

# R for Statistical Learning

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# Introduction

Welcome to R for Statistical Learning!

## 0.1 About This Book

This book will serve as a supplement to An Introduction to Statistical Learning for STAT 430 - Basics of Statistical Learning at the University of Illinois at Urbana-Champaign.

Chapters will come in roughly three flavors:

- **Notes** that discuss mathematics in greater detail.
- **Tutorials** that illustrate the use of R for statistical learning.
- **Analyses** that show end-to-end analysis of a particular dataset.

The end of each chapter will contain:

- Annotated links to additional information and resources.
- A link to the RMarkdown file that generates the chapter.

## 0.2 Caveat Emptor

**This “book” is under active development.** Chapters will be added as we move through the course in Spring 2017. Sometimes chapters will be more in the style of course notes than a fully narrative text.

When possible, it would be best to always access the text online to be sure you are using the most up-to-date version. Also, the html version provides additional features such as changing text size, font, and colors. If you are in need of a local copy, a **pdf version** is continuously maintained.

Since this book is under active development you may encounter errors ranging from typos, to broken code, to poorly explained topics. If you do, please let us know! Simply send an email and we will make the changes as soon as possible. (`dalpiazz2 AT illinois DOT edu`) Or, if you know RMarkdown and are familiar with GitHub, make a pull request and fix an issue yourself! This process is partially automated by the edit button in the top-left corner of the html version. If your suggestion or fix becomes part of the book, you will be added to the list at the end of this chapter. We’ll also link to your GitHub account, or personal website upon request.

## 0.3 Conventions

This text uses MathJax to render mathematical notation for the web. Occasionally, but rarely, a JavaScript error will prevent MathJax from rendering correctly. In this case, you will see the “code” instead of the

expected mathematical equations. From experience, this is almost always fixed by simply refreshing the page. You'll also notice that if you right-click any equation you can obtain the MathML Code (for copying into Microsoft Word) or the TeX command used to generate the equation.

$$a^2 + b^2 = c^2$$

R code will be typeset using a `monospace` font which is syntax highlighted.

```
a = 3
b = 4
sqrt(a ^ 2 + b ^ 2)
```

R output lines, which would appear in the console will begin with `##`. They will generally not be syntax highlighted.

```
## [1] 5
```

Often the symbol  $\triangleq$  will be used to mean “is defined to be.”

We use the value  $p$  to mean the number of **predictors**.

## 0.4 Acknowledgements

Your name could be here! Suggest an edit! Correct a typo! If you submit a correction and would like to be listed below, please provide your name as you would like it to appear, as well as a link to a GitHub, LinkedIn, or personal website.

- James Balamuta, Summer 2016 - ???
- Korawat Tanwisuth, Spring 2017
- Yiming Gao, Spring 2017

## 0.5 License



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# Chapter 1

## Probability Review

We give a very brief review of some necessary probability concepts. As the treatment is less than complete, a list of references is given at the end of the chapter. For example, we ignore the usual recap of basic set theory and omit proofs and examples.

### 1.1 Probability Models

When discussing probability models, we speak of random **experiments** that produce one of a number of possible **outcomes**.

A **probability model** that describes the uncertainty of an experiment consists of two elements:

- The **sample space**, often denoted as  $\Omega$ , which is a set that contains all possible outcomes.
- A **probability function** that assigns to an event  $A$  a nonnegative number,  $P[A]$ , that represents how likely it is that event  $A$  occurs as a result of the experiment.

We call  $P[A]$  the **probability** of event  $A$ . An **event**  $A$  could be any subset of the sample space, not necessarily a single possible outcome. The probability law must follow a number of rules, which are the result of a set of axioms that we introduce now.

### 1.2 Probability Axioms

Given a sample space  $\Omega$  for a particular experiment, the **probability function** associated with the experiment must satisfy the following axioms.

1. *Nonnegativity*:  $P[A] \geq 0$  for any event  $A \subset \Omega$ .
2. *Normalization*:  $P[\Omega] = 1$ . That is, the probability of the entire space is 1.
3. *Additivity*: For mutually exclusive events  $E_1, E_2, \dots$

$$P\left[\bigcup_{i=1}^{\infty} E_i\right] = \sum_{i=1}^{\infty} P[E_i]$$

Using these axioms, many additional probability rules can easily be derived.

### 1.3 Probability Rules

Given an event  $A$ , and its complement,  $A^c$ , that is, the outcomes in  $\Omega$  which are not in  $A$ , we have the **complement rule**:

$$P[A^c] = 1 - P[A]$$

In general, for two events  $A$  and  $B$ , we have the **addition rule**:

$$P[A \cup B] = P[A] + P[B] - P[A \cap B]$$

If  $A$  and  $B$  are also *disjoint*, then we have:

$$P[A \cup B] = P[A] + P[B]$$

If we have  $n$  mutually exclusive events,  $E_1, E_2, \dots, E_n$ , then we have:

$$P[\bigcup_{i=1}^n E_i] = \sum_{i=1}^n P[E_i]$$

Often, we would like to understand the probability of an event  $A$ , given some information about the outcome of event  $B$ . In that case, we have the **conditional probability rule** provided  $P[B] > 0$ .

$$P[A | B] = \frac{P[A \cap B]}{P[B]}$$

Rearranging the conditional probability rule, we obtain the **multiplication rule**:

$$P[A \cap B] = P[B] \cdot P[A | B].$$

For a number of events  $E_1, E_2, \dots, E_n$ , the multiplication rule can be expanded into the **chain rule**:

$$P[\bigcap_{i=1}^n E_i] = P[E_1] \cdot P[E_2 | E_1] \cdot P[E_3 | E_1 \cap E_2] \cdots P\left[E_n | \bigcap_{i=1}^{n-1} E_i\right]$$

Define a **partition** of a sample space  $\Omega$  to be a set of disjoint events  $A_1, A_2, \dots, A_n$  whose union is the sample space  $\Omega$ . That is

$$A_i \cap A_j = \emptyset$$

for all  $i \neq j$ , and

$$\bigcup_{i=1}^n A_i = \Omega.$$

Now, let  $A_1, A_2, \dots, A_n$  form a partition of the sample space where  $P[A_i] > 0$  for all  $i$ . Then for any event  $B$  with  $P[B] > 0$  we have **Bayes' Rule**:

$$P[A_i | B] = \frac{P[A_i]P[B | A_i]}{P[B]} = \frac{P[A_i]P[B | A_i]}{\sum_{i=1}^n P[A_i]P[B | A_i]}$$

The denominator of the latter equality is often called the **law of total probability**:

$$P[B] = \sum_{i=1}^n P[A_i]P[B|A_i]$$

Two events  $A$  and  $B$  are said to be **independent** if they satisfy

$$P[A \cap B] = P[A] \cdot P[B]$$

This becomes the new multiplication rule for independent events.

A collection of events  $E_1, E_2, \dots, E_n$  is said to be independent if

$$P\left[\bigcup_{i \in S} E_i\right] = \prod_{i \in S} P[A_i]$$

for every subset  $S$  of  $\{1, 2, \dots, n\}$ .

If this is the case, then the chain rule is greatly simplified to:

$$P\left[\bigcap_{i=1}^n E_i\right] = \prod_{i=1}^n P[A_i]$$

## 1.4 Random Variables

A **random variable** is simply a *function* which maps outcomes in the sample space to real numbers.

### 1.4.1 Distributions

We often talk about the **distribution** of a random variable, which can be thought of as:

$$\text{distribution} = \text{list of possible values} + \text{associated probabilities}$$

This is not a strict mathematical definition, but is useful for conveying the idea.

If the possible values of a random variables are *discrete*, it is called a *discrete random variable*. If the possible values of a random variables are *continuous*, it is called a *continuous random variable*.

### 1.4.2 Discrete Random Variables

The distribution of a discrete random variable  $X$  is most often specified by a list of possible values and a probability **mass** function,  $p(x)$ . The mass function directly gives probabilities, that is,

$$p(x) = p_X(x) = P[X = x].$$

Note we almost always drop the subscript from the more correct  $p_X(x)$  and simply refer to  $p(x)$ . The relevant random variable is discerned from context

The most common example of a discrete random variable is a **binomial** random variable. The mass function of a binomial random variable  $X$ , is given by

$$p(x|n,p) = \binom{n}{x} p^x (1-p)^{n-x}, \quad x = 0, 1, \dots, n, \quad n \in \mathbb{N}, \quad 0 < p < 1.$$

This line conveys a large amount of information.

- The function  $p(x|n,p)$  is the mass function. It is a function of  $x$ , the possible values of the random variable  $X$ . It is conditional on the parameters  $n$  and  $p$ . Different values of these parameters specify different binomial distributions.
- $x = 0, 1, \dots, n$  indicates the **sample space**, that is, the possible values of the random variable.
- $n \in \mathbb{N}$  and  $0 < p < 1$  specify the **parameter spaces**. These are the possible values of the parameters that give a valid binomial distribution.

Often all of this information is simply encoded by writing

$$X \sim \text{bin}(n, p).$$

### 1.4.3 Continuous Random Variables

The distribution of a continuous random variable  $X$  is most often specified by a set of possible values and a probability **density** function,  $f(x)$ . (A cumulative density or moment generating function would also suffice.)

The probability of the event  $a < X < b$  is calculated as

$$P[a < X < b] = \int_a^b f(x) dx.$$

Note that densities are **not** probabilities.

The most common example of a continuous random variable is a **normal** random variable. The density of a normal random variable  $X$ , is given by

$$f(x|\mu, \sigma^2) = \frac{1}{\sigma\sqrt{2\pi}} \cdot \exp\left[\frac{-1}{2} \left(\frac{x-\mu}{\sigma}\right)^2\right], \quad -\infty < x < \infty, \quad -\infty < \mu < \infty, \quad \sigma > 0.$$

- The function  $f(x|\mu, \sigma^2)$  is the density function. It is a function of  $x$ , the possible values of the random variable  $X$ . It is conditional on the parameters  $\mu$  and  $\sigma^2$ . Different values of these parameters specify different normal distributions.
- $-\infty < x < \infty$  indicates the sample space. In this case, the random variable may take any value on the real line.
- $-\infty < \mu < \infty$  and  $\sigma > 0$  specify the parameter space. These are the possible values of the parameters that give a valid normal distribution.

Often all of this information is simply encoded by writing

$$X \sim N(\mu, \sigma^2)$$

### 1.4.4 Several Random Variables

Consider two random variables  $X$  and  $Y$ . We say they are independent if

$$f(x, y) = f(x) \cdot f(y)$$

for all  $x$  and  $y$ . Here  $f(x, y)$  is the **joint** density (mass) function of  $X$  and  $Y$ . We call  $f(x)$  the **marginal** density (mass) function of  $X$ . Then  $f(y)$  the marginal density (mass) function of  $Y$ . The joint density (mass) function  $f(x, y)$  together with the possible  $(x, y)$  values specify the joint distribution of  $X$  and  $Y$ .

Similar notions exist for more than two variables.

## 1.5 Expectations

For discrete random variables, we define the **expectation** of the function of a random variable  $X$  as follows.

$$\mathbb{E}[g(X)] \triangleq \sum_x g(x)p(x)$$

For continuous random variables we have a similar definition.

$$\mathbb{E}[g(X)] \triangleq \int g(x)f(x)dx$$

For specific functions  $g$ , expectations are given names.

The **mean** of a random variable  $X$  is given by

$$\mu_X = \text{mean}[X] \triangleq \mathbb{E}[X].$$

So for a discrete random variable, we would have

$$\text{mean}[X] = \sum_x x \cdot p(x)$$

For a continuous random variable we would simply replace the sum by an integral.

The **variance** of a random variable  $X$  is given by

$$\sigma_X^2 = \text{var}[X] \triangleq \mathbb{E}[(X - \mathbb{E}[X])^2] = \mathbb{E}[X^2] - (\mathbb{E}[X])^2.$$

The \*\*standard deviation of a random variable  $X$  is given by

$$\sigma_X = \text{sd}[X] \triangleq \sqrt{\sigma_X^2} = \sqrt{\text{var}[X]}.$$

The **covariance** of random variables  $X$  and  $Y$  is given by

$$\text{cov}[X, Y] \triangleq \mathbb{E}[(X - \mathbb{E}[X])(Y - \mathbb{E}[Y])] = \mathbb{E}[XY] - \mathbb{E}[X] \cdot \mathbb{E}[Y].$$

## 1.6 Likelihood

Consider  $n$  iid random variables  $X_1, X_2, \dots, X_n$ . We can then write their **likelihood** as

$$\mathcal{L}(\theta | x_1, x_2, \dots, x_n) = \prod_{i=1}^n f(x_i; \theta)$$

where  $f(x_i; \theta)$  is the density (or mass) function of random variable  $X_i$  evaluated at  $x_i$  with parameter  $\theta$ .

Whereas a probability is a function of a possible observed value given a particular parameter value, a likelihood is the opposite. It is a function of a possible parameter value given observed data.

Maximizing likelihood is a common technique for fitting a model to data.

## 1.7 References

Any of the following are either dedicated to, or contain a good coverage of the details of the topics above.

- Probability Texts
  - Introduction to Probability by Dimitri P. Bertsekas and John N. Tsitsiklis
  - A First Course in Probability by Sheldon Ross
- Machine Learning Texts with Probability Focus
  - Probability for Statistics and Machine Learning by Anirban DasGupta
  - Machine Learning: A Probabilistic Perspective by Kevin P. Murphy
- Statistics Texts with Introduction to Probability
  - Probability and Statistical Inference by Robert V. Hogg, Elliot Tanis, and Dale Zimmerman
  - Introduction to Mathematical Statistics by Robert V. Hogg, Joseph McKean, and Allen T. Craig

# Chapter 2

## Introduction to R

After reading this chapter you will be able to:

- Interact with R using RStudio.
- Use R as a calculator.
- Work with data as vectors, lists, and data frames.
- Make basic data visualizations.
- Write your own R functions.
- Perform hypothesis tests using R.
- Perform basic simulations in R.

### 2.1 Getting Started

R is both a programming language and software environment for statistical computing, which is *free* and *open-source*. To get started, you will need to install two pieces of software:

- R, the actual programming language.
  - Choose your operating system, and select the most recent version, 3.3.2.
- RStudio, an excellent IDE for working with R.
  - Note, you must have R installed to use RStudio. RStudio is simply an interface used to interact with R.

The popularity of R is on the rise, and everyday it becomes a better tool for statistical analysis. It even generated this book! (A skill you will learn in this course.) There are many good resources for learning R.

The following few chapters will serve as a whirlwind introduction to R. They are by no means meant to be a complete reference for the R language, but simply an introduction to the basics that we will need along the way. Several of the more important topics will be re-stressed as they are actually needed for analyses.

These introductory R chapters may feel like an overwhelming amount of information. You are not expected to pick up everything the first time through. You should try all of the code from these chapters, then return to them a number of times as you return to the concepts when performing analyses.

R is used both for software development and data analysis. We will operate in a grey area, somewhere between these two tasks. Our main goal will be to analyze data, but we will also perform programming exercises that help illustrate certain concepts.

RStudio has a large number of useful keyboard shortcuts. A list of these can be found using a keyboard shortcut – the keyboard shortcut to rule them all:

- On Windows: **Alt + Shift + K**
- On Mac: **Option + Shift + K**

The RStudio team has developed a number of “cheatsheets” for working with both R and RStudio. This particular cheatsheet for Base R will summarize many of the concepts in this document.

When programming, it is often a good practice to follow a style guide. (Where do spaces go? Tabs or spaces? Underscores or CamelCase when naming variables?) No style guide is “correct” but it helps to be aware of what others do. The more important thing is to be consistent within your own code.

- Hadley Wickham Style Guide from Advanced R
- Google Style Guide

For this course, our main deviation from these two guides is the use of `=` in place of `<-`. (More on that later.)

## 2.2 Basic Calculations

To get started, we’ll use R like a simple calculator.

### Addition, Subtraction, Multiplication and Division

Math	R	Result
$3 + 2$	<code>3 + 2</code>	5
$3 - 2$	<code>3 - 2</code>	1
$3 \cdot 2$	<code>3 * 2</code>	6
$3/2$	<code>3 / 2</code>	1.5

### Exponents

Math	R	Result
$3^2$	<code>3 ^ 2</code>	9
$2^{(-3)}$	<code>2 ^ (-3)</code>	0.125
$100^{1/2}$	<code>100 ^ (1 / 2)</code>	10
$\sqrt{100}$	<code>sqrt(100)</code>	10

### Mathematical Constants

Math	R	Result
$\pi$	<code>pi</code>	3.1415927
$e$	<code>exp(1)</code>	2.7182818

### Logarithms

Note that we will use `ln` and `log` interchangeably to mean the natural logarithm. There is no `ln()` in R, instead it uses `log()` to mean the natural logarithm.

Math	R	Result
$\log(e)$	<code>log(exp(1))</code>	1
$\log_{10}(1000)$	<code>log10(1000)</code>	3
$\log_2(8)$	<code>log2(8)</code>	3
$\log_4(16)$	<code>log(16, base = 4)</code>	2

## Trigonometry

Math	R	Result
$\sin(\pi/2)$	<code>sin(pi / 2)</code>	1
$\cos(0)$	<code>cos(0)</code>	1

## 2.3 Getting Help

In using R as a calculator, we have seen a number of functions: `sqrt()`, `exp()`, `log()` and `sin()`. To get documentation about a function in R, simply put a question mark in front of the function name and RStudio will display the documentation, for example:

```
?log
?sin
?paste
?lm
```

Frequently one of the most difficult things to do when learning R is asking for help. First, you need to decide to ask for help, then you need to know *how* to ask for help. Your very first line of defense should be to Google your error message or a short description of your issue. (The ability to solve problems using this method is quickly becoming an extremely valuable skill.) If that fails, and it eventually will, you should ask for help. There are a number of things you should include when emailing an instructor, or posting to a help website such as Stack Exchange.

- Describe what you expect the code to do.
- State the end goal you are trying to achieve. (Sometimes what you expect the code to do, is not what you want to actually do.)
- Provide the full text of any errors you have received.
- Provide enough code to recreate the error. Often for the purpose of this course, you could simply email your entire .R or .Rmd file.
- Sometimes it is also helpful to include a screenshot of your entire RStudio window when the error occurs.

If you follow these steps, you will get your issue resolved much quicker, and possibly learn more in the process. Do not be discouraged by running into errors and difficulties when learning R. (Or any technical skill.) It is simply part of the learning process.

## 2.4 Installing Packages

R comes with a number of built-in functions and datasets, but one of the main strengths of R as an open-source project is its package system. Packages add additional functions and data. Frequently if you want to

do something in R, and it is not available by default, there is a good chance that there is a package that will fulfill your needs.

To install a package, use the `install.packages()` function. Think of this as buying a recipe book from the store, bringing it home, and putting it on your shelf.

```
install.packages("ggplot2")
```

Once a package is installed, it must be loaded into your current R session before being used. Think of this as taking the book off of the shelf and opening it up to read.

```
library(ggplot2)
```

Once you close R, all the packages are closed and put back on the imaginary shelf. The next time you open R, you do not have to install the package again, but you do have to load any packages you intend to use by invoking `library()`.

# Chapter 3

# Data and Programming

## 3.1 Data Types

R has a number of basic data *types*.

- Numeric
  - Also known as Double. The default type when dealing with numbers.
  - Examples: 1, 1.0, 42.5
- Integer
  - Examples: 1L, 2L, 42L
- Complex
  - Example: 4 + 2i
- Logical
  - Two possible values: TRUE and FALSE
  - You can also use T and F, but this is *not* recommended.
  - NA is also considered logical.
- Character
  - Examples: "a", "Statistics", "1 plus 2."

## 3.2 Data Structures

R also has a number of basic data *structures*. A data structure is either homogeneous (all elements are of the same data type) or heterogeneous (elements can be of more than one data type).

Dimension	Homogeneous	Heterogeneous
1	Vector	List
2	Matrix	Data Frame
3+	Array	

### 3.2.1 Vectors

Many operations in R make heavy use of **vectors**. Vectors in R are indexed starting at 1. That is what the [1] in the output is indicating, that the first element of the row being displayed is the first element of the vector. Larger vectors will start additional rows with [\*] where \* is the index of the first element of the row.

Possibly the most common way to create a vector in R is using the `c()` function, which is short for “combine.” As the name suggests, it combines a list of elements separated by commas.

```
c(1, 3, 5, 7, 8, 9)
```

```
## [1] 1 3 5 7 8 9
```

Here R simply outputs this vector. If we would like to store this vector in a **variable** we can do so with the **assignment** operator `=`. In this case the variable `x` now holds the vector we just created, and we can access the vector by typing `x`.

```
x = c(1, 3, 5, 7, 8, 9)
x
```

```
## [1] 1 3 5 7 8 9
```

As an aside, there is a long history of the assignment operator in R, partially due to the keys available on the keyboards of the creators of the S language. (Which preceded R.) For simplicity we will use `=`, but know that often you will see `<-` as the assignment operator.

The pros and cons of these two are well beyond the scope of this book, but know that for our purposes you will have no issue if you simply use `=`. If you are interested in the weird cases where the difference matters, check out The R Inferno.

If you wish to use `<-`, you will still need to use `=`, however only for argument passing. Some users like to keep assignment (`<-`) and argument passing (`=`) separate. No matter what you choose, the more important thing is that you **stay consistent**. Also, if working on a larger collaborative project, you should use whatever style is already in place.

- TODO: coercion

```
c(42, "Statistics", TRUE)
```

```
## [1] "42"           "Statistics"    "TRUE"
```

```
c(42, TRUE)
```

```
## [1] 42  1
```

Frequently you may wish to create a vector based on a sequence of numbers. The quickest and easiest way to do this is with the `:` operator, which creates a sequence of integers between two specified integers.

```
(y = 1:100)
```

```
## [1] 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17
## [18] 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34
## [35] 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51
## [52] 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68
## [69] 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85
## [86] 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100
```

- TODO: style note

Here we see R labeling the rows after the first since this is a large vector. Also, we see that by putting parentheses around the assignment, R both stores the vector in a variable called `y` and automatically outputs `y` to the console.

Note that scalars do not exists in R. They are simply vectors of length 1.

```
2
```

```
## [1] 2
```

If we want to create a sequence that isn't limited to integers and increasing by 1 at a time, we can use the `seq()` function.

```
seq(from = 1.5, to = 4.2, by = 0.1)
```

```
## [1] 1.5 1.6 1.7 1.8 1.9 2.0 2.1 2.2 2.3 2.4 2.5 2.6 2.7 2.8 2.9 3.0 3.1
## [18] 3.2 3.3 3.4 3.5 3.6 3.7 3.8 3.9 4.0 4.1 4.2
```

We will discuss functions in detail later, but note here that the input labels `from`, `to`, and `by` are optional.

```
seq(1.5, 4.2, 0.1)
```

```
## [1] 1.5 1.6 1.7 1.8 1.9 2.0 2.1 2.2 2.3 2.4 2.5 2.6 2.7 2.8 2.9 3.0 3.1
## [18] 3.2 3.3 3.4 3.5 3.6 3.7 3.8 3.9 4.0 4.1 4.2
```

Another common operation to create a vector is `rep()`, which can repeat a single value a number of times.

```
rep("A", times = 10)
```

```
## [1] "A" "A" "A" "A" "A" "A" "A" "A" "A" "A"
```

The `rep()` function can be used to repeat a vector some number of times.

```
rep(x, times = 3)
```

```
## [1] 1 3 5 7 8 9 1 3 5 7 8 9 1 3 5 7 8 9
```

We have now seen four different ways to create vectors:

- `c()`
- `:`
- `seq()`
- `rep()`

So far we have mostly used them in isolation, but they are often used together.

```
c(x, rep(seq(1, 9, 2), 3), c(1, 2, 3), 42, 2:4)
```

```
## [1] 1 3 5 7 8 9 1 3 5 7 9 1 3 5 7 9 1 3 5 7 9 1 2
## [24] 3 42 2 3 4
```

The length of a vector can be obtained with the `length()` function.

```
length(x)
```

```
## [1] 6
```

```
length(y)
```

```
## [1] 100
```

### 3.2.1.1 Subsetting

To subset a vector, we use square brackets, `[]`.

```
x
```

```
## [1] 1 3 5 7 8 9
```

```
x[1]
```

```
## [1] 1
```

```
x[3]
```

```
## [1] 5
```

We see that `x[1]` returns the first element, and `x[3]` returns the third element.

```
x[-2]
```

```
## [1] 1 5 7 8 9
```

We can also exclude certain indexes, in this case the second element.

```
x[1:3]
```

```
## [1] 1 3 5
```

```
x[c(1,3,4)]
```

```
## [1] 1 5 7
```

Lastly we see that we can subset based on a vector of indices.

All of the above are subsetting a vector using a vector of indexes. (Remember a single number is still a vector.) We could instead use a vector of logical values.

```
z = c(TRUE, TRUE, FALSE, TRUE, TRUE, FALSE)
z
```

```
## [1] TRUE TRUE FALSE TRUE TRUE FALSE
```

```
x[z]
```

```
## [1] 1 3 7 8
```

### 3.2.2 Vectorization

One of the biggest strengths of R is its use of vectorized operations. (Frequently the lack of understanding of this concept leads of a belief that R is *slow*. R is not the fastest language, but it has a reputation for being slower than it really is.)

```
x = 1:10
x + 1
```

```
## [1] 2 3 4 5 6 7 8 9 10 11
```

```
2 * x
```

```
## [1] 2 4 6 8 10 12 14 16 18 20
```

```
2 ^ x
```

```
## [1] 2 4 8 16 32 64 128 256 512 1024
```

```
sqrt(x)
```

```
## [1] 1.000000 1.414214 1.732051 2.000000 2.236068 2.449490 2.645751
## [8] 2.828427 3.000000 3.162278
```

```
log(x)
```

```
## [1] 0.0000000 0.6931472 1.0986123 1.3862944 1.6094379 1.7917595 1.9459101
## [8] 2.0794415 2.1972246 2.3025851
```

We see that when a function like `log()` is called on a vector `x`, a vector is returned which has applied the function to each element of the vector `x`.

Operator	Summary	Example	Result
----------	---------	---------	--------

### 3.2.3 Logical Operators

Operator	Summary	Example	Result
<code>x &lt; y</code>	x less than y	<code>3 &lt; 42</code>	TRUE
<code>x &gt; y</code>	x greater than y	<code>3 &gt; 42</code>	FALSE
<code>x &lt;= y</code>	x less than or equal to y	<code>3 &lt;= 42</code>	TRUE
<code>x &gt;= y</code>	x greater than or equal to y	<code>3 &gt;= 42</code>	FALSE
<code>x == y</code>	x equal to y	<code>3 == 42</code>	FALSE
<code>x != y</code>	x not equal to y	<code>3 != 42</code>	TRUE
<code>!x</code>	not x	<code>!(3 &gt; 42)</code>	TRUE
<code>x   y</code>	x or y	<code>(3 &gt; 42)   TRUE</code>	TRUE
<code>x &amp; y</code>	x and y	<code>(3 &lt; 4) &amp; ( 42 &gt; 13)</code>	TRUE

- TODO: add narrative, split chunks

In R, logical operators are vectorized.

```
x = c(1, 3, 5, 7, 8, 9)

x > 3
## [1] FALSE FALSE  TRUE  TRUE  TRUE  TRUE

x < 3
## [1]  TRUE FALSE FALSE FALSE FALSE FALSE

x == 3
## [1] FALSE  TRUE FALSE FALSE FALSE FALSE

x != 3
## [1]  TRUE FALSE  TRUE  TRUE  TRUE  TRUE

x == 3 & x != 3
## [1] FALSE FALSE FALSE FALSE FALSE FALSE

x == 3 | x != 3
## [1]  TRUE  TRUE  TRUE  TRUE  TRUE  TRUE
```

This is extremely useful for subsetting.

```
x[x > 3]
```

```
## [1] 5 7 8 9
```

```
x[x != 3]
```

```
## [1] 1 5 7 8 9
```

- TODO: coercion

```
sum(x > 3)
```

```
## [1] 4
```

```
as.numeric(x > 3)
```

```
## [1] 0 0 1 1 1 1
```

```
which(x > 3)
```

```
## [1] 3 4 5 6
```

```
x[which(x > 3)]
```

```
## [1] 5 7 8 9
```

```
max(x)
```

```
## [1] 9
```

```
which(x == max(x))
```

```
## [1] 6
```

```
which.max(x)
```

```
## [1] 6
```

### 3.2.4 More Vectorization

```
x = c(1, 3, 5, 7, 8, 9)
```

```
y = 1:100
```

```
x + 2

## [1] 3 5 7 9 10 11

x + rep(2, 6)

## [1] 3 5 7 9 10 11

x > 3

## [1] FALSE FALSE TRUE TRUE TRUE TRUE

x > rep(3, 6)

## [1] FALSE FALSE TRUE TRUE TRUE TRUE

x + y

## Warning in x + y: longer object length is not a multiple of shorter object
## length

## [1] 2 5 8 11 13 15 8 11 14 17 19 21 14 17 20 23 25
## [18] 27 20 23 26 29 31 33 26 29 32 35 37 39 32 35 38 41
## [35] 43 45 38 41 44 47 49 51 44 47 50 53 55 57 50 53 56
## [52] 59 61 63 56 59 62 65 67 69 62 65 68 71 73 75 68 71
## [69] 74 77 79 81 74 77 80 83 85 87 80 83 86 89 91 93 86
## [86] 89 92 95 97 99 92 95 98 101 103 105 98 101 104 107

length(x)

## [1] 6

length(y)

## [1] 100

length(y) / length(x)

## [1] 16.66667

(x + y) - y

## Warning in x + y: longer object length is not a multiple of shorter object
## length

## [1] 1 3 5 7 8 9 1 3 5 7 8 9 1 3 5 7 8 9 1 3 5 7 8 9 1 3 5 7 8 9 1 3 5 7 8
## [36] 9 1 3 5 7 8 9 1 3 5 7 8 9 1 3 5 7 8 9 1 3 5 7 8 9 1 3 5 7 8 9 1 3 5 7
## [71] 8 9 1 3 5 7 8 9 1 3 5 7 8 9 1 3 5 7 8 9 1 3 5 7 8 9 1 3 5 7
```

```

y = 1:60
x + y

## [1]  2  5  8 11 13 15  8 11 14 17 19 21 14 17 20 23 25 27 20 23 26 29 31
## [24] 33 26 29 32 35 37 39 32 35 38 41 43 45 38 41 44 47 49 51 44 47 50 53
## [47] 55 57 50 53 56 59 61 63 56 59 62 65 67 69

length(y) / length(x)

## [1] 10

rep(x, 10) + y

## [1]  2  5  8 11 13 15  8 11 14 17 19 21 14 17 20 23 25 27 20 23 26 29 31
## [24] 33 26 29 32 35 37 39 32 35 38 41 43 45 38 41 44 47 49 51 44 47 50 53
## [47] 55 57 50 53 56 59 61 63 56 59 62 65 67 69

all(x + y == rep(x, 10) + y)

## [1] TRUE

identical(x + y, rep(x, 10) + y)

## [1] TRUE

# ?any
# ?all.equal

```

### 3.2.5 Matrices

R can also be used for **matrix** calculations. Matrices have rows and columns containing a single data type. In a matrix, the order of rows and columns is important. (This is not true of *data frames*, which we will see later.)

Matrices can be created using the **matrix** function.

```

x = 1:9
x

## [1] 1 2 3 4 5 6 7 8 9

X = matrix(x, nrow = 3, ncol = 3)
X

##      [,1] [,2] [,3]
## [1,]    1    4    7
## [2,]    2    5    8
## [3,]    3    6    9

```

Note here that we are using two different variables: lower case `x`, which stores a vector and capital `X`, which stores a matrix. (Following the usual mathematical convention.) We can do this because R is case sensitive.

By default the `matrix` function reorders a vector into columns, but we can also tell R to use rows instead.

```
Y = matrix(x, nrow = 3, ncol = 3, byrow = TRUE)
Y
```

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

We can also create a matrix of a specified dimension where every element is the same, in this case 0.

```
Z = matrix(0, 2, 4)
Z
```

```
##      [,1] [,2] [,3] [,4]
## [1,]    0    0    0    0
## [2,]    0    0    0    0
```

Like vectors, matrices can be subsetted using square brackets, `[]`. However, since matrices are two-dimensional, we need to specify both a row and a column when subsetting.

```
X
```

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

```
X[1, 2]
```

```
## [1] 4
```

Here we accessed the element in the first row and the second column. We could also subset an entire row or column.

```
X[1, ]
```

```
## [1] 1 4 7
```

```
X[, 2]
```

```
## [1] 4 5 6
```

We can also use vectors to subset more than one row or column at a time. Here we subset to the first and third column of the second row.

```
x[2, c(1, 3)]
```

```
## [1] 2 8
```

Matrices can also be created by combining vectors as columns, using `cbind`, or combining vectors as rows, using `rbind`.

- TODO: some subsetting returns vectors.

```
x = 1:9
rev(x)
```

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

```
rep(1, 9)
```

```
## [1] 1 1 1 1 1 1 1 1 1
```

```
rbind(x, rev(x), rep(1, 9))
```

```
## [,1] [,2] [,3] [,4] [,5] [,6] [,7] [,8] [,9]
## x     1     2     3     4     5     6     7     8     9
##         9     8     7     6     5     4     3     2     1
##         1     1     1     1     1     1     1     1     1
```

```
cbind(col_1 = x, col_2 = rev(x), col_3 = rep(1, 9))
```

```
##      col_1 col_2 col_3
## [1,]     1     9     1
## [2,]     2     8     1
## [3,]     3     7     1
## [4,]     4     6     1
## [5,]     5     5     1
## [6,]     6     4     1
## [7,]     7     3     1
## [8,]     8     2     1
## [9,]     9     1     1
```

- TODO: named columns

R can then be used to perform matrix calculations.

```
x = 1:9
y = 9:1
X = matrix(x, 3, 3)
Y = matrix(y, 3, 3)
X
```

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

Y

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

X + Y

```
##      [,1] [,2] [,3]
## [1,]   10   10   10
## [2,]   10   10   10
## [3,]   10   10   10
```

X - Y

```
##      [,1] [,2] [,3]
## [1,]   -8   -2    4
## [2,]   -6    0    6
## [3,]   -4    2    8
```

X \* Y

```
##      [,1] [,2] [,3]
## [1,]    9   24   21
## [2,]   16   25   16
## [3,]   21   24    9
```

X / Y

```
##      [,1]      [,2]      [,3]
## [1,] 0.1111111 0.6666667 2.333333
## [2,] 0.2500000 1.0000000 4.000000
## [3,] 0.4285714 1.5000000 9.000000
```

Note that X \* Y is not matrix multiplication. It is element by element multiplication. (Same for X / Y). Instead, matrix multiplication uses %\*%. Other matrix functions include t() which gives the transpose of a matrix and solve() which returns the inverse of a square matrix if it is invertible.

X %\*% Y

```
##      [,1] [,2] [,3]
## [1,]   90   54   18
## [2,]  114   69   24
## [3,]  138   84   30
```

```
t(X)
```

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

Z = matrix(c(9, 2, -3, 2, 4, -2, -3, -2, 16), 3, byrow = TRUE)
Z
```

```
##      [,1] [,2] [,3]
## [1,]    9    2   -3
## [2,]    2    4   -2
## [3,]   -3   -2   16
```

```
solve(Z)
```

```
##                  [,1]          [,2]          [,3]
## [1,]  0.12931034 -0.05603448  0.01724138
## [2,] -0.05603448  0.29094828  0.02586207
## [3,]  0.01724138  0.02586207  0.06896552
```

- TODO: explain

```
solve(Z) %*% Z
```

```
##                  [,1]          [,2]          [,3]
## [1,] 1.000000e+00 -6.245005e-17  0.000000e+00
## [2,] 8.326673e-17  1.000000e+00  5.551115e-17
## [3,] 2.775558e-17  0.000000e+00  1.000000e+00
```

```
diag(3)
```

```
##      [,1] [,2] [,3]
## [1,]    1    0    0
## [2,]    0    1    0
## [3,]    0    0    1
```

```
all.equal(solve(Z) %*% Z, diag(3))
```

```
## [1] TRUE
```

R has a number of matrix specific functions for obtaining dimension and summary information.

```
X = matrix(1:6, 2, 3)
X
```

```
##      [,1] [,2] [,3]
## [1,]    1    3    5
## [2,]    2    4    6
```

```
dim(X)

## [1] 2 3

rowSums(X)

## [1] 9 12

colSums(X)

## [1] 3 7 11

rowMeans(X)

## [1] 3 4

colMeans(X)

## [1] 1.5 3.5 5.5
```

The `diag()` function can be used in a number of ways. We can extract the diagonal of a matrix.

```
diag(Z)

## [1] 9 4 16
```

Or create a matrix with specified elements on the diagonal. (And 0 on the off-diagonals.)

```
diag(1:5)

##      [,1] [,2] [,3] [,4] [,5]
## [1,]    1    0    0    0    0
## [2,]    0    2    0    0    0
## [3,]    0    0    3    0    0
## [4,]    0    0    0    4    0
## [5,]    0    0    0    0    5
```

Or, lastly, create a square matrix of a certain dimension with 1 for every element of the diagonal and 0 for the off-diagonals.

```
diag(5)

##      [,1] [,2] [,3] [,4] [,5]
## [1,]    1    0    0    0    0
## [2,]    0    1    0    0    0
## [3,]    0    0    1    0    0
## [4,]    0    0    0    1    0
## [5,]    0    0    0    0    1
```

### Calculations with Vectors and Matrices

Certain operations in R, for example `%*%` have different behavior on vectors and matrices. To illustrate this, we will first create two vectors.

```
a_vec = c(1, 2, 3)
b_vec = c(2, 2, 2)
```

Note that these are indeed vectors. They are not matrices.

```
c(is.vector(a_vec), is.vector(b_vec))
```

```
## [1] TRUE TRUE
```

```
c(is.matrix(a_vec), is.matrix(b_vec))
```

```
## [1] FALSE FALSE
```

When this is the case, the `%*%` operator is used to calculate the **dot product**, also known as the **inner product** of the two vectors.

The dot product of vectors  $\mathbf{a} = [a_1, a_2, \dots, a_n]$  and  $\mathbf{b} = [b_1, b_2, \dots, b_n]$  is defined to be

$$\mathbf{a} \cdot \mathbf{b} = \sum_{i=1}^n a_i b_i = a_1 b_1 + a_2 b_2 + \dots + a_n b_n.$$

```
a_vec %*% b_vec # inner product
```

```
##      [,1]
## [1,]    12
```

```
a_vec %o% b_vec # outer product
```

```
##      [,1] [,2] [,3]
## [1,]    2    2    2
## [2,]    4    4    4
## [3,]    6    6    6
```

The `%o%` operator is used to calculate the **outer product** of the two vectors.

When vectors are coerced to become matrices, they are column vectors. So a vector of length  $n$  becomes an  $n \times 1$  matrix after coercion.

```
as.matrix(a_vec)
```

```
##      [,1]
## [1,]    1
## [2,]    2
## [3,]    3
```

If we use the `%*%` operator on matrices, `%*%` again performs the expected matrix multiplication. So you might expect the following to produce an error, because the dimensions are incorrect.

```
as.matrix(a_vec) %*% b_vec
```

```
##      [,1] [,2] [,3]
## [1,]    2    2    2
## [2,]    4    4    4
## [3,]    6    6    6
```

At face value this is a  $3 \times 1$  matrix, multiplied by a  $3 \times 1$  matrix. However, when `b_vec` is automatically coerced to be a matrix, R decided to make it a “row vector”, a  $1 \times 3$  matrix, so that the multiplication has conformable dimensions.

If we had coerced both, then R would produce an error.

```
as.matrix(a_vec) %*% as.matrix(b_vec)
```

Another way to calculate a *dot product* is with the `crossprod()` function. Given two vectors, the `crossprod()` function calculates their dot product. The function has a rather misleading name.

```
crossprod(a_vec, b_vec) # inner product
```

```
##      [,1]
## [1,]    12
```

```
tcrossprod(a_vec, b_vec) # outer product
```

```
##      [,1] [,2] [,3]
## [1,]    2    2    2
## [2,]    4    4    4
## [3,]    6    6    6
```

These functions could be very useful later. When used with matrices  $X$  and  $Y$  as arguments, it calculates

$$X^\top Y.$$

When dealing with linear models, the calculation

$$X^\top X$$

is used repeatedly.

```
C_mat = matrix(c(1, 2, 3, 4, 5, 6), 2, 3)
D_mat = matrix(c(2, 2, 2, 2, 2, 2), 2, 3)
```

This is useful both as a shortcut for a frequent calculation and as a more efficient implementation than using `t()` and `%*%`.

```
crossprod(C_mat, D_mat)
```

```
##      [,1] [,2] [,3]
## [1,]    6    6    6
## [2,]   14   14   14
## [3,]   22   22   22
```

```
t(C_mat) %*% D_mat

##      [,1] [,2] [,3]
## [1,]     6     6     6
## [2,]    14    14    14
## [3,]    22    22    22

all.equal(crossprod(C_mat, D_mat), t(C_mat) %*% D_mat)

## [1] TRUE

crossprod(C_mat, C_mat)

##      [,1] [,2] [,3]
## [1,]     5    11    17
## [2,]    11    25    39
## [3,]    17    39    61

t(C_mat) %*% C_mat

##      [,1] [,2] [,3]
## [1,]     5    11    17
## [2,]    11    25    39
## [3,]    17    39    61

all.equal(crossprod(C_mat, C_mat), t(C_mat) %*% C_mat)

## [1] TRUE
```

### 3.2.6 Lists

- TODO: explain list stuff below:

```
# creation
list(42, "Hello", TRUE)

## [[1]]
## [1] 42
##
## [[2]]
## [1] "Hello"
##
## [[3]]
## [1] TRUE

ex_list = list(
  a = c(1, 2, 3, 4),
  b = TRUE,
  c = "Hello!",
  d = function(arg = 42) {print("Hello World!")},
  e = diag(5)
)
```

```
# subsetting
ex_list$e
```

```
##      [,1] [,2] [,3] [,4] [,5]
## [1,]    1    0    0    0    0
## [2,]    0    1    0    0    0
## [3,]    0    0    1    0    0
## [4,]    0    0    0    1    0
## [5,]    0    0    0    0    1
```

```
ex_list[1:2]
```

```
## $a
## [1] 1 2 3 4
##
## $b
## [1] TRUE
```

```
ex_list[1]
```

```
## $a
## [1] 1 2 3 4
```

```
ex_list[[1]]
```

```
## [1] 1 2 3 4
```

```
ex_list[c("e", "a")]
```

```
## $e
##      [,1] [,2] [,3] [,4] [,5]
## [1,]    1    0    0    0    0
## [2,]    0    1    0    0    0
## [3,]    0    0    1    0    0
## [4,]    0    0    0    1    0
## [5,]    0    0    0    0    1
##
## $a
## [1] 1 2 3 4
```

```
ex_list["e"]
```

```
## $e
##      [,1] [,2] [,3] [,4] [,5]
## [1,]    1    0    0    0    0
## [2,]    0    1    0    0    0
## [3,]    0    0    1    0    0
## [4,]    0    0    0    1    0
## [5,]    0    0    0    0    1
```

```

ex_list[["e"]]

##      [,1] [,2] [,3] [,4] [,5]
## [1,]    1    0    0    0    0
## [2,]    0    1    0    0    0
## [3,]    0    0    1    0    0
## [4,]    0    0    0    1    0
## [5,]    0    0    0    0    1

ex_list$d

## function(arg = 42) {print("Hello World!")}

ex_list$d(arg = 1)

## [1] "Hello World!"

```

### 3.2.7 Data Frames

We have previously seen vectors and matrices for storing data as we introduced R. We will now introduce a **data frame** which will be the most common way that we store and interact with data in this course.

```

example_data = data.frame(x = c(1, 3, 5, 7, 9, 1, 3, 5, 7, 9),
                          y = c(rep("Hello", 9), "Goodbye"),
                          z = rep(c(TRUE, FALSE), 5))

```

Unlike a matrix, which can be thought of as a vector rearranged into rows and columns, a data frame is not required to have the same data type for each element. A data frame is a **list** of vectors. So, each vector must contain the same data type, but the different vectors can store different data types.

```
example_data
```

```

##      x        y     z
## 1  1 Hello  TRUE
## 2  3 Hello FALSE
## 3  5 Hello  TRUE
## 4  7 Hello FALSE
## 5  9 Hello  TRUE
## 6  1 Hello FALSE
## 7  3 Hello  TRUE
## 8  5 Hello FALSE
## 9  7 Hello  TRUE
## 10 9 Goodbye FALSE

```

- TODO: explain below

```
example_data$x
```

```
## [1] 1 3 5 7 9 1 3 5 7 9
```

```

all.equal(length(example_data$x),
          length(example_data$y),
          length(example_data$z))

## [1] TRUE

str(example_data)

## 'data.frame':   10 obs. of  3 variables:
## $ x: num  1 3 5 7 9 1 3 5 7 9
## $ y: Factor w/ 2 levels "Goodbye","Hello": 2 2 2 2 2 2 2 2 2 1
## $ z: logi  TRUE FALSE TRUE FALSE TRUE FALSE ...
nrow(example_data)

## [1] 10

ncol(example_data)

## [1] 3

dim(example_data)

## [1] 10  3

```

The `data.frame()` function above is one way to create a data frame. We can also import data from various file types in into R, as well as use data stored in packages.

The example data above can also be found here as a .csv file. To read this data into R, we would use the `read_csv()` function from the `readr` package. Note that R has a built in function `read.csv()` that operates very similarly. The `readr` function `read_csv()` has a number of advantages. For example, it is much faster reading larger data. It also uses the `tibble` package to read the data as a tibble.

```

library(readr)
example_data_from_csv = read_csv("data/example-data.csv")

```

This particular line of code assumes that the file `example_data.csv` exists in a folder called `data` in your current working directory.

