125	0.750	0.000	0.000	1.000
5	0.407	0.000	0.000	0.000	0.093	0.093	0.000
6	0.000	0.000	1.200	0.100	0.000	0.000	0.600
7	0.200	0.067	0.000	0.000	0.000	0.000	1.000
8	0.111	0.000	0.000	0.000	0.444	0.444	0.000

	research	series	slides	social	time	tutorial	users
1	0.000	0.040	0.000	0.000	0.040	0.200	0.160
2	0.053	0.000	0.053	0.000	0.000	0.000	0.158
3	0.071	0.000	0.071	0.786	0.000	0.286	0.071
4	0.000	0.000	0.125	0.000	0.000	0.125	0.250
5	0.000	0.019	0.074	0.000	0.019	0.111	0.019
6	0.100	0.000	0.100	0.000	0.000	0.100	0.100
7	0.000	0.400	0.533	0.000	0.400	0.000	0.400
8	1.333	0.000	0.000	0.111	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 examples code
cluster 2:  data mining r
cluster 3:  network analysis social
cluster 4:  computing r parallel
cluster 5:  data mining tutorial
cluster 6:  package r examples
cluster 7:  r analysis slides
cluster 8:  research data positions
```

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, 2010], 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

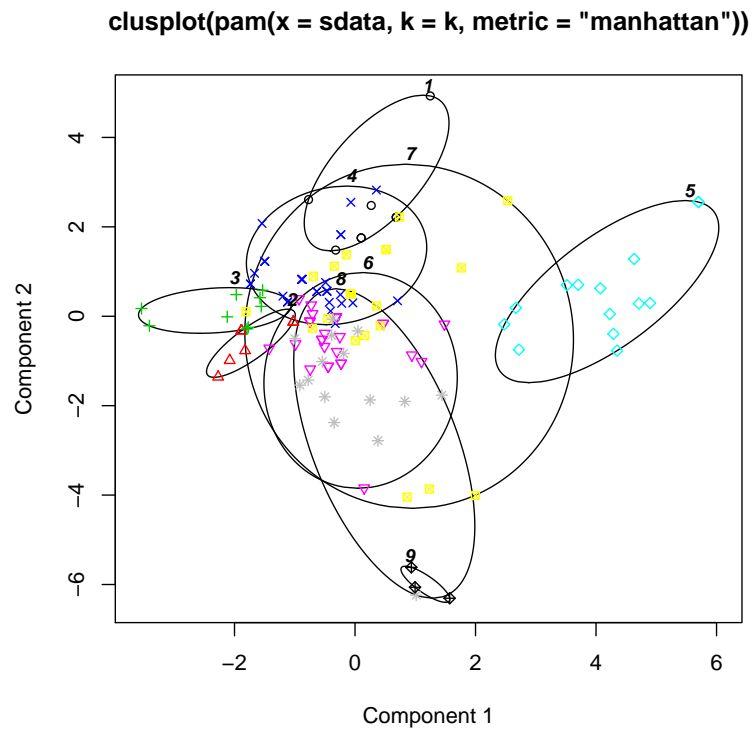
> pamResult <- pamResult$pamobject
> # print cluster medoids
> for (i in 1:k) {
+   cat(paste("cluster", i, ":  "))
+   cat(colnames(pamResult$medoids)[which(pamResult$medoids[i,]==1)], "\n")
+   # print tweets in cluster i
+   # print(rdmTweets[pamResult$clustering==i])
+ }
```

```
cluster 1 :  data positions research
cluster 2 :  computing parallel r
cluster 3 :  mining package r
cluster 4 :  data mining
cluster 5 :  analysis network social tutorial
cluster 6 :  r
cluster 7 :
cluster 8 :  examples r
cluster 9 :  analysis mining series time users
```

```

> # 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

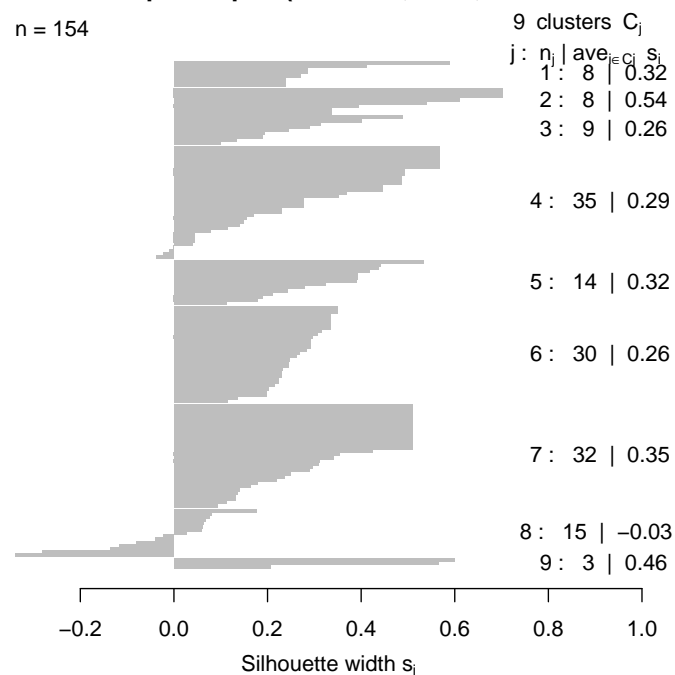
```



These two components explain 24.81 % of the point variability.

### Silhouette plot of pam(x = sdata, k = k, metric = "manhat

n = 154



Average silhouette width : 0.29

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 unstandable 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 the readers can try it with the code below.