```

example_data_from_csv

## # A tibble: 10 × 3
##       x     y     z
##   <int> <chr> <lgl>
## 1     1 Hello  TRUE
## 2     3 Hello FALSE
## 3     5 Hello  TRUE
## 4     7 Hello FALSE
## 5     9 Hello  TRUE

```

```
## 6      1 Hello FALSE
## 7      3 Hello TRUE
## 8      5 Hello FALSE
## 9      7 Hello TRUE
## 10     9 Goodbye FALSE
```

A tibble is simply a data frame that prints with sanity. Notice in the output above that we are given additional information such as dimension and variable type.

The `as_tibble()` function can be used to coerce a regular data frame to a tibble.

```
library(tibble)
example_data = as_tibble(example_data)
example_data
```

```
## # A tibble: 10 × 3
##       x     y     z
##   <dbl> <fctr> <lgl>
## 1     1 Hello  TRUE
## 2     3 Hello FALSE
## 3     5 Hello  TRUE
## 4     7 Hello FALSE
## 5     9 Hello  TRUE
## 6     1 Hello FALSE
## 7     3 Hello  TRUE
## 8     5 Hello FALSE
## 9     7 Hello  TRUE
## 10    9 Goodbye FALSE
```

Alternatively, we could use the “Import Dataset” feature in RStudio which can be found in the environment window. (By default, the top-right pane of RStudio.) Once completed, this process will automatically generate the code to import a file. The resulting code will be shown in the console window. In recent versions of RStudio, `read_csv()` is used by default, thus reading in a tibble.

Earlier we looked at installing packages, in particular the `ggplot2` package. (A package for visualization. While not necessary for this course, it is quickly growing in popularity.)

```
library(ggplot2)
```

Inside the `ggplot2` package is a dataset called `mpg`. By loading the package using the `library()` function, we can now access `mpg`.

When using data from inside a package, there are three things we would generally like to do:

- Look at the raw data.
- Understand the data. (Where did it come from? What are the variables? Etc.)
- Visualize the data.

To look at the data, we have two useful commands: `head()` and `str()`.

```
head(mpg, n = 10)
```

```
## # A tibble: 10 × 11
##   manufacturer     model  displ  year   cyl     trans  drv   cty   hwy
##   <chr>       <chr>   <dbl> <int> <int>    <chr> <chr> <int> <int>
## 1 audi         a4      1.8  1999     4 auto(15) f     18    29
## 2 audi         a4      1.8  1999     4 manual(m5) f     21    29
## 3 audi         a4      2.0  2008     4 manual(m6) f     20    31
## 4 audi         a4      2.0  2008     4 auto(av)  f     21    30
## 5 audi         a4      2.8  1999     6 auto(15)  f     16    26
## 6 audi         a4      2.8  1999     6 manual(m5) f     18    26
## 7 audi         a4      3.1  2008     6 auto(av)  f     18    27
## 8 audi a4 quattro 1.8  1999     4 manual(m5) 4     18    26
## 9 audi a4 quattro 1.8  1999     4 auto(15)  4     16    25
## 10 audi a4 quattro 2.0  2008    4 manual(m6) 4    20    28
## # ... with 2 more variables: fl <chr>, class <chr>
```

The function `head()` will display the first n observations of the data frame. The `head()` function was more useful before tibbles. Notice that `mpg` is a tibble already, so the output from `head()` indicates there are only 10 observations. Note that this applies to `head(mpg, n = 10)` and not `mpg` itself. Also note that tibbles print a limited number of rows and columns by default. The last line of the printed output indicates with rows and columns were omitted.

```
mpg
```

```
## # A tibble: 234 × 11
##   manufacturer     model  displ  year   cyl     trans  drv   cty   hwy
##   <chr>       <chr>   <dbl> <int> <int>    <chr> <chr> <int> <int>
## 1 audi         a4      1.8  1999     4 auto(15) f     18    29
## 2 audi         a4      1.8  1999     4 manual(m5) f     21    29
## 3 audi         a4      2.0  2008     4 manual(m6) f     20    31
## 4 audi         a4      2.0  2008     4 auto(av)  f     21    30
## 5 audi         a4      2.8  1999     6 auto(15)  f     16    26
## 6 audi         a4      2.8  1999     6 manual(m5) f     18    26
## 7 audi         a4      3.1  2008     6 auto(av)  f     18    27
## 8 audi a4 quattro 1.8  1999     4 manual(m5) 4     18    26
## 9 audi a4 quattro 1.8  1999     4 auto(15)  4     16    25
## 10 audi a4 quattro 2.0  2008    4 manual(m6) 4    20    28
## # ... with 224 more rows, and 2 more variables: fl <chr>, class <chr>
```

The function `str()` will display the “structure” of the data frame. It will display the number of **observations** and **variables**, list the variables, give the type of each variable, and show some elements of each variable. This information can also be found in the “Environment” window in RStudio.

```
str(mpg)
```

```
## Classes 'tbl_df', 'tbl' and 'data.frame': 234 obs. of 11 variables:
## $ manufacturer: chr "audi" "audi" "audi" "audi" ...
## $ model       : chr "a4" "a4" "a4" "a4" ...
## $ displ        : num 1.8 1.8 2 2 2.8 2.8 3.1 1.8 1.8 2 ...
## $ year         : int 1999 1999 2008 2008 1999 1999 2008 1999 1999 2008 ...
## $ cyl          : int 4 4 4 4 6 6 6 4 4 4 ...
## $ trans        : chr "auto(15)" "manual(m5)" "manual(m6)" "auto(av)" ...
## $ drv          : chr "f" "f" "f" "f" ...
## $ cty          : int 18 21 20 21 16 18 18 18 16 20 ...
```

```
## $ hwy      : int  29 29 31 30 26 26 27 26 25 28 ...
## $ fl       : chr  "p" "p" "p" "p" ...
## $ class    : chr  "compact" "compact" "compact" "compact" ...
```

It is important to note that while matrices have rows and columns, data frames (tibbles) instead have observations and variables. When displayed in the console or viewer, each row is an observation and each column is a variable. However generally speaking, their order does not matter, it is simply a side-effect of how the data was entered or stored.

In this dataset an observation is for a particular model-year of a car, and the variables describe attributes of the car, for example its highway fuel efficiency.

To understand more about the data set, we use the `?` operator to pull up the documentation for the data.

```
?mpg
```

R has a number of functions for quickly working with and extracting basic information from data frames. To quickly obtain a vector of the variable names, we use the `names()` function.

```
names(mpg)
```

```
## [1] "manufacturer" "model"          "displ"        "year"
## [5] "cyl"           "trans"          "drv"          "cty"
## [9] "hwy"           "fl"             "class"
```

To access one of the variables **as a vector**, we use the `$` operator.

```
mpg$year
```

```
## [1] 1999 1999 2008 2008 1999 1999 2008 1999 1999 2008 2008 1999 1999 2008
## [15] 2008 1999 2008 2008 2008 2008 1999 2008 1999 1999 2008 2008 2008 2008
## [29] 2008 2008 1999 1999 1999 2008 1999 2008 2008 1999 1999 1999 1999 2008
## [43] 2008 2008 1999 1999 2008 2008 2008 1999 1999 2008 2008 2008 2008 1999
## [57] 1999 1999 2008 2008 2008 1999 2008 1999 2008 2008 2008 2008 2008 2008
## [71] 1999 1999 2008 1999 1999 1999 2008 1999 1999 1999 2008 2008 2008 1999 1999
## [85] 1999 1999 1999 2008 1999 2008 1999 1999 2008 2008 1999 1999 2008 2008 2008
## [99] 2008 1999 1999 1999 1999 1999 2008 2008 2008 2008 1999 1999 2008 2008 2008
## [113] 1999 1999 2008 1999 1999 2008 2008 2008 2008 2008 2008 2008 1999 1999
## [127] 2008 2008 2008 1999 2008 2008 1999 1999 1999 2008 1999 2008 1999 2008 2008
## [141] 1999 1999 1999 2008 2008 2008 1999 1999 2008 1999 1999 2008 1999 2008 2008
## [155] 1999 1999 1999 2008 2008 1999 1999 2008 2008 2008 1999 1999 1999 1999
## [169] 1999 2008 2008 2008 1999 1999 1999 1999 2008 2008 2008 1999 1999 2008
## [183] 2008 1999 1999 2008 1999 1999 2008 2008 1999 1999 2008 1999 1999 1999 1999
## [197] 2008 2008 1999 2008 1999 1999 2008 1999 1999 2008 2008 1999 1999 1999 2008
## [211] 2008 1999 1999 1999 1999 2008 2008 2008 2008 1999 1999 1999 1999 1999 1999
## [225] 1999 2008 2008 1999 1999 2008 2008 1999 1999 2008
```

```
mpg$hwy
```

```
## [1] 29 29 31 30 26 26 27 26 25 28 27 25 25 25 25 24 25 23 20 15 20 17 17
## [24] 26 23 26 25 24 19 14 15 17 27 30 26 29 26 24 24 22 22 24 24 17 22 21
## [47] 23 23 19 18 17 17 19 19 12 17 15 17 17 12 17 16 18 15 16 12 17 17 16
```

```
## [70] 12 15 16 17 15 17 17 18 17 19 17 19 19 17 17 16 16 17 15 17 26 25
## [93] 26 24 21 22 23 22 20 33 32 32 29 32 34 36 36 29 26 27 30 31 26 26 28
## [116] 26 29 28 27 24 24 24 22 19 20 17 12 19 18 14 15 18 18 15 17 16 18 17
## [139] 19 19 17 29 27 31 32 27 26 26 25 25 17 17 20 18 26 26 27 28 25 25 24
## [162] 27 25 26 23 26 26 26 25 27 25 27 20 20 19 17 20 17 29 27 31 31 26
## [185] 26 28 27 29 31 31 26 26 27 30 33 35 37 35 15 18 20 20 22 17 19 18 20
## [208] 29 26 29 29 24 44 29 26 29 29 29 23 24 44 41 29 26 28 29 29 29 29 28
## [231] 29 26 26 26
```

We can use the `dim()`, `nrow()` and `ncol()` functions to obtain information about the dimension of the data frame.

```
dim(mpg)
```

```
## [1] 234 11
```

```
nrow(mpg)
```

```
## [1] 234
```

```
ncol(mpg)
```

```
## [1] 11
```

Here `nrow()` is also the number of observations, which in most cases is the *sample size*.

Subsetting data frames can work much like subsetting matrices using square brackets, `[,]`. Here, we find fuel efficient vehicles earning over 35 miles per gallon and only display `manufacturer`, `model` and `year`.

```
mpg[mpg$hwy > 35, c("manufacturer", "model", "year")]
```

```
## # A tibble: 6 × 3
##   manufacturer     model   year
##   <chr>        <chr> <int>
## 1 honda         civic  2008
## 2 honda         civic  2008
## 3 toyota        corolla 2008
## 4 volkswagen    jetta  1999
## 5 volkswagen    new beetle 1999
## 6 volkswagen    new beetle 1999
```

An alternative would be to use the `subset()` function, which has a much more readable syntax.

```
subset(mpg, subset = hwy > 35, select = c("manufacturer", "model", "year"))
```

Lastly, we could use the `filter` and `select` functions from the `dplyr` package which introduces the `%>%` operator from the `magrittr` package. This is not necessary for this course, however the `dplyr` package is something you should be aware of as it is becoming a popular tool in the R world.

```
library(dplyr)
mpg %>% filter(hwy > 35) %>% select(manufacturer, model, year)
```

All three approaches produce the same results. Which you use will be largely based on a given situation as well as user preference.

- TODO: general data.frame subsetting
- TODO: difference between data.frame (more like matrix) and tibble (more like list) subsetting

## 3.3 Programming Basics

### 3.3.1 Control Flow

In R, the if/else syntax is:

```
if (...) {
  some R code
} else {
  more R code
}
```

For example,

```
x = 1
y = 3
if (x > y) {
  z = x * y
  print("x is larger than y")
} else {
  z = x + 5 * y
  print("x is less than or equal to y")
}
```

```
## [1] "x is less than or equal to y"
```

```
z
```

```
## [1] 16
```

R also has a special function `ifelse()` which is very useful. It returns one of two specified values based on a conditional statement.

```
ifelse(4 > 3, 1, 0)
```

```
## [1] 1
```

The real power of `ifelse()` comes from its ability to be applied to vectors.

```

fib = c(1, 1, 2, 3, 5, 8, 13, 21)
ifelse(fib > 6, "Foo", "Bar")

## [1] "Bar" "Bar" "Bar" "Bar" "Bar" "Bar" "Foo" "Foo" "Foo"

```

Now a `for` loop example,

```

x = 11:15
for (i in 1:5) {
  x[i] = x[i] * 2
}

x

```

```
## [1] 22 24 26 28 30
```

Note that this `for` loop is very normal in many programming languages, but not in R. In R we would not use a loop, instead we would simply use a vectorized operation.

```

x = 11:15
x = x * 2
x

```

```
## [1] 22 24 26 28 30
```

### 3.3.2 Functions

So far we have been using functions, but haven't actually discussed some of their details.

```
function_name(arg1 = 10, arg2 = 20)
```

To use a function, you simply type its name, followed by an open parenthesis, then specify values of its arguments, then finish with a closing parenthesis.

An **argument** is a variable which is used in the body of the function. Specifying the values of the arguments is essentially providing the inputs to the function.

We can also write our own functions in R. For example, we often like to “standardize” variables, that is, subtracting the sample mean, and dividing by the sample standard deviation.

$$\frac{x - \bar{x}}{s}$$

In R we would write a function to do this. When writing a function, there are three thing you must do.

- Give the function a name. Preferably something that is short, but descriptive.
- Specify the arguments using `function()`
- Write the body of the function within curly braces, `{}`.

```
standardize = function(x) {
  m = mean(x)
  std = sd(x)
  result = (x - m) / std
  result
}
```

Here the name of the function is `standardize`, and the function has a single argument `x` which is used in the body of function. Note that the output of the final line of the body is what is returned by the function. In this case the function returns the vector stored in the variable `results`.

To test our function, we will take a random sample of size `n = 10` from a normal distribution with a mean of 2 and a standard deviation of 5.

```
(test_sample = rnorm(n = 10, mean = 2, sd = 5))

## [1] 2.6879133 7.0237063 3.9232644 0.4843381 2.2942529 1.2596067
## [7] -0.6475368 0.6246163 6.7156359 3.9787585

standardize(x = test_sample)

## [1] -0.05655214 1.61667394 0.42018228 -0.90693391 -0.20846964
## [6] -0.60774998 -1.34373583 -0.85279914 1.49778644 0.44159798
```

This function could be written much more succinctly, simply performing all the operations on one line and immediately returning the result, without storing any of the intermediate results.

```
standardize = function(x) {
  (x - mean(x)) / sd(x)
}
```

When specifying arguments, you can provide default arguments.

```
power_of_num = function(num, power = 2) {
  num ^ power
}
```

Let's look at a number of ways that we could run this function to perform the operation  $10^2$  resulting in 100.

```
power_of_num(10)
```

```
## [1] 100
```

```
power_of_num(10, 2)
```

```
## [1] 100
```

```
power_of_num(num = 10, power = 2)
```

```
## [1] 100
```

```
power_of_num(power = 2, num = 10)
```

```
## [1] 100
```

Note that without using the argument names, the order matters. The following code will not evaluate to the same output as the previous example.

```
power_of_num(2, 10)
```

```
## [1] 1024
```

Also, the following line of code would produce an error since arguments without a default value must be specified.

```
power_of_num(power = 5)
```

To further illustrate a function with a default argument, we will write a function that calculates sample variance two ways.

By default, it will calculate the unbiased estimate of  $\sigma^2$ , which we will call  $s^2$ .

$$s^2 = \frac{1}{n-1} \sum_{i=1}^n (x - \bar{x})^2$$

It will also have the ability to return the biased estimate (based on maximum likelihood) which we will call  $\hat{\sigma}^2$ .

$$\hat{\sigma}^2 = \frac{1}{n} \sum_{i=1}^n (x - \bar{x})^2$$

```
get_var = function(x, biased = FALSE) {
  n = length(x) - 1 * !biased
  (1 / n) * sum((x - mean(x)) ^ 2)
}
```

```
get_var(test_sample)
```

```
## [1] 6.714719
```

```
get_var(test_sample, biased = FALSE)
```

```
## [1] 6.714719
```

```
var(test_sample)
```

```
## [1] 6.714719
```

We see the function is working as expected, and when returning the unbiased estimate it matches R's built-in function `var()`. Finally, let's examine the biased estimate of  $\sigma^2$ .

```
get_var(test_sample, biased = TRUE)
```

```
## [1] 6.043247
```



# Chapter 4

## Summarizing Data

### 4.1 Summary Statistics

R has built in functions for a large number of summary statistics.

```
(y = 1:100)
```

```
## [1]  1  2  3  4  5  6  7  8  9 10 11 12 13 14 15 16 17
## [18] 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34
## [35] 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51
## [52] 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68
## [69] 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85
## [86] 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100
```

TODO: change to mpg\$cty, discuss what the results mean

#### Central Tendency

Measure	R	Result
Mean	<code>mean(y)</code>	50.5
Median	<code>median(y)</code>	50.5

#### Spread

Measure	R	Result
Variance	<code>var(y)</code>	841.6666667
Standard Deviation	<code>sd(y)</code>	29.011492
IQR	<code>IQR(y)</code>	49.5
Minimum	<code>min(y)</code>	1
Maximum	<code>max(y)</code>	100
Range	<code>range(y)</code>	1, 100

- TODO: categorical summary

```
table(mpg$drv)
```

```
##  
##   4     f     r  
## 103 106  25
```

```
table(mpg$drv) / nrow(mpg)
```

```
##  
##           4           f           r  
## 0.4401709 0.4529915 0.1068376
```

TODO: discuss relationships found in the data, look at the data.

## 4.2 Plotting

Now that we have some data to work with, and we have learned about the data at the most basic level, our next task is to visualize the data. Often, a proper visualization can illuminate features of the data that can inform further analysis.

We will look at four methods of visualizing data that we will use throughout the course:

- Histograms
- Barplots
- Boxplots
- Scatterplots

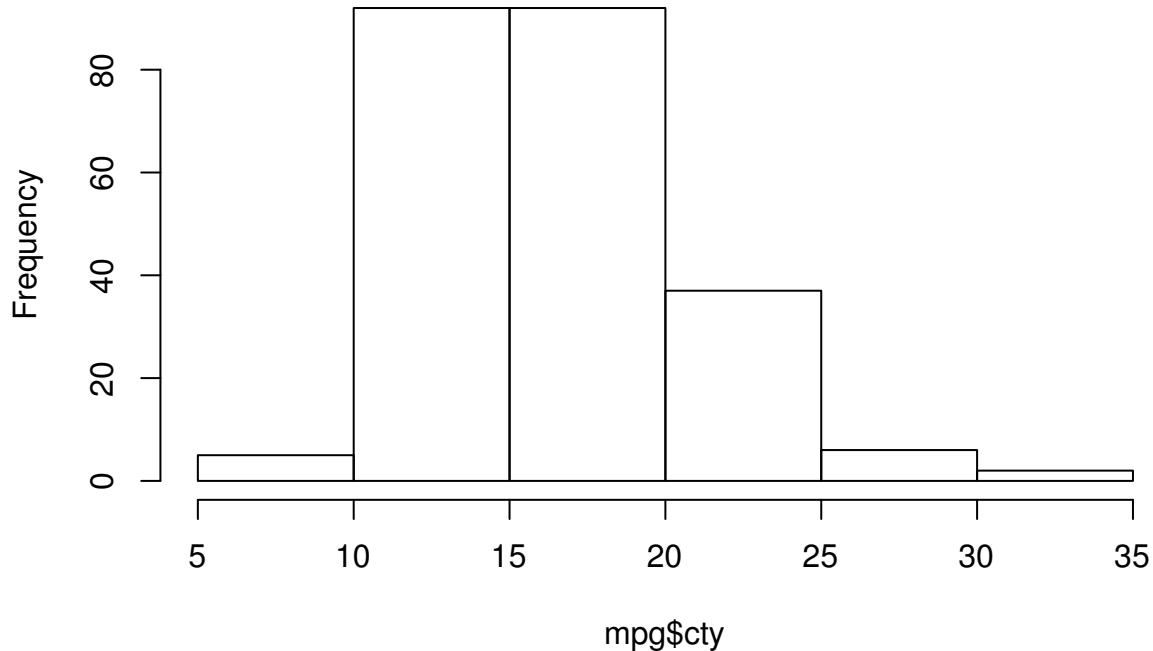
TODO: discuss relationships found in the data

### 4.2.1 Histograms

When visualizing a single numerical variable, a **histogram** will be our go-to tool, which can be created in R using the `hist()` function.

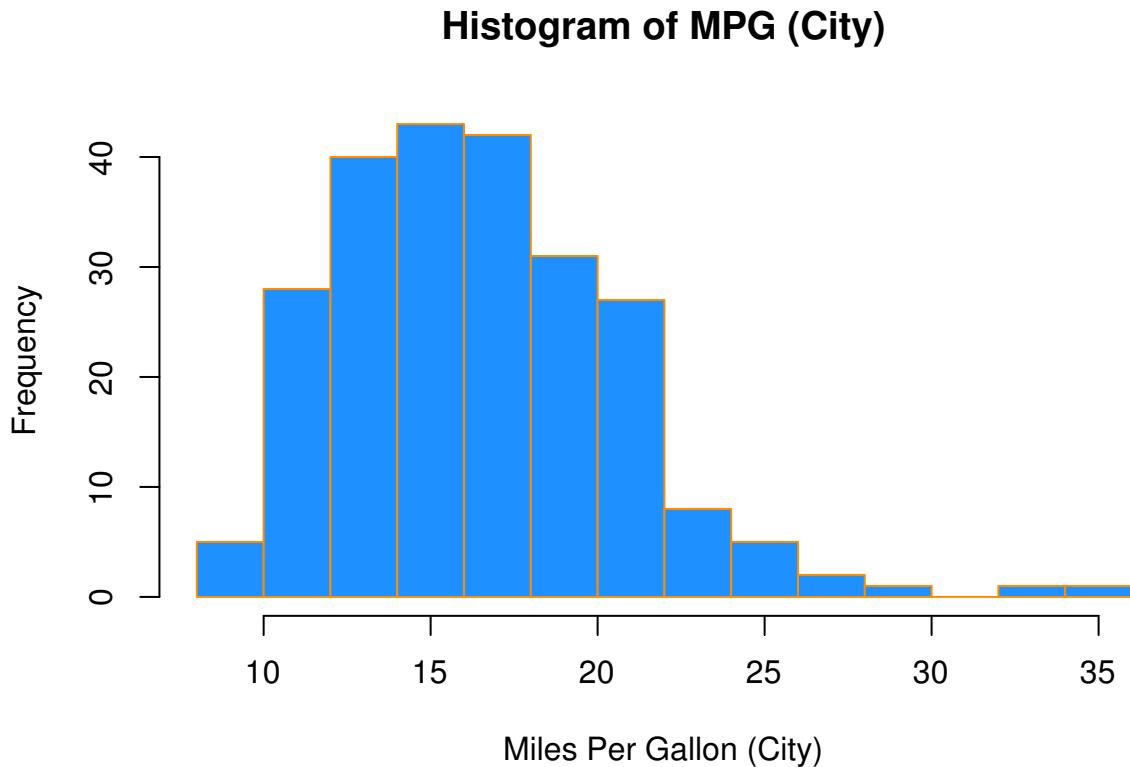
```
hist(mpg$cty)
```

### Histogram of mpg\$cty



The histogram function has a number of parameters which can be changed to make our plot look much nicer. Use the `? operator to read the documentation for the hist() to see a full list of these parameters.`

```
hist(mpg$cty,
      xlab = "Miles Per Gallon (City)",
      main = "Histogram of MPG (City)",
      breaks = 12,
      col = "dodgerblue",
      border = "darkorange")
```

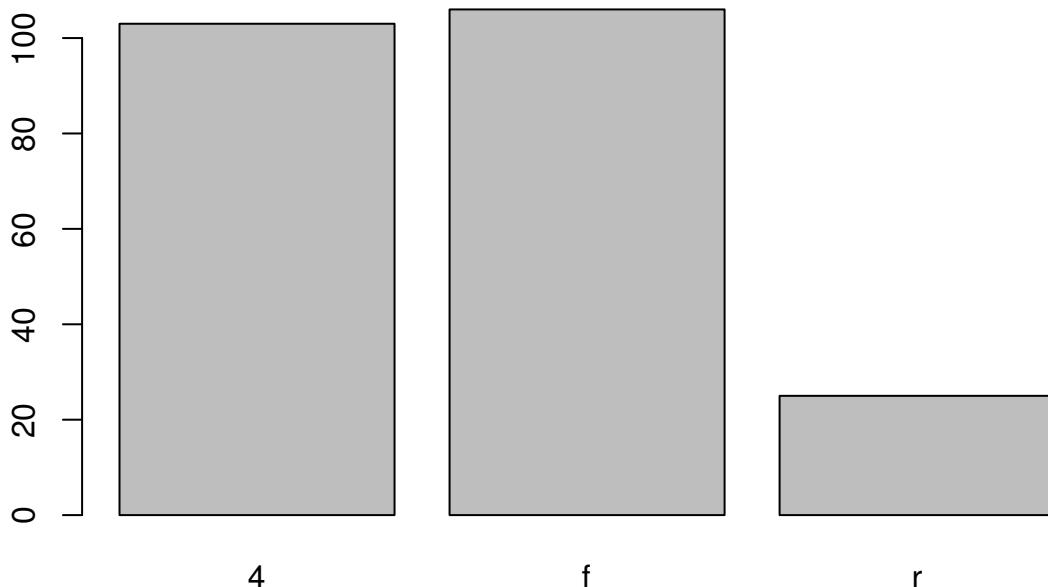


Importantly, you should always be sure to label your axes and give the plot a title. The argument `breaks` is specific to `hist()`. Entering an integer will give a suggestion to R for how many bars to use for the histogram. By default R will attempt to intelligently guess a good number of `breaks`, but as we can see here, it is sometimes useful to modify this yourself.

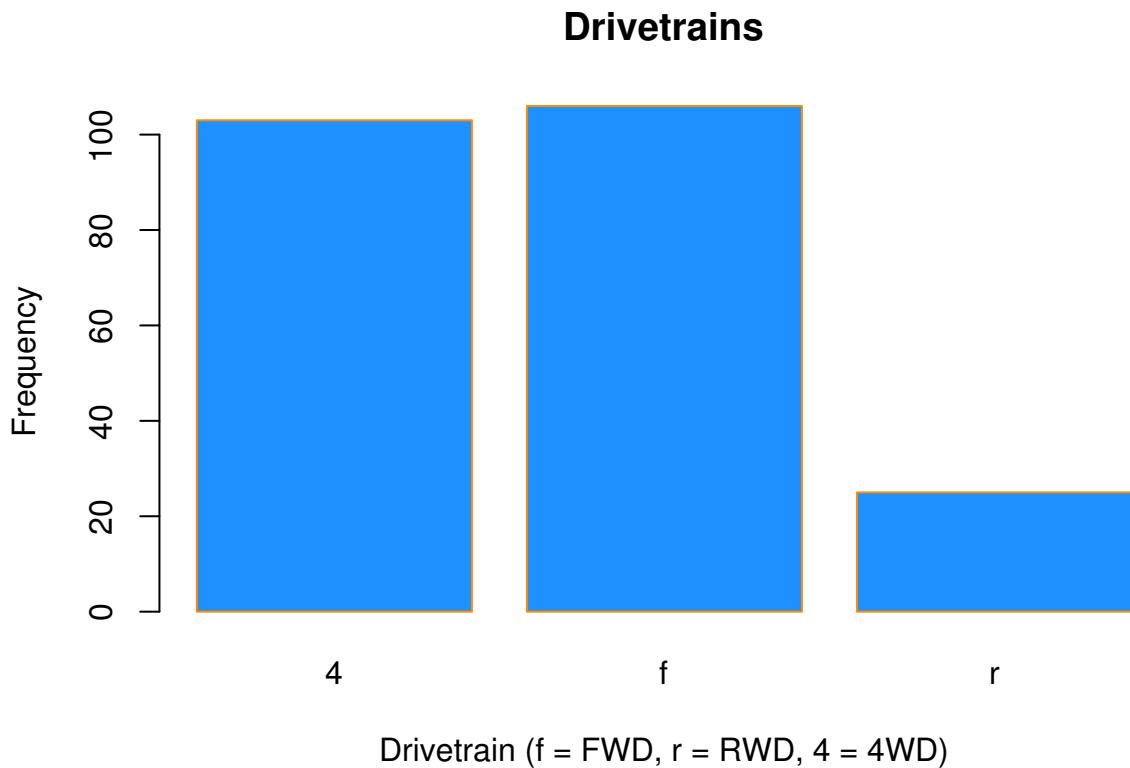
#### 4.2.2 Barplots

TODO: narrative

```
barplot(table(mpg$drv))
```



```
barplot(table(mpg$drv),
       xlab = "Drivetrain (f = FWD, r = RWD, 4 = 4WD)",
       ylab = "Frequency",
       main = "Drivetrains",
       col = "dodgerblue",
       border = "darkorange")
```



### 4.2.3 Boxplots

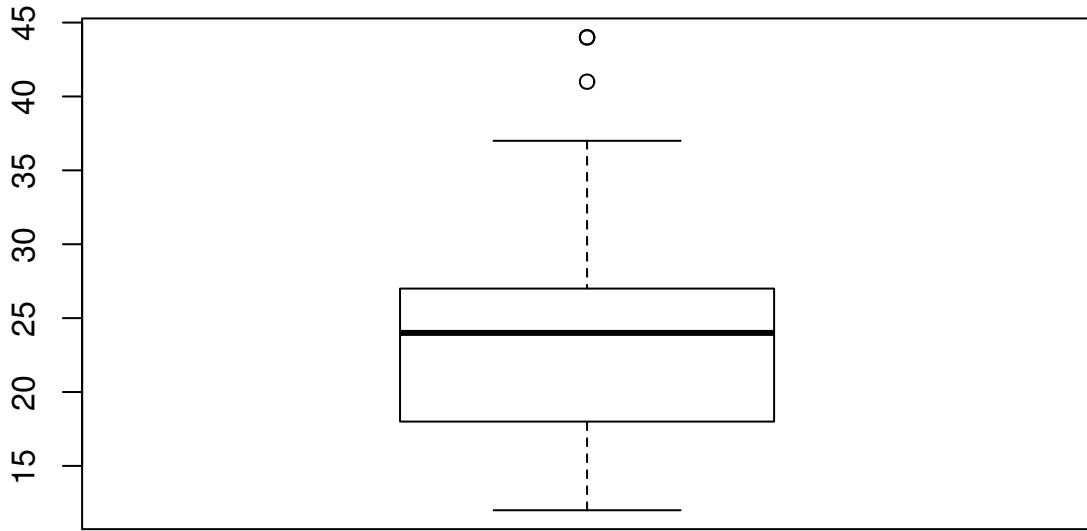
To visualize the relationship between a numerical and categorical variable, we will use a **boxplot**. In the `mpg` dataset, the `drv` variable takes a small, finite number of values. A car can only be front wheel drive, 4 wheel drive, or rear wheel drive.

```
unique(mpg$drv)
```

```
## [1] "f" "4" "r"
```

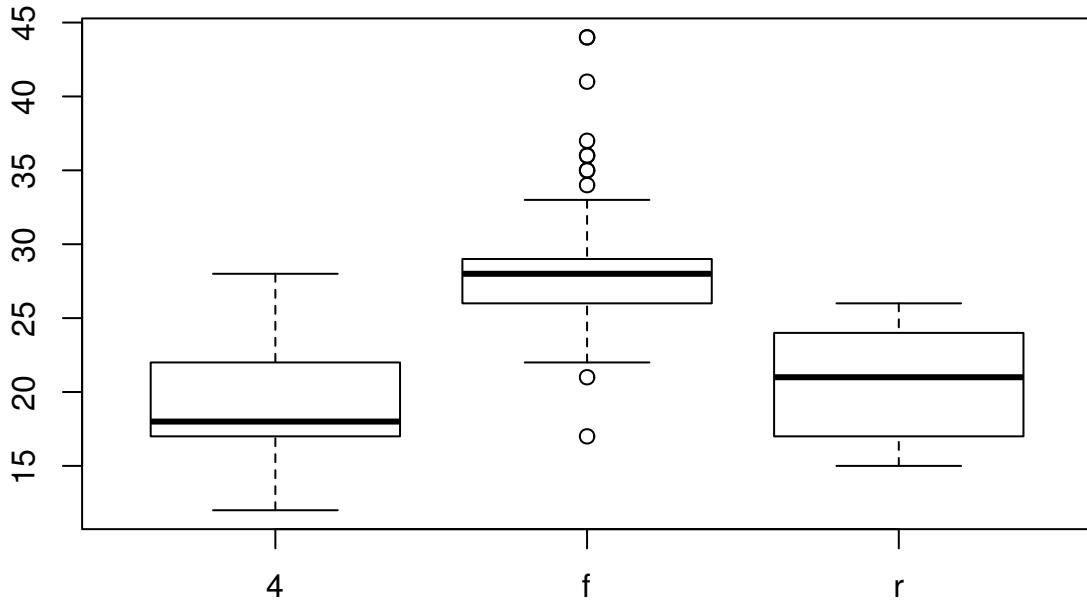
First note that we can use a single boxplot as an alternative to a histogram for visualizing a single numerical variable. To do so in R, we use the `boxplot()` function.

```
boxplot(mpg$hwy)
```



However, more often we will use boxplots to compare a numerical variable for different values of a categorical variable.

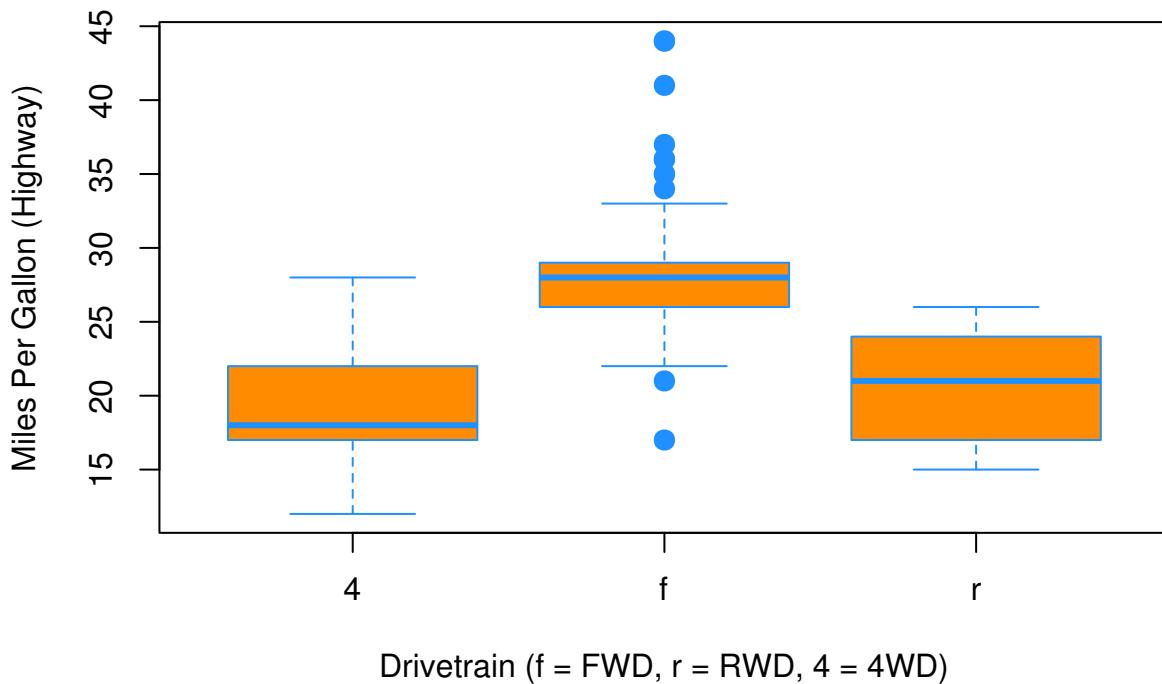
```
boxplot(hwy ~ drv, data = mpg)
```



Here used the `boxplot()` command to create side-by-side boxplots. However, since we are now dealing with two variables, the syntax has changed. The R syntax `hwy ~ drv, data = mpg` reads “Plot the `hwy` variable against the `drv` variable using the dataset `mpg`.” We see the use of a `~` (which specifies a formula) and also a `data =` argument. This will be a syntax that is common to many functions we will use in this course.

```
boxplot(hwy ~ drv, data = mpg,
        xlab = "Drivetrain (f = FWD, r = RWD, 4 = 4WD)",
        ylab = "Miles Per Gallon (Highway)",
        main = "MPG (Highway) vs Drivetrain",
        pch = 20,
        cex = 2,
        col = "darkorange",
        border = "dodgerblue")
```

## MPG (Highway) vs Drivetrain

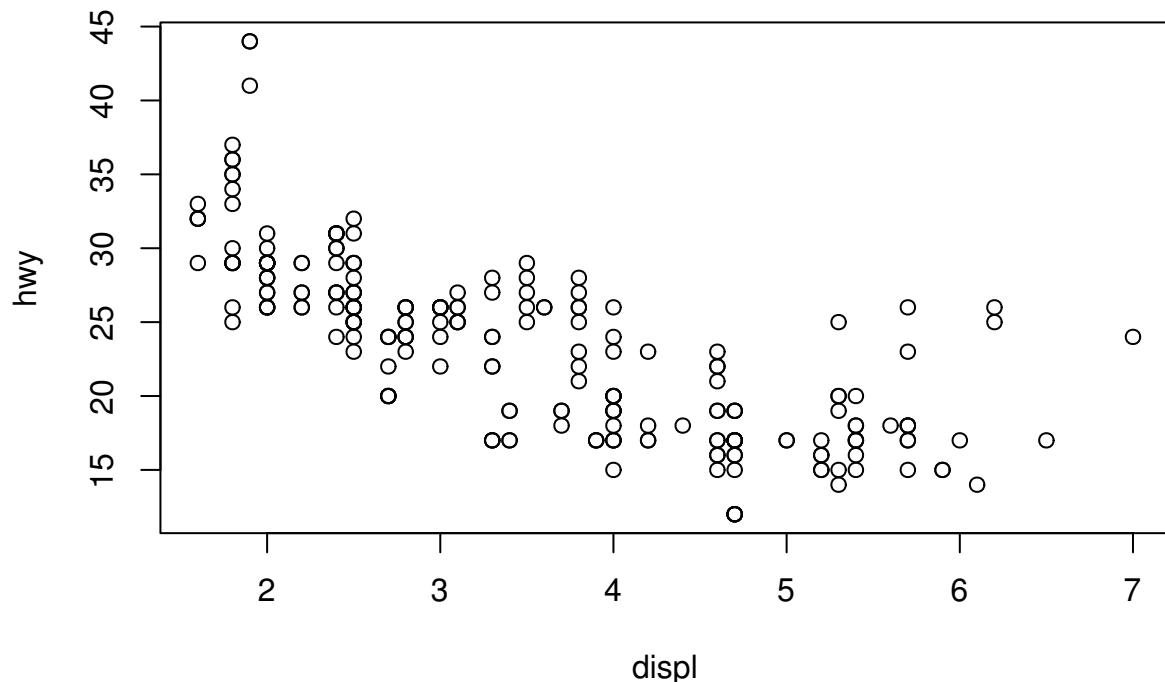


Again, `boxplot()` has a number of additional arguments which have the ability to make our plot more visually appealing.

### 4.2.4 Scatterplots

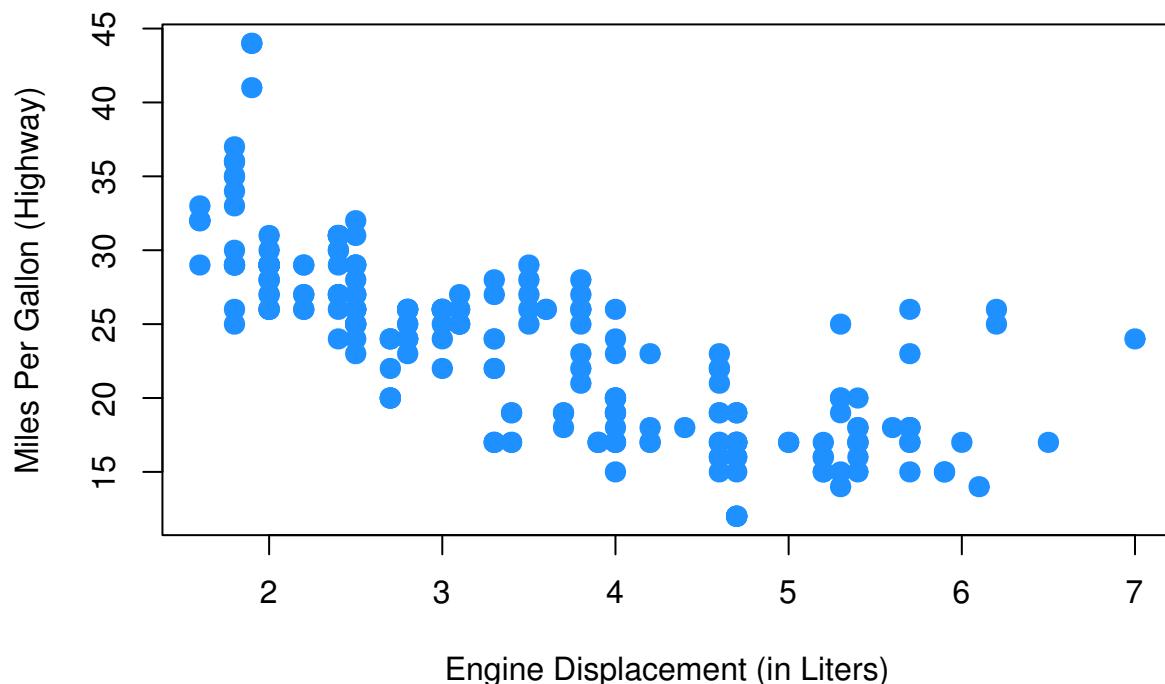
Lastly, to visualize the relationship between two numeric variables we will use a **scatterplot**. This can be done with the `plot()` function and the `~` syntax we just used with a boxplot. (The function `plot()` can also be used more generally; see the documentation for details.)

```
plot(hwy ~ displ, data = mpg)
```



```
plot(hwy ~ displ, data = mpg,
      xlab = "Engine Displacement (in Liters)",
      ylab = "Miles Per Gallon (Highway)",
      main = "MPG (Highway) vs Engine Displacement",
      pch = 20,
      cex = 2,
      col = "dodgerblue")
```

### MPG (Highway) vs Engine Displacement



# Chapter 5

## R Resources

So far, we have seen a lot of R, and a lot of R quickly. Again, the preceding chapters were in no way meant to be a complete reference for the R language, but rather an introduction to many of the concepts we will need in this text. The following resources are not necessary for the remainder of this text, but you may find them useful if you would like a deeper understanding of R:

### 5.1 Beginner Tutorials and References

- Try R from Code School.
  - An interactive introduction to the basics of R. Useful for getting up to speed on R's syntax.
- Quick-R by Robert Kabacoff.
  - A good reference for R basics.
- R Tutorial by Chi Yau.
  - A combination reference and tutorial for R basics.
- R Programming for Data Science by Roger Peng
  - A great text for R programming beginners. Discusses R from the ground up, highlighting programming details we might not discuss.

### 5.2 Intermediate References

- R for Data Science by Hadley Wickham and Garrett Grolemund.
  - Similar to Advanced R, but focuses more on data analysis, while still introducing programming concepts. Especially useful for working in the tidyverse.
- The Art of R Programming by Norman Matloff.
  - Gentle introduction to the programming side of R. (Whereas we will focus more on the data analysis side.) A free electronic version is available through the Illinois library.

### 5.3 Advanced References

- Advanced R by Hadley Wickham.
  - From the author of several extremely popular R packages. Good follow-up to The Art of R Programming. (And more up-to-date material.)
- The R Inferno by Patrick Burns.
  - Likens learning the tricks of R to descending through the levels of hell. Very advanced material, but may be important if R becomes a part of your everyday toolkit.
- Efficient R Programming by Colin Gillespie and Robin Lovelace
  - Discusses both efficient R programs, as well as programming in R efficiently.

# Chapter 6

## Probability in R

### 6.1 Distributions

When working with different statistical distributions, we often want to make probabilistic statements based on the distribution.

We typically want to know one of four things:

- The density (pdf) at a particular value.
- The distribution (cdf) at a particular value.
- The quantile value corresponding to a particular probability.
- A random draw of values from a particular distribution.

This used to be done with statistical tables printed in the back of textbooks. Now, R has functions for obtaining density, distribution, quantile and random values.

The general naming structure of the relevant R functions is:

- `dname` calculates density (pdf) at input `x`.
- `pname` calculates distribution (cdf) at input `x`.
- `qname` calculates the quantile at an input probability.
- `rname` generates a random draw from a particular distribution.

Note that `name` represents the name of the given distribution.

For example, consider a random variable  $X$  which is  $N(\mu = 2, \sigma^2 = 25)$ . (Note, we are parameterizing using the variance  $\sigma^2$ . R however uses the standard deviation.)

To calculate the value of the pdf at  $x = 3$ , that is, the height of the curve at  $x = 3$ , use:

```
dnorm(x = 3, mean = 2, sd = 5)
```

```
## [1] 0.07820854
```

To calculate the value of the cdf at  $x = 3$ , that is,  $P(X \leq 3)$ , the probability that  $X$  is less than or equal to 3, use:

```
pnorm(q = 3, mean = 2, sd = 5)
```

```
## [1] 0.5792597
```

Or, to calculate the quantile for probability 0.975, use:

```
qnorm(p = 0.975, mean = 2, sd = 5)
```

```
## [1] 11.79982
```

Lastly, to generate a random sample of size  $n = 10$ , use:

```
rnorm(n = 10, mean = 2, sd = 5)
```

```
## [1] 6.2577821 -8.5058812 4.5002065 0.9264441 1.1255433 -4.2306800
## [7] -3.2195377 -7.0833998 2.4675533 4.0577006
```

These functions exist for many other distributions, including but not limited to:

Command	Distribution
*binom	Binomial
*t	t
*pois	Poisson
*f	F
*chisq	Chi-Squared

Where \* can be d, p, q, and r. Each distribution will have its own set of parameters which need to be passed to the functions as arguments. For example, `dbinom()` would not have arguments for `mean` and `sd`, since those are not parameters of the distribution. Instead a binomial distribution is usually parameterized by  $n$  and  $p$ , however R chooses to call them something else. To find the names that R uses we would use `?dbinom` and see that R instead calls the arguments `size` and `prob`. For example:

```
dbinom(x = 6, size = 10, prob = 0.75)
```

```
## [1] 0.145998
```

Also note that, when using the `dname` functions with discrete distributions, they are the pmf of the distribution. For example, the above command is  $P(Y = 6)$  if  $Y \sim b(n = 10, p = 0.75)$ . (The probability of flipping an unfair coin 10 times and seeing 6 heads, if the probability of heads is 0.75.)

# Chapter 7

## Hypothesis Tests in R

A prerequisite for STAT 420 is an understanding of the basics of hypothesis testing. Recall the basic structure of hypothesis tests:

- An overall model and related assumptions are made. (The most common being observations following a normal distribution.)
- The **null** ( $H_0$ ) and **alternative** ( $H_1$  or  $H_A$ ) hypothesis are specified. Usually the null specifies a particular value of a parameter.
- With given data, the **value** of the *test statistic* is calculated.
- Under the general assumptions, as well as assuming the null hypothesis is true, the **distribution** of the *test statistic* is known.
- Given the distribution and value of the test statistic, as well as the form of the alternative hypothesis, we can calculate a **p-value** of the test.
- Based on the **p-value** and pre-specified level of significance, we make a decision. One of:
  - Fail to reject the null hypothesis.
  - Reject the null hypothesis.

We'll do some quick review of two of the most common tests to show how they are performed using R.

### 7.0.1 One Sample t-Test: Review

Suppose  $x_i \sim N(\mu, \sigma^2)$  and we want to test  $H_0 : \mu = \mu_0$  versus  $H_1 : \mu \neq \mu_0$ .

Assuming  $\sigma$  is unknown, we use the one-sample Student's *t* test statistic:

$$t = \frac{\bar{x} - \mu_0}{s/\sqrt{n}} \sim t_{n-1},$$

where  $\bar{x} = \frac{\sum_{i=1}^n x_i}{n}$  and  $s = \sqrt{\frac{1}{n-1} \sum_{i=1}^n (x_i - \bar{x})^2}$ .

A  $100(1 - \alpha)\%$  confidence interval for  $\mu$  is given by,

$$\bar{x} \pm t_{n-1}(\alpha/2) \frac{s}{\sqrt{n}}$$

where  $t_{n-1}(\alpha/2)$  is the critical value such that  $P(t > t_{n-1}(\alpha/2)) = \alpha/2$  for  $n - 1$  degrees of freedom.

### 7.0.2 One Sample t-Test: Example

Suppose a grocery store sells “16 ounce” boxes of *Captain Crisp* cereal. A random sample of 9 boxes was taken and weighed. The weight in ounces are stored in the data frame `capt_crisp`.

```
capt_crisp = data.frame(weight = c(15.5, 16.2, 16.1, 15.8, 15.6, 16.0, 15.8, 15.9, 16.2))
```

The company that makes *Captain Crisp* cereal claims that the average weight of a box is at least 16 ounces. We will assume the weight of cereal in a box is normally distributed and use a 0.05 level of significance to test the company’s claim.

To test  $H_0 : \mu \geq 16$  versus  $H_1 : \mu < 16$ , the test statistic is

$$t = \frac{\bar{x} - \mu_0}{s/\sqrt{n}}$$

The sample mean  $\bar{x}$  and the sample standard deviation  $s$  can be easily computed using R. We also create variables which store the hypothesized mean and the sample size.

```
x_bar = mean(capt_crisp$weight)
s      = sd(capt_crisp$weight)
mu_0   = 16
n      = 9
```

We can then easily compute the test statistic.

```
t = (x_bar - mu_0) / (s / sqrt(n))
t
```

```
## [1] -1.2
```

Under the null hypothesis, the test statistic has a  $t$  distribution with  $n - 1$  degrees of freedom, in this case 8.

To complete the test, we need to obtain the p-value of the test. Since this is a one-sided test with a less-than alternative, we need to area to the left of -1.2 for a  $t$  distribution with 8 degrees of freedom. That is,

$$P(t_8 < -1.2)$$

```
pt(t, df = n - 1)
```

```
## [1] 0.1322336
```

We now have the p-value of our test, which is greater than our significance level (0.05), so we fail to reject the null hypothesis.

Alternatively, this entire process could have been completed using one line of R code.

```
t.test(x = capt_crisp$weight, mu = 16, alternative = c("less"), conf.level = 0.95)
```

```
##  
##  One Sample t-test  
##  
## data:  capt_crisp$weight  
## t = -1.2, df = 8, p-value = 0.1322  
## alternative hypothesis: true mean is less than 16  
## 95 percent confidence interval:  
##       -Inf 16.05496  
## sample estimates:  
## mean of x  
##      15.9
```

We supply R with the data, the hypothesized value of  $\mu$ , the alternative, and the confidence level. R then returns a wealth of information including:

- The value of the test statistic.
- The degrees of freedom of the distribution under the null hypothesis.
- The p-value of the test.
- The confidence interval which corresponds to the test.
- An estimate of  $\mu$ .

Since the test was one-sided, R returned a one-sided confidence interval. If instead we wanted a two-sided interval for the mean weight of boxes of *Captain Crisp* cereal we could modify our code.

```
capt_test_results = t.test(capt_crisp$weight, mu = 16,  
                           alternative = c("two.sided"), conf.level = 0.95)
```

This time we have stored the results. By doing so, we can directly access portions of the output from `t.test()`. To see what information is available we use the `names()` function.

```
names(capt_test_results)
```

```
## [1] "statistic"    "parameter"    "p.value"      "conf.int"      "estimate"  
## [6] "null.value"   "alternative"  "method"       "data.name"
```

We are interested in the confidence interval which is stored in `conf.int`.

```
capt_test_results$conf.int
```

```
## [1] 15.70783 16.09217  
## attr(,"conf.level")  
## [1] 0.95
```

Let's check this interval "by hand." The one piece of information we are missing is the critical value,  $t_{n-1}(\alpha/2) = t_8(0.025)$ , which can be calculated in R using the `qt()` function.

```
qt(0.975, df = 8)
```

```
## [1] 2.306004
```

So, the 95% CI for the mean weight of a cereal box is calculated by plugging into the formula,

$$\bar{x} \pm t_{n-1}(\alpha/2) \frac{s}{\sqrt{n}}$$

```
c(mean(capt_crisp$weight) - qt(0.975, df = 8) * sd(capt_crisp$weight) / sqrt(9),
  mean(capt_crisp$weight) + qt(0.975, df = 8) * sd(capt_crisp$weight) / sqrt(9))
```

```
## [1] 15.70783 16.09217
```

### 7.0.3 Two Sample t-Test: Review

Suppose  $x_i \sim N(\mu_x, \sigma^2)$  and  $y_i \sim N(\mu_y, \sigma^2)$ .

Want to test  $H_0 : \mu_x - \mu_y = \mu_0$  versus  $H_1 : \mu_x - \mu_y \neq \mu_0$ .

Assuming  $\sigma$  is unknown, use the two-sample Student's  $t$  test statistic:

$$t = \frac{(\bar{x} - \bar{y}) - \mu_0}{s_p \sqrt{\frac{1}{n} + \frac{1}{m}}} \sim t_{n+m-2},$$

where  $\bar{x} = \frac{\sum_{i=1}^n x_i}{n}$ ,  $\bar{y} = \frac{\sum_{i=1}^m y_i}{m}$ , and  $s_p^2 = \frac{(n-1)s_x^2 + (m-1)s_y^2}{n+m-2}$ .

A  $100(1 - \alpha)\%$  CI for  $\mu_x - \mu_y$  is given by

$$(\bar{x} - \bar{y}) \pm t_{n+m-2}(\alpha/2) \left( s_p \sqrt{\frac{1}{n} + \frac{1}{m}} \right),$$

where  $t_{n+m-2}(\alpha/2)$  is the critical value such that  $P(t > t_{n+m-2}(\alpha/2)) = \alpha/2$ .

### 7.0.4 Two Sample t-Test: Example

Assume that the distributions of  $X$  and  $Y$  are  $N(\mu_1, \sigma^2)$  and  $N(\mu_2, \sigma^2)$ , respectively. Given the  $n = 6$  observations of  $X$ ,

```
x = c(70, 82, 78, 74, 94, 82)
n = length(x)
```

and the  $m = 8$  observations of  $Y$ ,

```
y = c(64, 72, 60, 76, 72, 80, 84, 68)
m = length(y)
```

we will test  $H_0 : \mu_1 = \mu_2$  versus  $H_1 : \mu_1 > \mu_2$ .

First, note that we can calculate the sample means and standard deviations.

```
x_bar = mean(x)
s_x    = sd(x)
y_bar = mean(y)
s_y    = sd(y)
```

We can then calculate the pooled standard deviation.

$$s_p = \sqrt{\frac{(n-1)s_x^2 + (m-1)s_y^2}{n+m-2}}$$

```
s_p = sqrt(((n - 1) * s_x ^ 2 + (m - 1) * s_y ^ 2) / (n + m - 2))
```

Thus, the relevant  $t$  test statistic is given by

$$t = \frac{(\bar{x} - \bar{y}) - \mu_0}{s_p \sqrt{\frac{1}{n} + \frac{1}{m}}}.$$

```
t = ((x_bar - y_bar) - 0) / (s_p * sqrt(1 / n + 1 / m))
t
```

```
## [1] 1.823369
```

Note that  $t \sim t_{n+m-2} = t_{12}$ , so we can calculate the p-value, which is

$$P(t_{12} > 1.8233692).$$

```
1 - pt(t, df = n + m - 2)
```

```
## [1] 0.04661961
```

But, then again, we could have simply performed this test in one line of R.

```
t.test(x, y, alternative = c("greater"), var.equal = TRUE)
```

```
##
##  Two Sample t-test
##
## data: x and y
## t = 1.8234, df = 12, p-value = 0.04662
## alternative hypothesis: true difference in means is greater than 0
## 95 percent confidence interval:
##  0.1802451      Inf
## sample estimates:
## mean of x mean of y
##       80        72
```

Recall that a two-sample  $t$ -test can be done with or without an equal variance assumption. Here `var.equal = TRUE` tells R we would like to perform the test under the equal variance assumption.

Above we carried out the analysis using two vectors `x` and `y`. In general, we will have a preference for using data frames.

```
t_test_data = data.frame(values = c(x, y),
                         group = c(rep("A", length(x)), rep("B", length(y))))
```

We now have the data stored in a single variables (`values`) and have created a second variable (`group`) which indicates which “sample” the value belongs to.

```
t_test_data
```

```
##   values group
## 1     70    A
## 2     82    A
## 3     78    A
## 4     74    A
## 5     94    A
## 6     82    A
## 7     64    B
## 8     72    B
## 9     60    B
## 10    76    B
## 11    72    B
## 12    80    B
## 13    84    B
## 14    68    B
```

Now to perform the test, we still use the `t.test()` function but with the `~` syntax and a `data` argument.

```
t.test(values ~ group, data = t_test_data,
       alternative = c("greater"), var.equal = TRUE)
```

```
##
##  Two Sample t-test
##
## data:  values by group
## t = 1.8234, df = 12, p-value = 0.04662
## alternative hypothesis: true difference in means is greater than 0
## 95 percent confidence interval:
##  0.1802451      Inf
## sample estimates:
## mean in group A mean in group B
##                 80                  72
```

# Chapter 8

## Simulation

Simulation and model fitting are related but opposite processes.

- In **simulation**, the *data generating process* is known. We will know the form of the model as well as the value of each of the parameters. In particular, we will often control the distribution and parameters which define the randomness, or noise in the data.
- In **model fitting**, the *data* is known. We will then assume a certain form of model and find the best possible values of the parameters given the observed data. Essentially we are seeking to uncover the truth. Often we will attempt to fit many models, and we will learn metrics to assess which model fits best.

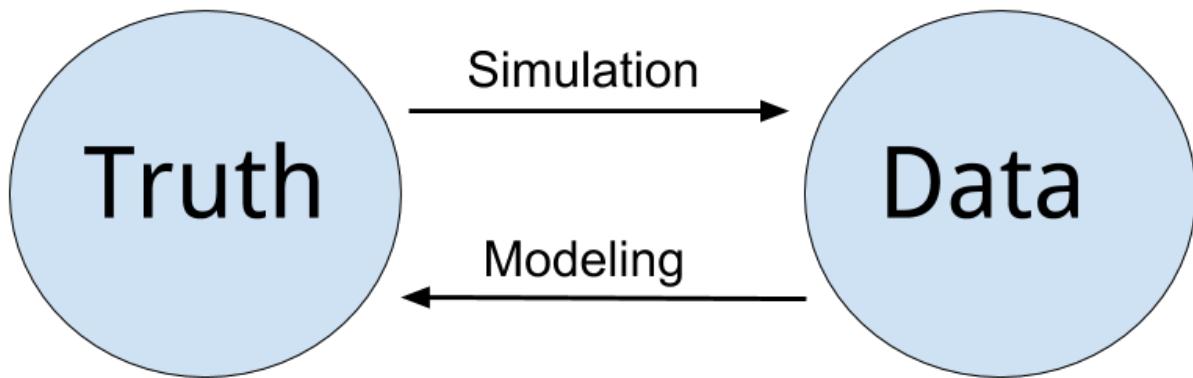


Figure 8.1: Simulation vs Modeling

Often we will simulate data according to a process we decide, then use a modeling method seen in class. We can then verify how well the method works, since we know the data generating process.

One of the biggest strengths of R is its ability to carry out simulations using built-in functions for generating random samples from certain distributions. We'll look at two very simple examples here, however simulation will be a topic we revisit several times throughout the course.

### 8.0.1 Paired Differences

Consider the model:

$$\begin{aligned} X_{11}, X_{12}, \dots, X_{1n} &\sim N(\mu_1, \sigma^2) \\ X_{21}, X_{22}, \dots, X_{2n} &\sim N(\mu_2, \sigma^2) \end{aligned}$$

Assume that  $\mu_1 = 6$ ,  $\mu_2 = 5$ ,  $\sigma^2 = 4$  and  $n = 25$ .

Let

$$\begin{aligned} \bar{X}_1 &= \frac{1}{n} \sum_{i=1}^n X_{1i} \\ \bar{X}_2 &= \frac{1}{n} \sum_{i=1}^n X_{2i} \\ D &= \bar{X}_1 - \bar{X}_2. \end{aligned}$$

Suppose we would like to calculate  $P(0 < D < 2)$ . First we will need to obtain the distribution of  $D$ .

Recall,

$$\bar{X}_1 \sim N\left(\mu_1, \frac{\sigma^2}{n}\right)$$

and

$$\bar{X}_2 \sim N\left(\mu_2, \frac{\sigma^2}{n}\right).$$

Then,

$$D = \bar{X}_1 - \bar{X}_2 \sim N\left(\mu_1 - \mu_2, \frac{\sigma^2}{n} + \frac{\sigma^2}{n}\right) = N\left(6 - 5, \frac{4}{25} + \frac{4}{25}\right).$$

So,

$$D \sim N(\mu = 1, \sigma^2 = 0.32).$$

Thus,

$$P(0 < D < 2) = P(D < 2) - P(D < 0).$$

This can then be calculated using R without a need to first standardize, or use a table.

```
pnorm(2, mean = 1, sd = sqrt(0.32)) - pnorm(0, mean = 1, sd = sqrt(0.32))
```

```
## [1] 0.9229001
```

An alternative approach, would be to **simulate** a large number of observations of  $D$  then use the **empirical distribution** to calculate the probability.

Our strategy will be to repeatedly:

- Generate a sample of 25 random observations from  $N(\mu_1 = 6, \sigma^2 = 4)$ . Call the mean of this sample  $\bar{x}_{1s}$ .
- Generate a sample of 25 random observations from  $N(\mu_1 = 5, \sigma^2 = 4)$ . Call the mean of this sample  $\bar{x}_{2s}$ .
- Calculate the differences of the means,  $d_s = \bar{x}_{1s} - \bar{x}_{2s}$ .

We will repeat the process a large number of times. Then we will use the distribution of the simulated observations of  $d_s$  as an estimate for the true distribution of  $D$ .

```
set.seed(42)
num_samples = 10000
differences = rep(0, num_samples)
```

Before starting our `for` loop to perform the operation, we set a seed for reproducibility, create and set a variable `num_samples` which will define the number of repetitions, and lastly create a variables `differences` which will store the simulate values,  $d_s$ .

By using `set.seed()` we can reproduce the random results of `rnorm()` each time starting from that line.

```
for (s in 1:num_samples) {
  x1 = rnorm(n = 25, mean = 6, sd = 2)
  x2 = rnorm(n = 25, mean = 5, sd = 2)
  differences[s] = mean(x1) - mean(x2)
}
```

To estimate  $P(0 < D < 2)$  we will find the proportion of values of  $d_s$  (among the  $10^{[4]}$  values of  $d_s$  generated) that are between 0 and 2.

```
mean(0 < differences & differences < 2)
```

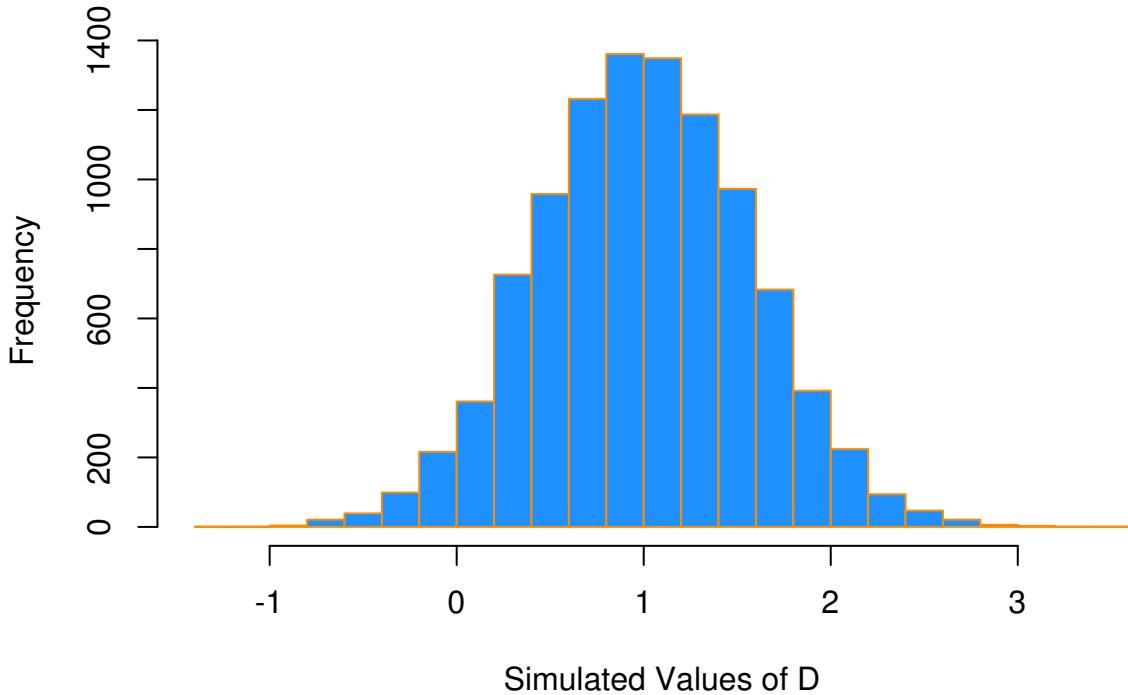
```
## [1] 0.9222
```

Recall that above we derived the distribution of  $D$  to be  $N(\mu = 1, \sigma^2 = 0.32)$

If we look at a histogram of the differences, we find that it looks very much like a normal distribution.

```
hist(differences, breaks = 20,
      main = "Empirical Distribution of D",
      xlab = "Simulated Values of D",
      col = "dodgerblue",
      border = "darkorange")
```

## Empirical Distribution of D



Also the sample mean and variance are very close to what we would expect.

```
mean(differences)
```

```
## [1] 1.001423
```

```
var(differences)
```

```
## [1] 0.3230183
```

We could have also accomplished this task with a single line of more “idiomatic” R.

```
set.seed(42)
diffs = replicate(10000, mean(rnorm(25, 6, 2)) - mean(rnorm(25, 5, 2)))
```

Use `?replicate` to take a look at the documentation for the `replicate` function and see if you can understand how this line performs the same operations that our `for` loop above executed.

```
mean(differences == diffs)
```

```
## [1] 1
```

We see that by setting the same seed for the randomization, we actually obtain identical results!

### 8.0.2 Distribution of a Sample Mean

For another example of simulation, we will simulate observations from a Poisson distribution, and examine the empirical distribution of the sample mean of these observations.

Recall, if

$$X \sim \text{Pois}(\mu)$$

then

$$E[X] = \mu$$

and

$$\text{Var}[X] = \mu.$$

Also, recall that for a random variable  $X$  with finite mean  $\mu$  and finite variance  $\sigma^2$ , the central limit theorem tells us that the mean,  $\bar{X}$  of a random sample of size  $n$  is approximately normal for *large* values of  $n$ . Specifically, as  $n \rightarrow \infty$ ,

$$\bar{X} \xrightarrow{d} N\left(\mu, \frac{\sigma^2}{n}\right).$$

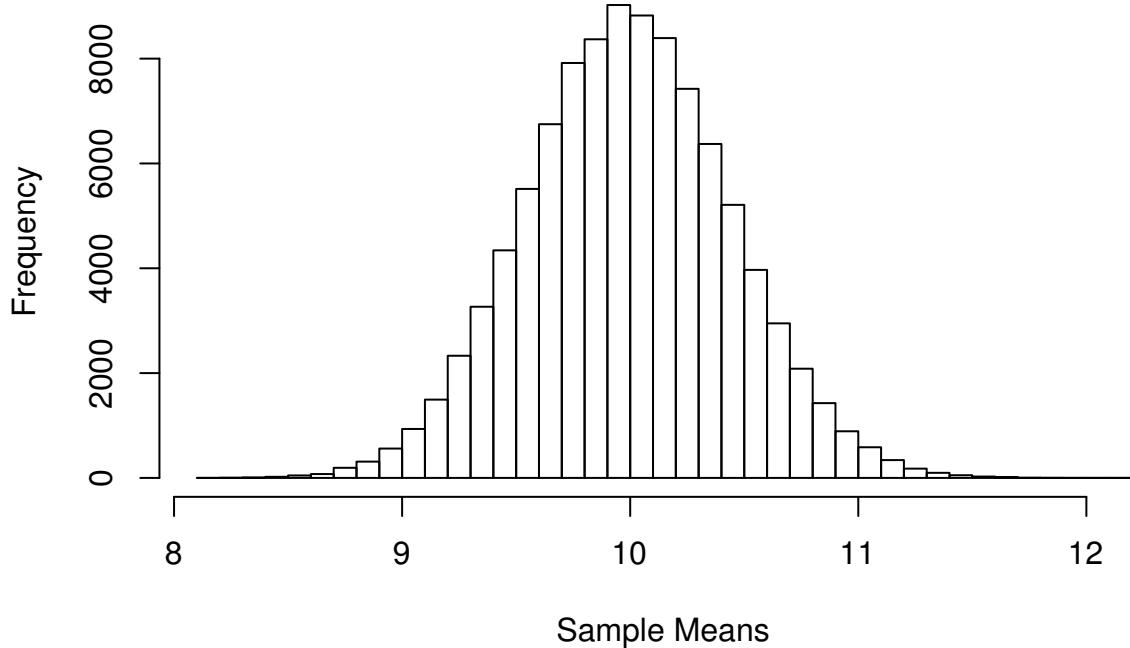
The following verifies this result for a Poisson distribution with  $\mu = 10$  and a sample size of  $n = 50$ .

```
set.seed(1337)
mu      = 10
sample_size = 50
samples   = 100000
x_bars    = rep(0, samples)

for(i in 1:samples){
  x_bars[i] = mean(rpois(sample_size, lambda = mu))
}

x_bar_hist = hist(x_bars, breaks = 50,
                  main = "Histogram of Sample Means",
                  xlab = "Sample Means")
```

## Histogram of Sample Means



Now we will compare sample statistics from the empirical distribution with their known values based on the parent distribution.

```
c(mean(x_bars), mu)

## [1] 10.00008 10.00000

c(var(x_bars), mu / sample_size)

## [1] 0.1989732 0.2000000

c(sd(x_bars), sqrt(mu) / sqrt(sample_size))

## [1] 0.4460641 0.4472136
```

And here, we will calculate the proportion of sample means that are within 2 standard deviations of the population mean.

```
mean(x_bars > mu - 2 * sqrt(mu) / sqrt(sample_size) &
      x_bars < mu + 2 * sqrt(mu) / sqrt(sample_size))

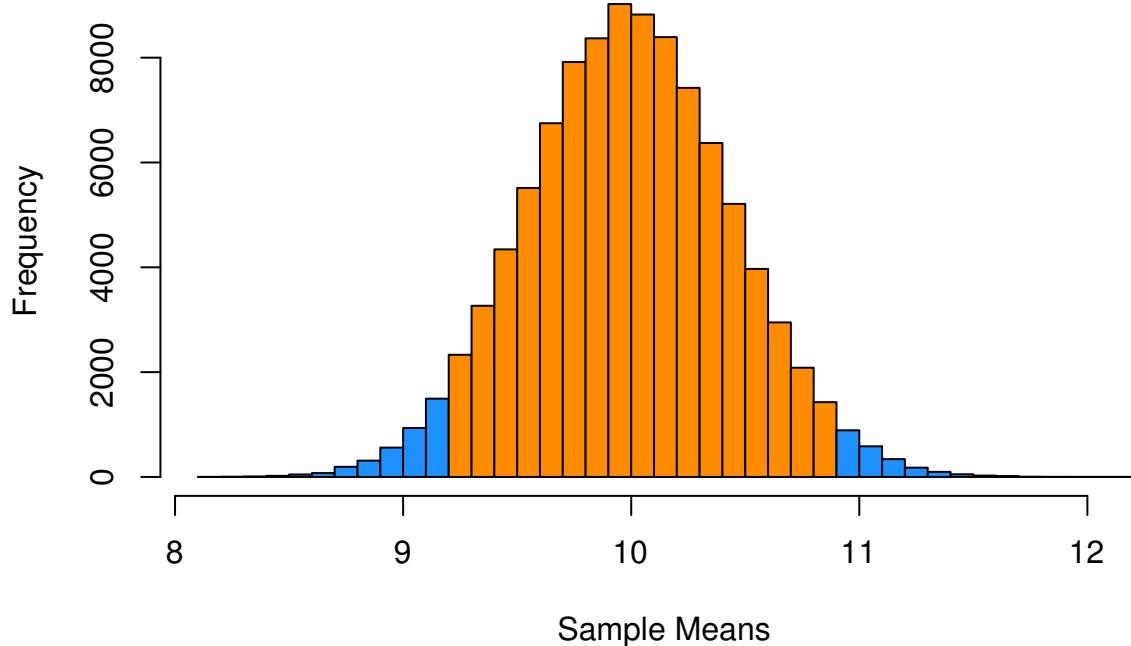
## [1] 0.95429
```

This last histogram uses a bit of a trick to approximately shade the bars that are within two standard deviations of the mean.)

```
shading = ifelse(x_bar_hist$breaks > mu - 2 * sqrt(mu) / sqrt(sample_size) &
                 x_bar_hist$breaks < mu + 2 * sqrt(mu) / sqrt(sample_size),
                 "darkorange", "dodgerblue")

x_bar_hist = hist(x_bars, breaks = 50, col = shading,
                  main = "Histogram of Sample Means, Two Standard Deviations",
                  xlab = "Sample Means")
```

## Histogram of Sample Means, Two Standard Deviations





# Chapter 9

## RStudio and RMarkdown

This chapter will serve as a (currently brief) collection of tutorials for using RStudio and RMarkdown. It will likely be expanded over time. At this time many resources also appear in the previous chapter. Over time some may be moved here.

The following videos were made as an introduction to R, RStudio, and RMarkdown for STAT 420 at UIUC.

- RStudio Basics
- RMarkdown Intro
- RMarkdown Basics
- RMarkdown Tips and Tricks

Note that RStudio and RMarkdown are constantly receiving excellent support and updates, so these videos already contain some outdated information. For example, as of recent RStudio versions, the “Import Dataset” functionality has been updated to utilize the `readr` and `tibble` packages. Additionally, working interactively with RMarkdown documents in RStudio has a long list of new functionality.

RStudio provides their own tutorial for RMarkdown. They also have an excellent RStudio “cheatsheets” which visually identifies many of the features available in the IDE.

### 9.1 Template

This `.zip` file contains the files necessary to produce this rendered document. This document is a more complete version of a template than what is seen in the above videos.



# Chapter 10

## Regression Basics in R

This chapter will recap the basics of performing regression analyses in R. For more detailed coverage, see Applied Statistics with R.

We will use the Advertising data associated with Introduction to Statistical Learning.

```
library(readr)
Advertising = read_csv("data/Advertising.csv")
```

After loading data into R, our first step should **always** be to inspect the data. We will start by simply printing some observations in order to understand the basic structure of the data.

```
Advertising
```

```
## # A tibble: 200 × 4
##       TV Radio Newspaper Sales
##   <dbl> <dbl>    <dbl> <dbl>
## 1 230.1 37.8     69.2  22.1
## 2 44.5  39.3     45.1  10.4
## 3 17.2  45.9     69.3   9.3
## 4 151.5 41.3     58.5  18.5
## 5 180.8 10.8     58.4  12.9
## 6  8.7  48.9     75.0   7.2
## 7 57.5  32.8     23.5  11.8
## 8 120.2 19.6     11.6  13.2
## 9  8.6  2.1      1.0   4.8
## 10 199.8  2.6     21.2  10.6
## # ... with 190 more rows
```

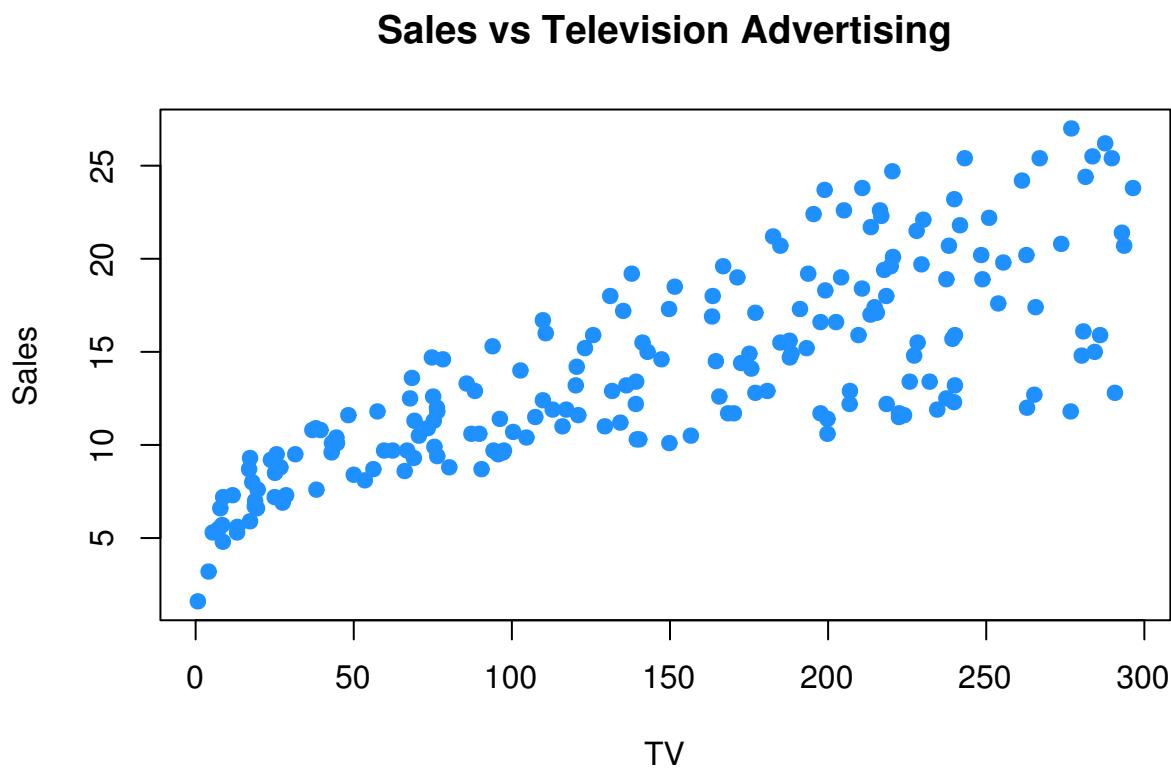
Because the data was read using `read_csv()`, `Advertising` is a tibble. We see that there are a total of 200 observations and 4 variables, each of which is numeric. (Specifically double-precision vectors, but more importantly they are numbers.) For the purpose of this analysis, `Sales` will be the **response variable**. That is, we seek to understand the relationship between `Sales`, and the **predictor variables**: `TV`, `Radio`, and `Newspaper`.

## 10.1 Visualization for Regression

After investigating the structure of the data, the next step should be to visualize the data. Since we have only numeric variables, we should consider **scatter plots**.

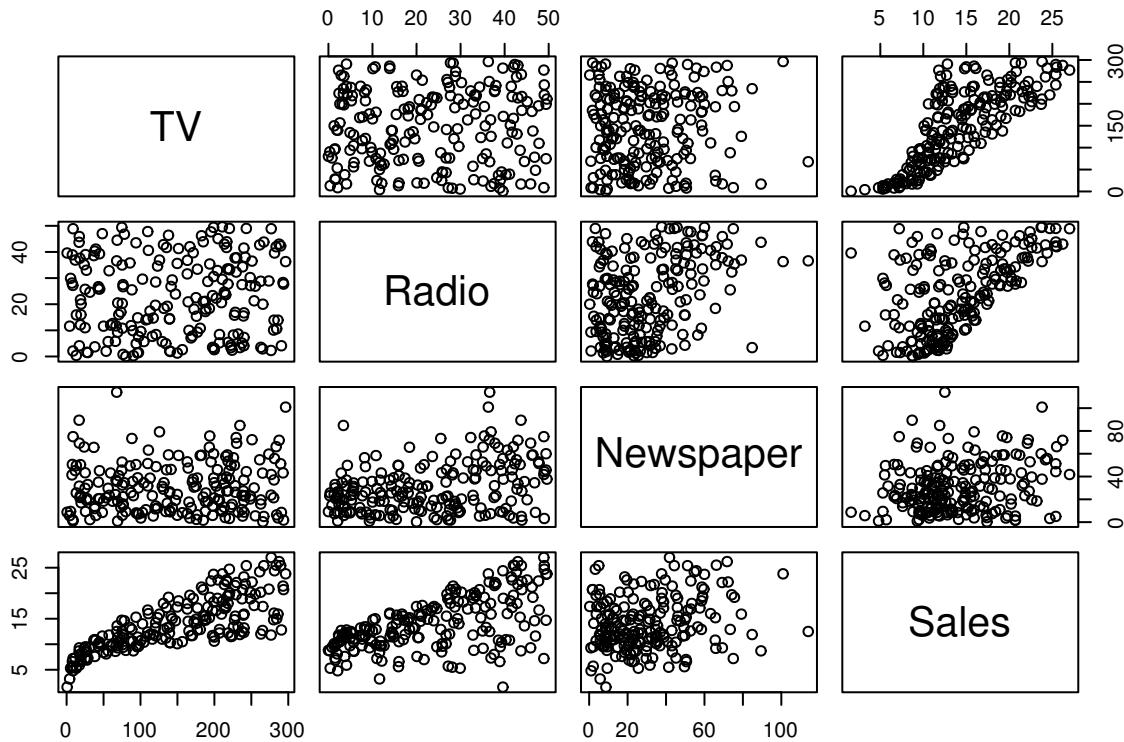
We could do so for any individual predictor.

```
plot(Sales ~ TV, data = Advertising, col = "dodgerblue", pch = 20, cex = 1.5,
      main = "Sales vs Television Advertising")
```



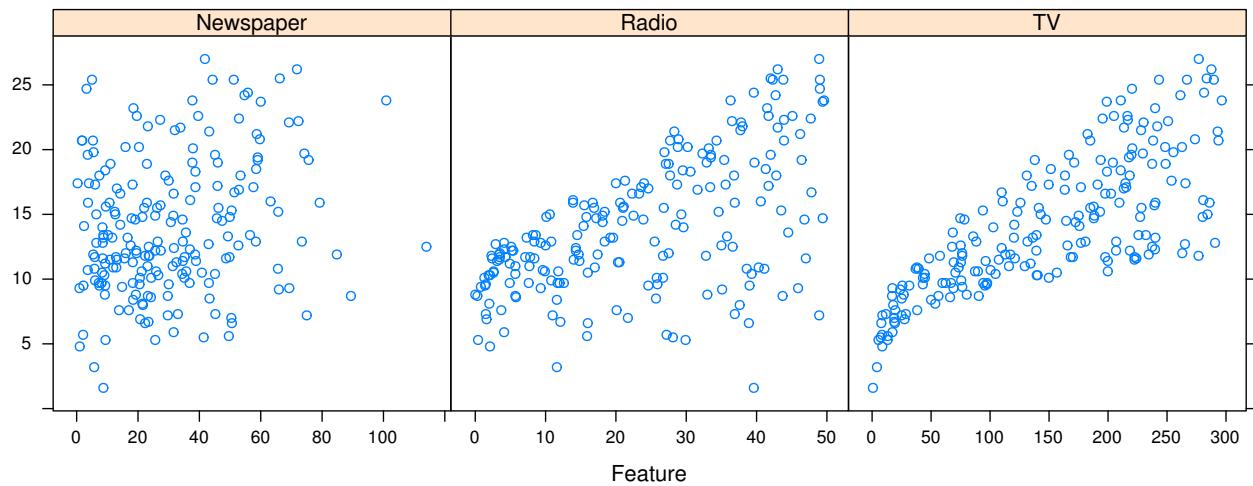
The `pairs()` function is a useful way to quickly visualize a number of scatter plots.

```
pairs(Advertising)
```



Often, we will be most interested in only the relationship between each predictor and the response. For this, we can use the `featurePlot()` function from the `caret` package. (We will use the `caret` package more and more frequently as we introduce new topics.)

```
library(caret)
featurePlot(x = Advertising[, c("TV", "Radio", "Newspaper")], y = Advertising$Sales)
```



We see that there is a clear increase in `Sales` as `Radio` or `TV` are increased. The relationship between `Sales` and `Newspaper` is less clear. How all of the predictors work together is also unclear, as there is some obvious correlation between `Radio` and `TV`. To investigate further, we will need to model the data.

## 10.2 The `lm()` Function

The following code fits an additive **linear model** with `Sales` as the response and each remaining variable as a predictor. Note, by not using `attach()` and instead specifying the `data =` argument, we are able to specify this model without using each of the variable names directly.

```
mod_1 = lm(Sales ~ ., data = Advertising)
# mod_1 = lm(Sales ~ TV + Radio + Newspaper, data = Advertising)
```

Note that the commented line is equivalent to the line that is run, but we will often use the `response ~ .` syntax when possible.

## 10.3 Hypothesis Testing

The `summary()` function will return a large amount of useful information about a model fit using `lm()`. Much of it will be helpful for hypothesis testing including individual tests about each predictor, as well as the significance of the regression test.

```
summary(mod_1)

##
## Call:
## lm(formula = Sales ~ ., data = Advertising)
##
## Residuals:
##      Min      1Q      Median      3Q      Max 
## -8.8277 -0.8908  0.2418  1.1893  2.8292 
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)    
## (Intercept) 2.938889  0.311908   9.422 <2e-16 ***
## TV          0.045765  0.001395  32.809 <2e-16 ***
## Radio       0.188530  0.008611  21.893 <2e-16 ***
## Newspaper   -0.001037  0.005871  -0.177    0.86  
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 1.686 on 196 degrees of freedom
## Multiple R-squared:  0.8972, Adjusted R-squared:  0.8956 
## F-statistic: 570.3 on 3 and 196 DF,  p-value: < 2.2e-16

mod_0 = lm(Sales ~ TV + Radio, data = Advertising)
```

The `anova()` function is useful for comparing two models. Here we compare the full additive model, `mod_1`, to a reduced model `mod_0`. Essentially we are testing for the significance of the `Newspaper` variable in the additive model.

```
anova(mod_0, mod_1)
```

```
## Analysis of Variance Table
##
## Model 1: Sales ~ TV + Radio
## Model 2: Sales ~ TV + Radio + Newspaper
##   Res.Df   RSS Df Sum of Sq    F Pr(>F)
## 1     197 556.91
## 2     196 556.83  1  0.088717 0.0312 0.8599
```

Note that hypothesis testing is *not* our focus, so we omit many details.

## 10.4 Prediction

The `predict()` function is an extremely versatile function, for, prediction. When used on the result of a model fit using `lm()` it will, by default, return predictions for each of the data points used to fit the model. (Here, we limit the printed result to the first 10.)

```
head(predict(mod_1), n = 10)

##          1          2          3          4          5          6          7
## 20.523974 12.337855 12.307671 17.597830 13.188672 12.478348 11.729760
##          8          9         10
## 12.122953  3.727341 12.550849
```

Note that the effect of the `predict()` function is dependent on the input to the function. Here, we are supplying as the first argument a model object of class `lm`. Because of this, `predict()` then runs the `predict.lm()` function. Thus, we should use `?predict.lm()` for details.

We could also specify new data, which should be a data frame or tibble with the same column names as the predictors.

```
new_obs = data.frame(TV = 150, Radio = 40, Newspaper = 1)
```

We can then use the `predict()` function for point estimates, confidence intervals, and prediction intervals. Using only the first two arguments, R will simply return a point estimate, that is, the “predicted value,”  $\hat{y}$ .

```
predict(mod_1, newdata = new_obs)
```

```
##          1
## 17.34375
```

If we specify an additional argument `interval` with a value of "confidence", R will return a 95% confidence interval for the mean response at the specified point. Note that here R also gives the point estimate as `fit`.

```
predict(mod_1, newdata = new_obs, interval = "confidence")
```

```
##      fit      lwr      upr
## 1 17.34375 16.77654 17.91096
```

Lastly, we can alter the level using the `level` argument. Here we report a prediction interval instead of a confidence interval.

```
predict(mod_1, newdata = new_obs, interval = "prediction", level = 0.99)
```

```
##      fit      lwr      upr
## 1 17.34375 12.89612 21.79138
```

## 10.5 Unusual Observations

R provides several functions for obtaining metrics related to unusual observations.

- `resid()` provides the residual for each observation
- `hatvalues()` gives the leverage of each observation
- `rstudent()` give the studentized residual for each observation
- `cooks.distance()` calculates the influence of each observation

```
head(resid(mod_1), n = 10)
```

```
##      1      2      3      4      5      6
## 1.57602559 -1.93785482 -3.00767078  0.90217049 -0.28867186 -5.27834763
##      7      8      9     10
## 0.07024005  1.07704683  1.07265914 -1.95084872
```

```
head(hatvalues(mod_1), n = 10)
```

```
##      1      2      3      4      5      6
## 0.025202848 0.019418228 0.039226158 0.016609666 0.023508833 0.047481074
##      7      8      9     10
## 0.014435091 0.009184456 0.030714427 0.017147645
```

```
head(rstudent(mod_1), n = 10)
```

```
##      1      2      3      4      5      6
## 0.94680369 -1.16207937 -1.83138947  0.53877383 -0.17288663 -3.28803309
##      7      8      9     10
## 0.04186991  0.64099269  0.64544184 -1.16856434
```

```
head(cooks.distance(mod_1), n = 10)
```

```
##      1      2      3      4      5
## 5.797287e-03 6.673622e-03 3.382760e-02 1.230165e-03 1.807925e-04
##      6      7      8      9     10
## 1.283058e-01 6.452021e-06 9.550237e-04 3.310088e-03 5.945006e-03
```

## 10.6 Adding Complexity

We have a number of ways to add complexity to a linear model, even allowing a linear model to be used to model non-linear relationships.

### 10.6.1 Interactions

Interactions can be introduced to the `lm()` procedure in a number of ways.

We can use the `:` operator to introduce a single interaction of interest.

```
mod_2 = lm(Sales ~ . + TV:Newspaper, data = Advertising)
coef(mod_2)

##   (Intercept)          TV          Radio        Newspaper  TV:Newspaper
##  3.8730824491  0.0392939602  0.1901312252 -0.0320449675  0.0002016962
```

The `response ~ . ^ k` syntax can be used to model all  $k$ -way interactions. (As well as the appropriate lower order terms.) Here we fit a model with all two-way interactions, and the lower order main effects.

```
mod_3 = lm(Sales ~ . ^ 2, data = Advertising)
coef(mod_3)

##   (Intercept)          TV          Radio        Newspaper
##  6.460158e+00  2.032710e-02  2.292919e-02  1.703394e-02
##  TV:Radio      TV:Newspaper  Radio:Newspaper
##  1.139280e-03 -7.971435e-05 -1.095976e-04
```

The `*` operator can be used to specify all interactions of a certain order, as well as all lower order terms according to the usual hierarchy. Here we see a three-way interaction and all lower order terms.

```
mod_4 = lm(Sales ~ TV * Radio * Newspaper, data = Advertising)
coef(mod_4)

##   (Intercept)          TV          Radio
##  6.555887e+00  1.971030e-02  1.962160e-02
##  Newspaper      TV:Radio      TV:Newspaper
##  1.310565e-02  1.161523e-03 -5.545501e-05
##  Radio:Newspaper TV:Radio:Newspaper
##  9.062944e-06 -7.609955e-07
```

Note that, we have only been dealing with numeric predictors. **Categorical predictors** are often recorded as **factor** variables in R.