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

## 10.9 Packages, Further Readings and Discussions

Some R packages for text mining are listed below.

- Package *tm* [Feinerer, 2012]: A framework for text mining applications within R.
- Package *tm.plugin.mail* [Feinerer, 2010]: Text Mining E-Mail Plug-In. A plug-in for the *tm* text mining framework providing mail handling functionality.
- package *textcat* [Hornik et al., 2012] provides n-Gram Based Text Categorization.
- *lda* [Chang, 2011] 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](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/>

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.



## Chapter 11

# Social Network Analysis

This chapter presents examples of social network analysis with R. We will show how to build networks with package *igraph* [Csardi and Nepusz, 2006]. The data to analyze is Twitter text data used in Chapter 10: Text Mining. We will 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 will build a two-mode network composed of both terms and tweets. We will also demonstrate some tricks to plot nice network graphs.

Some of the work in this chapter is based on the examples given at <http://www.stanford.edu/~messaging/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, infrequent terms are removed from the document-term matrix. 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.

```
> # remove infrequent terms
> #myTdm2 <- removeSparseTerms(myTdm, sparse=0.95)
> #m <- as.matrix(myTdm2)
> load("data/termDocMatrix.rdata")
> m2 <- termDocMatrix
> # change it to a Boolean matrix
> m2[m2>=1] <- 1
> # transform into a term-term adjacency matrix
> m4 <- m2 %*% t(m2)
> # build a graph from the adjacency matrix
> library(igraph)
> g <- graph.adjacency(m4, 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)
```

```

> # set seed to make the layout reproducible
> set.seed(1852)
> layout1 <- layout.fruchterman.reingold(g)
> plot(g, layout=layout1)

```

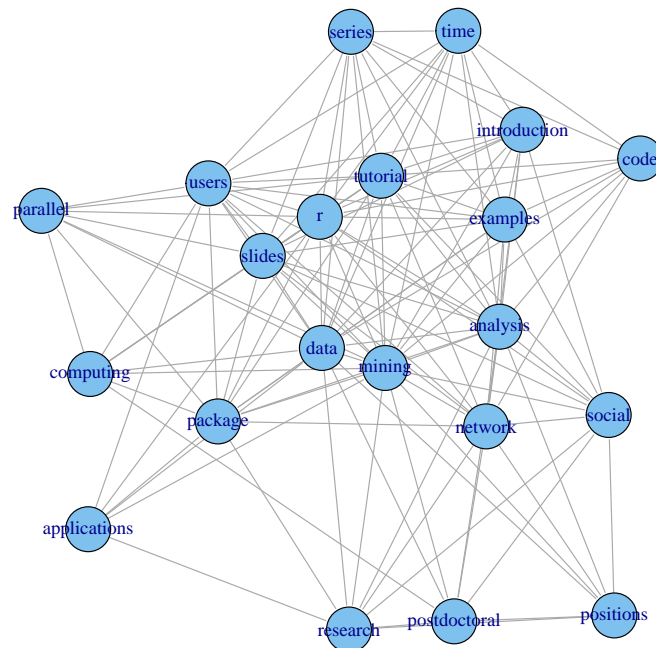


Figure 11.1: A Network of Terms - I

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)

```

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()

```

Next, we will 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 very crowded with many vertices and edges. In the code below, function `rgb(red, green, blue, alpha)` defines a color, with an `alpha` transparency. We plot the graph in the same layout as Figure 11.1.

```

> 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)+.2) / max(log(E(g)$weight)+.2)
> E(g)$color <- rgb(.5, .5, 0, egam)
> E(g)$width <- egam
> # plot the graph in layout1
> plot(g, layout=layout1)

```

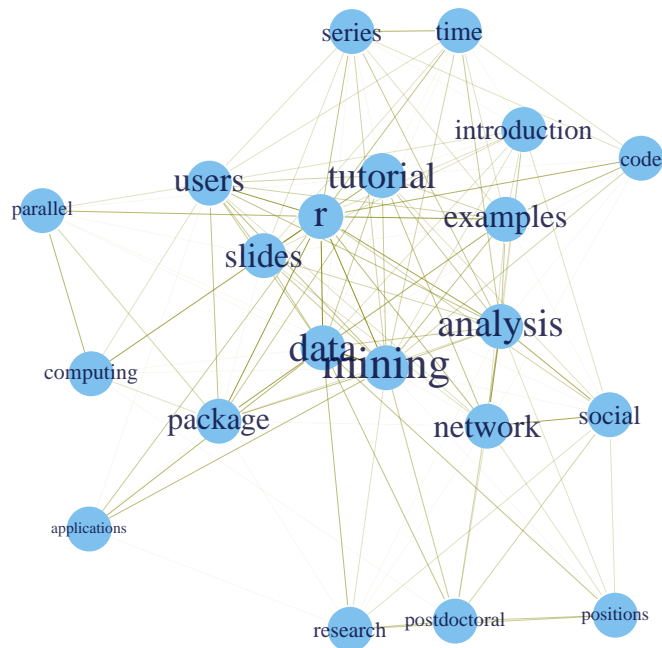


Figure 11.2: A Network of Terms - II

## 11.2 Network of Tweets

Similar to the previous section, we can also build a graph of tweets base on the number of terms they have in common. In the code below, the labels of vertices are set to the IDs and the first 10 characters of tweets.

```

> # remove "r"
> idx <- which(dimnames(myTdm)$Terms %in% c("r", "mining", "data"))
> myTdm3 <- myTdm[-idx,]
> m <- as.matrix(myTdm3)
> m[m>=1] <- 1
> m3 <- t(m) %*% m
> library(igraph)
> g <- graph.adjacency(m3, weighted=T, mode = "undirected")
> V(g)$degree <- degree(g)
> g <- simplify(g)
> # set labels to the IDs and the first 10 characters of tweets
> V(g)$label <- paste(V(g)$name, substr(df$text, 1, 10), sep=": ")
> V(g)$label.cex <- 1
> V(g)$size <- 2
> set.seed(3152)
> layout2 <- layout.fruchterman.reingold(g)
> plot(g, layout=layout2)

```

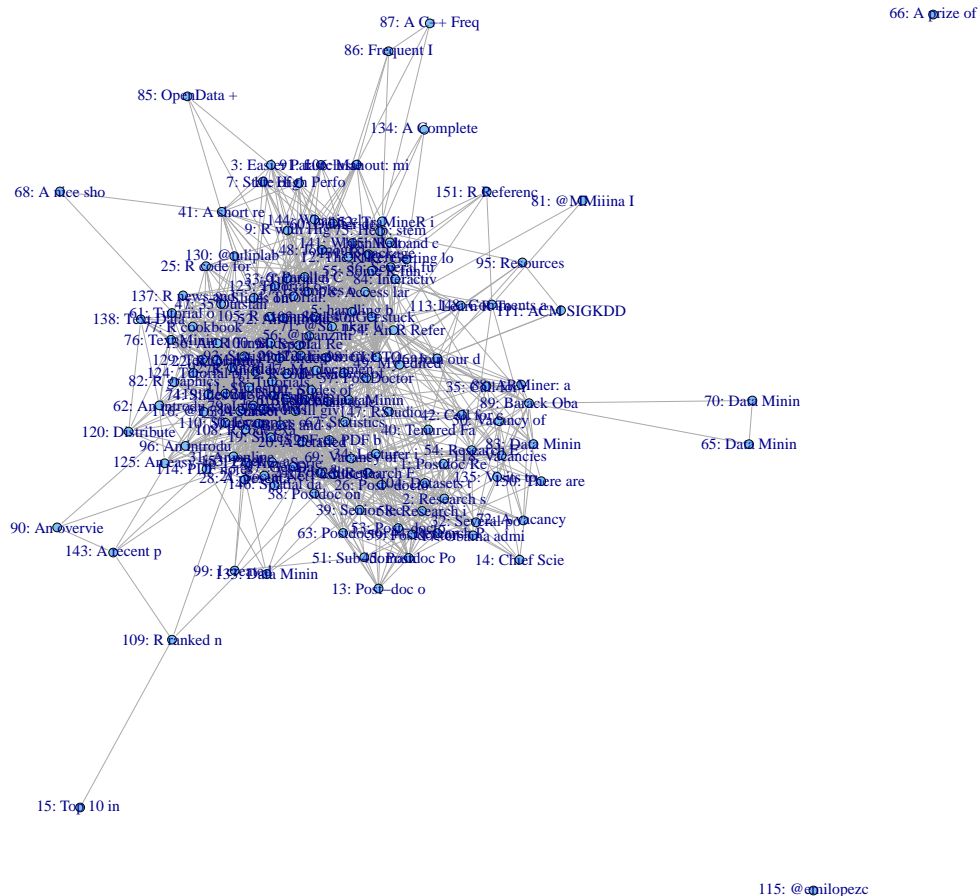


Figure 11.3: A Network of Tweets - I



```
> plot(density(V(g)$degree))
```

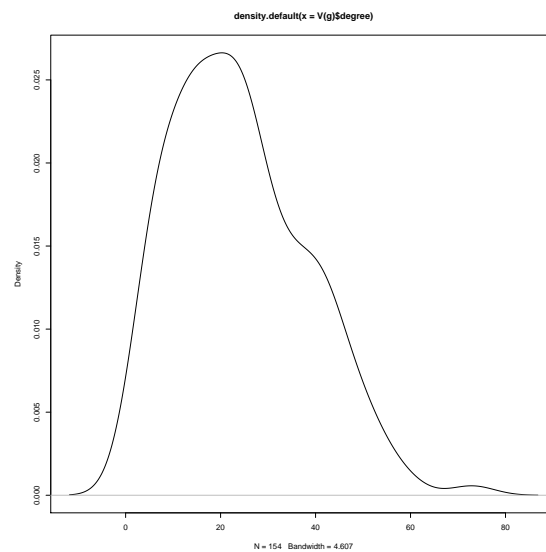


Figure 11.4: Density of Degree

```
> #V(g)$label.cex <- 0.5 * V(g)$degree / max(V(g)$degree) + .6
> alpha <- 0.4 * V(g)$degree / max(V(g)$degree) + .6
> idx1 <- V(g)$degree >= 25
> V(g)$label.color[idx1] <- rgb(0.8, 0, 0, alpha[idx1])
> idx2 <- V(g)$degree < 25 & V(g)$degree >= 10
> V(g)$label.color[idx2] <- rgb(0, 0.5, 0, alpha[idx2])
> idx3 <- V(g)$degree < 10
> V(g)$label.color[idx3] <- rgb(0, 0, 0.3, alpha[idx3])
> #V(g)$label.color <- rgb(0, 0, .2, alpha)
> V(g)$frame.color <- NA
> egam <- (log(E(g)$weight)+.2) / max(log(E(g)$weight)+.2)
> E(g)$color <- rgb(.5, .5, 0, egam)
> E(g)$width <- egam
```

```
> plot(g, layout=layout2)
```