```
library(tibble)
cat_pred = tibble(
  x1 = factor(c(rep("A", 10), rep("B", 10), rep("C", 10))),
  x2 = runif(n = 30),
  y   = rnorm(n = 30)
)
cat_pred

## # A tibble: 30 × 3
##       x1      x2       y
##   <fctr>    <dbl>    <dbl>
## 1     A  0.78494121 -0.4971619
```

```

## 2      A 0.27328751  0.7439579
## 3      A 0.80142765  0.7685171
## 4      A 0.65878720  1.4473288
## 5      A 0.68500647 -1.6572183
## 6      A 0.15101810 -1.2934777
## 7      A 0.20795060  0.3312560
## 8      A 0.51374619 -0.3715673
## 9      A 0.08174307  1.4112243
## 10     A 0.70793562 -2.0438214
## # ... with 20 more rows

```

Notice that in this simple simulated tibble, we have coerced `x1` to be a factor variable, although this is not strictly necessary since the variable took values A, B, and C. When using `lm()`, even if not a factor, R would have treated `x1` as such. Coercion to factor is more important if a categorical variable is coded for example as 1, 2 and 3. Otherwise it is treated as numeric, which creates a difference in the regression model.

The following two models illustrate the effect of factor variables on linear models.

```

cat_pred_mod_add = lm(y ~ x1 + x2, data = cat_pred)
coef(cat_pred_mod_add)

```

```

## (Intercept)          x1B          x1C          x2
## -0.05555776  0.17932815 -0.22033976 -0.12441520

```

```

cat_pred_mod_int = lm(y ~ x1 * x2, data = cat_pred)
coef(cat_pred_mod_int)

```

```

## (Intercept)          x1B          x1C          x2      x1B:x2      x1C:x2
##   0.4601419  -0.5589751  -1.0273326  -1.1842514   1.5277016   1.6357785

```

## 10.6.2 Polynomials

Polynomial terms can be specified using the inhibit function `I()` or through the `poly()` function. Note that these two methods produce different coefficients, but the same residuals! This is due to the `poly()` function using orthogonal polynomials by default.

```

mod_5 = lm(Sales ~ TV + I(TV ^ 2), data = Advertising)
coef(mod_5)

```

```

##   (Intercept)          TV      I(TV^2)
##  6.114120e+00  6.726593e-02 -6.846934e-05

```

```

mod_6 = lm(Sales ~ poly(TV, degree = 2), data = Advertising)
coef(mod_6)

```

```

##           (Intercept) poly(TV, degree = 2)1 poly(TV, degree = 2)2
## 14.022500          57.572721         -6.228802

```

```

all.equal(resid(mod_5), resid(mod_6))

```

```
## [1] TRUE
```

Polynomials and interactions can be mixed to create even more complex models.

```
mod_7 = lm(Sales ~ . ^ 2 + poly(TV, degree = 3), data = Advertising)
# mod_7 = lm(Sales ~ . ^ 2 + I(TV ^ 2) + I(TV ^ 3), data = Advertising)
coef(mod_7)
```

	(Intercept)	TV	Radio
##	6.206394e+00	2.092726e-02	3.766579e-02
##	Newspaper	poly(TV, degree = 3)1	poly(TV, degree = 3)2
##	1.405289e-02	NA	-9.925605e+00
##	poly(TV, degree = 3)3	TV:Radio	TV:Newspaper
##	5.309590e+00	1.082074e-03	-5.690107e-05
##	Radio:Newspaper		
##	-9.924992e-05		

Notice here that R ignores the first order term from `poly(TV, degree = 3)` as it is already in the model. We could consider using the commented line instead.

### 10.6.3 Transformations

Note that we could also create more complex models, which allow for non-linearity, using transformations. Be aware, when doing so to the response variable, that this will affect the units of said variable. You may need to un-transform to compare to non-transformed models.

```
mod_8 = lm(log(Sales) ~ ., data = Advertising)
sqrt(mean(resid(mod_8) ^ 2)) # incorrect RMSE for Model 8
```

```
## [1] 0.1849483
```

```
sqrt(mean(resid(mod_7) ^ 2)) # RMSE for Model 7
```

```
## [1] 0.4813215
```

```
sqrt(mean(exp(resid(mod_8)) ^ 2)) # correct RMSE for Model 8
```

```
## [1] 1.023205
```



# Chapter 11

## Regression for Statistical Learning

When using linear models in the past, we often emphasized distributional results, which were useful for creating and performing hypothesis tests. Frequently, when developing a linear regression model, part of our goal was to **explain** a relationship.

Now, we will ignore much of what we have learned and instead simply use regression as a tool to **predict**. Instead of a model which explains relationships, we seek a model which minimizes errors.

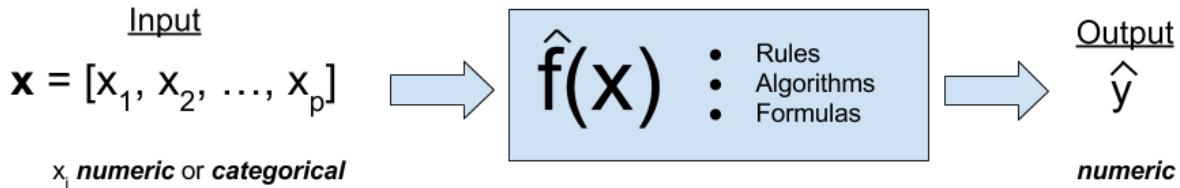


Figure 11.1:

First, note that a linear model is one of many methods used in regression. **Regression** is a form of **supervised learning**. Supervised learning deals with problems where there are both an input and an output. Regression problems are the subset of supervised learning problems with a **numeric** output.

Often one of the biggest differences between *statistical learning*, *machine learning*, *artificial intelligence* are the names used to describe variables and methods.

- The **input** can be called: input vector, feature vector, or predictors. The elements of these would be an input, feature, or predictor. The individual features can be either numeric or categorical.
- The **output** may be called: output, response, outcome, or target. The response must be numeric.

As an aside, some textbooks and statisticians use the terms independent and dependent variables to describe the response and the predictors. However, this practice can be confusing as those terms have specific meanings in probability theory.

*Our goal is to find a rule, algorithm, or function which takes as input a feature vector, and outputs a response which is as close to the true value as possible.* We often write the true, unknown relationship between the input and output  $f(\mathbf{x})$ . The relationship we learn, based on data, is written  $\hat{f}(\mathbf{x})$ .

From a statistical learning point-of-view, we write,

$$Y = f(\mathbf{x}) + \epsilon$$

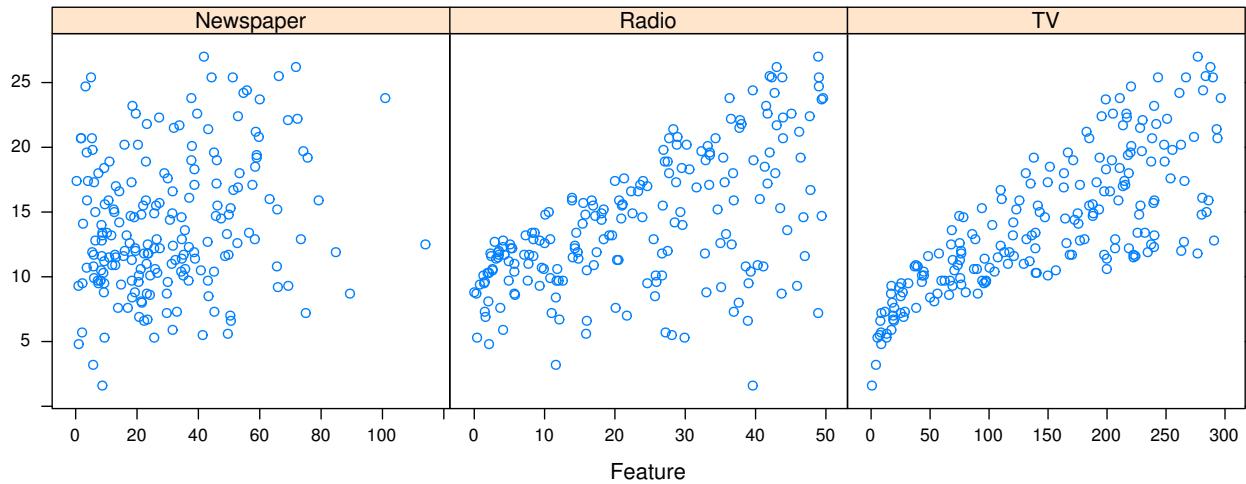
to indicate that the true response is a function of both the unknown relationship, as well as some unlearnable noise.

To discuss linear models in the context of prediction, we return to the `Advertising` data from the previous chapter.

### Advertising

```
## # A tibble: 200 × 4
##       TV Radio Newspaper Sales
##   <dbl> <dbl>    <dbl> <dbl>
## 1 230.1 37.8     69.2  22.1
## 2 44.5  39.3     45.1  10.4
## 3 17.2  45.9     69.3   9.3
## 4 151.5 41.3     58.5  18.5
## 5 180.8 10.8     58.4  12.9
## 6  8.7  48.9     75.0   7.2
## 7 57.5  32.8     23.5  11.8
## 8 120.2 19.6     11.6  13.2
## 9  8.6  2.1      1.0   4.8
## 10 199.8 2.6     21.2  10.6
## # ... with 190 more rows
```

```
library(caret)
featurePlot(x = Advertising[, c("TV", "Radio", "Newspaper")], y = Advertising$Sales)
```



## 11.1 Assessing Model Accuracy

There are many metrics to assess the accuracy of a regression model. Most of these measure in some way the average error that the model makes. The metric that we will be most interested in is the root-mean-square error.

$$\text{RMSE}(\hat{f}, \text{Data}) = \sqrt{\frac{1}{n} \sum_{i=1}^n (y_i - \hat{f}(\mathbf{x}_i))^2}$$

While for the sake of comparing models, the choice between RMSE and MSE is arbitrary, we have a preference for RMSE, as it has the same units as the response variable. Also, notice that in the prediction context MSE refers to an average, whereas in an ANOVA context, the denominator for MSE may not be  $n$ .

For a linear model , the estimate of  $f$ ,  $\hat{f}$ , is given by the fitted regression line.

$$\hat{y}_i = \hat{f}(\mathbf{x}_i)$$

We can write an R function that will be useful for performing this calculation.

```
rmse = function(actual, predicted) {
  sqrt(mean((actual - predicted) ^ 2))
}
```

## 11.2 Model Complexity

Aside from how well a model predicts, we will also be very interested in the complexity (flexibility) of a model. For now, we will only considered nested linear models for simplicity. Then in that case, the more predictors that a model has, the more complex the model. For the sake of assigning a numerical value to the complexity of a linear model, we will use the number of predictors,  $p$ .

We write a simple R function to extract this information from a model.

```
get_complexity = function(model) {
  length(coef(model)) - 1
}
```

## 11.3 Test-Train Split

There is an issue with fitting a model to all available data then using RMSE to determine how well the model predicts. It is essentially cheating! As a linear model becomes more complex, the RSS, thus RMSE, can never go up. It will only go down, or in very specific cases, stay the same.

This would suggest that to predict well, we should use the largest possible model! However, in reality we have hard fit to a specific dataset, but as soon as we see new data, a large model may in fact predict poorly. This is called **overfitting**.

Frequently we will take a dataset of interest and split it in two. One part of the datasets will be used to fit (train) a model, which we will call the **training** data. The remainder of the original data will be used to assess how well the model is predicting, which we will call the **test** data. Test data should *never* be used to train a model.

Note that sometimes the terms *evaluation set* and *test set* are used interchangeably. We will give somewhat specific definitions to these later. For now we will simply use a single test set for a training set.

Here we use the `sample()` function to obtain a random sample of the rows of the original data. We then use those row numbers (and remaining row numbers) to split the data accordingly. Notice we used the `set.seed()` function to allow use to reproduce the same random split each time we perform this analysis.

```
set.seed(9)
num_obs = nrow(Advertising)

train_index = sample(num_obs, size = trunc(0.50 * num_obs))
train_data = Advertising[train_index, ]
test_data = Advertising[-train_index, ]
```

We will look at two measures that assess how well a model is predicting, the **train RMSE** and the **test RMSE**.

$$\text{RMSE}_{\text{Train}} = \text{RMSE}(\hat{f}, \text{Train Data}) = \sqrt{\frac{1}{n_{\text{Tr}}} \sum_{i \in \text{Train}} (y_i - \hat{f}(\mathbf{x}_i))^2}$$

Here  $n_{Tr}$  is the number of observations in the train set. Train RMSE will still always go down (or stay the same) as the complexity of a linear model increases. That means train RMSE will not be useful for comparing models, but checking that it decreases is a useful sanity check.

$$\text{RMSE}_{\text{Test}} = \text{RMSE}(\hat{f}, \text{Train Data}) = \sqrt{\frac{1}{n_{\text{Te}}} \sum_{i \in \text{Test}} (y_i - \hat{f}(\mathbf{x}_i))^2}$$

Here  $n_{Te}$  is the number of observations in the test set. Test RMSE uses the model fit to the training data, but evaluated on the unused test data. This is a measure of how well the fitted model will predict **in general**, not simply how well it fits data used to train the model, as is the case with train RMSE. What happens to test RMSE as the size of the model increases? That is what we will investigate.

We will start with the simplest possible linear model, that is, a model with no predictors.

```
fit_0 = lm(Sales ~ 1, data = train_data)
get_complexity(fit_0)

## [1] 0

# train RMSE
sqrt(mean((train_data$Sales - predict(fit_0, train_data)) ^ 2))

## [1] 4.788513

# test RMSE
sqrt(mean((test_data$Sales - predict(fit_0, test_data)) ^ 2))

## [1] 5.643574
```

The previous two operations obtain the train and test RMSE. Since these are operations we are about to use repeatedly, we should use the function that we happen to have already written.

```
# train RMSE
rmse(actual = train_data$Sales, predicted = predict(fit_0, train_data))

## [1] 4.788513
```

```
# test RMSE
rmse(actual = test_data$Sales, predicted = predict(fit_0, test_data))

## [1] 5.643574
```

This function can actually be improved for the inputs that we are using. We would like to obtain train and test RMSE for a fitted model, given a train or test dataset, and the appropriate response variable.

```
get_rmse = function(model, data, response) {
  rmse(actual = data[, response],
       predicted = predict(model, data))
}
```

By using this function, our code becomes easier to read, and it is more obvious what task we are accomplishing.

```
get_rmse(model = fit_0, data = train_data, response = "Sales") # train RMSE

## [1] 4.788513

get_rmse(model = fit_0, data = test_data, response = "Sales") # test RMSE

## [1] 5.643574
```

## 11.4 Adding Flexibility to Linear Models

Each successive model we fit will be more and more flexible using both interactions and polynomial terms. We will see the training error decrease each time the model is made more flexible. We expect the test error to decrease a number of times, then eventually start going up, as a result of overfitting.

```
fit_1 = lm(Sales ~ ., data = train_data)
get_complexity(fit_1)

## [1] 3

get_rmse(model = fit_1, data = train_data, response = "Sales") # train RMSE

## [1] 1.637699

get_rmse(model = fit_1, data = test_data, response = "Sales") # test RMSE

## [1] 1.737574

fit_2 = lm(Sales ~ Radio * Newspaper * TV, data = train_data)
get_complexity(fit_2)

## [1] 7
```

```
get_rmse(model = fit_2, data = train_data, response = "Sales") # train RMSE
```

```
## [1] 0.7797226
```

```
get_rmse(model = fit_2, data = test_data, response = "Sales") # test RMSE
```

```
## [1] 1.110372
```

```
fit_3 = lm(Sales ~ Radio * Newspaper * TV + I(TV ^ 2), data = train_data)
get_complexity(fit_3)
```

```
## [1] 8
```

```
get_rmse(model = fit_3, data = train_data, response = "Sales") # train RMSE
```

```
## [1] 0.4960149
```

```
get_rmse(model = fit_3, data = test_data, response = "Sales") # test RMSE
```

```
## [1] 0.7320758
```

```
fit_4 = lm(Sales ~ Radio * Newspaper * TV +
           I(TV ^ 2) + I(Radio ^ 2) + I(Newspaper ^ 2), data = train_data)
get_complexity(fit_4)
```

```
## [1] 10
```

```
get_rmse(model = fit_4, data = train_data, response = "Sales") # train RMSE
```

```
## [1] 0.488771
```

```
get_rmse(model = fit_4, data = test_data, response = "Sales") # test RMSE
```

```
## [1] 0.7466312
```

```
fit_5 = lm(Sales ~ Radio * Newspaper * TV +
           I(TV ^ 2) * I(Radio ^ 2) * I(Newspaper ^ 2), data = train_data)
get_complexity(fit_5)
```

```
## [1] 14
```

```
get_rmse(model = fit_5, data = train_data, response = "Sales") # train RMSE
```

```
## [1] 0.4705201
```

```
get_rmse(model = fit_5, data = test_data, response = "Sales") # test RMSE
```

```
## [1] 0.8425384
```

## 11.5 Choosing a Model

To better understand the relationship between train RMSE, test RMSE, and model complexity, we summarize our results, as the above is somewhat cluttered.

First, we recap the models that we have fit.

```
fit_1 = lm(Sales ~ ., data = train_data)
fit_2 = lm(Sales ~ Radio * Newspaper * TV, data = train_data)
fit_3 = lm(Sales ~ Radio * Newspaper * TV + I(TV ^ 2), data = train_data)
fit_4 = lm(Sales ~ Radio * Newspaper * TV +
           I(TV ^ 2) + I(Radio ^ 2) + I(Newspaper ^ 2), data = train_data)
fit_5 = lm(Sales ~ Radio * Newspaper * TV +
           I(TV ^ 2) * I(Radio ^ 2) * I(Newspaper ^ 2), data = train_data)
```

Next, we create a list of the models fit.

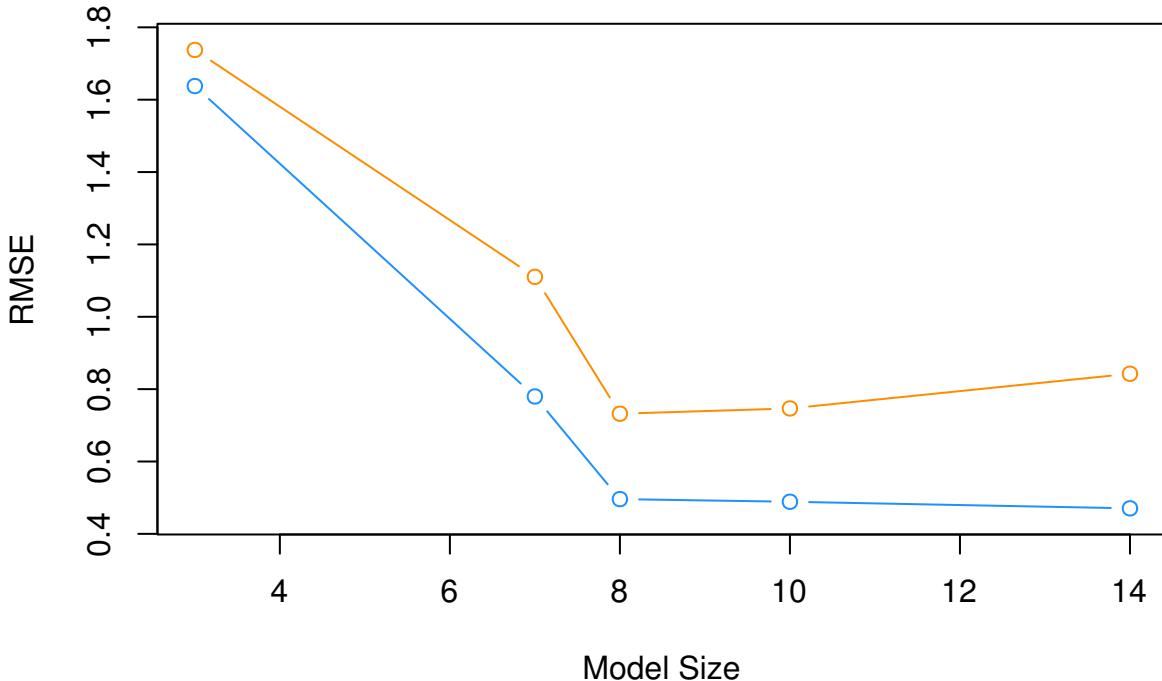
```
model_list = list(fit_1, fit_2, fit_3, fit_4, fit_5)
```

We then obtain train RMSE, test RMSE, and model complexity for each.

```
train_rmse = sapply(model_list, get_rmse, data = train_data, response = "Sales")
test_rmse = sapply(model_list, get_rmse, data = test_data, response = "Sales")
model_complexity = sapply(model_list, get_complexity)
```

We then plot the results. The train RMSE can be seen in blue, while the test RMSE is given in orange.

```
plot(model_complexity, train_rmse, type = "b",
      ylim = c(min(c(train_rmse, test_rmse)) - 0.02,
               max(c(train_rmse, test_rmse)) + 0.02),
      col = "dodgerblue",
      xlab = "Model Size",
      ylab = "RMSE")
lines(model_complexity, test_rmse, type = "b", col = "darkorange")
```



We also summarize the results as a table. `fit_1` is the least flexible, and `fit_5` is the most flexible. We see the Train RMSE decrease as flexibility increases. We see that the Test RMSE is smallest for `fit_3`, thus is the model we believe will perform the best on future data not used to train the model. Note this may not be the best model, but it is the best model of the models we have seen in this example.

Model	Train RMSE	Test RMSE	Predictors
<code>fit_1</code>	1.6376991	1.7375736	3
<code>fit_2</code>	0.7797226	1.1103716	7
<code>fit_3</code>	0.4960149	0.7320758	8
<code>fit_4</code>	0.488771	0.7466312	10
<code>fit_5</code>	0.4705201	0.8425384	14

To summarize:

- **Underfitting models:** In general *High* Train RMSE, *High* Test RMSE. Seen in `fit_1` and `fit_2`.
- **Overfitting models:** In general *Low* Train RMSE, *High* Test RMSE. Seen in `fit_4` and `fit_5`.

Specifically, we say that a model is overfitting if there exists a less complex model with lower Test RMSE. Then a model is underfitting if there exists a more complex model with lower Test RMSE.

A number of notes on these results:

- The labels of under and overfitting are *relative* to the best model we see, `fit_3`. Any model more complex with higher Test RMSE is overfitting. Any model less complex with higher Test RMSE is underfitting.
- The train RMSE is guaranteed to follow this non-increasing pattern. The same is not true of test RMSE. Here we see a nice U-shaped curve. There are theoretical reasons why we should expect this, but that is on average. Because of the randomness of one test-train split, we may not always see this result. Re-perform this analysis with a different seed value and the pattern may not hold. We will discuss why we expect this next chapter. We will discuss how we can help create this U-shape much later.

- Often we expect train RMSE to be lower than test RMSE. Again, due to the randomness of the split, you may get lucky and this will not be true.

A final note on the analysis performed here; we paid no attention whatsoever to the “assumptions” of a linear model. We only sought a model that **predicted** well, and paid no attention to a model for **explanation**. Hypothesis testing did not play a role in deciding the model, only prediction accuracy. Collinearity? We don’t care. Assumptions? Still don’t care. Diagnostics? Never heard of them. (These statements are a little over the top, and not completely true, but just to drive home the point that we only care about prediction. Often we latch onto methods that we have seen before, even when they are not needed.)



# Chapter 12

## Simulating the Bias–Variance Tradeoff

Consider the general regression setup

$$y = f(\mathbf{x}) + \epsilon$$

with

$$E[\epsilon] = 0 \quad \text{and} \quad \text{var}(\epsilon) = \sigma^2.$$

### 12.1 Bias–Variance Decomposition

Using  $\hat{f}(\mathbf{x})$ , trained with data, to estimate  $f(\mathbf{x})$ , we are interested in the expected prediction error. Specifically, considered making a prediction of  $y_0 = \hat{f}(\mathbf{x}_0) + \epsilon$  at the point  $\mathbf{x}_0$ .

In that case, we have

$$E \left[ (y_0 - \hat{f}(\mathbf{x}_0))^2 \right] = \text{bias} \left( \hat{f}(\mathbf{x}_0) \right)^2 + \text{var} \left( \hat{f}(\mathbf{x}_0) \right) + \sigma^2.$$

Recall the definition of the bias of an estimate.

$$\text{bias} \left( \hat{f}(\mathbf{x}_0) \right) = E \left[ \hat{f}(\mathbf{x}_0) \right] - f(\mathbf{x}_0)$$

So, we have decomposed the error into two types; **reducible** and **irreducible**. The reducible can be further decomposed into the squared **bias** and **variance** of the estimate. We can “control” these through our choice of model. The irreducible, is noise, that should not and cannot be modeled.

### 12.2 Simulation

We will illustrate this decomposition, and the resulting bias-variance tradeoff through simulation. Suppose we would like a train a model to learn the function  $f(x) = x^2$ .

```
f = function(x) {  
  x ^ 2  
}
```

More specifically,

$$y = x^2 + \epsilon$$

where

$$\epsilon \sim N(\mu = 0, \sigma^2 = 0.3^2).$$

We write a function which generates data accordingly.

```
get_sim_data = function(f, sample_size = 100) {
  x = runif(n = sample_size, min = 0, max = 1)
  y = f(x) + rnorm(n = sample_size, mean = 0, sd = 0.3)
  data.frame(x, y)
}
```

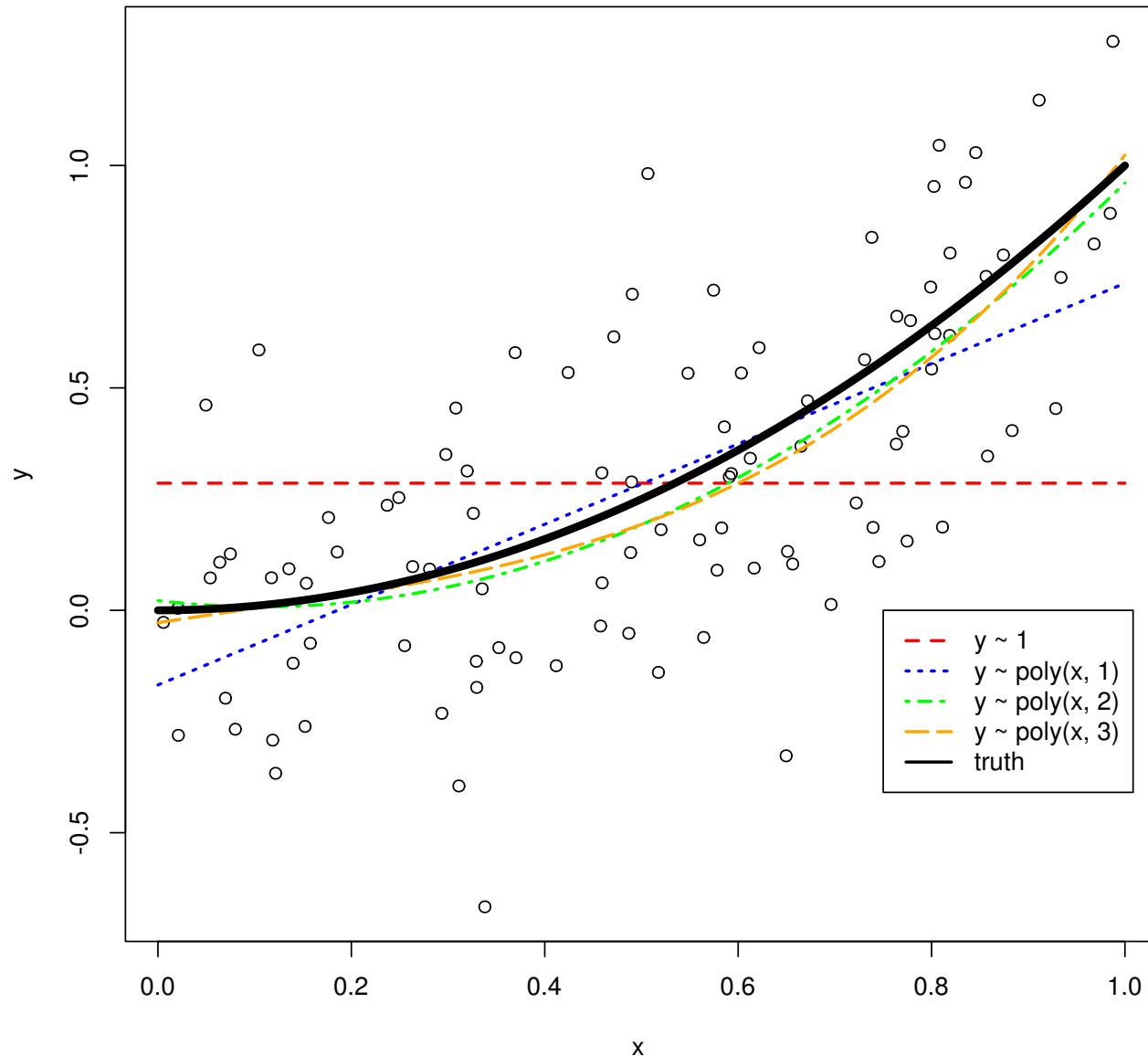
To get a sense of the data, we generate one simulated dataset, and fit the four models that we will be of interest.

```
sim_data = get_sim_data(f, sample_size = 100)

fit_1 = lm(y ~ 1, data = sim_data)
fit_2 = lm(y ~ poly(x, degree = 1), data = sim_data)
fit_3 = lm(y ~ poly(x, degree = 2), data = sim_data)
fit_4 = lm(y ~ poly(x, degree = 3), data = sim_data)
```

Plotting these four trained models, we see that the zero predictor model (red) does very poorly. The single predictor model (blue) is reasonable, but we can see that the two (green) and three (orange) predictor models seem more appropriate. Between these latter two, it is hard to see which seems more appropriate.

```
set.seed(430)
plot(y ~ x, data = sim_data)
grid = seq(from = 0, to = 1, by = 0.01)
lines(grid, predict(fit_1, newdata = data.frame(x = grid)),
      col = "red", lwd = 2, lty = 2)
lines(grid, predict(fit_2, newdata = data.frame(x = grid)),
      col = "blue", lwd = 2, lty = 3)
lines(grid, predict(fit_3, newdata = data.frame(x = grid)),
      col = "green", lwd = 2, lty = 4)
lines(grid, predict(fit_4, newdata = data.frame(x = grid)),
      col = "orange", lwd = 2, lty = 5)
lines(grid, f(grid), col = "black", lwd = 5)
legend(x = 0.75, y = 0,
       c("y ~ 1", "y ~ poly(x, 1)", "y ~ poly(x, 2)", "y ~ poly(x, 3)", "truth"),
       col = c("red", "blue", "green", "orange", "black"), lty = c(2, 3, 4, 5, 1), lwd = 2)
```



We will now use simulation to estimate the bias, variance, and mean squared error for the estimates for  $f(x)$  given by these models at the point  $x_0 = 0.95$ . We use simulation to complete this task, as performing the exact calculations are always difficult, and often impossible.

```
set.seed(1)
n_sims = 1000
n_models = 4
x0 = 0.95
predictions = matrix(0, nrow = n_sims, ncol = n_models)
sim_data = get_sim_data(f, sample_size = 100)
plot(y ~ x, data = sim_data, col = "white", xlim = c(0.75, 1), ylim = c(0, 1.5))

for (i in 1:n_sims) {

  sim_data = get_sim_data(f, sample_size = 100)

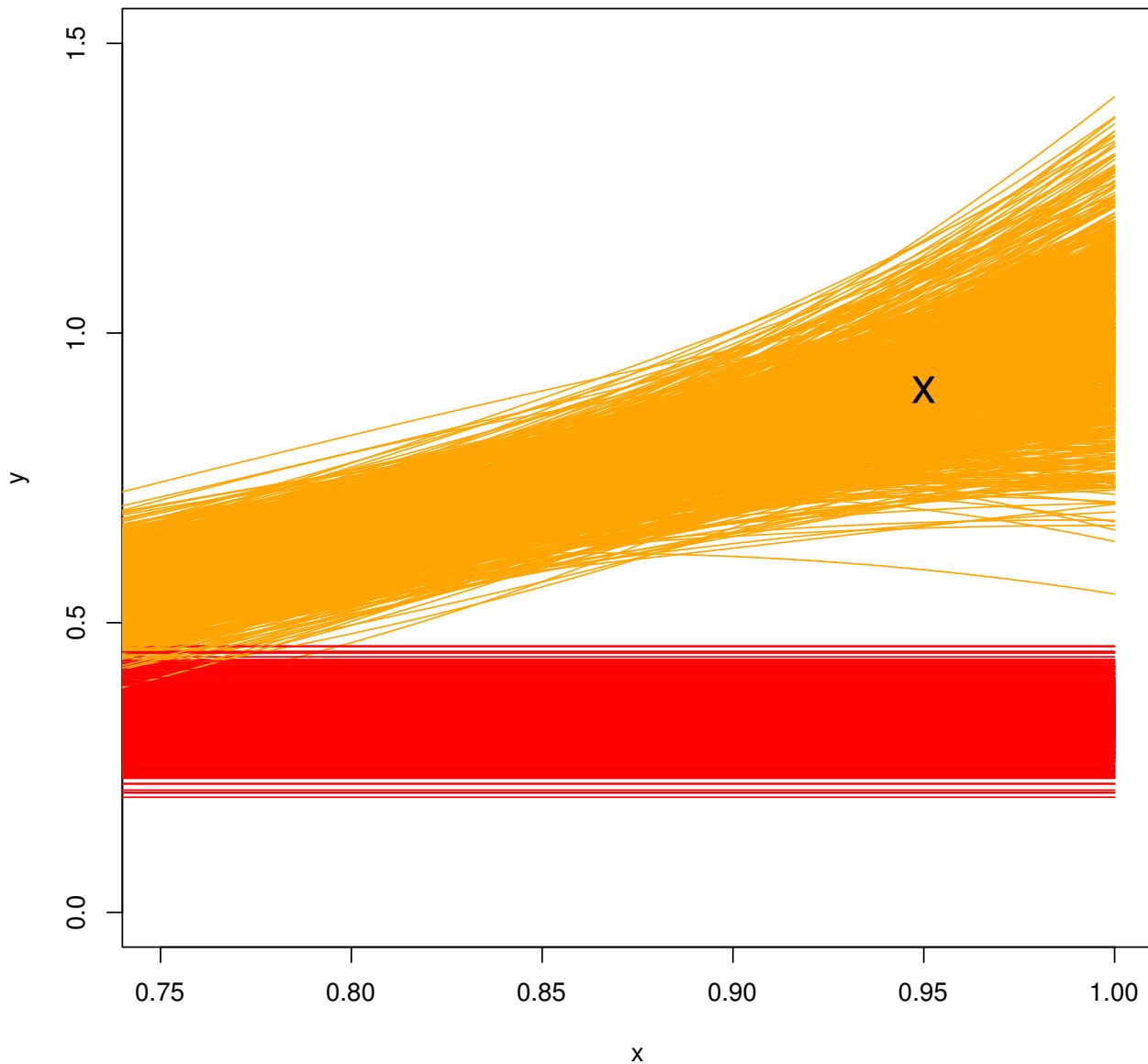
  fit_1 = lm(y ~ 1, data = sim_data)
```

```
fit_2 = lm(y ~ poly(x, degree = 1), data = sim_data)
fit_3 = lm(y ~ poly(x, degree = 2), data = sim_data)
fit_4 = lm(y ~ poly(x, degree = 3), data = sim_data)

lines(grid, predict(fit_1, newdata = data.frame(x = grid)), col = "red", lwd = 1)
# lines(grid, predict(fit_2, newdata = data.frame(x = grid)), col = "blue", lwd = 1)
# lines(grid, predict(fit_3, newdata = data.frame(x = grid)), col = "green", lwd = 1)
lines(grid, predict(fit_4, newdata = data.frame(x = grid)), col = "orange", lwd = 1)

predictions[i, ] = c(
  predict(fit_1, newdata = data.frame(x = x0)),
  predict(fit_2, newdata = data.frame(x = x0)),
  predict(fit_3, newdata = data.frame(x = x0)),
  predict(fit_4, newdata = data.frame(x = x0))
)
}

points(x0, f(x0), col = "black", pch = "x", cex = 2)
```



The above plot shows the 1000 trained models for each of the zero predictor and three predictor models. (We have excluded the one and two predictor models for clarity of the plot.) The truth at  $x_0 = 0.95$  is given by a black “X”. We see that the red lines for the zero predictor model are on average wrong, with some variability. The orange lines for the three predictor model are on average correct, but with more variance.

## 12.3 Bias-Variance Tradeoff

To evaluate the bias and variance, we simulate values for the response  $y$  at  $x_0 = 0.95$  according to the true model.

```
eps = rnorm(n = n_sims, mean = 0, sd = 0.3)
y0 = f(x0) + eps
```

R already has a function to calculate variance, however, we add functions for bias and mean squared error.

```
get_bias = function(estimate, truth) {
  mean(estimate) - truth
}

get_mse = function(estimate, truth) {
  mean((estimate - truth) ^ 2)
}
```

When then use the predictions obtained from the above simulation to estimate the bias, variance and mean squared error for estimating  $f(x)$  at  $x_0 = 0.95$  for the four models.

```
bias = apply(predictions, 2, get_bias, f(x0))
variance = apply(predictions, 2, var)
mse = apply(predictions, 2, get_mse, y0)
```

We summarize these results in the following table.

Model	Squared Bias	Variance (Of Estimate)	MSE
fit_1	0.322916	0.001784	0.4201411
fit_2	0.0136794	0.0036355	0.1145159
fit_3	0.0000036	0.0058178	0.1031294
fit_4	0.0000009	0.0079906	0.1053599

A number of things to notice here:

- We use squared bias in this table. Since bias can be positive or negative, squared bias is more useful for observing the trend as complexity increases.
- The squared bias trend which we see here is **decreasing** bias as complexity increases, which we expect to see in general.
- The exact opposite is true of variance. As model complexity increases, variance **increases**.
- The mean squared error, which is a function of the bias and variance, decreases, then increases. This is a result of the bias-variance tradeoff. We can decrease bias, by increases variance. Or, we can decrease variance by increasing bias. By striking the correct balance, we can find a good mean squared error.

We can check for these trends with the `diff()` function in R.

```
all(diff(bias ^ 2) < 0)

## [1] TRUE

all(diff(variance) > 0)

## [1] TRUE

diff(mse)

## [1] -0.305625170 -0.011386537  0.002230515
```

Notice that the table lacks a column for the variance of the noise. Add this to squared bias and variance would give the mean squared error. However, notice that we are simulation to estiamte the bias and variance, so the relationship is not exact. If we used more replications of the simulation, these two values would move closer together.

```
bias ^ 2 + variance + var(eps)

## [1] 0.4209744 0.1135892 0.1020958 0.1042659

mse

## [1] 0.4201411 0.1145159 0.1031294 0.1053599
```



# Chapter 13

## Classification

**Classification** is a form of **supervised learning** where the response variable is categorical, as opposed to numeric for regression. *Our goal is to find a rule, algorithm, or function which takes as input a feature vector, and outputs a category which is the true category as often as possible.*

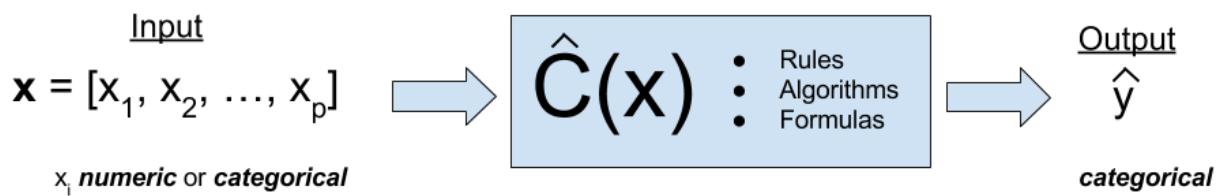


Figure 13.1:

That is, the classifier  $\hat{C}$  returns the predicted category  $\hat{y}$ .

$$\hat{y}_i = \hat{C}(\mathbf{x}_i)$$

To build our first classifier, we will use the `Default` dataset from the `ISLR` package.

```
library(ISLR)
library(tibble)
as_tibble(Default)
```

```
## # A tibble: 10,000 × 4
##   default student  balance    income
##   <fctr>  <fctr>     <dbl>     <dbl>
## 1 No      No    729.5265 44361.625
## 2 No      Yes   817.1804 12106.135
## 3 No      No    1073.5492 31767.139
## 4 No      No    529.2506 35704.494
## 5 No      No    785.6559 38463.496
## 6 No      Yes   919.5885 7491.559
## 7 No      No    825.5133 24905.227
## 8 No      Yes   808.6675 17600.451
```

```
## 9      No      No 1161.0579 37468.529
## 10     No      No  0.0000 29275.268
## # ... with 9,990 more rows
```

Our goal is to properly classify individuals as defaulters based on student status, credit card balance, and income. Be aware that the response `default` is a factor, as is the predictor `student`.

```
is.factor(Default$default)
```

```
## [1] TRUE
```

```
is.factor(Default$student)
```

```
## [1] TRUE
```

As we did with regression, we test-train split our data. In this case, using 50% for each.

```
set.seed(42)
train_index = sample(nrow(Default), 5000)
train_default = Default[train_index, ]
test_default = Default[-train_index, ]
```

## 13.1 Visualization for Classification

Often, some simple visualizations can suggest simple classification rules. To quickly create some useful visualizations, we use the `featurePlot()` function from the `caret()` package.

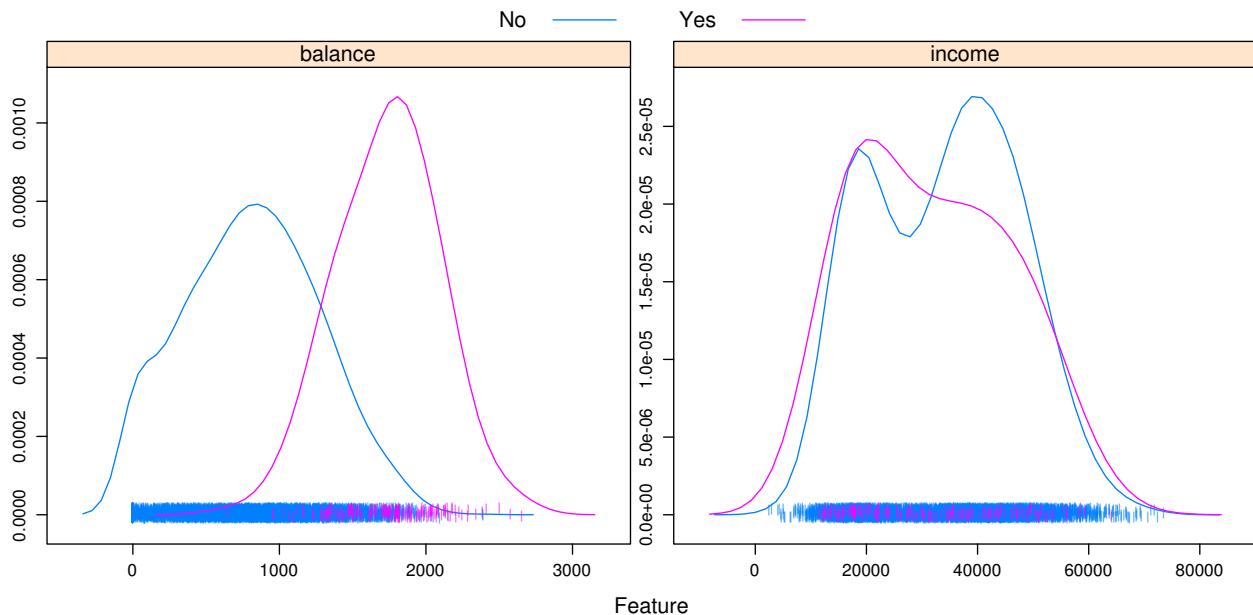
```
library(caret)
```

A density plot can often suggest a simple split based on a numeric predictor. Essentially this plot graphs a density estimate

$$f_{X_i}(x_i \mid y = k)$$

for each numeric predictor  $x_i$  and each category  $k$  of the response  $y$ .