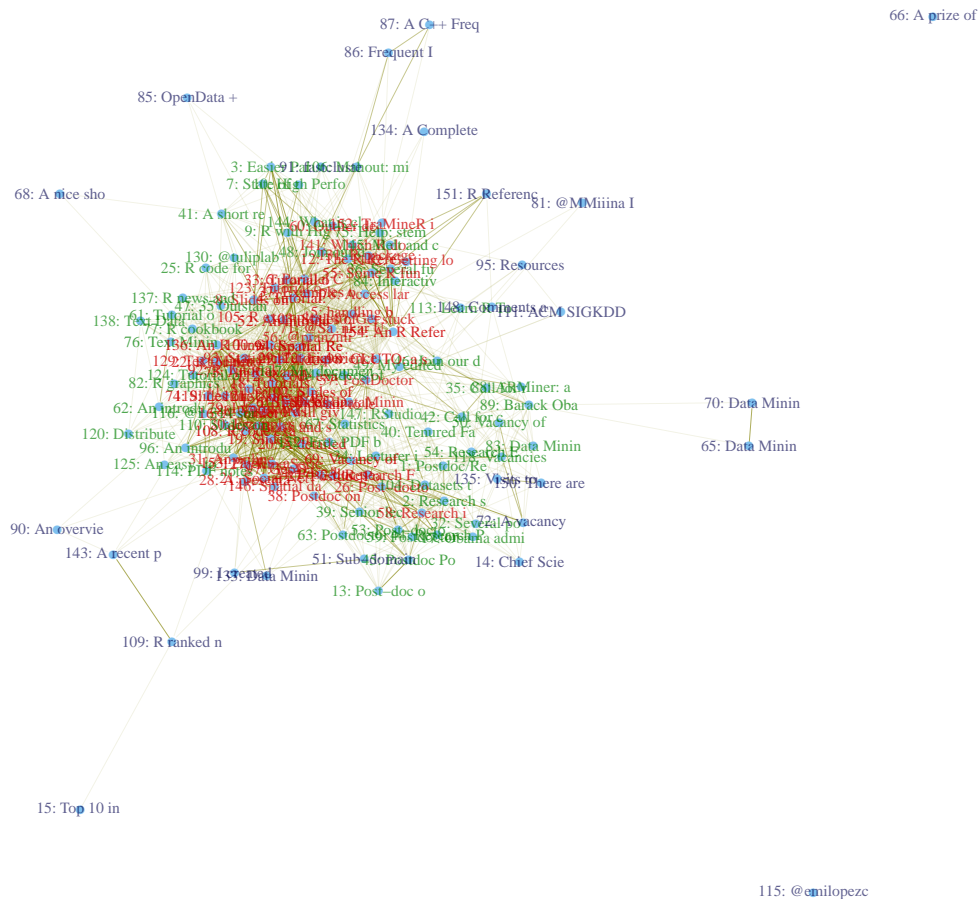


Figure 11.5: A Network of Tweets - II

Remove vertices with low degrees

```
> g2 <- delete.vertices(g, V(g)[V(g)$degree <= 15])
```



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

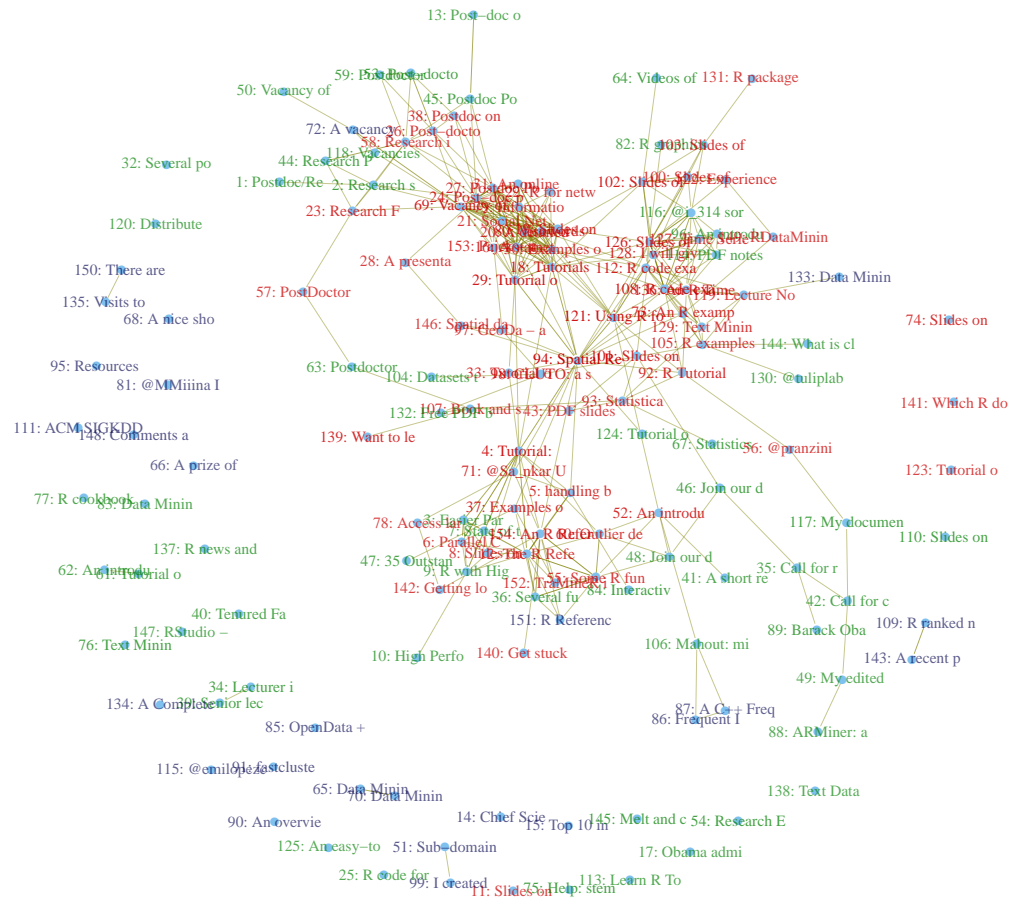


Figure 11.7: A Network of Tweets - IV

## 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 create a matrix  $M$  directly from the document-term matrix `myTdm`, and generate a graph  $g$  from it. 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`.

```
> # create a graph
> M <- as.matrix(myTdm)
> g <- graph.incidence(M, 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 different colors and sizes for vertices and edges
> V(g)$size[idx.terms] <- 6
> V(g)$color[idx.docs] <- rgb(1, 0, 0, .4)
> V(g)$size[idx.docs] <- 4
> V(g)$label <- V(g)$name
> V(g)$label.color <- rgb(0, 0, 0, .5)
> V(g)$label.cex <- .8
> V(g)$frame.color <- NA
> # set edge width and color
> E(g)$width <- .3
> E(g)$color <- rgb(.5, .5, 0, .3)
> # plot the graph
> set.seed(5365)
> layout3 <- layout.fruchterman.reingold(g)
> plot(g, layout=layout3)
```

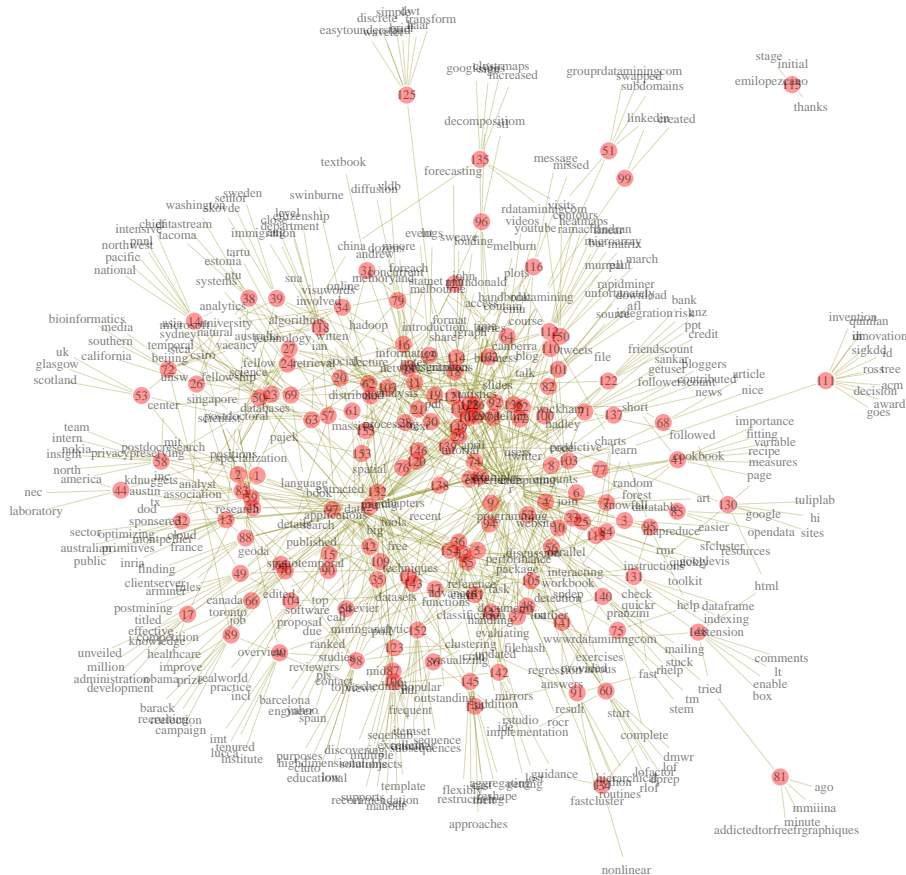


Figure 11.8: A Two-Mode Network of Terms and Tweets - I

To make the graph easy to read, we remove the terms which appears in no more than two tweets using `delete.vertices()`.

```
> # remove low-frequency terms
> set.seed(5365)
> V(g)$degree <- degree(g)
> V(g)$color[idx.terms] <- rgb(0, 1, 0, .5)
> V(g)$label.cex <- 0.8*V(g)$degree/max(V(g)$degree) + 1
> idx <- degree(g)<=2 & c(rep(T, nTerms), rep(F,nDocs))
> g.sim <- delete.vertices(g, V(g)[idx])
> plot(g.sim, layout=layout.fruchterman.reingold)
```