```
featurePlot(x = train_default[, c("balance", "income")],
            y = train_default$default,
            plot = "density",
            scales = list(x = list(relation = "free"),
                          y = list(relation = "free")),
            adjust = 1.5,
            pch = "|",
            layout = c(2, 1),
            auto.key = list(columns = 2))
```

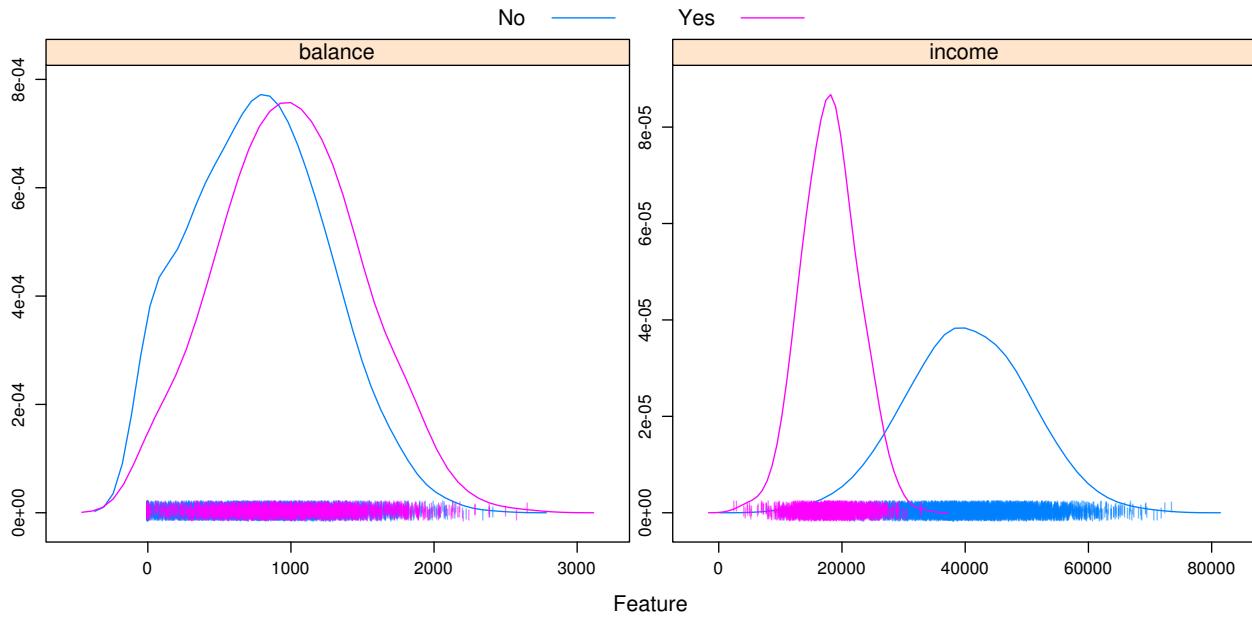


Some notes about the arguments to this function:

- `x` is a data frame containing only **numeric predictors**. It would be nonsensical to estimate a density for a categorical predictor.
- `y` is the response variable. It needs to be a factor variable. If coded as 0 and 1, you will need to coerce to factor for plotting.
- `plot` specifies the type of plot, here `density`.
- `scales` defines the scale of the axes for each plot. By default, the axis of each plot would be the same, which often is not useful, so the arguments here, a different axis for each plot, will almost always be used.
- `adjust` specifies the amount of smoothing used for the density estimate.
- `pch` specifies the `plot` character used for the bottom of the plot.
- `layout` places the individual plots into rows and columns. For some odd reason, it is given as `(col, row)`.
- `auto.key` defines the key at the top of the plot. The number of columns should be the number of categories.

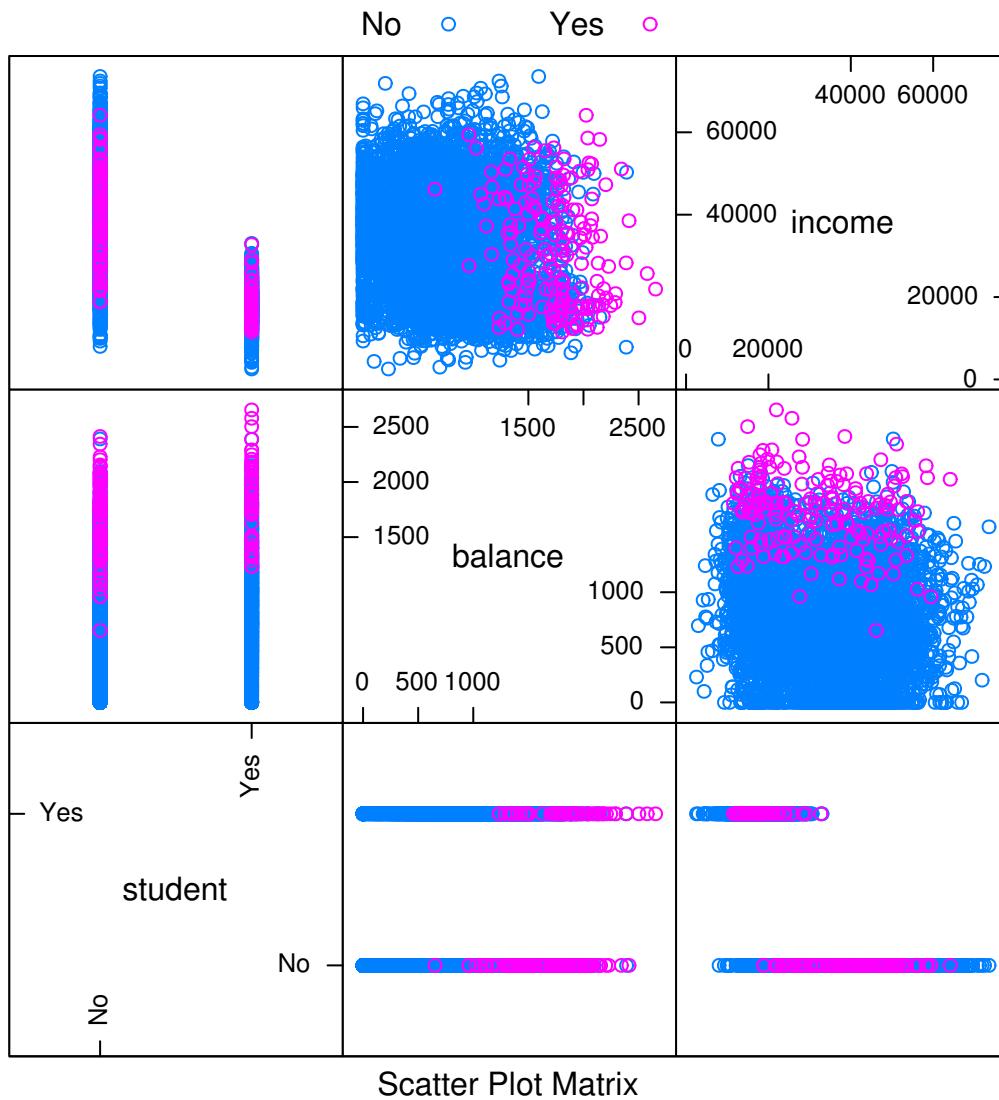
It seems that the income variable by itself is not particularly useful. However, there seems to be a big difference in default status at a `balance` of about 1400. We will use this information shortly.

```
featurePlot(x = train_default[, c("balance", "income")],
            y = train_default$student,
            plot = "density",
            scales = list(x = list(relation = "free"),
                          y = list(relation = "free")),
            adjust = 1.5,
            pch = "|",
            layout = c(2, 1),
            auto.key = list(columns = 2))
```



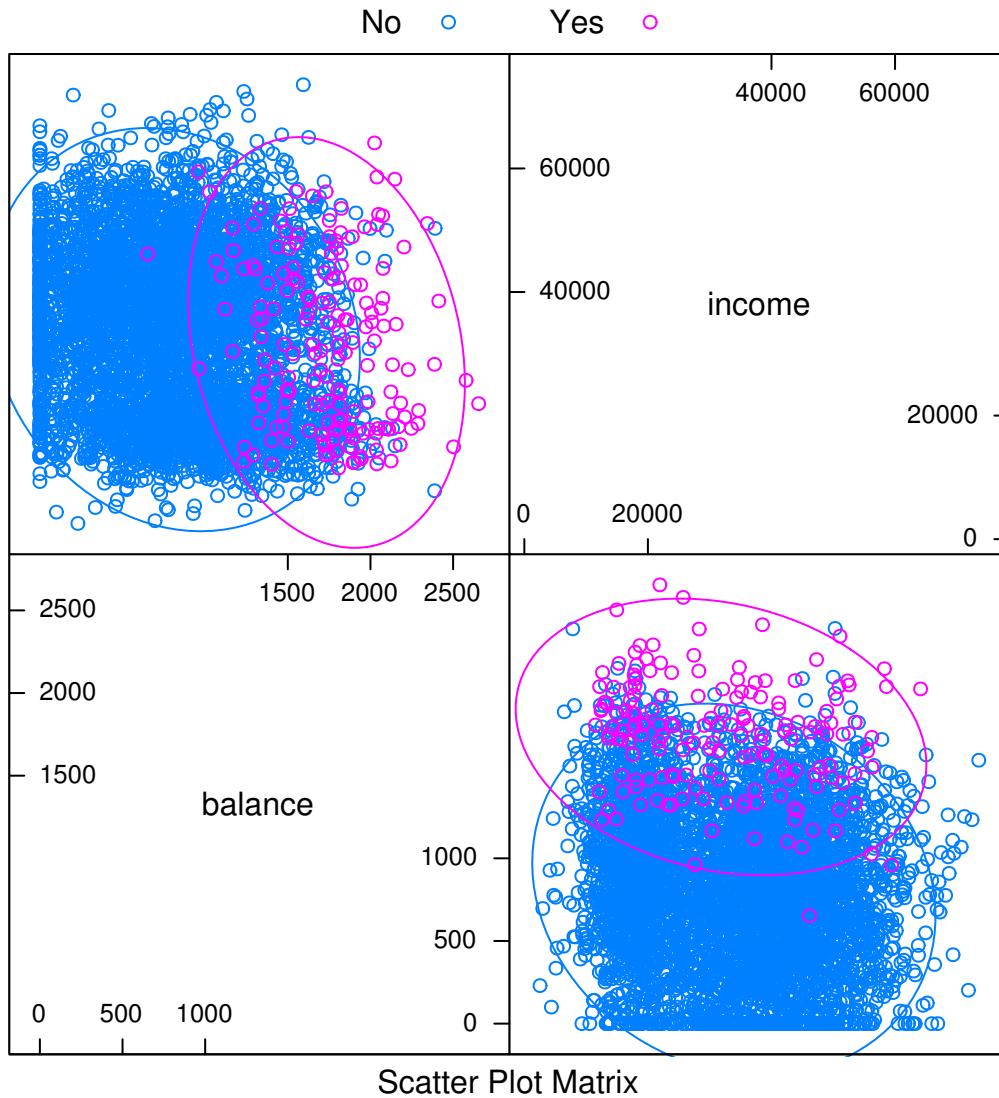
Above, we create a similar plot, except with `student` as the response. We see that students often carry a slightly larger balance, and have far lower income. This will be useful to know when making more complicated classifiers.

```
featurePlot(x = train_default[, c("student", "balance", "income")],
            y = train_default$default,
            plot = "pairs",
            auto.key = list(columns = 2))
```



We can use `plot = "pairs"` to consider multiple variables at the same time. This plot reinforces using `balance` to create a classifier, and again shows that `income` seems not that useful.

```
library(ellipse)
featurePlot(x = train_default[, c("balance", "income")],
            y = train_default$default,
            plot = "ellipse",
            auto.key = list(columns = 2))
```



Similar to `pairs` is a plot of type `ellipse`, which requires the `ellipse` package. Here we only use numeric predictors, as essentially we are assuming multivariate normality. The ellipses mark points of equal density. This will be useful later when discussing LDA and QDA.

## 13.2 A Simple Classifier

A very simple classifier is a rule based on a boundary  $b$  for a particular input variable  $x$ .

$$\hat{C}(\mathbf{x}) = \begin{cases} 1 & x > b \\ 0 & x \leq b \end{cases}$$

Based on the first plot, we believe we can use `balance` to create a reasonable classifier. In particular,

$$\hat{C}(\text{balance}) = \begin{cases} \text{Yes} & \text{balance} > 1400 \\ \text{No} & \text{balance} \leq 1400 \end{cases}$$

So we predict an individual is a defaulter if their `balance` is above 1400, and not a defaulter if the balance is 1400 or less.

```
simple_class = function(x, boundary, above = 1, below = 0) {
  ifelse(x > boundary, above, below)
}
```

We write a simple R function that compares a variable to a boundary, then use it to make predictions on the train and test sets with our chosen variable and boundary.

```
train_pred = simple_class(x = train_default$balance,
                         boundary = 1400, above = "Yes", below = "No")
test_pred = simple_class(x = test_default$balance,
                         boundary = 1400, above = "Yes", below = "No")
head(train_pred, n = 10)

## [1] "No"  "Yes" "No"  "No"  "No"  "No"  "No"  "No"  "No"  "No"
```

### 13.3 Metrics for Classification

In the classification setting, there are a large number of metrics to asses how well a classifier is performing.

One of the most obvious things to do is arrange predictions and true values in a cross table.

```
(train_tab = table(predicted = train_pred, actual = train_default$default))
```

```
##           actual
## predicted   No  Yes
##       No  4319   29
##       Yes  513  139
```

```
(test_tab = table(predicted = test_pred, actual = test_default$default))
```

```
##           actual
## predicted   No  Yes
##       No  4361   23
##       Yes  474  142
```

Often we give specific names to individual cells of these tables, and in the predictive setting, we would call this table a **confusion matrix**. Be aware, that the placement of Actual and Predicted values affects the names of the cells, and often the matrix may be presented transposed.

In statistics, we label the errors Type I and Type II, but these are hard to remember. False Positive and False Negative are more descriptive, so we choose to use these.

The `confusionMatrix()` function from the `caret` package can be used to obtain a wealth of additional information, which we see output below for the test data. Note that we specify which category is considered “positive.”

		Actual	
		False (0)	True (1)
Predicted	False (0)	True Negative ( <b>TN</b> )	False Negative ( <b>FN</b> )
	True (1)	False Positive ( <b>FP</b> )	True Positive ( <b>TP</b> )

Figure 13.2:

```
train_con_mat = confusionMatrix(train_tab, positive = "Yes")
(test_con_mat = confusionMatrix(test_tab, positive = "Yes"))
```

```
## Confusion Matrix and Statistics
##
##           actual
## predicted   No  Yes
##       No 4361   23
##       Yes 474  142
##
##           Accuracy : 0.9006
##                 95% CI : (0.892, 0.9088)
##       No Information Rate : 0.967
##       P-Value [Acc > NIR] : 1
##
##           Kappa : 0.3287
##   Mcnemar's Test P-Value : <2e-16
##
##           Sensitivity : 0.8606
##           Specificity : 0.9020
##       Pos Pred Value : 0.2305
##       Neg Pred Value : 0.9948
##           Prevalence : 0.0330
##       Detection Rate : 0.0284
##   Detection Prevalence : 0.1232
##       Balanced Accuracy : 0.8813
##
##       'Positive' Class : Yes
##
```

The most common, and most important metric is the **classification accuracy**.

$$\text{Acc}(\hat{C}, \text{Data}) = \frac{1}{n} \sum_{i=1}^n I(y_i = \hat{C}(\mathbf{x}_i))$$

Here,  $I$  is an indicator function, so we are essentially calculating the proportion of predicted classes that match the true class.

$$I(y_i = \hat{C}(x)) = \begin{cases} 1 & y_i = \hat{C}(x) \\ 0 & y_i \neq \hat{C}(x) \end{cases}$$

It is also common to discuss the **misclassification rate**, or classification error, which is simply one minus the accuracy.

Like regression, we often split the data, and then consider Train Accuracy and Test Accuracy. Test Accuracy will be used as a measure of how well a classifier will work on unseen future data.

$$\text{Acc}_{\text{Train}}(\hat{C}, \text{Train Data}) = \frac{1}{n_{Tr}} \sum_{i \in \text{Train}} I(y_i = \hat{C}(\mathbf{x}_i))$$

$$\text{Acc}_{\text{Test}}(\hat{C}, \text{Test Data}) = \frac{1}{n_{Te}} \sum_{i \in \text{Test}} I(y_i = \hat{C}(\mathbf{x}_i))$$

These accuracy values are given by calling `confusionMatrix()`, or, if stored, can be accessed directly.

```
train_con_mat$overall["Accuracy"]
```

```
## Accuracy
## 0.8916
```

```
test_con_mat$overall["Accuracy"]
```

```
## Accuracy
## 0.9006
```

Sometimes guarding against making certain errors, FP or FN, are more important than simply finding the best accuracy. Thus, sometimes we will consider **sensitivity** and **specificity**.

$$\text{Sens} = \text{True Positive Rate} = \frac{\text{TP}}{\text{P}} = \frac{\text{TP}}{\text{TP} + \text{FN}}$$

```
test_con_mat$byClass["Sensitivity"]
```

```
## Sensitivity
## 0.8606061
```

$$\text{Spec} = \text{True Negative Rate} = \frac{\text{TN}}{\text{N}} = \frac{\text{TN}}{\text{TN} + \text{FP}}$$

```
test_con_mat$byClass["Specificity"]
```

```
## Specificity
## 0.9019648
```

Like accuracy, these can easily be found using `confusionMatrix()`.

When considering how well a classifier is performing, often, it is understandable to assume that any accuracy in a binary classification problem above 0.50, is a reasonable classifier. This however is not the case. We need to consider the **balance** of the classes. To do so, we look at the **prevalence** of positive cases.

$$\text{Prev} = \frac{P}{\text{Total Obs}} = \frac{\text{TP} + \text{FN}}{\text{Total Obs}}$$

```
train_con_mat$byClass["Prevalence"]
```

```
## Prevalence
##      0.0336
```

```
test_con_mat$byClass["Prevalence"]
```

```
## Prevalence
##      0.033
```

Here, we see an extremely low prevalence, which suggests an even simpler classifier than our current based on **balance**.

$$\hat{C}(\text{balance}) = \begin{cases} \text{No} & \text{balance} > 1400 \\ \text{Yes} & \text{balance} \leq 1400 \end{cases}$$

This classifier simply classifies all observations as negative cases.

```
pred_all_no = simple_class(test_default$balance,
                            boundary = 1400, above = "No", below = "No")
table(predicted = pred_all_no, actual = test_default$default)
```

```
##           actual
## predicted   No   Yes
##       No 4835  165
```

The `confusionMatrix()` function won't even accept this table as input, because it isn't a full matrix, only one row, so we calculate some metrics “by hand”.

```
4835 / (4835 + 165) # test accuracy
```

```
## [1] 0.967
```

```
1 - 0.0336 # 1 - (train prevalence)
```

```
## [1] 0.9664
```

```
1 - 0.033 # 1 - (test prevalence)
```

```
## [1] 0.967
```

This classifier does better than the previous. But the point is, in reality, to create a good classifier, we should obtain a test accuracy better than 0.967, which is obtained by simply manipulating the prevalence. Next chapter, we'll introduce much better classifiers which should have no problem accomplishing this task.

# Chapter 14

## Logistic Regression

In this chapter, we continue our discussion of classification. We introduce our first model for classification, logistic regression. To begin, we return to the `Default` dataset from the previous chapter.

```
library(ISLR)
library(tibble)
as_tibble(Default)

## # A tibble: 10,000 × 4
##   default student    balance    income
##   <fctr>  <fctr>     <dbl>     <dbl>
## 1      No      No  729.5265 44361.625
## 2      No     Yes  817.1804 12106.135
## 3      No      No 1073.5492 31767.139
## 4      No      No  529.2506 35704.494
## 5      No      No  785.6559 38463.496
## 6      No     Yes  919.5885  7491.559
## 7      No      No  825.5133 24905.227
## 8      No     Yes  808.6675 17600.451
## 9      No      No 1161.0579 37468.529
## 10     No      No     0.0000 29275.268
## # ... with 9,990 more rows
```

We also repeat the test-train split from the previous chapter.

```
set.seed(42)
default_index = sample(nrow(Default), 5000)
default_train = Default[default_index, ]
default_test = Default[-default_index, ]
```

### 14.1 Linear Regression

Before moving on to logistic regression, why not plain, old, linear regression?

```
default_train_lm = default_train
default_test_lm = default_test
```

Since linear regression expects a numeric response variable, we coerce the response to be numeric. (Notice that we also shift the results, as we require 0 and 1, not 1 and 2.) Notice we have also copied the dataset so that we can return the original data with factors later.

```
default_train_lm$default = as.numeric(default_train_lm$default) - 1
default_test_lm$default = as.numeric(default_test_lm$default) - 1
```

Why would we think this should work? Recall that,

$$\hat{E}[Y | X = x] = X\hat{\beta}.$$

Since  $Y$  is limited to values of 0 and 1, we have

$$E[Y | X = x] = P[Y = 1 | X = x].$$

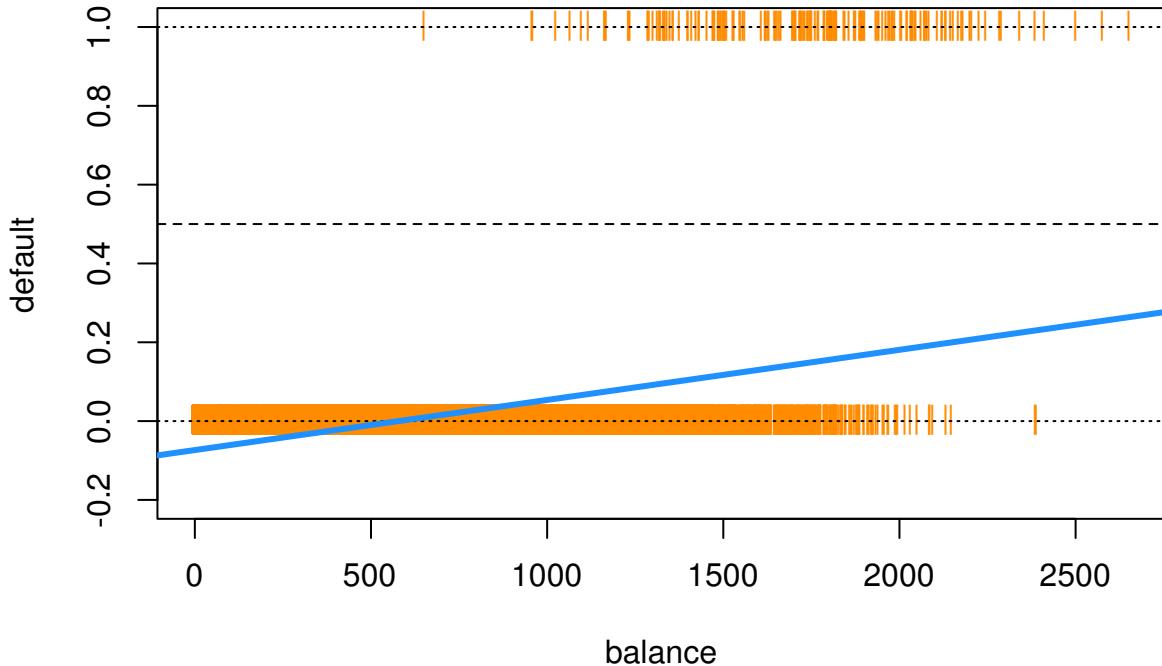
It would then seem reasonable that  $X\hat{\beta}$  is a reasonable estimate of  $P[Y = 1 | X = x]$ . We test this on the Default data.

```
model_lm = lm(default ~ balance, data = default_train_lm)
```

Everything seems to be working, until we plot the results.

```
plot(default ~ balance, data = default_train_lm,
      col = "darkorange", pch = "|", ylim = c(-0.2, 1),
      main = "Using Linear Regression for Classification")
abline(h = 0, lty = 3)
abline(h = 1, lty = 3)
abline(h = 0.5, lty = 2)
abline(model_lm, lwd = 3, col = "dodgerblue")
```

## Using Linear Regression for Classification



Two issues arise. First, all of the predicted probabilities are below 0.5. That means, we would classify every observation as a "No". This is certainly possible, but not what we would expect.

```
all(predict(model_lm) < 0.5)
```

```
## [1] TRUE
```

The next, and bigger issue, is predicted probabilities less than 0.

```
any(predict(model_lm) < 0)
```

```
## [1] TRUE
```

## 14.2 Bayes Classifier

Why are we using a predicted probability of 0.5 as the cutoff for classification? Recall, the Bayes Classifier, which minimizes the classification error:

$$C^B(\mathbf{x}) = \operatorname{argmax}_k P[Y = k | \mathbf{X} = \mathbf{x}]$$

So, in the binary classification problem, we will use predicted probabilities

$$\hat{p}(\mathbf{x}) = \hat{P}[Y = 1 | \mathbf{X} = \mathbf{x}]$$

and

$$\hat{P}[Y = 0 \mid \mathbf{X} = \mathbf{x}]$$

and then classify to the larger of the two. We actually only need to consider a single probability, usually for  $\hat{P}[Y = 1 \mid \mathbf{X} = \mathbf{x}]$ . Since we use it so often, we give it the shorthand notation,  $\hat{p}(\mathbf{x})$ . Then the classifier is written,

$$\hat{C}(\mathbf{x}) = \begin{cases} 1 & \hat{p}(\mathbf{x}) > 0.5 \\ 0 & \hat{p}(\mathbf{x}) \leq 0.5 \end{cases}$$

## 14.3 Logistic Regression with `glm()`

To better estimate the probability

$$p(\mathbf{x}) = P[Y = 1 \mid \mathbf{X} = \mathbf{x}]$$

we turn to logistic regression. The model is written

$$\log\left(\frac{p(\mathbf{x})}{1 - p(\mathbf{x})}\right) = \beta_0 + \beta_1 x_1 + \beta_2 x_2 + \cdots + \beta_p x_p.$$

Rearranging, we see the probabilities can be written as

$$p(\mathbf{x}) = \frac{1}{1 + e^{-(\beta_0 + \beta_1 x_1 + \beta_2 x_2 + \cdots + \beta_p x_p)}} = \sigma(\beta_0 + \beta_1 x_1 + \beta_2 x_2 + \cdots + \beta_p x_p)$$

Notice, we use the sigmoid function as shorthand notation, which appears often in deep learning literature. It takes any real input, and outputs a number between 0 and 1. How useful!

$$\sigma(x) = \frac{1}{1 + e^{-x}}$$

The model is fit by numerically maximizing the likelihood, which we will let R take care of.

We start with a single predictor example, again using `balance` as our single predictor.

```
model_glm = glm(default ~ balance, data = default_train, family = "binomial")
```

Fitting this model looks very similar to fitting a simple linear regression. Instead of `lm()` we use `glm()`. The only other difference is the use of `family = "binomial"` which indicates that we have a two-class categorical response. Using `glm()` with `family = "gaussian"` would perform the usual linear regression.

First, we can obtain the fitted coefficients the same way we did with linear regression.

```
coef(model_glm)
```

```
## (Intercept)      balance
## -10.45218276   0.005367655
```

The next thing we should understand is how the `predict()` function works with `glm()`. So, let's look at some predictions.

```
head(predict(model_glm))
```

```
##      9149      9370      2861      8302      6415      5189
## -6.9616496 -0.7089539 -4.8936916 -9.4123620 -9.0416096 -7.3600645
```

By default, `predict.glm()` uses `type = "link"`.

```
head(predict(model_glm, type = "link"))
```

```
##      9149      9370      2861      8302      6415      5189
## -6.9616496 -0.7089539 -4.8936916 -9.4123620 -9.0416096 -7.3600645
```

That is, R is returning

$$\hat{\beta}_0 + \hat{\beta}_1 x_1 + \hat{\beta}_2 x_2 + \cdots + \hat{\beta}_p x_p$$

for each observation.

Importantly, these are **not** predicted probabilities. To obtain the predicted probabilities

$$\hat{p}(\mathbf{x}) = \hat{P}[Y = 1 | \mathbf{X} = \mathbf{x}]$$

we need to use `type = "response"`

```
head(predict(model_glm, type = "response"))
```

```
##      9149      9370      2861      8302      6415
## 9.466353e-04 3.298300e-01 7.437969e-03 8.170105e-05 1.183661e-04
##      5189
## 6.357530e-04
```

Note that these are probabilities, **not** classifications. To obtain classifications, we will need to compare to the correct cutoff value with an `ifelse()` statement.

```
model_glm_pred = ifelse(predict(model_glm, type = "link") > 0, "Yes", "No")
# model_glm_pred = ifelse(predict(model_glm, type = "response") > 0.5, "Yes", "No")
```

The line that is run is performing

$$\hat{C}(\mathbf{x}) = \begin{cases} 1 & \hat{f}(\mathbf{x}) > 0 \\ 0 & \hat{f}(\mathbf{x}) \leq 0 \end{cases}$$

where

$$\hat{f}(\mathbf{x}) = \hat{\beta}_0 + \hat{\beta}_1 x_1 + \hat{\beta}_2 x_2 + \cdots + \hat{\beta}_p x_p.$$

The commented line, which would give the same results, is performing

$$\hat{C}(\mathbf{x}) = \begin{cases} 1 & \hat{p}(\mathbf{x}) > 0.5 \\ 0 & \hat{p}(\mathbf{x}) \leq 0.5 \end{cases}$$

where

$$\hat{p}(\mathbf{x}) = \hat{P}[Y = 1 \mid \mathbf{X} = \mathbf{x}].$$

Once we have classifications, we can calculate metrics such as accuracy.

```
mean(model_glm_pred == default_train$default) # train accuracy
## [1] 0.9722
```

As we saw previously, the `table()` and `confusionMatrix()` functions can be used to quickly obtain many more metrics.

```
train_tab = table(predicted = model_glm_pred, actual = default_train$default)
library(caret)
train_con_mat = confusionMatrix(train_tab, positive = "Yes")
c(train_con_mat$overall[["Accuracy"]],
  train_con_mat$byClass[["Sensitivity"]],
  train_con_mat$byClass[["Specificity"]])

##      Accuracy Sensitivity Specificity
## 0.9722000  0.2738095  0.9964818
```

As we did with regression, we could also write a custom function for accuracy.

```
get_accuracy = function(mod, data, res = "y", pos = 1, neg = 0, cut = 0.5) {
  probs = predict(mod, newdata = data, type = "response")
  preds = ifelse(probs > cut, pos, neg)
  mean(data[, res] == preds)
}
```

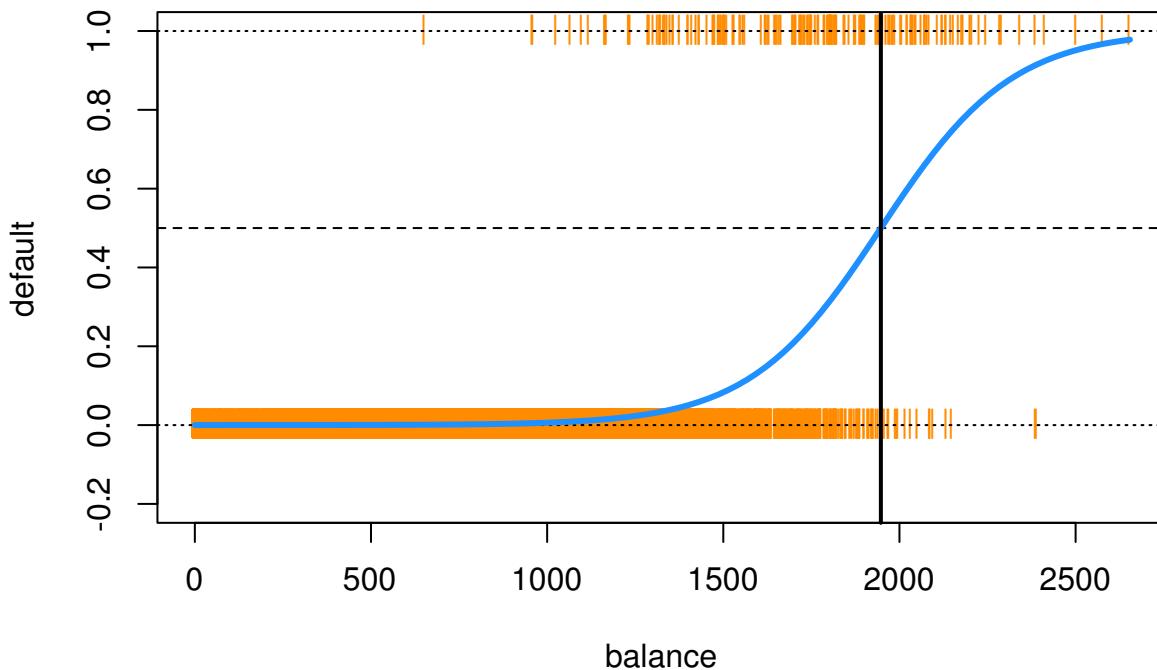
This function will be useful later when calculating train and test accuracies for several models at the same time.

```
get_accuracy(model_glm, data = default_train,
             res = "default", pos = "Yes", neg = "No", cut = 0.5)
## [1] 0.9722
```

To see how much better logistic regression is for this task, we create the same plot we used for linear regression.

```
plot(default ~ balance, data = default_train_lm,
      col = "darkorange", pch = "|", ylim = c(-0.2, 1),
      main = "Using Logistic Regression for Classification")
abline(h = 0, lty = 3)
abline(h = 1, lty = 3)
abline(h = 0.5, lty = 2)
curve(predict(model_glm, data.frame(balance = x), type = "response"),
      add = TRUE, lwd = 3, col = "dodgerblue")
abline(v = -coef(model_glm)[1] / coef(model_glm)[2], lwd = 2)
```

## Using Logistic Regression for Classification



This plot contains a wealth of information.

- The orange | characters are the data,  $(x_i, y_i)$ .
- The blue “curve” is the predicted probabilities given by the fitted logistic regression. That is,

$$\hat{p}(\mathbf{x}) = \hat{P}[Y = 1 \mid \mathbf{X} = \mathbf{x}]$$

- The solid vertical black line represents the **decision boundary**, the `balance` that obtains a predicted probability of 0.5. In this case `balance` = 1947.252994.

The decision boundary is found by solving for points that satisfy

$$\hat{p}(\mathbf{x}) = \hat{P}[Y = 1 \mid \mathbf{X} = \mathbf{x}] = 0.5$$

This is equivalent to point that satisfy

$$\hat{\beta}_0 + \hat{\beta}_1 x_1 = 0.$$

Thus, for logistic regression with a single predictor, the decision boundary is given by the *point*

$$x_1 = \frac{-\hat{\beta}_0}{\hat{\beta}_1}.$$

The following is not run, but an alternative way to add the logistic curve to the plot.

```
grid = seq(0, max(default_train$balance), by = 0.01)

sigmoid = function(x) {
  1 / (1 + exp(-x))
```

```

}

lines(grid, sigmoid(coef(model_glm)[1] + coef(model_glm)[2] * grid), lwd = 3)

```

Using the usual formula syntax, it is easy to add complexity to logistic regressions.

```

model_1 = glm(default ~ 1, data = default_train, family = "binomial")
model_2 = glm(default ~ ., data = default_train, family = "binomial")
model_3 = glm(default ~ . ^ 2 + I(balance ^ 2),
              data = default_train, family = "binomial")

```

Note that, using polynomial transformations of predictors will allow a linear model to have non-linear decision boundaries.

```

model_list = list(model_1, model_2, model_3)

train_error = 1 - sapply(model_list, get_accuracy, data = default_train,
                        res = "default", pos = "Yes", neg = "No", cut = 0.5)
test_error = 1 - sapply(model_list, get_accuracy, data = default_test,
                        res = "default", pos = "Yes", neg = "No", cut = 0.5)

```

Here we see the misclassification error rates for each model. The train decreases, and the test decreases, until it starts to increases. Everything we learned about the bias-variance tradeoff for regression also applies here.

```
diff(train_error)
```

```
## [1] -0.0058 -0.0002
```

```
diff(test_error)
```

```
## [1] -0.0068  0.0004
```

We call `model_2` the **additive** logistic model, which we will use quite often.

## 14.4 ROC Curves

Let's return to our simple model with only balance as a predictor.

```
model_glm = glm(default ~ balance, data = default_train, family = "binomial")
```

We write a function which allows use to make predictions based on different probability cutoffs.

```

get_pred = function(mod, data, res = "y", pos = 1, neg = 0, cut = 0.5) {
  probs = predict(mod, newdata = data, type = "response")
  ifelse(probs > cut, pos, neg)
}

```

$$\hat{C}(\mathbf{x}) = \begin{cases} 1 & \hat{f}(\mathbf{x}) > c \\ 0 & \hat{f}(\mathbf{x}) \leq c \end{cases}$$

Let's use this to obtain predictions using a low, medium, and high cutoff. (0.1, 0.5, and 0.9)

```
test_pred_10 = get_pred(model_glm, data = default_test, res = "default", pos = "Yes", neg = "No", cut =
test_pred_50 = get_pred(model_glm, data = default_test, res = "default", pos = "Yes", neg = "No", cut =
test_pred_90 = get_pred(model_glm, data = default_test, res = "default", pos = "Yes", neg = "No", cut =
```

Now we evaluate accuracy, sensitivity, and specificity for these classifiers.

```
test_tab_10 = table(predicted = test_pred_10, actual = default_test$default)
test_tab_50 = table(predicted = test_pred_50, actual = default_test$default)
test_tab_90 = table(predicted = test_pred_90, actual = default_test$default)
```

```
test_con_mat_10 = confusionMatrix(test_tab_10, positive = "Yes")
test_con_mat_50 = confusionMatrix(test_tab_50, positive = "Yes")
test_con_mat_90 = confusionMatrix(test_tab_90, positive = "Yes")
```

```
metrics = rbind(
```

```
c(test_con_mat_10$overall["Accuracy"],
  test_con_mat_10$byClass["Sensitivity"],
  test_con_mat_10$byClass["Specificity"]),

c(test_con_mat_50$overall["Accuracy"],
  test_con_mat_50$byClass["Sensitivity"],
  test_con_mat_50$byClass["Specificity"]),

c(test_con_mat_90$overall["Accuracy"],
  test_con_mat_90$byClass["Sensitivity"],
  test_con_mat_90$byClass["Specificity"]))
```

```
)
```

```
rownames(metrics) = c("c = 0.10", "c = 0.50", "c = 0.90")
metrics
```

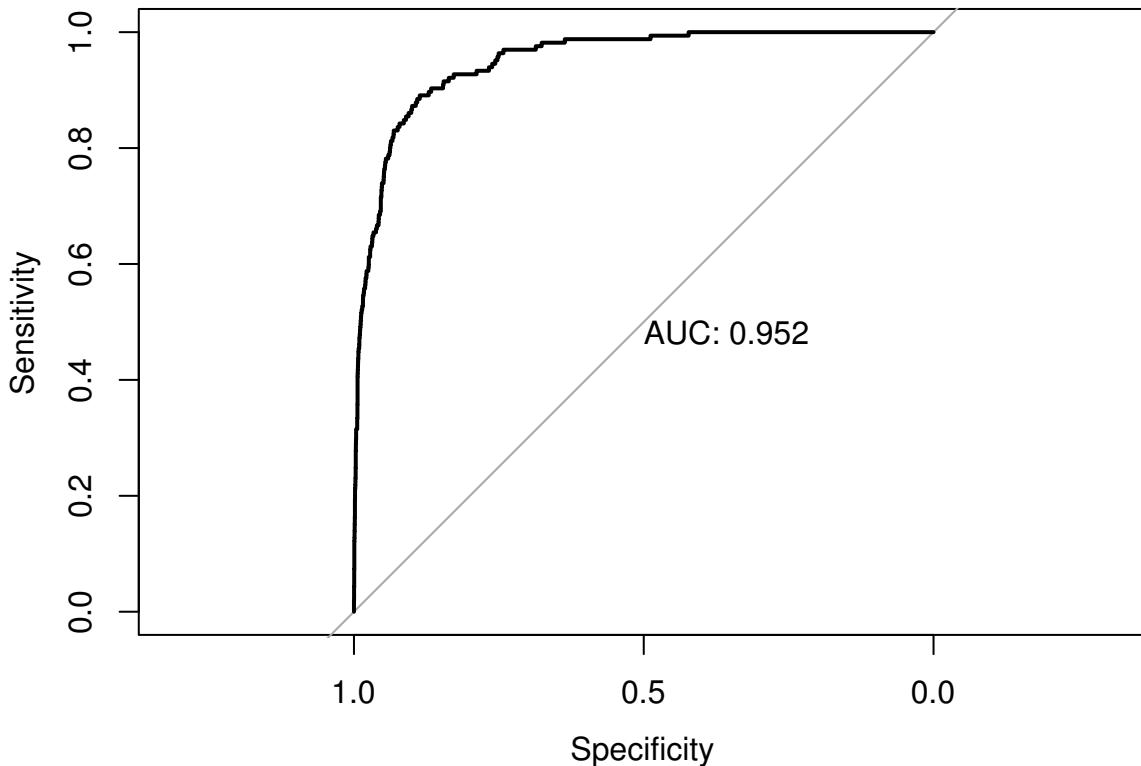
```
##          Accuracy Sensitivity Specificity
## c = 0.10    0.9404    0.77575758    0.9460186
## c = 0.50    0.9738    0.31515152    0.9962771
## c = 0.90    0.9674    0.01818182    0.9997932
```

We see then sensitivity decreases as the cutoff is increased. Conversely, specificity increases as the cutoff increases. This is useful if we are more interested in a particular error, instead of giving them equal weight.

Note that usually the best accuracy will be seen near  $c = 0.50$ .

Instead of manually checking cutoffs, we can create an ROC curve (receiver operating characteristic curve) which will sweep through all possible cutoffs, and plot the sensitivity and specificity.

```
library(pROC)
test_prob = predict(model_glm, newdata = default_test, type = "response")
test_roc = roc(default_test$default ~ test_prob, plot = TRUE, print.auc = TRUE)
```



```
as.numeric(test_roc$auc)
```

```
## [1] 0.9515076
```

A good model will have a high AUC, that is as often as possible a high sensitivity and specificity.

## 14.5 Multinomial Logistic Regression

What if the response contains more than two categories? For that we need multinomial logistic regression.

$$P[Y = k \mid \mathbf{X} = \mathbf{x}] = \frac{e^{\beta_{0k} + \beta_{1k}x_1 + \dots + \beta_{pk}x_p}}{\sum_{j=1}^K e^{\beta_{0j} + \beta_{1j}x_1 + \dots + \beta_{pj}x_p}}$$

We will omit the details, as ISL has as well. If you are interested, the Wikipedia page provides a rather thorough coverage. Also note that the above is an example of the softmax function.

As an example of a dataset with a three category response, we use the `iris` dataset, which is so famous, it has its own Wikipedia entry. It is also a default dataset in R, so no need to load it.

Before proceeding, we test-train split this data.

```
set.seed(430)
iris_obs = nrow(iris)
iris_index = sample(iris_obs, size = trunc(0.50 * iris_obs))
iris_train = iris[iris_index, ]
iris_test = iris[-iris_index, ]
```

To perform multinomial logistic regression, we use the `multinom` function from the `nnet` package. Training using `multinom()` is done using similar syntax to `lm()` and `glm()`. We add the `trace = FALSE` argument to suppress information about updates to the optimization routine as the model is trained.

```
library(nnet)
model_multi = multinom(Species ~ ., data = iris_train, trace = FALSE)
summary(model_multi)$coefficients
```

```
##           (Intercept) Sepal.Length Sepal.Width Petal.Length Petal.Width
## versicolor    26.81602     -6.983313   -16.24574    20.35750    3.218787
## virginica    -34.24228     -8.398869   -17.03985    31.94659   11.594518
```

Notice we are only given coefficients for two of the three class, much like only needing coefficients for one class in logistic regression.

A difference between `glm()` and `multinom()` is how the `predict()` function operates.

```
head(predict(model_multi, newdata = iris_train))

## [1] setosa      virginica   setosa      setosa      virginica setosa
## Levels: setosa versicolor virginica
```

```
head(predict(model_multi, newdata = iris, type = "prob"))
```

```
##   setosa  versicolor  virginica
## 1 1 1.386333e-16 1.137629e-39
## 2 1 1.888634e-12 3.059666e-35
## 3 1 3.868198e-14 2.226923e-37
## 4 1 2.315067e-11 1.687874e-33
## 5 1 5.490420e-17 4.794326e-40
## 6 1 2.196721e-17 1.482366e-38
```

Notice that by default, classifications are returned. When obtaining probabilities, we are given the predicted probability for **each** class.

Interestingly, you've just fit a neural network, and you didn't even know it! (Hence the `nnet` package.) Later we will discuss the connections between logistic regression, multinomial logistic regression, and simple neural networks.



# Chapter 15

## Generative Models

In this chapter, we continue our discussion of classification methods. We introduce three new methods, each a **generative** method. This in comparison to logistic regression, which is a **discriminative** method.

Generative methods model the joint probability,  $p(x, y)$ , often by assuming some distribution for the conditional distribution of  $X$  given  $Y$ ,  $f(x | y)$ . Bayes theorem is then applied to classify according to  $p(y | x)$ . Discriminative methods directly model this conditional,  $p(y | x)$ . A detailed discussion and analysis can be found in Ng and Jordan, 2002.

Each of the methods in this chapter will use Bayes theorem to build a classifier.

$$p_k(x) = P[Y = k | \mathbf{X} = \mathbf{x}] = \frac{\pi_k \cdot f_k(\mathbf{x})}{\sum_{i=1}^K \pi_i \cdot f_i(\mathbf{x})}$$

We call  $p_k(x)$  the **posterior** probability, which we will estimate then use to create classifications. The  $\pi_k$  are called the **prior** probabilities for each class  $k$ . That is,  $P[y = k]$ , unconditioned on  $X$ . The  $f_k(\mathbf{x})$  are called the **likelihoods**, which are indexed by  $k$  to denote that they are conditional on the classes. The denominator is often referred to as a **normalizing constant**.

The methods will differ by placing different modeling assumptions on the likelihoods,  $f_k(\mathbf{x})$ . For each method, the priors could be learned from data or pre-specified.

For each method, classifications are made to the class with the highest estimated posterior probability, which is equivalent to the class with the largest

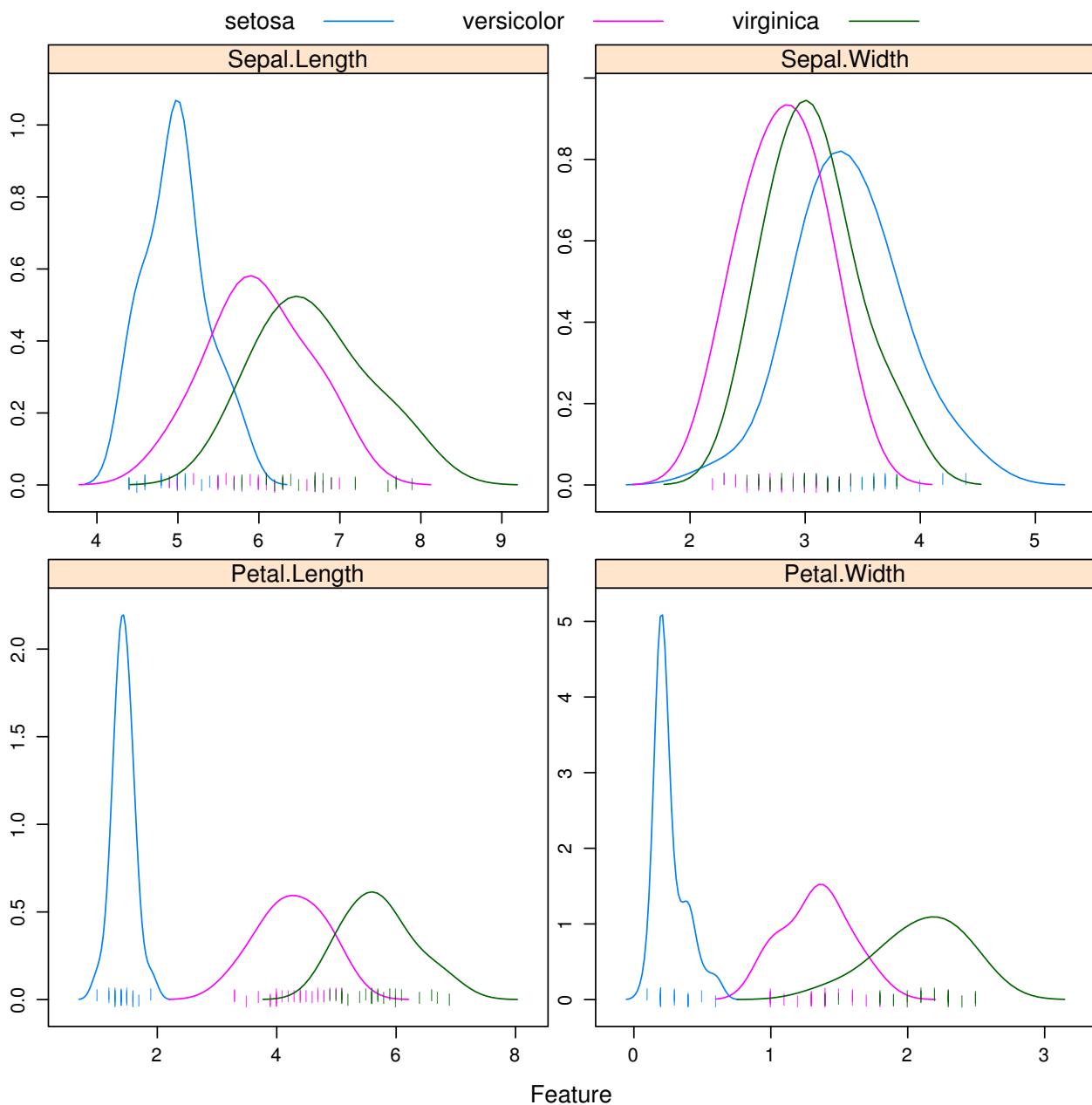
$$\log(\hat{\pi}_k \cdot \hat{f}_k(\mathbf{x})).$$

By substituting the corresponding likelihoods, simplifying, and eliminating unnecessary terms, we could derive the discriminant function for each.

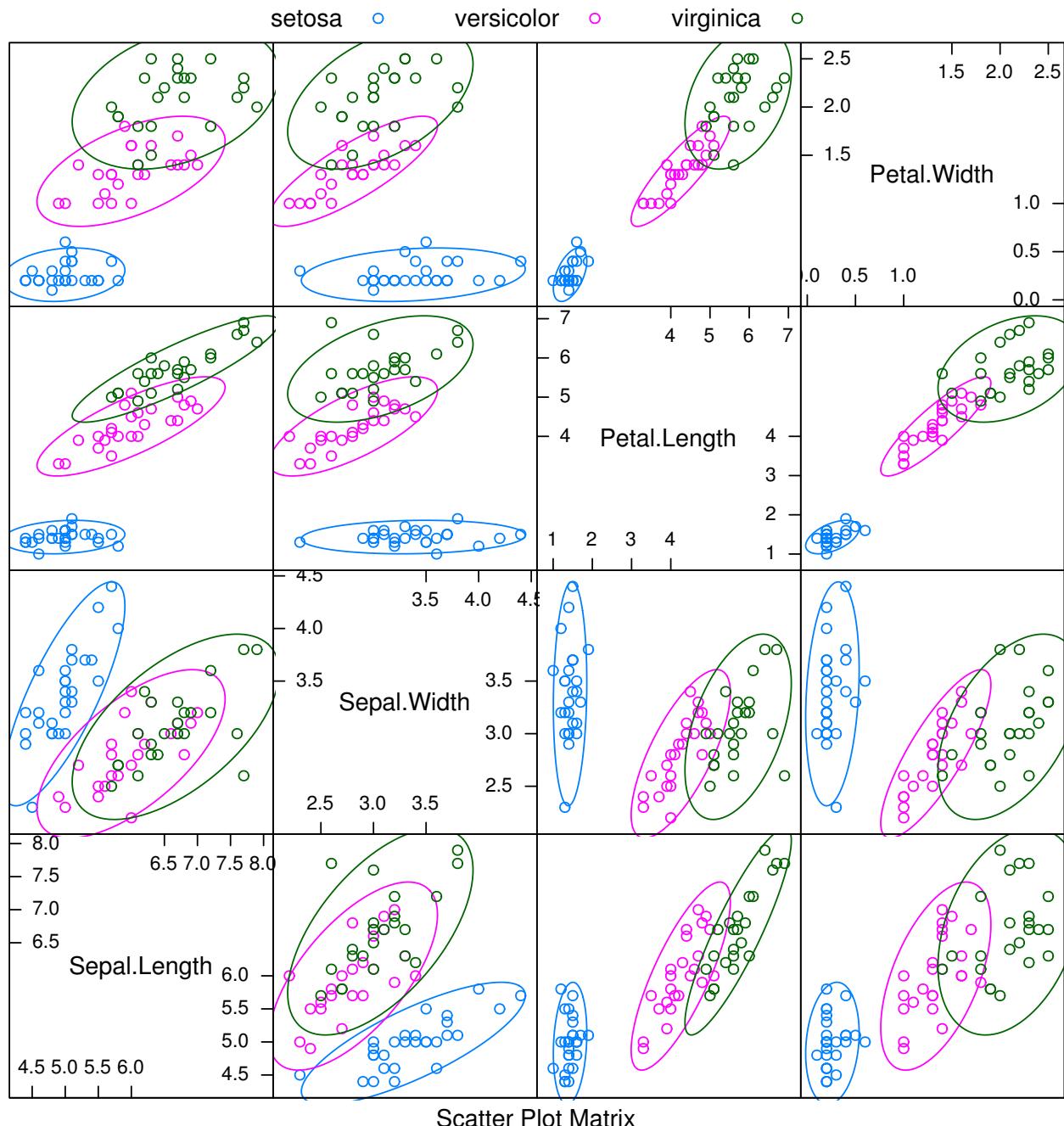
To illustrate these new methods, we return to the iris data, which you may remember has three classes. After a test-train split, we create a number of plots to refresh our memory.

```
set.seed(430)
iris_obs = nrow(iris)
iris_index = sample(iris_obs, size = trunc(0.50 * iris_obs))
# iris_index = sample(iris_obs, size = trunc(0.10 * iris_obs))
iris_train = iris[iris_index, ]
iris_test = iris[-iris_index, ]
```

```
caret::featurePlot(x = iris_train[, c("Sepal.Length", "Sepal.Width",
                                    "Petal.Length", "Petal.Width")],
                  y = iris_train$Species,
                  plot = "density",
                  scales = list(x = list(relation = "free"),
                                y = list(relation = "free")),
                  adjust = 1.5,
                  pch = "|",
                  layout = c(2, 2),
                  auto.key = list(columns = 3))
```

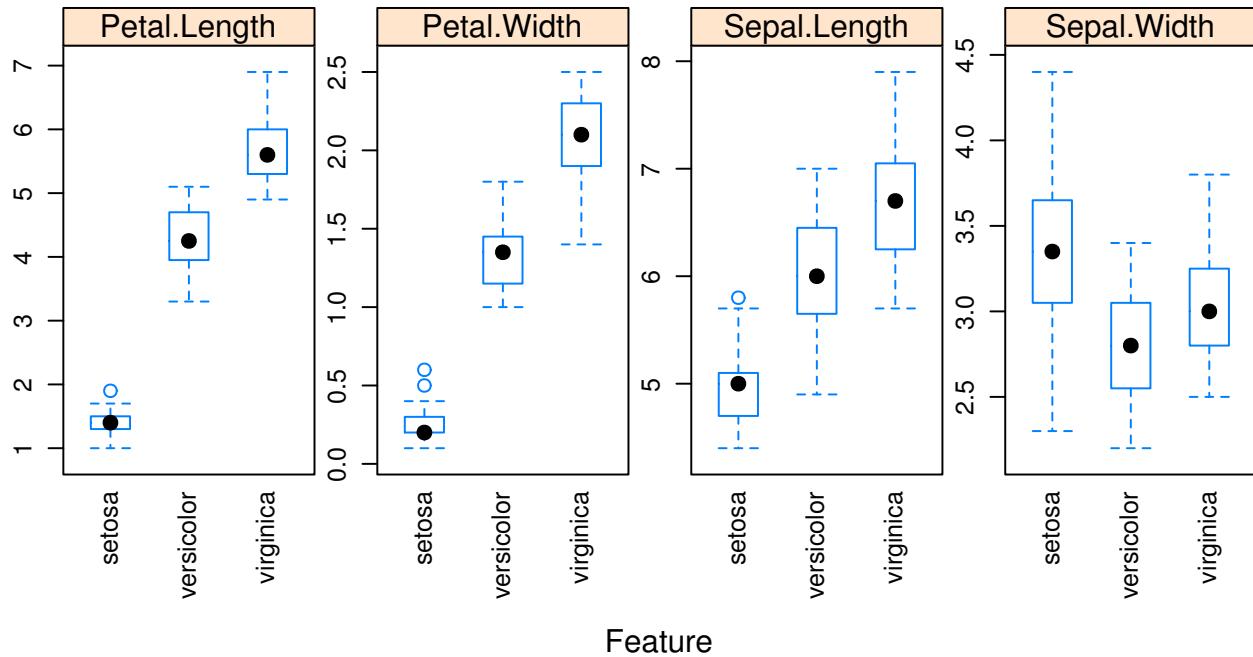


```
caret::featurePlot(x = iris_train[, c("Sepal.Length", "Sepal.Width",
                                     "Petal.Length", "Petal.Width")],
                  y = iris_train$Species,
                  plot = "ellipse",
                  auto.key = list(columns = 3))
```



```
caret::featurePlot(x = iris_train[, c("Sepal.Length", "Sepal.Width",
                                     "Petal.Length", "Petal.Width")],
                  y = iris_train$Species,
                  plot = "box",
                  scales = list(y = list(relation="free"),
```

```
x = list(rot = 90),
layout = c(4, 1))
```



Especially based on the pairs plot, we see that it should not be too difficult to find a good classifier.

Notice that we use `caret::featurePlot` to access the `featurePlot()` function without loading the entire `caret` package.

## 15.1 Linear Discriminant Analysis

LDA assumes that the predictors are multivariate normal conditioned on the classes.

$$\mathbf{X} \mid Y = k \sim N(\mu_k, \Sigma)$$

$$f_k(\mathbf{x}) = \frac{1}{(2\pi)^{p/2} |\Sigma|^{1/2}} \exp \left[ -\frac{1}{2} (\mathbf{x} - \mu_k)' \Sigma^{-1} (\mathbf{x} - \mu_k) \right]$$

Notice that  $\Sigma$  does **not** depend on  $k$ , that is, we are assuming the same  $\Sigma$  for each class. We then use information from all the classes to estimate  $\Sigma$ .

To fit an LDA model, we use the `lda()` function from the `MASS` package.

```
library(MASS)
iris_lda = lda(Species ~ ., data = iris_train)
iris_lda
```

```
## Call:
## lda(Species ~ ., data = iris_train)
##
## Prior probabilities of groups:
```

```

##      setosa versicolor  virginica
##  0.3733333  0.3200000  0.3066667
##
## Group means:
##           Sepal.Length Sepal.Width Petal.Length Petal.Width
## setosa      4.978571    3.378571   1.432143   0.2607143
## versicolor   5.995833    2.808333   4.254167   1.3333333
## virginica    6.669565    3.065217   5.717391   2.0956522
##
## Coefficients of linear discriminants:
##           LD1        LD2
## Sepal.Length 0.7100013 -0.8446128
## Sepal.Width  1.2435532  2.4773120
## Petal.Length -2.3419418 -0.4065865
## Petal.Width  -1.8502355  2.3234441
##
## Proportion of trace:
##       LD1       LD2
## 0.9908 0.0092

```

Here we see the estimated  $\hat{\pi}_k$  and  $\hat{\mu}_k$  for each class.

```

is.list(predict(iris_lda, iris_train))

## [1] TRUE

names(predict(iris_lda, iris_train))

## [1] "class"      "posterior"   "x"

head(predict(iris_lda, iris_train)$class, n = 10)

## [1] setosa      virginica   setosa      setosa      virginica   setosa
## [7] virginica   setosa      versicolor  setosa
## Levels: setosa versicolor virginica

head(predict(iris_lda, iris_train)$posterior, n = 10)

##           setosa  versicolor  virginica
## 23  1.000000e+00 1.517145e-21 1.717663e-41
## 106 2.894733e-43 1.643603e-06 9.999984e-01
## 37  1.000000e+00 2.169066e-20 1.287216e-40
## 40  1.000000e+00 3.979954e-17 8.243133e-36
## 145 1.303566e-37 4.335258e-06 9.999957e-01
## 36  1.000000e+00 1.947567e-18 5.996917e-38
## 119 2.220147e-51 9.587514e-09 1.000000e+00
## 16  1.000000e+00 5.981936e-23 1.344538e-42
## 94  1.599359e-11 9.999999e-01 1.035129e-07
## 27  1.000000e+00 8.154612e-15 4.862249e-32

```

As we should come to expect, the `predict()` function operates in a new way when called on an `lda` object. By default, it returns an entire list. Within that list `class` stores the classifications and `posterior` contains the estimated probability for each class.

```
iris_lda_train_pred = predict(iris_lda, iris_train)$class
iris_lda_test_pred = predict(iris_lda, iris_test)$class
```

We store the predictions made on the train and test sets.

```
accuracy = function(actual, predicted) {
  mean(actual == predicted)
}

accuracy(predicted = iris_lda_train_pred, actual = iris_train$Species)

## [1] 0.96

accuracy(predicted = iris_lda_test_pred, actual = iris_test$Species)

## [1] 0.9866667
```

As expected, LDA performs well on both the train and test data.

```
table(predicted = iris_lda_test_pred, actual = iris_test$Species)

##          actual
## predicted   setosa versicolor virginica
##   setosa      22       0       0
##   versicolor    0      26       1
##   virginica     0       0      26
```

Looking at the test set, we see that we are perfectly predicting both setosa and versicolor. The only error is labeling a virginica as a versicolor.

```
iris_lda_flat = lda(Species ~ ., data = iris_train, prior = c(1, 1, 1) / 3)
iris_lda_flat

## Call:
## lda(Species ~ ., data = iris_train, prior = c(1, 1, 1)/3)
##
## Prior probabilities of groups:
##   setosa versicolor virginica
## 0.3333333 0.3333333 0.3333333
##
## Group means:
##           Sepal.Length Sepal.Width Petal.Length Petal.Width
## setosa        4.978571   3.378571    1.432143   0.2607143
## versicolor    5.995833   2.808333    4.254167   1.3333333
## virginica     6.669565   3.065217    5.717391   2.0956522
##
```

```
## Coefficients of linear discriminants:
##          LD1      LD2
## Sepal.Length  0.7136357 -0.8415442
## Sepal.Width   1.2328623  2.4826497
## Petal.Length -2.3401674 -0.4166784
## Petal.Width  -1.8602343  2.3154465
##
## Proportion of trace:
##      LD1      LD2
## 0.9901  0.0099
```

Instead of learning (estimating) the proportion of the three species from the data, we could instead specify them ourselves. Here we choose a uniform distributions over the possible species. We would call this a “flat” prior.

```
iris_lda_flat_train_pred = predict(iris_lda_flat, iris_train)$class
iris_lda_flat_test_pred = predict(iris_lda_flat, iris_test)$class

accuracy(predicted = iris_lda_flat_train_pred, actual = iris_train$Species)

## [1] 0.96

accuracy(predicted = iris_lda_flat_test_pred, actual = iris_test$Species)

## [1] 1
```

This actually gives a better test accuracy!

## 15.2 Quadratic Discriminant Analysis

QDA also assumes that the predictors are multivariate normal conditioned on the classes.

$$\mathbf{X} \mid Y = k \sim N(\boldsymbol{\mu}_k, \boldsymbol{\Sigma}_k)$$

$$f_k(\mathbf{x}) = \frac{1}{(2\pi)^{p/2} |\boldsymbol{\Sigma}_k|^{1/2}} \exp \left[ -\frac{1}{2} (\mathbf{x} - \boldsymbol{\mu}_k)' \boldsymbol{\Sigma}_k^{-1} (\mathbf{x} - \boldsymbol{\mu}_k) \right]$$

Notice that now  $\boldsymbol{\Sigma}_k$  **does** depend on  $k$ , that is, we are allowing a different  $\boldsymbol{\Sigma}_k$  for each class. We only use information from class  $k$  to estimate  $\boldsymbol{\Sigma}_k$ .

```
iris_qda = qda(Species ~ ., data = iris_train)
iris_qda

## Call:
## qda(Species ~ ., data = iris_train)
##
## Prior probabilities of groups:
##       setosa versicolor  virginica
```

```

##  0.3733333 0.3200000 0.3066667
##
## Group means:
##           Sepal.Length Sepal.Width Petal.Length Petal.Width
## setosa      4.978571    3.378571    1.432143   0.2607143
## versicolor  5.995833    2.808333    4.254167   1.3333333
## virginica   6.669565    3.065217    5.717391   2.0956522

```

Here the output is similar to LDA, again giving the estimated  $\hat{\pi}_k$  and  $\hat{\mu}_k$  for each class. Like `lda()`, the `qda()` function is found in the MASS package.

Consider trying to fit QDA again, but this time with a smaller training set. (Use the commented line above to obtain a smaller test set.) This will cause an error because there are not enough observations within each class to estimate the large number of parameters in the  $\Sigma_k$  matrices. This is less of a problem with LDA, since all observations, no matter the class, are being used to estimate the shared  $\Sigma$  matrix.

```

iris_qda_train_pred = predict(iris_qda, iris_train)$class
iris_qda_test_pred = predict(iris_qda, iris_test)$class

```

The `predict()` function operates the same as the `predict()` function for LDA.

```
accuracy(predicted = iris_qda_train_pred, actual = iris_train$Species)
```

```
## [1] 0.9866667
```

```
accuracy(predicted = iris_qda_test_pred, actual = iris_test$Species)
```

```
## [1] 0.96
```

```
table(predicted = iris_qda_test_pred, actual = iris_test$Species)
```

	actual	setosa	versicolor	virginica
predicted	setosa	versicolor	virginica	
setosa	22	0	0	
versicolor	0	23	0	
virginica	0	3	27	

Here we find that QDA is not performing as well as LDA. It is misclassifying versicolors. Since QDA is a more complex model than LDA (many more parameters) we would say that QDA is overfitting here.

Also note that, QDA creates quadratic decision boundaries, while LDA creates linear decision boundaries. We could also add quadratic terms to LDA to allow it to create quadratic decision boundaries.

### 15.3 Naive Bayes

Naive Bayes comes in many forms. With only numeric predictors, it often assumes a multivariate normal conditioned on the classes, but a very specific multivariate normal.

$$\mathbf{X} \mid Y = k \sim N(\boldsymbol{\mu}_k, \boldsymbol{\Sigma}_k)$$

Naive Bayes assumes that the predictors  $X_1, X_2, \dots, X_p$  are independent. This is the “naive” part of naive Bayes. The Bayes part is nothing new. Since  $X_1, X_2, \dots, X_p$  are assumed independent, each  $\Sigma_k$  is diagonal, that is, we assume no correlation between predictors. Independence implies zero correlation.

This will allow us to write the (joint) likelihood as a product of univariate distributions. In this case, the product of univariate normal distributions instead of a (joint) multivariate distribution.

$$f_k(\mathbf{x}) = \prod_{j=1}^{j=p} f_{kj}(x_j)$$

Here,  $f_{kj}(x_j)$  is the density for the  $j$ -th predictor conditioned on the  $k$ -th class. Notice that there is a  $\sigma_{kj}$  for each predictor for each class.

$$f_{kj}(x_j) = \frac{1}{\sigma_{kj}\sqrt{2\pi}} \exp \left[ -\frac{1}{2} \left( \frac{x_j - \mu_{kj}}{\sigma_{kj}} \right)^2 \right]$$

When  $p = 1$ , this version of naive Bayes is equivalent to QDA.

```
library(e1071)
iris_nb = naiveBayes(Species ~ ., data = iris_train)
iris_nb

##
## Naive Bayes Classifier for Discrete Predictors
##
## Call:
## naiveBayes.default(x = X, y = Y, laplace = laplace)
##
## A-priori probabilities:
## Y
##     setosa versicolor virginica
## 0.3733333 0.3200000 0.3066667
##
## Conditional probabilities:
##             Sepal.Length
## Y      [,1]      [,2]
## setosa 4.978571 0.3774742
## versicolor 5.995833 0.5812125
## virginica 6.669565 0.6392003
##
##             Sepal.Width
## Y      [,1]      [,2]
## setosa 3.378571 0.4349177
## versicolor 2.808333 0.3269313
## virginica 3.065217 0.3600615
##
##             Petal.Length
## Y      [,1]      [,2]
## setosa 1.432143 0.1743848
## versicolor 4.254167 0.5166608
## virginica 5.717391 0.5540366
##
```

```

##          Petal.Width
## Y      [,1]      [,2]
##   setosa    0.2607143 0.1133310
##   versicolor 1.3333333 0.2334368
##   virginica  2.0956522 0.3022315

```

Many packages implement naive Bayes. Here we choose to use `naiveBayes()` from the package `e1071`. (The name of this package has an interesting history. Based on the name you wouldn't know it, but the package contains many functions related to machine learning.)

The **Conditional probabilities:** portion of the output gives the mean and standard deviation of the normal distribution for each predictor in each class. Notice how these mean estimates match those for LDA and QDA above.

Note that `naiveBayes()` will work without a factor response, but functions much better with one. (Especially when making predictions.) If you are using a 0 and 1 response, you might consider coercing to a factor first.

```

head(predict(iris_nb, iris_train))

## [1] setosa     virginica setosa     setosa     virginica setosa
## Levels: setosa versicolor virginica

head(predict(iris_nb, iris_train, type = "class"))

## [1] setosa     virginica setosa     setosa     virginica setosa
## Levels: setosa versicolor virginica

head(predict(iris_nb, iris_train, type = "raw"))

##          setosa     versicolor     virginica
## [1,] 1.000000e+00 3.134201e-16 2.948226e-27
## [2,] 4.400050e-257 5.188308e-08 9.999999e-01
## [3,] 1.000000e+00 2.263278e-14 1.168760e-24
## [4,] 1.000000e+00 4.855740e-14 2.167253e-24
## [5,] 1.897732e-218 6.189883e-08 9.999999e-01
## [6,] 1.000000e+00 8.184097e-15 6.816322e-26

```

Oh look, `predict()` has another new mode of operation. If only there were a way to unify the `predict()` function across all of these methods...

```

iris_nb_train_pred = predict(iris_nb, iris_train)
iris_nb_test_pred = predict(iris_nb, iris_test)

accuracy(predicted = iris_nb_train_pred, actual = iris_train$Species)

## [1] 0.9466667

accuracy(predicted = iris_nb_test_pred, actual = iris_test$Species)

## [1] 0.9466667

```

```
table(predicted = iris_nb_test_pred, actual = iris_test$Species)
```

```
##           actual
## predicted   setosa versicolor virginica
##   setosa      22        0        0
##   versicolor    0       26        4
##   virginica     0        0       23
```

Like LDA, naive Bayes is having trouble with virginica.

Method	Train Accuracy	Test Accuracy
LDA	0.9600000	0.9866667
LDA, Flat Prior	0.9600000	1.0000000
QDA	0.9866667	0.9600000
Naive Bayes	0.9466667	0.9466667

Summarizing the results, we see that Naive Bayes is the worst of LDA, QDA, and NB for this data. So why should we care about naive Bayes?

The strength of naive Bayes comes from its ability to handle a large number of predictors,  $p$ , even with a limited sample size  $n$ . Even with the naive independence assumption, naive Bayes works rather well in practice. Also because of this assumption, we can often train naive Bayes where LDA and QDA may be impossible to train because of the large number of parameters relative to the number of observations.

Here naive Bayes doesn't get a chance to show its strength since LDA and QDA already perform well, and the number of predictors is low. The choice between LDA and QDA is mostly down to a consideration about the amount of complexity needed.

## 15.4 Discrete Inputs

So far, we have assumed that all predictors are numeric. What happens with categorical predictors?

```
iris_train_mod = iris_train

iris_train_mod$Sepal.Width = ifelse(iris_train$Sepal.Width > 3,
                                    ifelse(iris_train$Sepal.Width > 4,
                                          "Large", "Medium"),
                                    "Small")

unique(iris_train_mod$Sepal.Width)

## [1] "Medium" "Small"  "Large"
```

Here we make a new dataset where `Sepal.Width` is categorical, with levels `Small`, `Medium`, and `Large`. We then try to train classifiers using only the sepal variables.

```
naiveBayes(Species ~ Sepal.Length + Sepal.Width, data = iris_train_mod)
```

```
##
## Naive Bayes Classifier for Discrete Predictors
##
## Call:
```

```
## naiveBayes.default(x = X, y = Y, laplace = laplace)
##
## A-priori probabilities:
## Y
##   setosa versicolor virginica
## 0.3733333 0.3200000 0.3066667
##
## Conditional probabilities:
## Sepal.Length
## Y      [,1]      [,2]
## setosa 4.978571 0.3774742
## versicolor 5.995833 0.5812125
## virginica 6.669565 0.6392003
##
## Sepal.Width
## Y      Large     Medium    Small
## setosa 0.07142857 0.67857143 0.25000000
## versicolor 0.00000000 0.25000000 0.75000000
## virginica 0.00000000 0.43478261 0.56521739
```

Naive Bayes makes a somewhat obvious and intelligent choice to model the categorical variable as a multinomial. It then estimates the probability parameters of a multinomial distribution.

```
lda(Species ~ Sepal.Length + Sepal.Width, data = iris_train_mod)
```

```
## Call:
## lda(Species ~ Sepal.Length + Sepal.Width, data = iris_train_mod)
##
## Prior probabilities of groups:
##   setosa versicolor virginica
## 0.3733333 0.3200000 0.3066667
##
## Group means:
##           Sepal.Length Sepal.WidthMedium Sepal.WidthSmall
## setosa        4.978571       0.6785714       0.2500000
## versicolor    5.995833       0.2500000       0.7500000
## virginica     6.669565       0.4347826       0.5652174
##
## Coefficients of linear discriminants:
##                 LD1         LD2
## Sepal.Length    2.051602  0.4768608
## Sepal.WidthMedium 1.728698 -0.4433340
## Sepal.WidthSmall  3.173903 -2.2804034
##
## Proportion of trace:
##   LD1     LD2
## 0.9764 0.0236
```

LDA however creates dummy variables, here with `Large` is the reference level, then continues to model them as normally distributed. Not great, but better than not using a categorical variable.

## 15.5 RMarkdown

The RMarkdown file for this chapter can be found [here](#). The file was created using R version 3.3.2 and the following packages:

- Base Packages, Attached

```
## [1] "stats"      "graphics"    "grDevices"   "utils"       "datasets"    "base"
```

- Additional Packages, Attached

```
## [1] "e1071"     "MASS"
```

- Additional Packages, Not Attached

```
## [1] "Rcpp"        "nloptr"      "plyr"        "class" 
## [5] "methods"     "iterators"   "tools"       "digest" 
## [9] "lme4"        "evaluate"    "tibble"      "gttable" 
## [13] "nlme"        "lattice"     "mgcv"       "Matrix" 
## [17] "foreach"     "yaml"        "parallel"    "SparseM" 
## [21] "stringr"     "knitr"       "MatrixModels" "stats4" 
## [25] "rprojroot"   "grid"        "caret"       "nnet" 
## [29] "ellipse"     "rmarkdown"   "bookdown"    "minqa" 
## [33] "ggplot2"     "reshape2"    "car"         "magrittr" 
## [37] "backports"   "scales"      "codetools"   "ModelMetrics" 
## [41] "htmltools"   "splines"     "assertthat" "pbkrtest" 
## [45] "colorspace"  "quantreg"    "stringi"    "lazyeval" 
## [49] "munsell"
```



# Chapter 16

## k-Nearest Neighbors

In this chapter we introduce our first **non-parametric** method,  $k$ -nearest neighbors, which can be used for both classification and regression.

Each method we have seen so far has been parametric. For example, logistic regression had the form

$$\log\left(\frac{p(\mathbf{x})}{1 - p(\mathbf{x})}\right) = \beta_0 + \beta_1 x_1 + \beta_2 x_2 + \cdots + \beta_p x_p.$$

In this case, the  $\beta_i$  are the parameters of the model, which we learned (estimated) by training (fitting) the model.

$k$ -nearest neighbors has no such parameters. Instead, it has a **tuning parameter**,  $k$ . This is a parameter which determines *how* the model is trained, instead of a parameter that is *learned* through training. Note that tuning parameters are not used exclusively used with non-parametric methods. Later we will see examples of tuning parameters for parametric methods.

### 16.1 Classification

```
library(ISLR)
library(class)
library(MASS)
```

We first load some necessary libraries. We'll begin discussing classification by returning to the `Default` data from the `ISLR` package. To illustrate regression, we'll also return to the `Boston` data from the `MASS` package. To perform  $k$ -nearest neighbors, we will use the `knn()` function from the `class` package.

#### 16.1.1 Default Data

Unlike many of our previous methods, `knn()` requires that all predictors be numeric, so we coerce `student` to be a 0 and 1 variable instead of a factor. (We can leave the response as a factor.)

```
set.seed(42)
Default$student = as.numeric(Default$student) - 1
default_index = sample(nrow(Default), 5000)
default_train = Default[default_index, ]
default_test = Default[-default_index, ]
```

Also unlike previous methods, `knn()` does not utilize the formula syntax, rather, requires the predictors be their own data frame or matrix, and the class labels be a separate factor variable. Note that the `y` data should be a factor vector, **not** a data frame containing a factor vector.

```
# training data
X_default_train = default_train[, -1]
y_default_train = default_train$default

# testing data
X_default_test = default_test[, -1]
y_default_test = default_test$default
```

There is very little “training” with  $k$ -nearest neighbors. Essentially the only training is to simply remember the inputs. Because of this, we say that  $k$ -nearest neighbors is fast at training time. However, at test time,  $k$ -nearest neighbors is very slow. For each test case, the method must find the  $k$ -nearest neighbors, which is not computationally cheap. (Note that `knn()` uses Euclidean distance.)

```
head(knn(train = X_default_train,
          test = X_default_test,
          cl = y_default_train,
          k = 3),
       n = 25)

## [1] No No
## [24] No No
## Levels: No Yes
```

Because of the lack of any need for training, the `knn()` function essentially replaces the `predict()` function, and immediately returns classifications. Here, `knn()` used four arguments:

- `train`, the predictors for the train set.
- `test`, the predictors for the test set. `knn()` will output results for these cases.
- `cl`, the true class labels for the train set.
- `k`, the number of neighbors to consider.

```
accuracy = function(actual, predicted) {
  mean(actual == predicted)
}
```

We'll use our usual `accuracy()` function to asses how well `knn()` works with this data.

```
accuracy(actual = y_default_test,
         predicted = knn(train = X_default_train,
                         test = X_default_test,
                         cl = y_default_train, k = 5))

## [1] 0.9684
```

Often with `knn()` we need to consider the scale of the predictors variables. If one variable is contains much larger numbers because of the units or range of the variable, it will dominate other variables in the distance measurements. But this doesn't necessarily mean that it should be such an important variable. It is common practice to scale the predictors to have 0 mean and unit variance. Be sure to apply the scaling to both the train and test data.

```
accuracy(actual = y_default_test,
         predicted = knn(train = scale(X_default_train),
                         test = scale(X_default_test),
                         cl = y_default_train, k = 5))
```

```
## [1] 0.9722
```

Here we see the scaling improves the classification accuracy. This may not always be the case, and often, it is normal to attempt classification with and without scaling.

How do we choose  $k$ ? Try different values and see which works best.

```
set.seed(42)
k_to_try = 1:100
acc_k = rep(x = 0, times = length(k_to_try))

for(i in seq_along(k_to_try)) {
  pred = knn(train = scale(X_default_train),
             test = scale(X_default_test),
             cl = y_default_train,
             k = k_to_try[i])
  acc_k[i] = accuracy(y_default_test, pred)
}
```

The `seq_along()` function can be very useful for looping over a vector that stores non-consecutive numbers. It often removes the need for an additional counter variable. We actually didn't need it in the above `knn()` example, but it is still a good habit. Here we see an example where we would have otherwise needed another variable.

```
ex_seq = seq(from = 1, to = 100, by = 5)
seq_along(ex_seq)
```

```
## [1] 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20
```

```
ex_storage = rep(x = 0, times = length(ex_seq))
for(i in seq_along(ex_seq)) {
  ex_storage[i] = mean(rnorm(n = 10, mean = ex_seq[i], sd = 1))
}

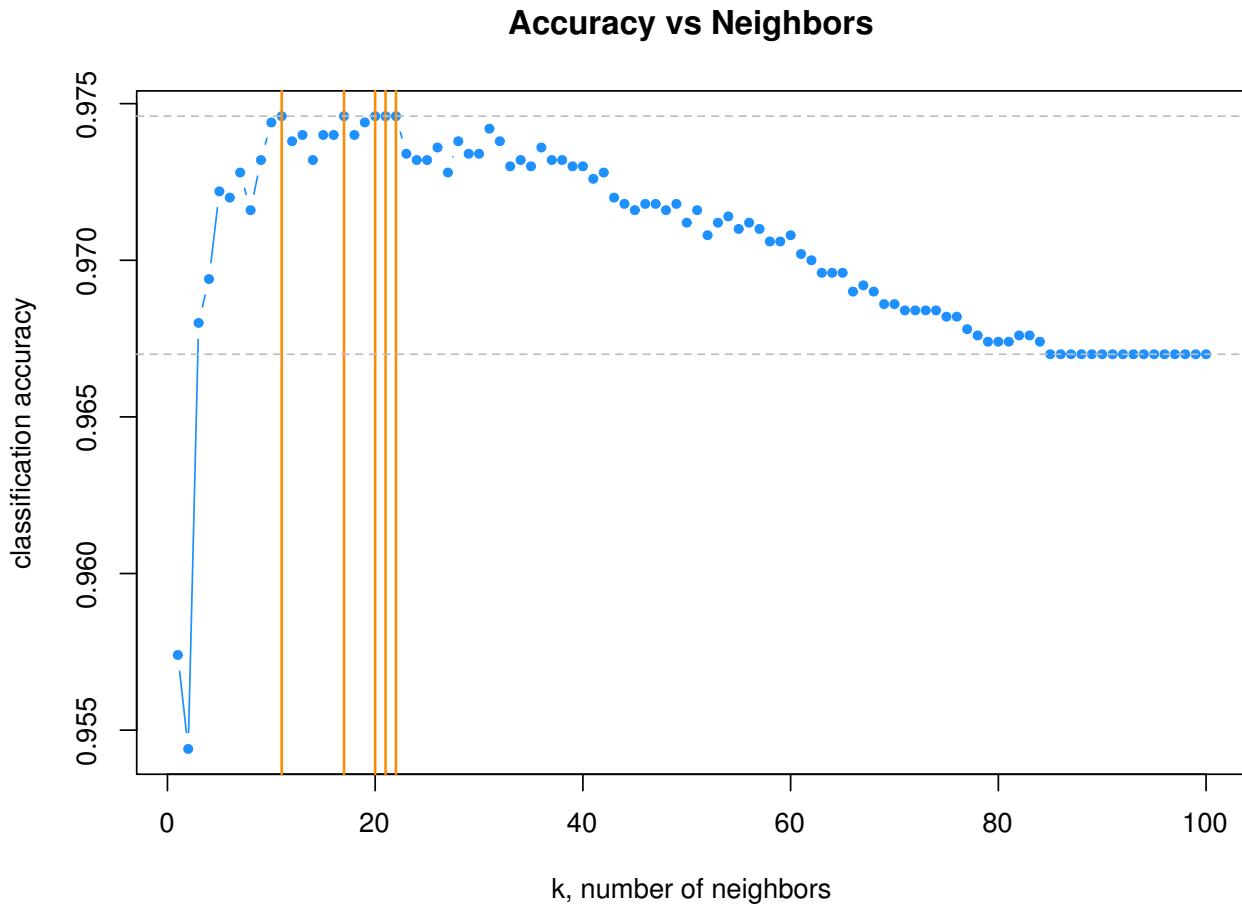
ex_storage
```

```
## [1] 0.948629 5.792671 11.090760 15.915397 21.422372 26.106009 30.857772
## [8] 35.593119 40.958334 46.338667 50.672116 55.733392 60.387860 65.747387
## [15] 71.037306 76.066974 80.956349 85.173316 91.077993 95.882329
```

Naturally, we plot the  $k$ -nearest neighbor results.

```
# plot accuracy vs choice of k
plot(acc_k, type = "b", col = "dodgerblue", cex = 1, pch = 20,
      xlab = "k, number of neighbors", ylab = "classification accuracy",
      main = "Accuracy vs Neighbors")
```

```
# add lines indicating k with best accuracy
abline(v = which(acc_k == max(acc_k)), col = "darkorange", lwd = 1.5)
# add line for max accuracy seen
abline(h = max(acc_k), col = "grey", lty = 2)
# add line for prevalence in test set
abline(h = mean(y_default_test == "No"), col = "grey", lty = 2)
```



```
max(acc_k)

## [1] 0.9746

max(which(acc_k == max(acc_k)))

## [1] 22
```

We see that four different values of  $k$  are tied for the highest accuracy. Given a choice of these four values of  $k$ , we select the largest, as it is the least variable, and has the least chance of overfitting.

Also notice that, as  $k$  increases, eventually the accuracy approaches the test prevalence.

```
mean(y_default_test == "No")

## [1] 0.967
```

### 16.1.2 Iris Data

Like LDA and QDA, KNN can be used for both binary and multi-class problems. As an example, we return to the iris data.

```
set.seed(430)
iris_obs = nrow(iris)
iris_index = sample(iris_obs, size = trunc(0.50 * iris_obs))
iris_train = iris[iris_index, ]
iris_test = iris[-iris_index, ]
```

All the predictors here are numeric, so we proceed to splitting the data into predictors and classes.

```
# training data
X_iris_train = iris_train[, -5]
y_iris_train = iris_train$Species

# testing data
X_iris_test = iris_test[, -5]
y_iris_test = iris_test$Species
```

Like previous methods, we can obtain predicted probabilities given test predictors. To do so, we add an argument, `prob = TRUE`

```
iris_pred = knn(train = scale(X_iris_train),
                 test = scale(X_iris_test),
                 cl = y_iris_train,
                 k = 10,
                 prob = TRUE)

iris_pred

## [1] setosa    setosa    setosa    setosa    setosa    setosa
## [7] setosa    setosa    setosa    setosa    setosa    setosa
## [13] setosa    setosa    setosa    setosa    setosa    setosa
## [19] setosa    setosa    setosa    setosa    versicolor versicolor
## [25] versicolor versicolor versicolor versicolor versicolor
## [31] versicolor versicolor versicolor versicolor versicolor
## [37] versicolor versicolor versicolor versicolor versicolor
## [43] versicolor versicolor versicolor versicolor versicolor
## [49] virginica versicolor virginica virginica virginica virginica
## [55] virginica virginica virginica versicolor versicolor virginica
## [61] virginica virginica virginica versicolor virginica virginica
## [67] virginica virginica virginica versicolor virginica virginica
## [73] virginica virginica versicolor
## attr("prob")
## [1] 1.0000000 1.0000000 1.0000000 1.0000000 1.0000000 1.0000000
## [8] 1.0000000 1.0000000 1.0000000 1.0000000 1.0000000 1.0000000
## [15] 1.0000000 1.0000000 1.0000000 1.0000000 1.0000000 1.0000000
## [22] 1.0000000 0.9000000 1.0000000 0.8000000 1.0000000 0.9000000 0.9000000
## [29] 0.9000000 0.8000000 1.0000000 0.9000000 1.0000000 0.8000000 0.5000000
## [36] 0.8000000 0.9000000 0.8000000 1.0000000 1.0000000 0.7272727 0.9000000
```

```
## [43] 0.8000000 0.9000000 1.0000000 1.0000000 0.9000000 0.9000000 0.9000000
## [50] 0.7000000 0.8000000 0.7272727 0.8000000 0.8000000 0.8000000 0.9000000
## [57] 0.6000000 0.6000000 0.5000000 0.9000000 0.6000000 1.0000000 0.6000000
## [64] 0.5000000 0.7000000 0.9000000 1.0000000 0.9000000 0.6000000 0.7000000
## [71] 0.8000000 0.9000000 0.8000000 0.9000000 0.5000000
## Levels: setosa versicolor virginica
```

Unfortunately, this only returns the predicted probability of the most common class. In the binary case, this would be sufficient, however, for multi-class problems, we cannot recover each of the probabilities of interest.

```
attributes(iris_pred)$prob
```

```
## [1] 1.0000000 1.0000000 1.0000000 1.0000000 1.0000000 1.0000000 1.0000000
## [8] 1.0000000 1.0000000 1.0000000 1.0000000 1.0000000 1.0000000 1.0000000
## [15] 1.0000000 1.0000000 1.0000000 1.0000000 1.0000000 1.0000000 1.0000000
## [22] 1.0000000 0.9000000 1.0000000 0.8000000 1.0000000 0.9000000 0.9000000
## [29] 0.9000000 0.8000000 1.0000000 0.9000000 1.0000000 0.8000000 0.5000000
## [36] 0.8000000 0.9000000 0.8000000 1.0000000 1.0000000 0.7272727 0.9000000
## [43] 0.8000000 0.9000000 1.0000000 1.0000000 0.9000000 0.9000000 0.9000000
## [50] 0.7000000 0.8000000 0.7272727 0.8000000 0.8000000 0.8000000 0.9000000
## [57] 0.6000000 0.6000000 0.5000000 0.9000000 0.6000000 1.0000000 0.6000000
## [64] 0.5000000 0.7000000 0.9000000 1.0000000 0.9000000 0.6000000 0.7000000
## [71] 0.8000000 0.9000000 0.8000000 0.9000000 0.5000000
```

## 16.2 Regression

We quickly illustrate KNN for regression using the Boston data. We'll only use `lstat` as a predictor, and `medv` as the response. We won't test-train split for this example since won't be checking RMSE, but instead plotting fitted models. There is also no need to worry about scaling since there is only one predictor.

```
X_boston = Boston["lstat"]
y_boston = Boston$medv
```

We create a “test” set, that is a grid of `lstat` values at which we will predict `medv`.

```
lstat_grid = data.frame(lstat = seq(range(X_boston$lstat)[1], range(X_boston$lstat)[2], by = 0.01))
```

Unfortunately, `knn()` from `class` only handles classification. To perform regression, we will need `knn.reg()` from the `FNN` package. Notice that, we do **not** load this package, but instead use `FNN::knn.reg` to access the function. This is useful since `FNN` also contains a function `knn()` and would then mask `knn()` from `class`.

```
pred_001 = FNN::knn.reg(train = X_boston, test = lstat_grid, y = y_boston, k = 1)
pred_005 = FNN::knn.reg(train = X_boston, test = lstat_grid, y = y_boston, k = 5)
pred_010 = FNN::knn.reg(train = X_boston, test = lstat_grid, y = y_boston, k = 10)
pred_050 = FNN::knn.reg(train = X_boston, test = lstat_grid, y = y_boston, k = 50)
pred_100 = FNN::knn.reg(train = X_boston, test = lstat_grid, y = y_boston, k = 100)
pred_506 = FNN::knn.reg(train = X_boston, test = lstat_grid, y = y_boston, k = 506)
```

We make predictions for various values of `k`. Note that 506 is the number of observations in this dataset.