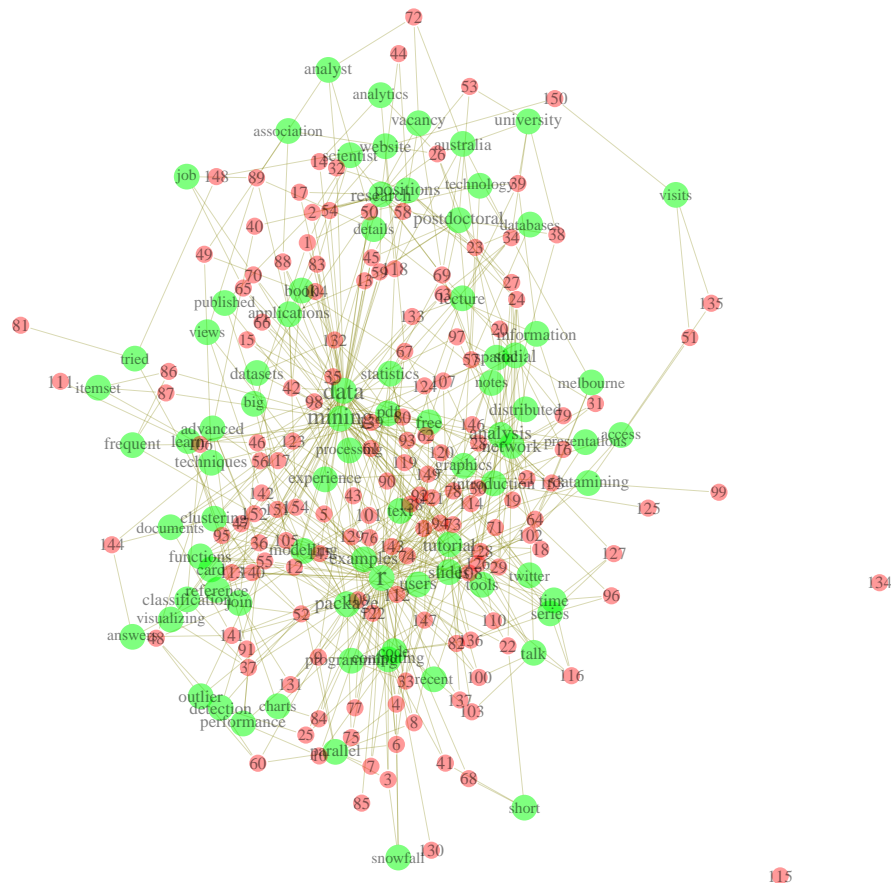


Figure 11.9: A Two-Mode Network of Terms and Tweets - II

The graph above 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")]
```

Vertex sequence:

```
[1] "3" "4" "5" "6" "7" "8" "9" "10" "12" "19" "21"
[12] "22" "25" "28" "30" "33" "35" "36" "41" "42" "55" "64"
[23] "67" "68" "73" "74" "75" "77" "78" "82" "84" "85" "91"
[34] "92" "94" "95" "100" "101" "102" "105" "108" "109" "110" "112"
[45] "113" "114" "117" "118" "119" "120" "121" "122" "126" "128" "129"
[56] "131" "136" "137" "138" "140" "141" "142" "143" "145" "146" "147"
[67] "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")])
```

Vertex sequence:

```
[1] "12" "35" "36" "42" "55" "78" "117" "119" "138" "143" "149"
[12] "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.
```

To make it short, only the first five tweets are shown in the 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.

## 11.4 Further Readings

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/~messaging/RforSNA.html>. There is a detailed introduction to Social Network Analysis with package *sna* [Butts, 2010] 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., 2003] for network analysis can be found at <http://csde.washington.edu/statnet/resources.shtml>. There is a short tutorial on package *network* [Butts et al., 2012] 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](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 version. They are reserved exclusively for a book version to be published by Elsevier Inc.



## Chapter 13

# Case Study II: Customer Response Prediction

This chapter and the other case studies are not available in this version. They are reserved exclusively for a book version to be published by Elsevier Inc.



## Chapter 14

# Case Study III: Risk Rating on Big Data with Limited Memory

This chapter and the other case studies are not available in this version. They are reserved exclusively for a book version to be published by Elsevier Inc.



## Chapter 15

# Case Study IV: Customer Behavior Prediction and Intervention

This chapter and the other case studies are not available in this version. They are reserved exclusively for a book version to be published by Elsevier Inc.





# Chapter 16

## Online Resources

This chapter presents links to online resources on data mining with R, includes books, documents, tutorials and slides.

### 16.1 R Reference Cards

- *R Reference Card*, by Tom Short  
[http://rpad.googlecode.com/svn-history/r76/Rpad\\_homepage/R-refcard.pdf](http://rpad.googlecode.com/svn-history/r76/Rpad_homepage/R-refcard.pdf)
- *R Reference Card for Data Mining*  
<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>

### 16.2 R

- *Quick-R*  
<http://www.statmethods.net/>
- *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 for Beginners*  
[http://cran.r-project.org/doc/contrib/Paradis-rdebuts\\_en.pdf](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>

### 16.3 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>
- *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/>
- Tutorial on Spatial and Spatio-Temporal Data Mining  
[http://www.inf.ufsc.br/%7Evania/tutorial\\_icdm.html](http://www.inf.ufsc.br/%7Evania/tutorial_icdm.html)
- Tutorial on Discovering Multiple Clustering Solutions  
<http://dme.rwth-aachen.de/en/DMCS>
- *A Complete Guide to Nonlinear Regression*  
<http://www.curvefit.com/>
- A paper on *Open-Source Tools for Data Mining*, published in 2008  
<http://eprints.fri.uni-lj.si/893/1/2008-OpenSourceDataMining.pdf>

### 16.4 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](http://en.wikibooks.org/wiki/Data_Mining_Algorithms_In_R)
- *Data Mining Desktop Survival Guide*  
<http://www.togaware.com/datamining/survivor/>

### 16.5 Decision Trees

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

### 16.6 Time Series Analysis

- *An R Time Series Tutorial*  
[http://www.stat.pitt.edu/stoffer/tsa2/R\\_time\\_series\\_quick\\_fix.htm](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](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>
- *Time Series Analysis for Business Forecasting*  
<http://home.ubalt.edu/ntsbarsh/stat-data/Forecast.htm>

## 16.7 Spatial Data Analysis

- *Applied Spatio-temporal Data Analysis with FOSS: R+OSGeo*  
[http://www.geostat-course.org/GeoSciences\\_AU\\_2011](http://www.geostat-course.org/GeoSciences_AU_2011)

## 16.8 Text Mining

- *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](http://www.casact.org/pubs/forum/10spforum/Francis_Flynn.pdf)
- *Distributed Text Mining in R*  
<http://epub.wu.ac.at/3034/>

## 16.9 Regression

- *A Complete Guide to Nonlinear Regression*  
<http://www.curvefit.com/>



# Bibliography

- [Adler and Murdoch, 2012] Adler, D. and Murdoch, D. (2012). *rgl: 3D visualization device system (OpenGL)*. R package version 0.92.879.
- [Agrawal et al., 1993] Agrawal, R., Faloutsos, C., and Swami, A. N. (1993). Efficient similarity search in sequence databases. In Lomet, D., editor, *Proceedings of the 4th International Conference of Foundations of Data Organization and Algorithms (FODO)*, pages 69–84, Chicago, Illinois. Springer Verlag.
- [Aldrich, 2010] Aldrich, E. (2010). wavelets: A package of funtions for computing wavelet filters, wavelet transforms and multiresolution analyses. <http://cran.r-project.org/web/packages/wavelets/index.html>.
- [Burrus et al., 1998] Burrus, C. S., Gopinath, R. A., and Guo, H. (1998). *Introduction to Wavelets and Wavelet Transforms: A Primer*. Prentice-Hall, Inc.
- [Butts, 2010] Butts, C. T. (2010). *sna: Tools for Social Network Analysis*. R package version 2.2-0.
- [Butts et al., 2012] Butts, C. T., Handcock, M. S., and Hunter, D. R. (March 1, 2012). *network: Classes for Relational Data*. Irvine, CA. R package version 1.7-1.
- [Chan et al., 2003] Chan, F. K., Fu, A. W., and Yu, C. (2003). Harr wavelets for efficient similarity search of time-series: with and without time warping. *IEEE Trans. on Knowledge and Data Engineering*, 15(3):686–705.
- [Chan and Fu, 1999] Chan, K.-p. and Fu, A. W.-c. (1999). Efficient time series matching by wavelets. In *Internation Conference on Data Engineering (ICDE '99)*, Sydney.
- [Chang, 2011] Chang, J. (2011). *lda: Collapsed Gibbs sampling methods for topic models*. R package version 1.3.1.
- [Csardi and Nepusz, 2006] Csardi, G. and Nepusz, T. (2006). The igraph software package for complex network research. *InterJournal, Complex Systems*:1695.
- [Ester et al., 1996] Ester, M., Kriegel, H.-P., Sander, J., and Xu, X. (1996). A density-based algorithm for discovering clusters in large spatial databases with noise. In *KDD*, pages 226–231.
- [Feinerer, 2010] Feinerer, I. (2010). *tm.plugin.mail: Text Mining E-Mail Plug-In*. R package version 0.0-4.
- [Feinerer, 2012] Feinerer, I. (2012). *tm: Text Mining Package*. R package version 0.5-7.1.
- [Feinerer et al., 2008] Feinerer, I., Hornik, K., and Meyer, D. (2008). Text mining infrastructure in r. *Journal of Statistical Software*, 25(5).
- [Fellows, 2012] Fellows, I. (2012). *wordcloud: Word Clouds*. R package version 2.0.