```
par(mfrow = c(3, 2))

plot(medv ~ lstat, data = Boston, cex = .8, col = "dodgerblue", main = "k = 1")
lines(lstat_grid$lstat, pred_001$pred, col = "darkorange", lwd = 0.25)

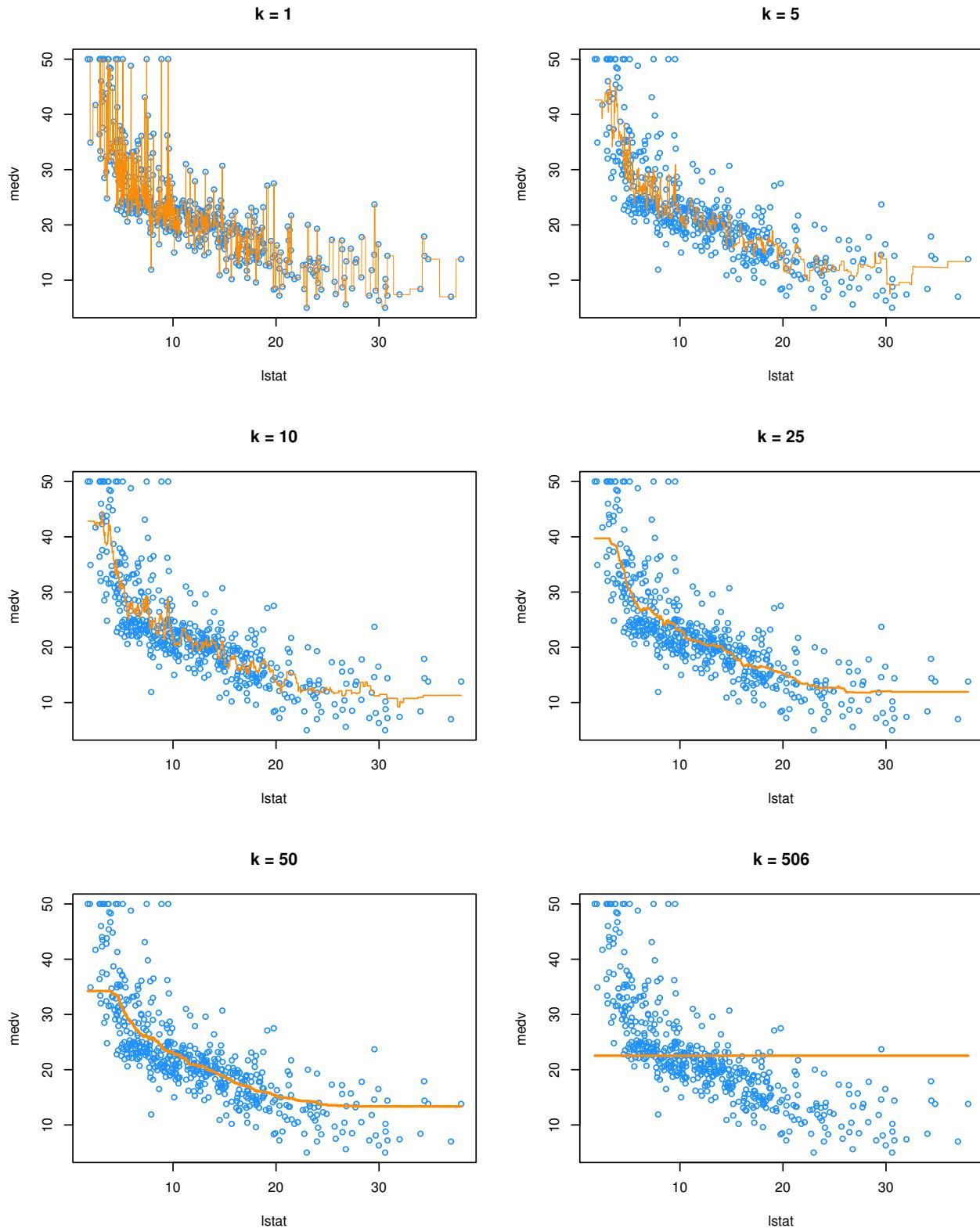
plot(medv ~ lstat, data = Boston, cex = .8, col = "dodgerblue", main = "k = 5")
lines(lstat_grid$lstat, pred_005$pred, col = "darkorange", lwd = 0.75)

plot(medv ~ lstat, data = Boston, cex = .8, col = "dodgerblue", main = "k = 10")
lines(lstat_grid$lstat, pred_010$pred, col = "darkorange", lwd = 1)

plot(medv ~ lstat, data = Boston, cex = .8, col = "dodgerblue", main = "k = 25")
lines(lstat_grid$lstat, pred_050$pred, col = "darkorange", lwd = 1.5)

plot(medv ~ lstat, data = Boston, cex = .8, col = "dodgerblue", main = "k = 50")
lines(lstat_grid$lstat, pred_100$pred, col = "darkorange", lwd = 2)

plot(medv ~ lstat, data = Boston, cex = .8, col = "dodgerblue", main = "k = 506")
lines(lstat_grid$lstat, pred_506$pred, col = "darkorange", lwd = 2)
```



We see that  $k = 1$  is clearly overfitting, as  $k = 1$  is a very complex, highly variable model. Conversely,  $k = 506$  is clearly underfitting the data, as  $k = 506$  is a very simple, low variance model. In fact, here it is predicting a simple average of all the data at each point.

## 16.3 External Links

- YouTube: *k*-Nearest Neighbor Classification Algorithm - Video from user “mathematicalmonk” which gives a brief but thorough introduction to the method.

## 16.4 RMarkdown

The RMarkdown file for this chapter can be found [here](#). The file was created using R version 3.3.2 and the following packages:

- Base Packages, Attached

```
## [1] "stats"      "graphics"    "grDevices"   "utils"       "datasets"    "base"
```

- Additional Packages, Attached

```
## [1] "MASS"      "class"      "ISLR"
```

- Additional Packages, Not Attached

```
## [1] "Rcpp"        "bookdown"    "FNN"         "digest"      "rprojroot"
## [6] "backports"   "magrittr"    "evaluate"    "stringi"    "rmarkdown"
## [11] "tools"       "stringr"     "yaml"        "htmltools"   "knitr"
## [16] "methods"
```



# Chapter 17

## Resampling

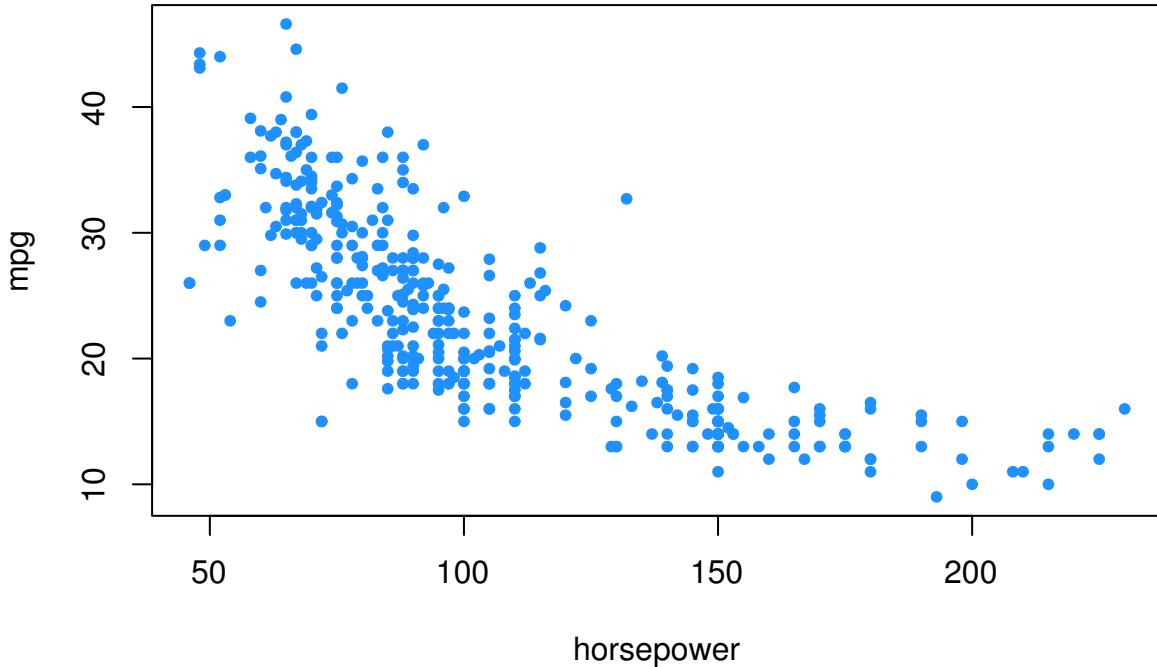
In this chapter we introduce resampling methods including cross-validation and the bootstrap.

```
library(ISLR)
```

Here, we will use the `Auto` data from `ISLR` and attempt to predict `mpg` (a numeric variable) from `horsepower`.

```
## # A tibble: 392 × 9
##   mpg cylinders displacement horsepower weight acceleration year
## * <dbl>     <dbl>        <dbl>       <dbl>    <dbl>        <dbl> <dbl>
## 1 18         8            307        130    3504        12.0  70
## 2 15         8            350        165    3693        11.5  70
## 3 18         8            318        150    3436        11.0  70
## 4 16         8            304        150    3433        12.0  70
## 5 17         8            302        140    3449        10.5  70
## 6 15         8            429        198    4341        10.0  70
## 7 14         8            454        220    4354         9.0  70
## 8 14         8            440        215    4312         8.5  70
## 9 14         8            455        225    4425        10.0  70
## 10 15        8            390        190    3850         8.5  70
## # ... with 382 more rows, and 2 more variables: origin <dbl>, name <fctr>
```

## MPG vs Horsepower



### 17.1 Test-Train Split

First, let's return to the usual test-train split procedure that we have used so far. Let's evaluate what happens if we repeat the process a large number of times, each time storing the test RMSE. We'll consider three models:

- An underfitting model: `mpg ~ horsepower`
- A reasonable model: `mpg ~ poly(horsepower, 2)`
- A ridiculous, overfitting model: `mpg ~ poly(horsepower, 8)`

```
set.seed(42)
num_reps = 100

lin_rmse  = rep(0, times = num_reps)
quad_rmse = rep(0, times = num_reps)
huge_rmse = rep(0, times = num_reps)

for(i in 1:100) {

  train_idx = sample(392, size = 196)

  lin_fit = lm(mpg ~ horsepower, data = Auto, subset = train_idx)
  lin_rmse[i] = sqrt(mean((Auto$mpg - predict(lin_fit, Auto))[-train_idx]^2))

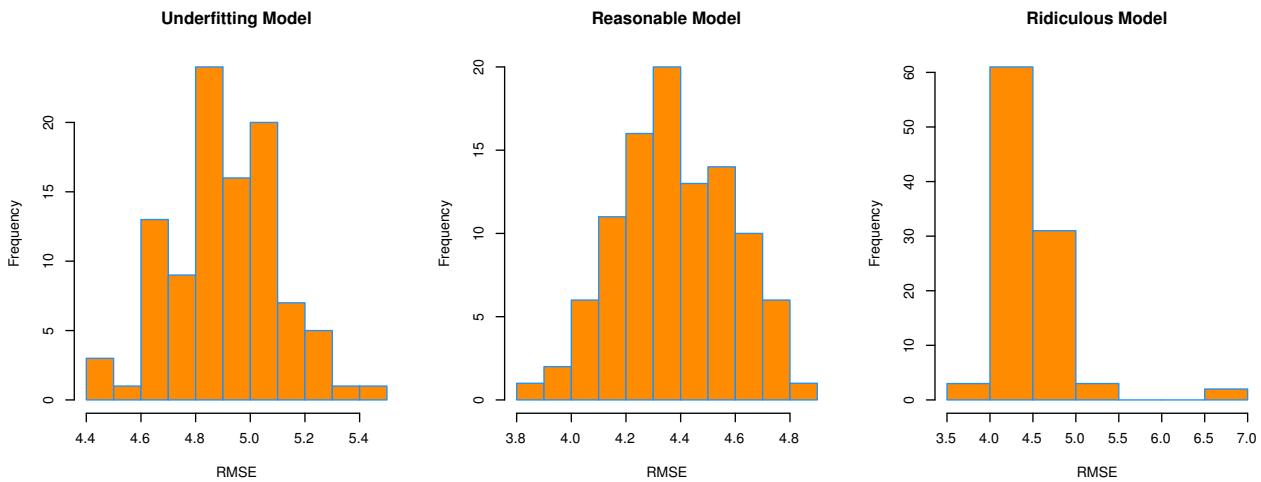
  quad_fit = lm(mpg ~ poly(horsepower, 2), data = Auto, subset = train_idx)
  quad_rmse[i] = sqrt(mean((Auto$mpg - predict(quad_fit, Auto))[-train_idx]^2))

  huge_fit = lm(mpg ~ poly(horsepower, 8), data = Auto, subset = train_idx)
  huge_rmse[i] = sqrt(mean((Auto$mpg - predict(huge_fit, Auto))[-train_idx]^2))
}
```

```

huge_fit = lm(mpg ~ poly(horsepower, 8), data = Auto, subset = train_idx)
huge_rmse[i] = sqrt(mean((Auto$mpg - predict(huge_fit, Auto))[-train_idx]^2))
}

```



Notice two things, first that the “Reasonable” model has on average the smallest error. Second, notice large variability in the RMSE. We see this in the “Reasonable” model, but it is very clear in the “Ridiculous” model. Here it is very clear that if we use an “unlucky” split, our test error will be much larger than the likely reality.

## 17.2 Cross-Validation

Instead of using a single test-train split, we instead look to use cross-validation. There are many ways to perform cross-validation R, depending on the method of interest.

### 17.2.1 Method Specific

Some methods, for example `glm()` through `cv.glm()` and `knn()` through `knn.cv()` have cross-validation capabilities built-in. We'll use `glm()` for illustration. First we need to convince ourselves that `glm()` can be used to perform the same tasks as `lm()`.

```

glm_fit = glm(mpg ~ horsepower, data = Auto)
coef(glm_fit)

```

```

## (Intercept) horsepower
## 39.9358610 -0.1578447

```

```

lm_fit = lm(mpg ~ horsepower, data = Auto)
coef(lm_fit)

```

```

## (Intercept) horsepower
## 39.9358610 -0.1578447

```

By default, `cv.glm()` will report leave-one-out cross-validation (LOOCV).

```

library(boot)
glm_fit = glm(mpg ~ horsepower, data = Auto)
loocv_rmse = sqrt(cv.glm(Auto, glm_fit)$delta)
loocv_rmse

## [1] 4.922552 4.922514

loocv_rmse[1]

## [1] 4.922552

```

We are actually given two values. The first is exactly the LOOCV-RMSE. The second is a minor correct that we will not worry about. We take a square root to obtain LOOCV-RMSE.

```

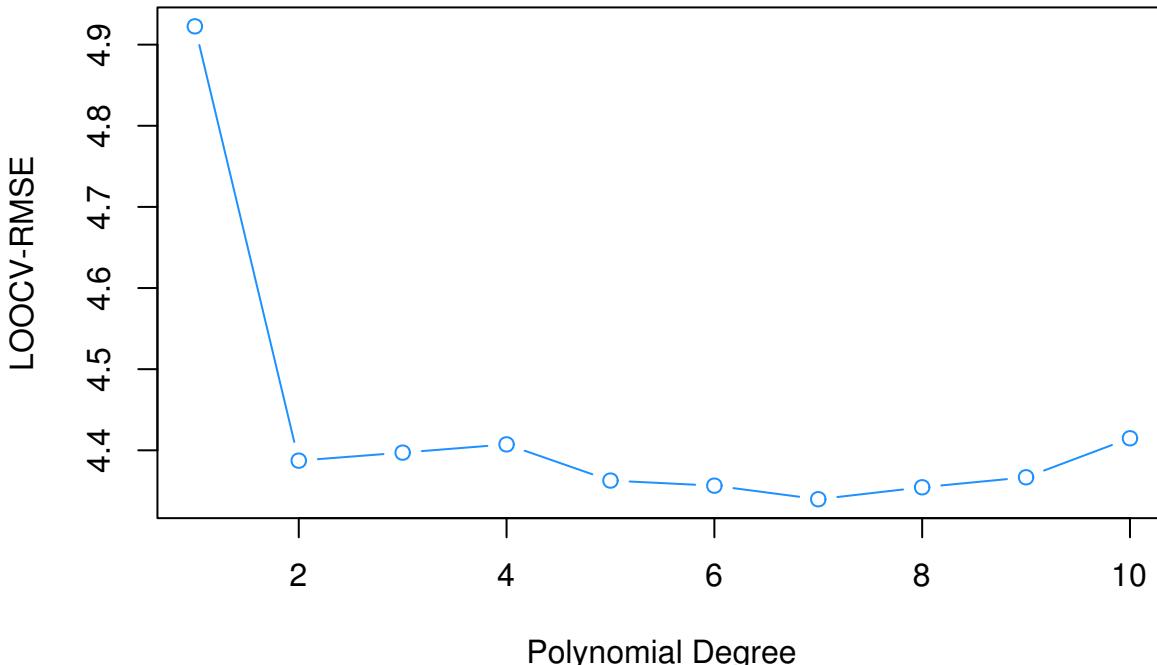
loocv_rmse_poly = rep(0, times = 10)
for (i in seq_along(loocv_rmse_poly)) {
  glm_fit = glm(mpg ~ poly(horsepower, i), data = Auto)
  loocv_rmse_poly[i] = sqrt(cv.glm(Auto, glm_fit)$delta[1])
}
loocv_rmse_poly

## [1] 4.922552 4.387279 4.397156 4.407316 4.362707 4.356449 4.339706
## [8] 4.354440 4.366764 4.414854

plot(loocv_rmse_poly, type = "b", col = "dodgerblue",
     main = "LOOCV-RMSE vs Polynomial Degree",
     ylab = "LOOCV-RMSE", xlab = "Polynomial Degree")

```

## LOOCV-RMSE vs Polynomial Degree



If you run the above code locally, you will notice that is painfully slow. We are fitting each of the 10 models 392 times, that is, each model  $n$  times, once with each data point left out. (Note: in this case, for a linear model, there is actually a shortcut formula which would allow us to obtain LOOCV-RMSE from a single fit to the data. See details in ISL as well as a link below.)

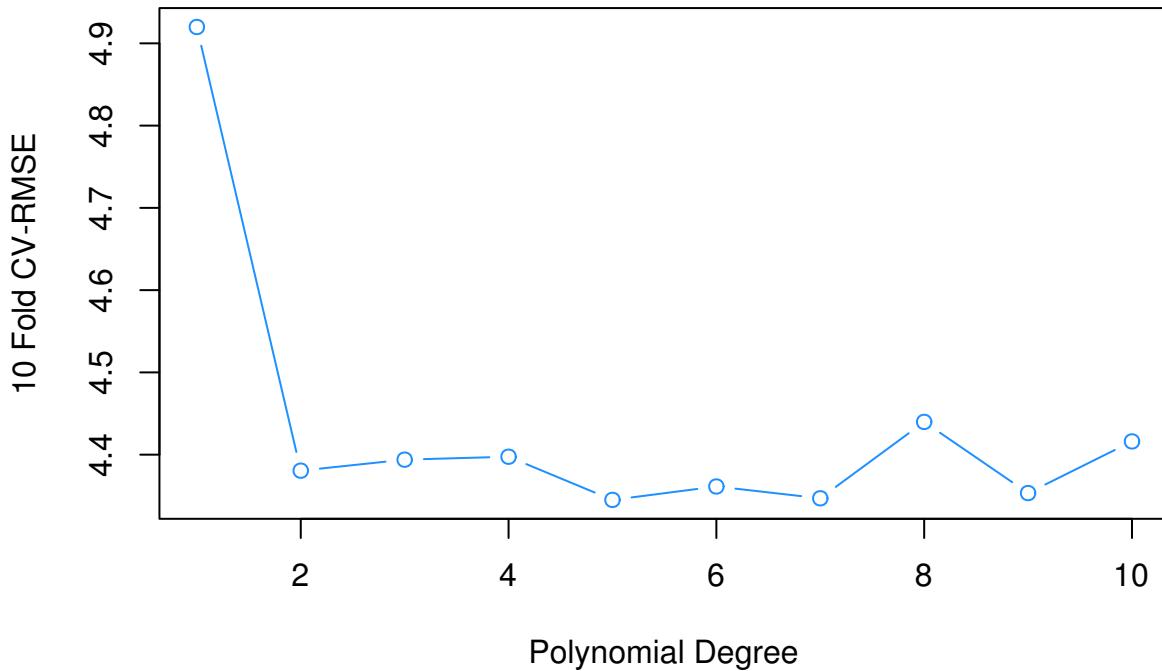
We could instead use  $k$ -fold cross-validation.

```
set.seed(17)
cv_10_rmse_poly = rep(0, times = 10)
for (i in seq_along(cv_10_rmse_poly)){
  glm_fit = glm(mpg ~ poly(horsepower, i), data = Auto)
  cv_10_rmse_poly[i] = sqrt(cv.glm(Auto, glm_fit, K = 10)$delta[1])
}
cv_10_rmse_poly
```

```
## [1] 4.919878 4.380552 4.393929 4.397498 4.345010 4.361311 4.346963
## [8] 4.439821 4.353321 4.416102
```

```
plot(cv_10_rmse_poly, type = "b", col = "dodgerblue",
     main = "10 Fold CV-RMSE vs Polynomial Degree",
     ylab = "10 Fold CV-RMSE", xlab = "Polynomial Degree")
```

## 10 Fold CV-RMSE vs Polynomial Degree



Here we chose 10-fold cross-validation. Notice it is **much** faster. In practice, we usually stick to 5 or 10-fold CV.

```
set.seed(42)
num_reps = 100
```

```

lin_rmse_10_fold = rep(0, times = num_reps)
quad_rmse_10_fold = rep(0, times = num_reps)
huge_rmse_10_fold = rep(0, times = num_reps)

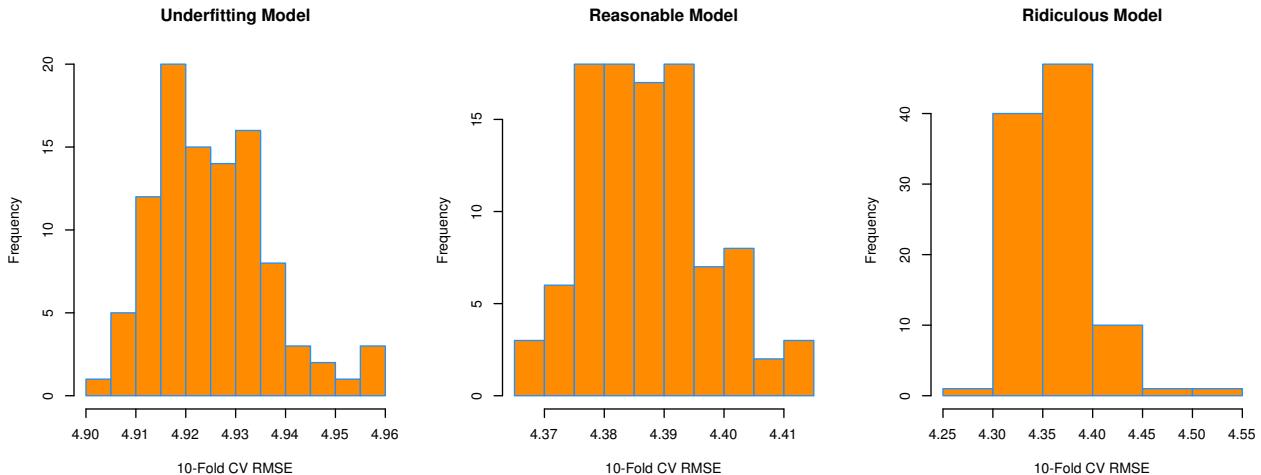
for(i in 1:100) {

  lin_fit = glm(mpg ~ poly(horsepower, 1), data = Auto)
  quad_fit = glm(mpg ~ poly(horsepower, 2), data = Auto)
  huge_fit = glm(mpg ~ poly(horsepower, 8), data = Auto)

  lin_rmse_10_fold[i] = sqrt(cv.glm(Auto, lin_fit, K = 10)$delta[1])
  quad_rmse_10_fold[i] = sqrt(cv.glm(Auto, quad_fit, K = 10)$delta[1])
  huge_rmse_10_fold[i] = sqrt(cv.glm(Auto, huge_fit, K = 10)$delta[1])
}

```

Repeating the test-train split analysis from above, this time with 10-fold CV, see that that the resulting RMSE are much less variable. That means, will cross-validation still has some inherent randomness, it has a much smaller effect on the results.



### 17.2.2 Manual Cross-Validation

For methods that do not have a built-in ability to perform cross-validation, or for methods that have limited cross-validation capability, we will need to write our own code for cross-validation. (Spoiler: This is not true, but let's pretend it is, so we can see how to perform cross-validation from scratch.)

This essentially amounts to randomly splitting the data, then looping over the splits. The `createFolds()` function from the `caret()` package will make this much easier.

```
caret::createFolds(Auto$mpg)
```

```

## $Fold01
## [1] 8 16 23 34 38 43 57 73 81 107 123 127 141 162 174 177 180
## [18] 187 188 218 221 227 232 238 244 258 273 281 282 284 287 305 307 318
## [35] 321 331 337 341 376 385 388
##
## $Fold02
## [1] 18 20 35 58 67 75 78 95 96 125 126 142 154 157 159 168 170

```

```

## [18] 172 182 186 215 241 249 255 271 277 288 289 292 298 301 304 310 311
## [35] 315 322 328 352 370 373
##
## $Fold03
## [1] 11 21 22 25 30 39 44 45 46 47 63 65 69 79 90 112 137
## [18] 147 165 167 173 204 209 213 216 217 239 247 267 279 308 313 329 338
## [35] 339 351 359 361 379
##
## $Fold04
## [1] 1 28 29 59 61 85 92 121 136 143 145 146 148 153 155 163 193
## [18] 198 202 206 212 224 231 233 246 266 269 280 295 303 323 326 336 343
## [35] 364 375 382 387
##
## $Fold05
## [1] 7 17 31 41 48 49 51 53 71 80 86 87 93 94 100 120 132
## [18] 135 169 176 200 214 219 225 229 236 250 256 278 296 297 306 319 332
## [35] 349 354 356 381 391 392
##
## $Fold06
## [1] 6 12 14 42 50 60 68 82 91 99 101 102 105 108 139 158 160
## [18] 171 179 183 185 208 226 240 243 245 251 252 253 254 309 320 325 330
## [35] 348 350 365 378 383
##
## $Fold07
## [1] 24 52 64 72 83 84 88 131 133 138 150 161 175 189 190 191 201
## [18] 211 230 261 262 264 265 272 275 285 286 294 312 317 333 342 355 358
## [35] 360 362 363 374 380
##
## $Fold08
## [1] 2 5 10 40 54 56 62 76 77 89 104 109 118 119 128 129 130
## [18] 134 181 184 194 197 220 228 257 259 263 268 270 276 290 293 300 347
## [35] 357 366 368 369 371
##
## $Fold09
## [1] 3 9 26 32 37 55 66 74 103 106 113 116 140 149 152 156 164
## [18] 166 178 195 199 203 207 210 234 235 237 248 283 299 302 314 316 327
## [35] 334 340 345 372 384
##
## $Fold10
## [1] 4 13 15 19 27 33 36 70 97 98 110 111 114 115 117 122 124
## [18] 144 151 192 196 205 222 223 242 260 274 291 324 335 344 346 353 367
## [35] 377 386 389 390

```

Can you use this to verify the 10-fold CV results from above?

### 17.2.3 Test Data

The following example illustrates the need for a test set which is **never** used in model training. If for no other reason, it gives us a quick sanity check that we have cross-validated correctly.

To be specific we will test-train split the data, then perform cross-validation on the training data.

```

accuracy = function(actual, predicted) {
  mean(actual == predicted)
}

# simulate data
# y is 0/1
# X are independent  $N(0, 1)$  variables
# X has no relationship with the response
# p >> n
set.seed(430)
n = 400
p = 5000
X = replicate(p, rnorm(n))
y = c(rep(0, times = n / 4), rep(1, times = n / 4),
      rep(0, times = n / 4), rep(1, times = n / 4))

# first n/2 observations are used for training
# last n/2 observations used for testing
# both are 50% 0s and 50% 1s
# cv will be done inside train data
full_data = data.frame(y, X)
train = full_data[1:(n / 2), ]
test = full_data[((n / 2) + 1):n, ]

```

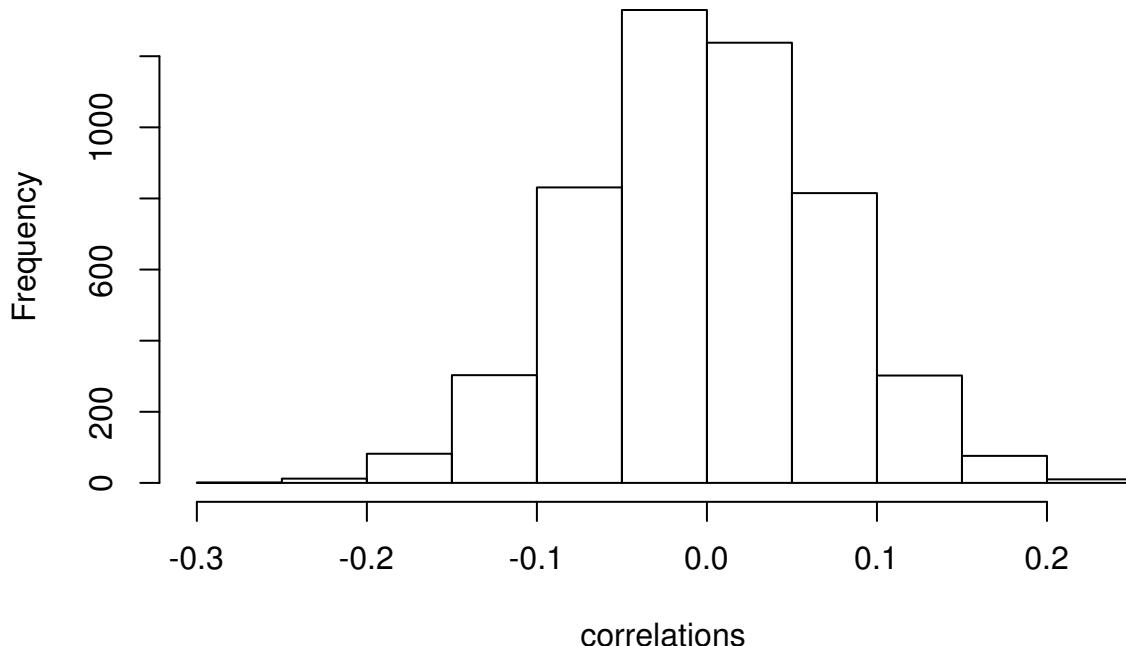
First, we use the screen-then-validate approach.

```

# find correlation between y and each predictor variable
correlations = apply(train[, -1], 2, cor, y = train$y)
hist(correlations)

```

## Histogram of correlations



```

# select the 25 largest (absolute) correlation
# these should be "useful" for prediction
selected = order(abs(correlations), decreasing = TRUE)[1:25]
correlations[selected]

##          X424      X4779      X2484      X1154      X2617      X1603
## -0.2577389  0.2491598  0.2379113 -0.2373367  0.2336055  0.2327971
##          X2963      X1091      X2806      X4586      X2569      X4532
##  0.2318932 -0.2281451 -0.2271382  0.2252979  0.2239974 -0.2225698
##          X3167      X741       X3329      X3862      X1741      X654
## -0.2201853 -0.2188919 -0.2186248 -0.2174146 -0.2150666  0.2130732
##          X3786      X4617      X3296      X2295      X999       X4349
##  0.2090650 -0.2086551 -0.2075271 -0.2072127  0.2055167 -0.1995252
##          X1409
##  0.1977006

# subset the test and training data based on the selected predictors
train_screen = train[c(1, selected)]
test_screen = test[c(1, selected)]

# fit an additive logistic regression
# use 10-fold cross-validation to obtain an estimate of test accuracy
# horribly optimistic
library(boot)
glm_fit = glm(y ~ ., data = train_screen, family = "binomial")
1 - cv.glm(train_screen, glm_fit, K = 10)$delta[1]

```

```
## [1] 0.709234
```

```

# get test accuracy, which we expect to be 0.50
# no better than guessing
glm_pred = (predict(glm_fit, newdata = test_screen, type = "response") > 0.5) * 1
accuracy(predicted = glm_pred, actual = test_screen$y)

```

```
## [1] 0.46
```

Now, we will correctly screen-while-validating.

```

# use the caret package to obtain 10 "folds"
folds = caret::createFolds(train_screen$y)

# for each fold
# - pre-screen variables on the 9 training folds
# - fit model to these variables
# - get accuracy on validation fold
fold_acc = rep(0, length(folds))

for(i in seq_along(folds)) {

  # split for fold i
  train_fold = train[-folds[[i]], ]

```

```

validate_fold = train[folds[[i]],]

# screening for fold i
correlations = apply(train_fold[, -1], 2, cor, y = train_fold[,1])
selected = order(abs(correlations), decreasing = TRUE)[1:25]
train_fold_screen = train_fold[ ,c(1,selected)]
validate_fold_screen = validate_fold[ ,c(1,selected)]

# accuracy for fold i
glm_fit = glm(y ~ ., data = train_fold_screen, family = "binomial")
glm_pred = (predict(glm_fit, newdata = validate_fold_screen, type = "response") > 0.5)*1
fold_acc[i] = mean(glm_pred == validate_fold_screen$y)

}

# report all 10 validation fold accuracies
fold_acc

## [1] 0.45 0.40 0.50 0.35 0.50 0.35 0.45 0.50 0.60 0.50

# properly cross-validated error
# this roughly matches what we expect in the test set
mean(fold_acc)

## [1] 0.46

```

### 17.3 Bootstrap

ISL also discusses the bootstrap, which is another resampling method. However, it is less relevant to the statistical learning tasks we will encounter. It could be useful if we were to attempt to calculate the bias and variance of a prediction (estimate) without access to the data generating process. Return to the bias-variance tradeoff chapter and think about how the bootstrap could be used to obtain estimates of bias and variance with a single dataset, instead of repeated simulated datasets.

For fun, write-up a simulation study which compares the strategy in the bias-variance tradeoff chapter to a strategy using bootstrap resampling of a single dataset. Submit it to be added to this chapter!

### 17.4 External Links

- YouTube: Cross-Validation, Part 1 - Video from user “mathematicalmonk” which introduces  $K$ -fold cross-validation in greater detail.
  - YouTube: Cross-Validation, Part 2 - Continuation which discusses selection and resampling strategies.
  - YouTube: Cross-Validation, Part 3 - Continuation which discusses choice of  $K$ .
- Blog: Fast Computation of Cross-Validation in Linear Models - Details for using leverage to speed-up LOOCV for linear models.
- OTexts: Bootstrap - Some brief mathematical details of the bootstrap.

## 17.5 RMarkdown

The RMarkdown file for this chapter can be found [here](#). The file was created using R version 3.3.2 and the following packages:

- Base Packages, Attached

```
## [1] "stats"      "graphics"    "grDevices"   "utils"       "datasets"    "base"
```

- Additional Packages, Attached

```
## [1] "boot"       "ISLR"
```

- Additional Packages, Not Attached

```
## [1] "Rcpp"        "nloptr"      "plyr"        "methods" 
## [5] " iterators"   " tools"      " digest"     " lme4"    
## [9] " evaluate"    " tibble"     " gtable"     " nlme"    
## [13] " lattice"    " mgcv"      " Matrix"     " foreach"  
## [17] " parallel"   " yaml"      " SparseM"   " stringr" 
## [21] " knitr"      " MatrixModels" " stats4"    " rprojroot" 
## [25] " grid"       " caret"      " nnet"       " rmarkdown" 
## [29] " bookdown"   " minqa"     " ggplot2"    " reshape2" 
## [33] " car"        " magrittr"   " backports"  " scales"   
## [37] " codetools"   " ModelMetrics" " htmltools"  " MASS"    
## [41] " splines"    " assertthat" " pbkrtest"   " colorspace" 
## [45] " quantreg"   " stringi"    " lazyeval"   " munsell"
```



# Chapter 18

## Classification Overview

At this point, you should know...

### Bayes Classifier

- Classify to the class with the highest probability given a particular input  $x$ .

$$C^B(\mathbf{x}) = \operatorname{argmax}_k P[Y = k \mid \mathbf{X} = \mathbf{x}]$$

- Since we rarely, if ever, know the true probabilities, use a classification method to estimate them using data.

### The Bias-Variance Tradeoff

- As model complexity increases, **bias** decreases.
- As model complexity increases, **variance** increases.
- As a result, there is a model somewhere in the middle with the best accuracy. (Or lowest RMSE for regression.)

### The Test-Train Split

- **Never use test data to train a model.** Test accuracy is a measure of how well a method works in general.
- We can identify underfitting and overfitting models relative to the best test accuracy.
  - A less complex model than the model with the best test accuracy is **underfitting**.
  - A more complex model than the model with the best test accuracy is **overfitting**.

### Classification Methods

- Logistic Regression
- Linear Discriminant Analysis (LDA)
- Quadratic Discriminant Analysis (QDA)

- Naive Bayes (NB)
- $k$ -Nearest Neighbors (KNN)
- For each, we can:
  - Obtain predicted probabilities.
  - Make classifications.
  - Find decision boundaries. (Seen only for some.)

## Discriminative versus Generative Methods

- **Discriminative** methods learn the conditional distribution  $p(y | x)$ , thus could only simulate  $y$  given a fixed  $x$ .
- **Generative** methods learn the joint distribution  $p(x, y)$ , thus could only simulate new data  $(x, y)$ .

## Parametric and Non-Parametric Methods

- **Parametric** methods models  $P[Y = k | X = x]$  as a specific function of parameters which are learned through data.
- **Non-Parametric** use an algorithmic approach to estimate  $P[Y = k | X = x]$  for each possible input  $x$ .

## Tuning Parameters

- Specify **how** to train a model. This in contrast to model parameters, which are learned through training.

## Cross-Validation

- A method to estimate test metrics with training data. Repeats the train-validate split inside the training data.

## Curse of Dimensionality

- As feature space grows, that is as  $p$  grows, “neighborhoods” must become much larger to contain “neighbors,” thus local methods are not so local.

## No-Free-Lunch Theorem

- There is no one classifier that will be best across all datasets.

### 18.1 External Links

- Wikipedia: No-Free-Lunch
- Do we Need Hundreds of Classifiers to Solve Real World Classification Problems? - A paper that argues that No-Free-Lunch may be true in theory, but in practice there are only a few classifiers that outperform most others.

## 18.2 RMarkdown

The RMarkdown file for this chapter can be found [here](#). The file was created using R version 3.3.2.



# Chapter 19

## The caret Package

**Instructor's Note:** This chapter is currently missing the usual narrative text. Hopefully it will be added later.

Now that we have seen a number of classification (and regression) methods, and introduced cross-validation, we see the general outline of a predictive analysis:

- Select a method
- Test-train split the available data
- Decide on a set of candidate models via tuning parameters
- Select the best model (tuning parameters) using a cross-validated metric
- Use chosen model to make predictions
- Calculate relevant metrics on the test data

At face value it would seem like it should be easy to repeat this process for a number of different methods, however we have run into a number of difficulties attempting to do so with R.

- The `predict()` function seems to have a different behavior for each new method we see.
- Many methods have different cross-validation functions, or worse yet, no built-in process for cross-validation.
- Not all methods expect the same data format. Some methods do not use formula syntax.
- Different methods have different handling of categorical predictors.

Thankfully, the R community has essentially provided a silver bullet for these issues, the `caret` package. Returning to the above list, we will see that a number of these tasks are directly addressed in the `caret` package.

- Test-train split the available data
  - `createDataPartition()` will take the place of our manual data splitting. It will also do some extra work to ensure that the train and test samples are somewhat similar.
- Decide on a set of candidate models via tuning parameters
  - `expand.grid()` is not a function in `caret`, but we will get in the habit of using it to specify a grid of tuning parameters.
- Select the best model (tuning parameters) using a cross-validated metric
  - `trainControl()` will setup cross-validation

- `train()` is the workhorse of `caret`. It takes the following information then trains the requested model:

```
* form, a formula, such as y ~ .
* data
* method, from a long list of possibilities
* preprocess which allows for specification of things such as centering and scaling
* tuneGrid which specifies the tuning parameters to train over
* trControl which specifies the resampling scheme, that is, how cross-validation should be performed
```

- Use chosen model to make predictions
  - `predict()` used on objects of type `train` will be magical!

To illustrate `caret`, we return to our familiar `Default` data.

```
data(Default, package = "ISLR")
```

```
library(caret)
```

We first test-train split the data using `createDataPartition`. Here we are using 75% of the data for training.

```
set.seed(430)
default_idx = createDataPartition(Default$default, p = 0.75, list = FALSE)
default_trn = Default[default_idx, ]
default_tst = Default[-default_idx, ]
```

```
default_glm = train(
  form = default ~ .,
  data = default_trn,
  method = "glm",
  family = "binomial",
  trControl = trainControl(method = "cv", number = 5)
)
```

```
default_glm
```

```
## Generalized Linear Model
##
## 7501 samples
##     3 predictor
##     2 classes: 'No', 'Yes'
##
## No pre-processing
## Resampling: Cross-Validated (5 fold)
## Summary of sample sizes: 6000, 6001, 6001, 6001, 6001
## Resampling results:
##
##     Accuracy    Kappa
##     0.9729372  0.4147209
##
```

```

names(default_glm)

## [1] "method"         "modelInfo"       "modelType"       "results"
## [5] "pred"           "bestTune"        "call"           "dots"
## [9] "metric"          "control"         "finalModel"      "preProcess"
## [13] "trainingData"    "resample"        "resampledCM"    "perfNames"
## [17] "maximize"        "yLimits"         "times"          "levels"
## [21] "terms"          "coefnames"      "contrasts"      "xlevels"

default_glm$results

##   parameter Accuracy   Kappa AccuracySD   KappaSD
## 1      none 0.9729372 0.4147209 0.001527574 0.04620646

default_glm$finalModel

##
## Call:  NULL
##
## Coefficients:
## (Intercept) studentYes      balance      income
## -1.066e+01   -6.254e-01   5.647e-03   1.395e-06
##
## Degrees of Freedom: 7500 Total (i.e. Null);  7497 Residual
## Null Deviance:      2192
## Residual Deviance: 1204  AIC: 1212

accuracy = function(actual, predicted) {
  mean(actual == predicted)
}

# make predictions
head(predict(default_glm, newdata = default_trn))

## [1] No No No No No No
## Levels: No Yes

# train acc
accuracy(actual = default_trn$default,
          predicted = predict(default_glm, newdata = default_trn))

## [1] 0.9730703

# test acc
accuracy(actual = default_tst$default,
          predicted = predict(default_glm, newdata = default_tst))

## [1] 0.9739896

```

```
# get probs
head(predict(default_glm, newdata = default_trn, type = "prob"))
```

```
##          No        Yes
## 1 0.9984674 0.001532637
## 3 0.9895850 0.010414985
## 5 0.9979141 0.002085863
## 6 0.9977233 0.002276746
## 8 0.9987645 0.001235527
## 9 0.9829081 0.017091877
```

```
default_knn = train(
  default ~ .,
  data = default_trn,
  method = "knn",
  trControl = trainControl(method = "cv", number = 5)
)
```

```
default_knn
```

```
## k-Nearest Neighbors
##
## 7501 samples
##     3 predictor
##     2 classes: 'No', 'Yes'
##
## No pre-processing
## Resampling: Cross-Validated (5 fold)
## Summary of sample sizes: 6000, 6001, 6001, 6001, 6001
## Resampling results across tuning parameters:
##
##     k  Accuracy   Kappa
##     5  0.9656046  0.1770996
##     7  0.9657378  0.1295425
##     9  0.9676045  0.1092291
##
## Accuracy was used to select the optimal model using the largest value.
## The final value used for the model was k = 9.
```

```
default_knn = train(
  default ~ .,
  data = default_trn,
  method = "knn",
  trControl = trainControl(method = "cv", number = 5),
  preProcess = c("center", "scale"),
  tuneGrid = expand.grid(k = seq(1, 100, by = 1))
)
```