- [Frank and Asuncion, 2010] Frank, A. and Asuncion, A. (2010). UCI machine learning repository. university of california, irvine, school of information and computer sciences. <http://archive.ics.uci.edu/ml>.
- [Gentry, 2012] Gentry, J. (2012). *twitteR: R based Twitter client*. R package version 0.99.19.
- [Giorgino, 2009] Giorgino, T. (2009). Computing and visualizing dynamic timewarping alignments in R: The dtw package. *Journal of Statistical Software*, 31(7):1–24.
- [Grün and Hornik, 2011] Grün, B. and Hornik, K. (2011). topicmodels: An R package for fitting topic models. *Journal of Statistical Software*, 40(13):1–30.
- [Han and Kamber, 2000] Han, J. and Kamber, M. (2000). *Data Mining: Concepts and Techniques*. Morgan Kaufmann Publishers Inc., San Francisco, CA, USA.
- [Hand et al., 2001] Hand, D. J., Mannila, H., and Smyth, P. (2001). *Principles of Data Mining (Adaptive Computation and Machine Learning)*. The MIT Press.
- [Handcock et al., 2003] Handcock, M. S., Hunter, D. R., Butts, C. T., Goodreau, S. M., and Morris, M. (2003). *statnet: Software tools for the Statistical Modeling of Network Data*. Seattle, WA. Version 2.0.
- [Hennig, 2010] Hennig, C. (2010). *fpc: Flexible procedures for clustering*. R package version 2.0-3.
- [Hornik et al., 2012] Hornik, K., Rauch, J., Buchta, C., and Feinerer, I. (2012). *textcat: N-Gram Based Text Categorization*. R package version 0.1-1.
- [Hothorn et al., 2010] Hothorn, T., Hornik, K., Strobl, C., and Zeileis, A. (2010). Party: A laboratory for recursive partytioning. <http://cran.r-project.org/web/packages/party/>.
- [Keogh et al., 2000] Keogh, E., Chakrabarti, K., Pazzani, M., and Mehrotra, S. (2000). Dimensionality reduction for fast similarity search in large time series databases. *Knowledge and Information Systems*, 3(3):263–286.
- [Keogh and Pazzani, 1998] Keogh, E. J. and Pazzani, M. J. (1998). An enhanced representation of time series which allows fast and accurate classification, clustering and relevance feedback. In *KDD 1998*, pages 239–243.
- [Keogh and Pazzani, 2000] Keogh, E. J. and Pazzani, M. J. (2000). A simple dimensionality reduction technique for fast similarity search in large time series databases. In *PAKDD*, pages 122–133.
- [Keogh and Pazzani, 2001] Keogh, E. J. and Pazzani, M. J. (2001). Derivative dynamic time warping. In *the 1st SIAM Int. Conf. on Data Mining (SDM-2001)*, Chicago, IL, USA.
- [Liaw and Wiener, 2002] Liaw, A. and Wiener, M. (2002). Classification and regression by randomforest. *R News*, 2(3):18–22.
- [Ligges and Mächler, 2003] Ligges, U. and Mächler, M. (2003). Scatterplot3d - an r package for visualizing multivariate data. *Journal of Statistical Software*, 8(11):1–20.
- [Mörchen, 2003] Mörchen, F. (2003). Time series feature extraction for data mining using DWT and DFT. Technical report, Departement of Mathematics and Computer Science Philipps-University Marburg. DWT & DFT.
- [R Development Core Team, 2010a] R Development Core Team (2010a). *R: A Language and Environment for Statistical Computing*. R Foundation for Statistical Computing, Vienna, Austria. ISBN 3-900051-07-0.

- [R Development Core Team, 2010b] R Development Core Team (2010b). *R Data Import/Export*. R Foundation for Statistical Computing, Vienna, Austria. ISBN 3-900051-10-0.
- [R Development Core Team, 2010c] R Development Core Team (2010c). *R Language Definition*. R Foundation for Statistical Computing, Vienna, Austria. ISBN 3-900051-13-5.
- [Rafiei and Mendelzon, 1998] Rafiei, D. and Mendelzon, A. O. (1998). Efficient retrieval of similar time sequences using DFT. In Tanaka, K. and Ghandeharizadeh, S., editors, *FODO*, pages 249–257.
- [Sarkar, 2008] Sarkar, D. (2008). *Lattice: Multivariate Data Visualization with R*. Springer, New York. ISBN 978-0-387-75968-5.
- [Therneau et al., 2010] Therneau, T. M., Atkinson, B., and Ripley, B. (2010). *rpart: Recursive Partitioning*. R package version 3.1-46.
- [Venables et al., 2010] Venables, W. N., Smith, D. M., and R Development Core Team (2010). *An Introduction to R*. R Foundation for Statistical Computing, Vienna, Austria. ISBN 3-900051-12-7.
- [Vlachos et al., 2003] Vlachos, M., Lin, J., Keogh, E., and Gunopulos, D. (2003). A wavelet-based anytime algorithm for k-means clustering of time series. In *Workshop on Clustering High Dimensionality Data and Its Applications, at the 3rd SIAM International Conference on Data Mining*, San Francisco, CA, USA.
- [Wickham, 2009] Wickham, H. (2009). *ggplot2: elegant graphics for data analysis*. Springer New York.
- [Witten and Frank, 2005] Witten, I. and Frank, E. (2005). *Data mining: Practical machine learning tools and techniques*. Morgan Kaufmann, San Francisco, CA., USA, second edition.
- [Wu et al., 2008] Wu, H. C., Luk, R. W. P., Wong, K. F., and Kwok, K. L. (2008). Interpreting tf-idf term weights as making relevance decisions. *ACM Transactions on Information Systems*, 26(3):13:1–13:37.
- [Wu et al., 2000] Wu, Y.-l., Agrawal, D., and Abbadi, A. E. (2000). A comparison of DFT and DWT based similarity search in time-series databases. In *Proceedings of the 9th ACM CIKM Int'l Conference on Information and Knowledge Management*, pages 488–495, McLean, VA.
- [Zhao and Zhang, 2006] Zhao, Y. and Zhang, S. (2006). Generalized dimension-reduction framework for recent-biased time series analysis. *IEEE Transactions on Knowledge and Data Engineering*, 18(2):231–244.

# Index

- ARIMA, 58
- CLARA, 47
- clustering, 45, 78, 79
- data exploration, 11
- data mining, 1
- DBSCAN, 49
- decision tree, 27
- density-based clustering, 49
- discrete wavelet transform, 66
- document-term matrix, *see* term-document matrix
- DTW, *see* dynamic time warping
- DWT, *see* discrete wavelet transform
- dynamic time warping, 59
- forecasting, 58
- generalized linear model, 42
- generalized linear regression, 42
- hierarchical clustering, 48, 61, 64, 78
- k-means, *see* k-means clustering
- k-means clustering, 45, 80
- k-medoids, *see* k-medoids clustering
- k-medoids clustering, 46, 81
- k-NN classification, 68
- linear regression, 37
- logistic regression, 41
- non-linear regression, 43
- PAM, 47, 81
- parallel coordinates, 24
- R, 1
- random forest, 33
- regression, 37
- seasonal component, 56
- silhouette, 48, 83
- social network analysis, 85
- stemming, *see* word stemming
- tag cloud, *see* word cloud
- term-document matrix, 74
- text mining, 71
- TF-IDF, 75
- time series, 55
- time series classification, 65
- time series clustering, 59
- time series decomposition, 56
- time series forecasting, 58
- topic model, 83
- Twitter, 71, 85
- word cloud, 71, 77
- word stemming, 73