```
default_knn
```

```
## k-Nearest Neighbors
```

```

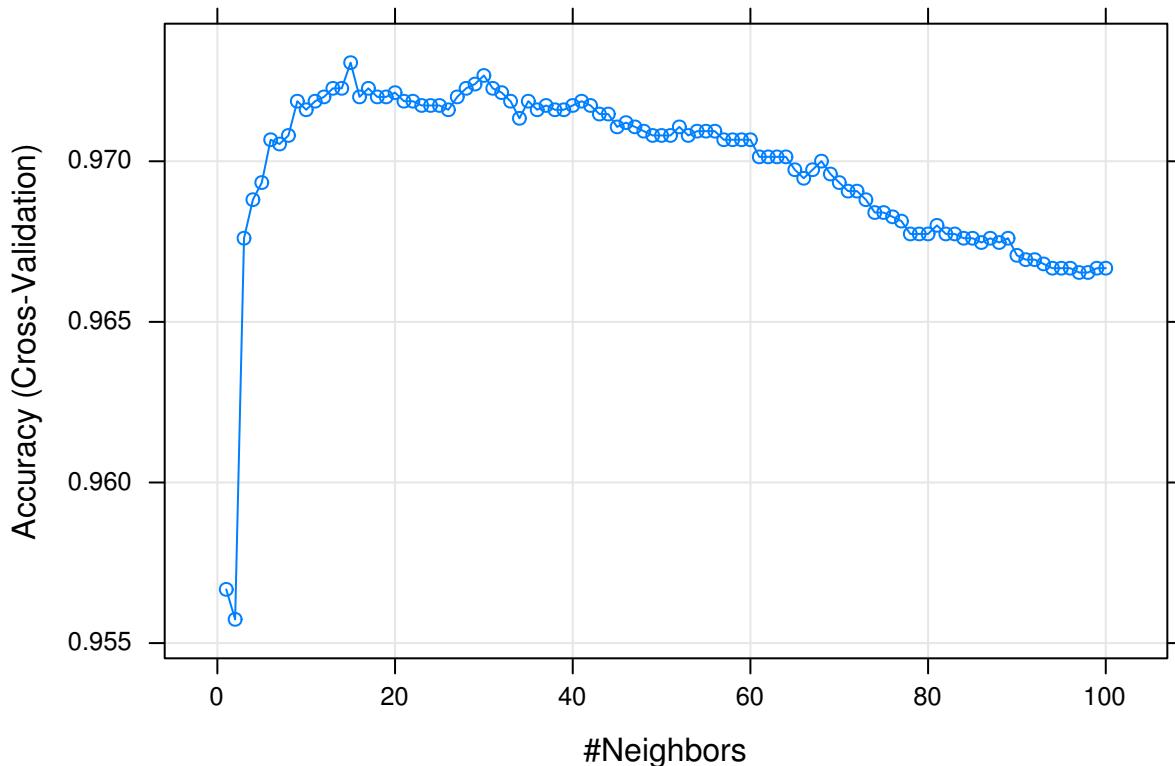
## 
## 7501 samples
##   3 predictor
##   2 classes: 'No', 'Yes'
##
## Pre-processing: centered (3), scaled (3)
## Resampling: Cross-Validated (5 fold)
## Summary of sample sizes: 6001, 6001, 6001, 6001, 6000
## Resampling results across tuning parameters:
##
##   k    Accuracy   Kappa
##   1    0.9566725  0.3102526809
##   2    0.9557393  0.3105592402
##   3    0.9676047  0.3737110726
##   4    0.9688045  0.3905217578
##   5    0.9693378  0.3720650032
##   6    0.9706708  0.3878199028
##   7    0.9705374  0.3805478527
##   8    0.9708038  0.3847869416
##   9    0.9718704  0.4008912524
##  10   0.9716037  0.3887596806
##  11   0.9718702  0.3893164746
##  12   0.9720036  0.4017431900
##  13   0.9722702  0.3885361750
##  14   0.9722703  0.3944481266
##  15   0.9730702  0.4007241418
##  16   0.9720039  0.3811342289
##  17   0.9722703  0.3792775497
##  18   0.9720038  0.3788523329
##  19   0.9720038  0.3697985519
##  20   0.9721370  0.3740347410
##  21   0.9718704  0.3615639366
##  22   0.9718705  0.3680145319
##  23   0.9717371  0.3539511129
##  24   0.9717371  0.3541232524
##  25   0.9717371  0.3499644208
##  26   0.9716037  0.3455285320
##  27   0.9720037  0.3528854219
##  28   0.9722703  0.3638828006
##  29   0.9724036  0.3687985599
##  30   0.9726703  0.3779447479
##  31   0.9722704  0.3584335333
##  32   0.9721371  0.3547676501
##  33   0.9718704  0.3473184965
##  34   0.9713372  0.3291867049
##  35   0.9718703  0.3367666962
##  36   0.9716038  0.3260879521
##  37   0.9717371  0.3320811820
##  38   0.9716037  0.3215128939
##  39   0.9716037  0.3219513284
##  40   0.9717371  0.3276712249
##  41   0.9718704  0.3277674417
##  42   0.9717371  0.3188637072
##  43   0.9714704  0.3066997114

```

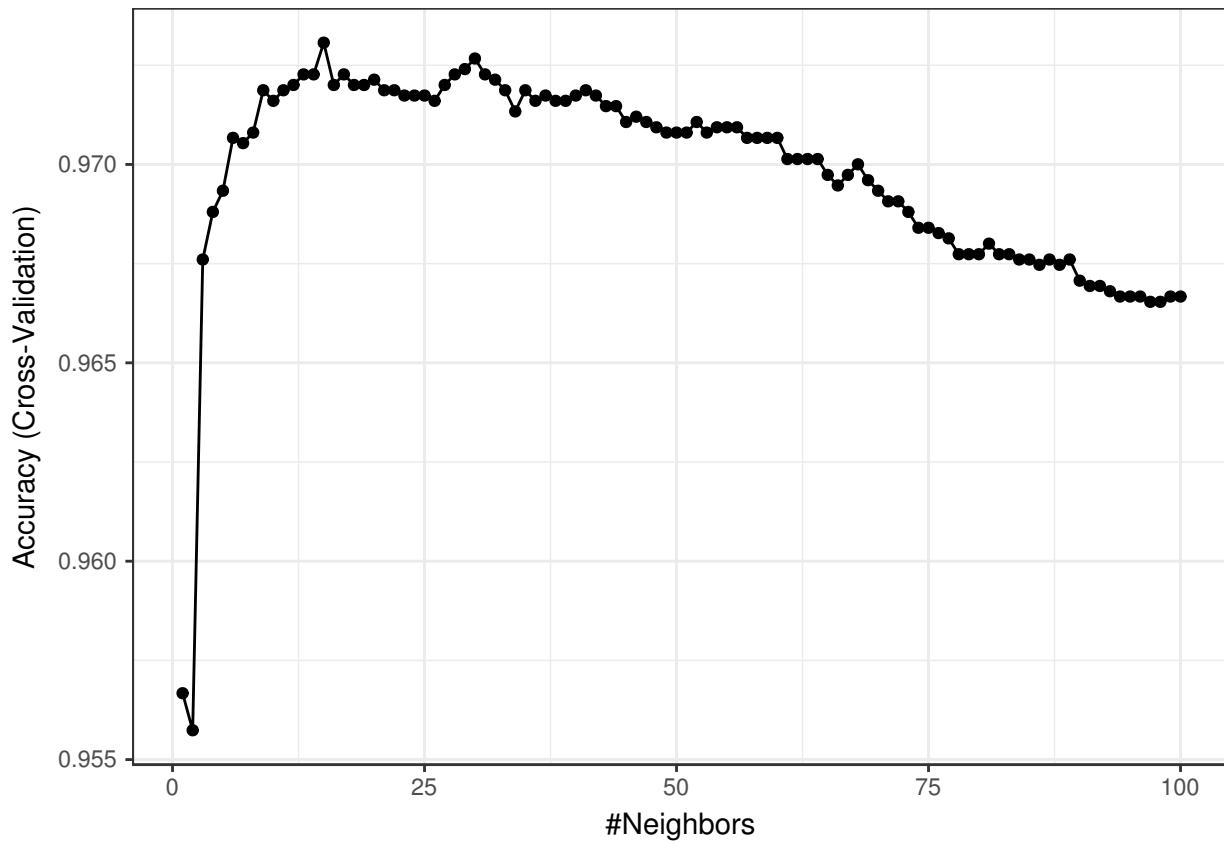
```
##   44  0.9714704  0.3077206051
##   45  0.9710704  0.2961400483
##   46  0.9712037  0.2961184626
##   47  0.9710704  0.2914235196
##   48  0.9709372  0.2860070606
##   49  0.9708037  0.2847306864
##   50  0.9708037  0.2847306864
##   51  0.9708036  0.2812029517
##   52  0.9710703  0.2867649638
##   53  0.9708037  0.2771131971
##   54  0.9709372  0.2817510947
##   55  0.9709371  0.2781721329
##   56  0.9709371  0.2774089321
##   57  0.9706705  0.2714234284
##   58  0.9706704  0.2638759429
##   59  0.9706703  0.2638759634
##   60  0.9706703  0.2585241342
##   61  0.9701371  0.2368125620
##   62  0.9701372  0.2327890464
##   63  0.9701372  0.2327890464
##   64  0.9701372  0.2279714026
##   65  0.9697372  0.2110842159
##   66  0.9694708  0.1945370488
##   67  0.9697372  0.1951671666
##   68  0.9700038  0.2030358192
##   69  0.9696040  0.1849170701
##   70  0.9693373  0.1717143623
##   71  0.9690708  0.1588168415
##   72  0.9690708  0.1593832545
##   73  0.9688041  0.1399844247
##   74  0.9684042  0.1264961122
##   75  0.9684041  0.1201537186
##   76  0.9682708  0.1133391796
##   77  0.9681375  0.1068555860
##   78  0.9677375  0.0857547640
##   79  0.9677376  0.0921848301
##   80  0.9677376  0.0853775175
##   81  0.9680043  0.0866367370
##   82  0.9677377  0.0790611308
##   83  0.9677376  0.0725173945
##   84  0.9676043  0.0658085644
##   85  0.9676043  0.0651989918
##   86  0.9674709  0.0578805892
##   87  0.9676043  0.0651989918
##   88  0.9674709  0.0584901617
##   89  0.9676043  0.0651989918
##   90  0.9670710  0.0362615841
##   91  0.9669378  0.0277870004
##   92  0.9669377  0.0286699611
##   93  0.9668044  0.0210781703
##   94  0.9666711  0.0141321593
##   95  0.9666711  0.0073298429
##   96  0.9666711  0.0073298429
##   97  0.9665378  -0.0002617801
```

```
##      98  0.9665378 -0.0002617801
##      99  0.9666711   0.0000000000
##     100  0.9666711   0.0000000000
##
## Accuracy was used to select the optimal model using  the largest value.
## The final value used for the model was k = 15.
```

```
plot(default_knn)
```



```
ggplot(default_knn) + theme_bw()
```



```
default_knn$bestTune

##      k
## 15 15

get_best_result = function(caret_fit) {
  best_result = caret_fit$results[as.numeric(rownames(caret_fit$bestTune)), ]
  rownames(best_result) = NULL
  best_result
}

get_best_result(default_knn)

##      k Accuracy     Kappa AccuracySD    KappaSD
## 1 15 0.9730702 0.4007241 0.002241574 0.08402323

default_knn$finalModel

## 15-nearest neighbor classification model
## Training set class distribution:
##
##      No   Yes
## 7251   250
```

Notes to add later:

- Fewer ties with CV than simple test-train approach
- Default grid vs specified grid. `tuneLength`
- Create table summarizing results for `knn()` and `glm()`. Test, train, and CV accuracy. Maybe also show SD for CV.

## 19.1 External Links

- The `caret` Package - Reference documentation for the `caret` package in bookdown format.
- `caret` Model List - List of available models in `caret`.

## 19.2 RMarkdown

The RMarkdown file for this chapter can be found [here](#). The file was created using R version 3.3.2 and the following packages:

- Base Packages, Attached

```
## [1] "methods"    "stats"       "graphics"   "grDevices"  "utils"      "datasets"
## [7] "base"
```

- Additional Packages, Attached

```
## [1] "caret"      "ggplot2"    "lattice"
```

- Additional Packages, Not Attached

```
##  [1] "Rcpp"        "compiler"     "nloptr"      "plyr"
##  [5] "class"       " iterators"   " tools"      " digest"
##  [9] "lme4"        " evaluate"    " tibble"     " gtable"
## [13] "nlme"        " mgcv"       " Matrix"    " foreach"
## [17] "yaml"        " parallel"   " SparseM"   " e1071"
## [21] "stringr"     " knitr"      " MatrixModels" " stats4"
## [25] "rprojroot"   " grid"       " nnet"      " rmarkdown"
## [29] "bookdown"    " minqa"     " reshape2"   " car"
## [33] "magrittr"    " backports"  " scales"    " codetools"
## [37] "ModelMetrics" " htmltools"  " MASS"      " splines"
## [41] "assertthat"  " pbkrtest"   " colorspace" " labeling"
## [45] "quantreg"    " stringi"   " lazyeval"  " munsell"
```



# Chapter 20

## Subset Selection

Instructor's Note: This chapter is currently missing the usual narrative text. Hopefully it will be added later.

```
data(Hitters, package = "ISLR")
```

```
sum(is.na(Hitters))
```

```
## [1] 59
```

```
sum(is.na(Hitters$Salary))
```

```
## [1] 59
```

```
Hitters = na.omit(Hitters)
sum(is.na(Hitters))
```

```
## [1] 0
```

### 20.1 AIC, BIC, and Cp

#### 20.1.1 leaps Package

```
library(leaps)
```

#### 20.1.2 Best Subset

```
fit_all = regsubsets(Salary ~ ., Hitters)
summary(fit_all)
```

```

## Subset selection object
## Call: regsubsets.formula(Salary ~ ., Hitters)
## 19 Variables (and intercept)
##          Forced in Forced out
## AtBat      FALSE      FALSE
## Hits       FALSE      FALSE
## HmRun      FALSE      FALSE
## Runs       FALSE      FALSE
## RBI        FALSE      FALSE
## Walks      FALSE      FALSE
## Years      FALSE      FALSE
## CAtBat     FALSE      FALSE
## CHits      FALSE      FALSE
## CHmRun     FALSE      FALSE
## CRuns      FALSE      FALSE
## CRBI       FALSE      FALSE
## CWalks     FALSE      FALSE
## LeagueN    FALSE      FALSE
## DivisionW  FALSE      FALSE
## PutOuts    FALSE      FALSE
## Assists    FALSE      FALSE
## Errors     FALSE      FALSE
## NewLeagueN FALSE      FALSE
## 1 subsets of each size up to 8
## Selection Algorithm: exhaustive
##          AtBat Hits HmRun Runs RBI Walks Years CAtBat CHits CHmRun CRuns
## 1 ( 1 ) " "   " "   " "   " "   " "   " "   " "   " "   " "   " "
## 2 ( 1 ) " "   "*"  " "   " "   " "   " "   " "   " "   " "   " "
## 3 ( 1 ) " "   "*"  " "   " "   " "   " "   " "   " "   " "   " "
## 4 ( 1 ) " "   "*"  " "   " "   " "   " "   " "   " "   " "   " "
## 5 ( 1 ) "*"  "*"  " "   " "   " "   " "   " "   " "   " "   " "
## 6 ( 1 ) "*"  "*"  " "   " "   " "   "*"  " "   " "   " "   " "
## 7 ( 1 ) " "   "*"  " "   " "   " "   "*"  " "   "*"  "*"  " "
## 8 ( 1 ) "*"  "*"  " "   " "   " "   "*"  " "   " "   "*"  "*"
##          CRBI CWalks LeagueN DivisionW PutOuts Assists Errors NewLeagueN
## 1 ( 1 ) "*"  " "   " "   " "   " "   " "   " "   " "
## 2 ( 1 ) "*"  " "   " "   " "   " "   " "   " "   " "
## 3 ( 1 ) "*"  " "   " "   " "   "*"  " "   " "   " "
## 4 ( 1 ) "*"  " "   " "   "*"  "*"  " "   " "   " "
## 5 ( 1 ) "*"  " "   " "   "*"  "*"  " "   " "   " "
## 6 ( 1 ) "*"  " "   " "   "*"  "*"  " "   " "   " "
## 7 ( 1 ) " "   " "   " "   "*"  "*"  " "   " "   " "
## 8 ( 1 ) " "   "*"  " "   "*"  "*"  " "   " "   " "

fit_all = regsubsets(Salary ~ ., data = Hitters, nvmax = 19)
fit_all_sum = summary(fit_all)
names(fit_all_sum)

## [1] "which"   "rsq"     "rss"     "adjr2"   "cp"      "bic"      "outmat"  "obj"

fit_all_sum$bic

## [1] -90.84637 -128.92622 -135.62693 -141.80892 -144.07143 -147.91690

```

```

## [7] -145.25594 -147.61525 -145.44316 -143.21651 -138.86077 -133.87283
## [13] -128.77759 -123.64420 -118.21832 -112.81768 -107.35339 -101.86391
## [19] -96.30412

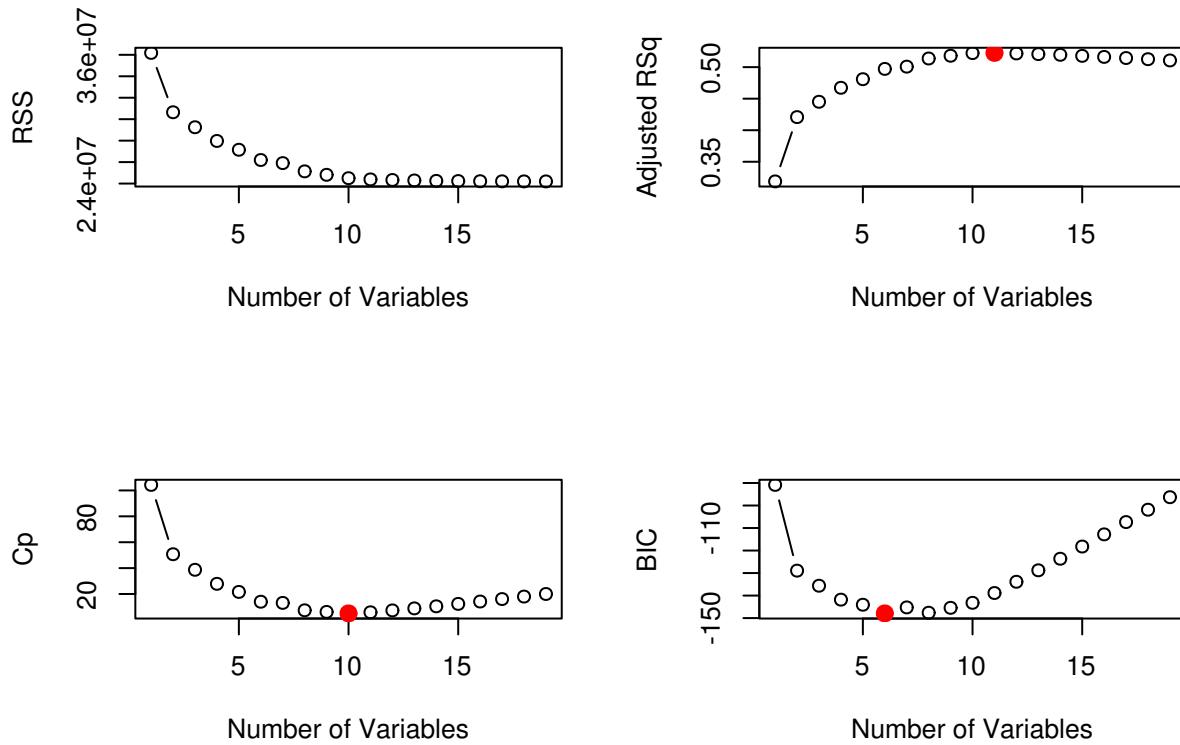
par(mfrow = c(2, 2))
plot(fit_all_sum$rss, xlab = "Number of Variables", ylab = "RSS", type = "b")

plot(fit_all_sum$adjr2, xlab = "Number of Variables", ylab = "Adjusted RSq", type = "b")
best_adj_r2 = which.max(fit_all_sum$adjr2)
points(best_adj_r2, fit_all_sum$adjr2[best_adj_r2],
       col = "red", cex = 2, pch = 20)

plot(fit_all_sum$cp, xlab = "Number of Variables", ylab = "Cp", type = 'b')
best_cp = which.min(fit_all_sum$cp)
points(best_cp, fit_all_sum$cp[best_cp],
       col = "red", cex = 2, pch = 20)

plot(fit_all_sum$bic, xlab = "Number of Variables", ylab = "BIC", type = 'b')
best_bic = which.min(fit_all_sum$bic)
points(best_bic, fit_all_sum$bic[best_bic],
       col = "red", cex = 2, pch = 20)

```



### 20.1.3 Stepwise Methods

```

fit_fwd = regsubsets(Salary ~ ., data = Hitters, nvmax = 19, method = "forward")
fit_fwd_sum = summary(fit_fwd)

```

```
fit_bwd = regsubsets(Salary ~ ., data = Hitters, nvmax = 19, method = "backward")
fit_bwd_sum = summary(fit_bwd)
```

```
coef(fit_fwd, 7)
```

	(Intercept)	AtBat	Hits	Walks	CRBI
##	109.7873062	-1.9588851	7.4498772	4.9131401	0.8537622
##	CWalks	DivisionW	PutOuts		
##	-0.3053070	-127.1223928	0.2533404		

```
coef(fit_bwd, 7)
```

	(Intercept)	AtBat	Hits	Walks	CRuns
##	105.6487488	-1.9762838	6.7574914	6.0558691	1.1293095
##	CWalks	DivisionW	PutOuts		
##	-0.7163346	-116.1692169	0.3028847		

```
coef(fit_all, 7)
```

	(Intercept)	Hits	Walks	CAtBat	CHits
##	79.4509472	1.2833513	3.2274264	-0.3752350	1.4957073
##	CHmRun	DivisionW	PutOuts		
##	1.4420538	-129.9866432	0.2366813		

```
fit_bwd_sum = summary(fit_bwd)
which.min(fit_bwd_sum$cp)
```

```
## [1] 10
```

```
coef(fit_bwd, which.min(fit_bwd_sum$cp))
```

	(Intercept)	AtBat	Hits	Walks	CAtBat
##	162.5354420	-2.1686501	6.9180175	5.7732246	-0.1300798
##	CRuns	CRBI	CWalks	DivisionW	PutOuts
##	1.4082490	0.7743122	-0.8308264	-112.3800575	0.2973726
##	Assists				
##	0.2831680				

```
fit = lm(Salary ~ ., data = Hitters)
fit_aic_back = step(fit, trace = FALSE)
coef(fit_aic_back)
```

	(Intercept)	AtBat	Hits	Walks	CAtBat
##	162.5354420	-2.1686501	6.9180175	5.7732246	-0.1300798
##	CRuns	CRBI	CWalks	DivisionW	PutOuts
##	1.4082490	0.7743122	-0.8308264	-112.3800575	0.2973726
##	Assists				
##	0.2831680				

## 20.2 Validated RMSE

```

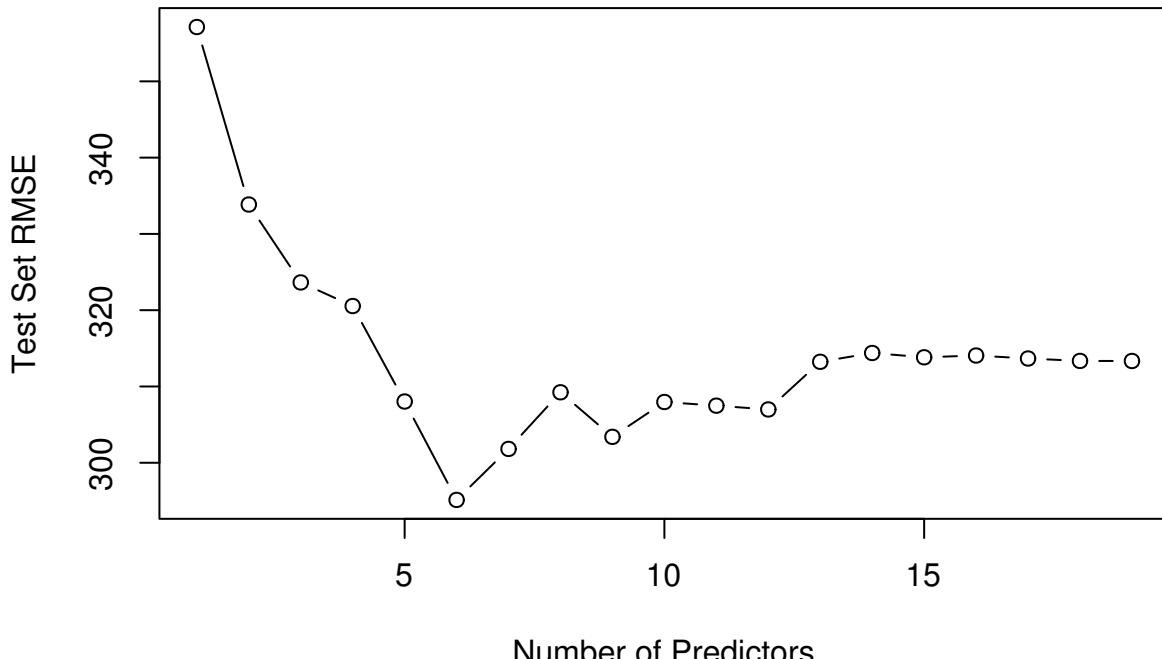
set.seed(42)
num_vars = ncol(Hitters) - 1
trn_idx = sample(c(TRUE, FALSE), nrow(Hitters), rep = TRUE)
tst_idx = (!trn_idx)

fit_all = regsubsets(Salary ~ ., data = Hitters[trn_idx, ], nvmax = num_vars)
test_mat = model.matrix(Salary ~ ., data = Hitters[tst_idx, ])

test_err = rep(0, times = num_vars)
for (i in seq_along(test_err)) {
  coefs = coef(fit_all, id = i)
  pred = test_mat[, names(coefs)] %*% coefs
  test_err[i] <- sqrt(mean((Hitters$Salary[tst_idx] - pred)^ 2))
}
test_err
## [1] 357.1226 333.8531 323.6408 320.5458 308.0303 295.1308 301.8142
## [8] 309.2389 303.3976 307.9660 307.4841 306.9883 313.2374 314.3905
## [15] 313.8258 314.0586 313.6674 313.3490 313.3424

plot(test_err, type='b', ylab = "Test Set RMSE", xlab = "Number of Predictors")

```



```
which.min(test_err)
```

```
## [1] 6
```

```

coef(fit_all, which.min(test_err))

##  (Intercept)      Walks      CAtBat      CHits      CRBI
##  171.2082504   5.0067050  -0.4005457   1.2951923   0.7894534
##  DivisionW     PutOuts
## -131.1212694   0.2682166

class(fit_all)

## [1] "regsubsets"

predict.regsubsets = function(object, newdata, id, ...) {

  form  = as.formula(object$call[[2]])
  mat   = model.matrix(form, newdata)
  coefs = coef(object, id = id)
  xvars = names(coefs)

  mat[, xvars] %*% coefs
}

rmse = function(actual, predicted) {
  sqrt(mean((actual - predicted) ^ 2))
}

num_folds = 5
num_vars  = 19
set.seed(1)
folds = caret::createFolds(Hitters$Salary, k = num_folds)
fold_error = matrix(0, nrow = num_folds, ncol = num_vars,
                    dimnames = list(paste(1:5), paste(1:19)))

for(j in 1:num_folds) {

  train_fold    = Hitters[-folds[[j]], ]
  validate_fold = Hitters[ folds[[j]], ]

  best_fit = regsubsets(Salary ~ ., data = train_fold, nvmax = 19)

  for (i in 1:num_vars) {

    pred = predict(best_fit, validate_fold, id = i)

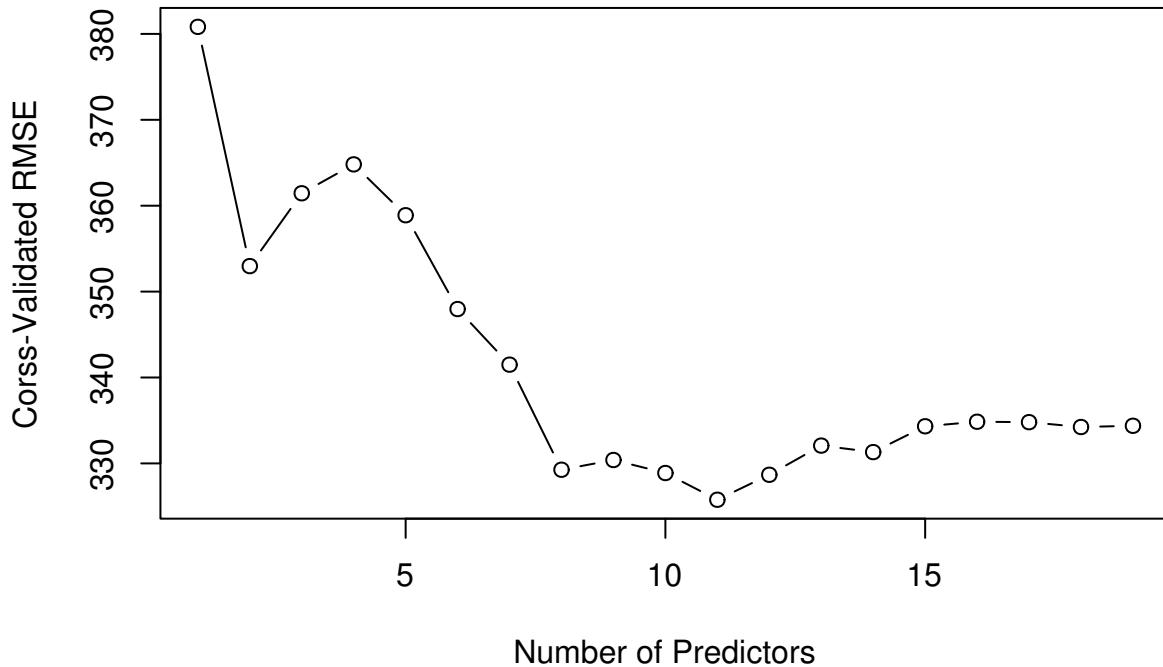
    fold_error[j, i] = rmse(actual = validate_fold$Salary,
                           predicted = pred)
  }
}

cv_error = apply(fold_error, 2, mean)
cv_error

```

```
##      1       2       3       4       5       6       7       8
## 380.8213 352.9698 361.4484 364.8120 358.8908 347.9691 341.4967 329.2623
##      9      10      11      12      13      14      15      16
## 330.3959 328.8812 325.7691 328.6772 332.0737 331.3155 334.3228 334.8503
##     17      18      19
## 334.8013 334.2359 334.3797

plot(cv_error, type='b', ylab = "Corss-Validated RMSE", xlab = "Number of Predictors")
```



```
fit_all = regsubsets(Salary ~ ., data = Hitters, nvmax = num_vars)
coef(fit_all, which.min(cv_error))
```

```
## (Intercept)          AtBat          Hits          Walks          CAtBat
## 135.7512195 -2.1277482   6.9236994   5.6202755 -0.1389914
## CRuns           CRBI           CWalks        LeagueN    DivisionW
## 1.4553310    0.7852528  -0.8228559  43.1116152 -111.1460252
## PutOuts         Assists
## 0.2894087    0.2688277
```

## 20.3 External Links

• -

## 20.4 RMarkdown

The RMarkdown file for this chapter can be found [here](#). The file was created using R version 3.3.2 and the following packages:

- Base Packages, Attached

```
## [1] "stats"      "graphics"    "grDevices"   "utils"       "datasets"    "base"
```

- Additional Packages, Attached

```
## [1] "leaps"
```

- Additional Packages, Not Attached

```
##  [1] "Rcpp"          "nloptr"        "plyr"         "methods"      "lme4"
##  [5] "iterators"     "tools"         "digest"       "nlme"        "foreach"
##  [9] "evaluate"      "tibble"        "gttable"      "stringr"     "grid"
## [13] "lattice"       "mgcv"         "Matrix"      "rprojroot"   "knitr"
## [17] "yaml"          "parallel"      "SparseM"     "rmarkdown"   "grid"
## [21] "grid"          "MatrixModels"  "stats4"      "reshape2"    "bookdown"
## [25] "grid"          "caret"         "nnet"        "scales"      "car"
## [29] "grid"          "minqa"         "ggplot2"     "MASS"        "codetools"
## [33] "grid"          "magrittr"      "backports"   "colorspace"  "splines"
## [37] "grid"          "ModelMetrics"  "htmltools"   "munsell"    "quantreg"
```

# Chapter 21

## Shrinkage Methods

We will use the **Hitters** dataset from the **ISLR** package to explore two shrinkage methods: **ridge** and **lasso**. These are otherwise known as **penalized regression** methods.

```
data(Hitters, package = "ISLR")
```

This dataset has some missing data in the response **Salary**. We use the **na.omit()** function to clean the dataset.

```
sum(is.na(Hitters))
```

```
## [1] 59
```

```
sum(is.na(Hitters$Salary))
```

```
## [1] 59
```

```
Hitters = na.omit(Hitters)
sum(is.na(Hitters))
```

```
## [1] 0
```

The predictor variables are offensive and defensive statistics for a number of baseball players.

```
names(Hitters)
```

```
## [1] "AtBat"      "Hits"       "HmRun"      "Runs"       "RBI"
## [6] "Walks"       "Years"      "CATBat"     "CHits"      "CChmRun"
## [11] "CRuns"      "CRBI"       "CWalks"     "League"     "Division"
## [16] "PutOuts"    "Assists"    "Errors"     "Salary"     "NewLeague"
```

We use the **glmnet()** and **cv.glmnet()** functions in the **glmnet** package to fit penalized regressions.

```
library(glmnet)
```

The `glmnet` function does not allow the use of model formulas, so we setup the data for ease of use with `glmnet`.

```
X = model.matrix(Salary ~ ., Hitters) [, -1]
y = Hitters$Salary
```

First, we fit a regular linear regression, and note the size of the predictors' coefficients, and predictors' coefficients squared. (The two penalties we will use.)

```
fit = lm(Salary ~ ., Hitters)
coef(fit)
```

	(Intercept)	AtBat	Hits	HmRun	Runs
##	163.1035878	-1.9798729	7.5007675	4.3308829	-2.3762100
##	RBI	Walks	Years	CAtBat	CHits
##	-1.04449620	6.2312863	-3.4890543	-0.1713405	0.1339910
##	CHmRun	CRuns	CRBI	CWalks	LeagueN
##	-0.1728611	1.4543049	0.8077088	-0.8115709	62.5994230
##	DivisionW	PutOuts	Assists	Errors	NewLeagueN
##	-116.8492456	0.2818925	0.3710692	-3.3607605	-24.7623251

```
sum(abs(coef(fit)[-1]))
```

```
## [1] 238.7295
```

```
sum(coef(fit)[-1] ^ 2)
```

```
## [1] 18337.3
```

## 21.1 Ridge Regression

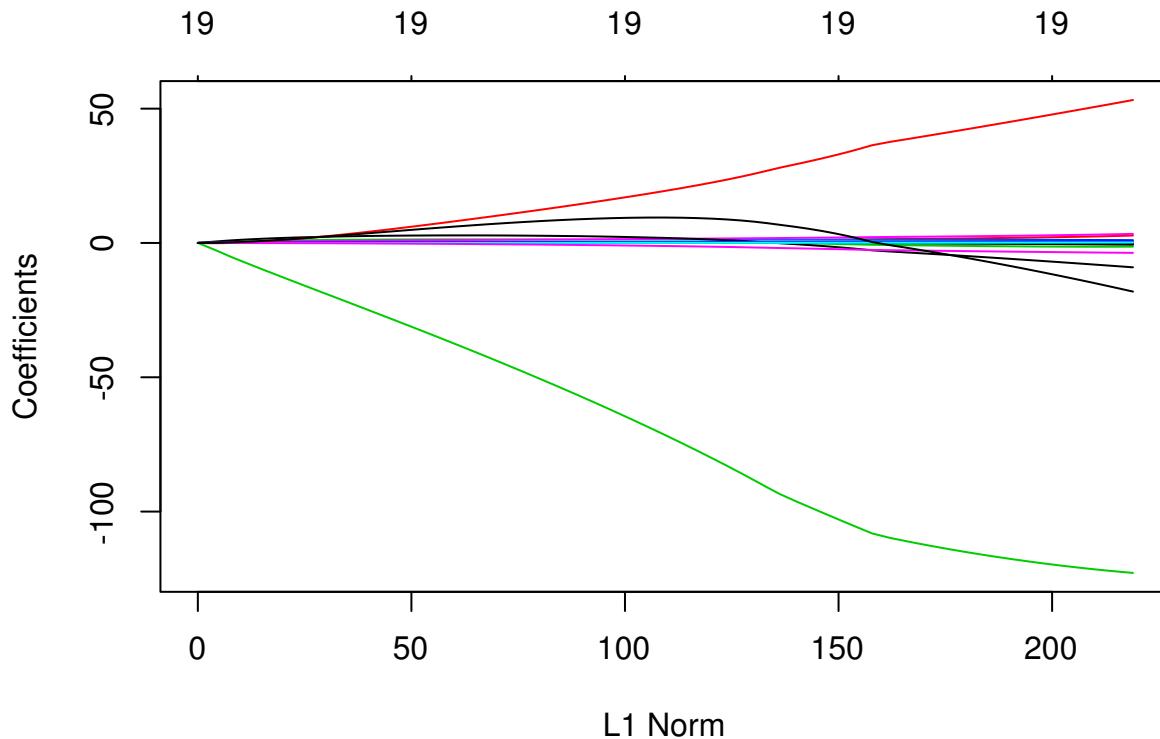
We first illustrate **ridge regression**, which can be fit using `glmnet()` with `alpha = 0` and seeks to minimize

$$\sum_{i=1}^n \left( y_i - \beta_0 - \sum_{j=1}^p \beta_j x_{ij} \right)^2 + \lambda \sum_{j=1}^p \beta_j^2.$$

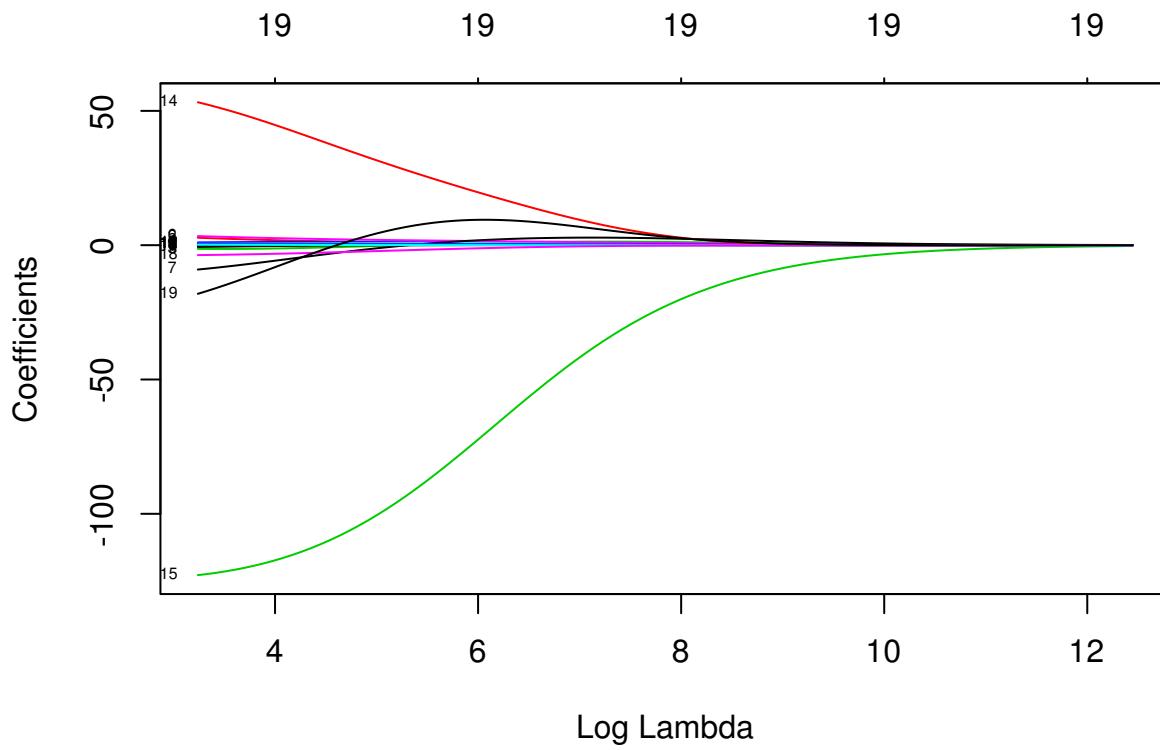
Notice that the intercept is **not** penalized. Also, note that that ridge regression is **not** scale invariant like the usual unpenalized regression. Thankfully, `glmnet()` takes care of this internally. It automatically standardizes input for fitting, then reports fitted coefficient using the original scale.

The two plots illustrate how much the coefficients are penalized for different values of  $\lambda$ . Notice none of the coefficients are forced to be zero.

```
fit_ridge = glmnet(X, y, alpha = 0)
plot(fit_ridge)
```



```
plot(fit_ridge, xvar = "lambda", label = TRUE)
```

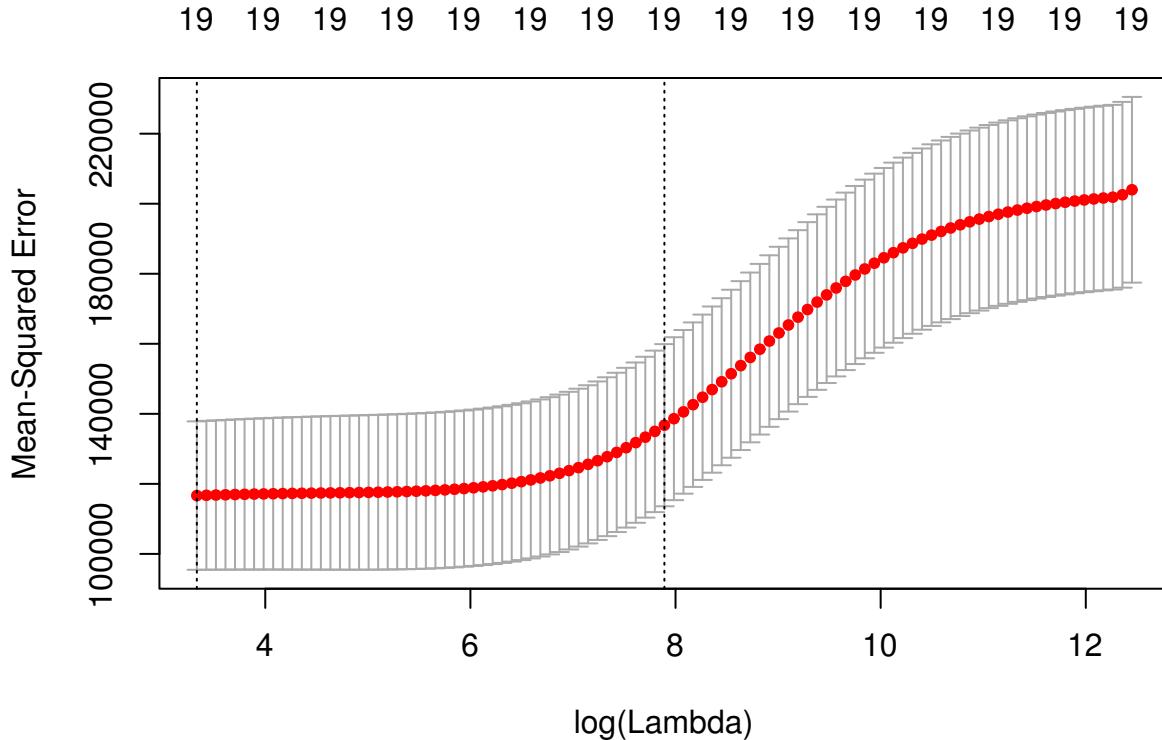


```
dim(coef(fit_ridge))
```

```
## [1] 20 100
```

We use cross-validation to select a good  $\lambda$  value. The `cv.glmnet()` function uses 10 folds by default. The plot illustrates the MSE for the  $\lambda$ s considered. Two lines are drawn. The first is the  $\lambda$  that gives the smallest MSE. The second is the  $\lambda$  that gives an MSE within one standard error of the smallest.

```
fit_ridge_cv = cv.glmnet(x, y, alpha = 0)
plot(fit_ridge_cv)
```



The `cv.glmnet()` function returns several details of the fit for both  $\lambda$  values in the plot. Notice the penalty terms are smaller than the full linear regression. (As we would expect.)

```
coef(fit_ridge_cv)
```

```
## 20 x 1 sparse Matrix of class "dgCMatrix"
##           1
## (Intercept) 213.066443434
## AtBat      0.090095728
## Hits       0.371252756
## HmRun      1.180126956
## Runs       0.596298287
## RBI        0.594502390
## Walks      0.772525466
## Years      2.473494238
## CAtBat     0.007597952
## CHits      0.029272172
## CHmRun     0.217335716
## CRuns      0.058705097
## CRBI       0.060722036
## CWalks     0.058698830
## LeagueN    3.276567828
```

```

## DivisionW   -21.889942619
## PutOuts      0.052667119
## Assists      0.007463678
## Errors       -0.145121336
## NewLeagueN   2.972759126

coef(fit_ridge_cv, s = "lambda.min")

## 20 x 1 sparse Matrix of class "dgCMatrix"
##                                         1
## (Intercept) 7.645824e+01
## AtBat      -6.315180e-01
## Hits       2.642160e+00
## HmRun      -1.388233e+00
## Runs       1.045729e+00
## RBI        7.315713e-01
## Walks      3.278001e+00
## Years      -8.723734e+00
## CAtBat     1.256354e-04
## CHits      1.318975e-01
## CHmRun     6.895578e-01
## CRuns      2.830055e-01
## CRBI       2.514905e-01
## CWalks     -2.599851e-01
## LeagueN    5.233720e+01
## DivisionW  -1.224170e+02
## PutOuts    2.623667e-01
## Assists    1.629044e-01
## Errors     -3.644002e+00
## NewLeagueN -1.702598e+01

sum(coef(fit_ridge_cv, s = "lambda.min")[-1] ^ 2) # penalty term for lambda minimum

## [1] 18126.85

coef(fit_ridge_cv, s = "lambda.1se")

## 20 x 1 sparse Matrix of class "dgCMatrix"
##                                         1
## (Intercept) 213.066443434
## AtBat      0.090095728
## Hits       0.371252756
## HmRun      1.180126956
## Runs       0.596298287
## RBI        0.594502390
## Walks      0.772525466
## Years      2.473494238
## CAtBat     0.007597952
## CHits      0.029272172
## CHmRun     0.217335716
## CRuns      0.058705097
## CRBI       0.060722036

```

```

## CWalks      0.058698830
## LeagueN    3.276567828
## DivisionW -21.889942619
## PutOuts     0.052667119
## Assists     0.007463678
## Errors      -0.145121336
## NewLeagueN  2.972759126

sum(coef(fit_ridge_cv, s = "lambda.1se")[-1] ^ 2) # penalty term for lambda one SE

## [1] 507.788

#predict(fit_ridge_cv, X, s = "lambda.min")
#predict(fit_ridge_cv, X)
mean((y - predict(fit_ridge_cv, X)) ^ 2) # "train error"

## [1] 132355.6

sqrt(fit_ridge_cv$cvm) # CV-RMSEs

## [1] 451.6471 450.0648 449.2948 449.0262 448.7327 448.4120 448.0616
## [8] 447.6792 447.2619 446.8068 446.3109 445.7706 445.1827 444.5433
## [15] 443.8484 443.0940 442.2760 441.3898 440.4311 439.3950 438.2772
## [22] 437.0728 435.7775 434.3869 432.8969 431.3037 429.6042 427.7956
## [29] 425.8762 423.8449 421.7017 419.4477 417.0856 414.6193 412.0542
## [36] 409.3976 406.6582 403.8462 400.9737 398.0543 395.1026 392.1347
## [43] 389.1670 386.2168 383.3012 380.4371 377.6406 374.9268 372.3094
## [50] 369.8004 367.4090 365.1429 363.0091 361.0107 359.1490 357.4237
## [57] 355.8327 354.3724 353.0379 351.8235 350.7226 349.7284 348.8338
## [64] 348.0301 347.3121 346.6785 346.1151 345.6162 345.1757 344.7911
## [71] 344.4597 344.1698 343.9198 343.7077 343.5244 343.3688 343.2399
## [78] 343.1277 343.0364 342.9533 342.8874 342.8224 342.7713 342.7174
## [85] 342.6699 342.6187 342.5680 342.5086 342.4548 342.3861 342.3229
## [92] 342.2405 342.1668 342.0700 341.9823 341.8766 341.7754 341.6630
## [99] 341.5505

sqrt(fit_ridge_cv$cvm[fit_ridge_cv$lambda == fit_ridge_cv$lambda.min]) # CV-RMSE minimum

## [1] 341.5505

sqrt(fit_ridge_cv$cvm[fit_ridge_cv$lambda == fit_ridge_cv$lambda.1se]) # CV-RMSE one SE

## [1] 369.8004

```

## 21.2 Lasso

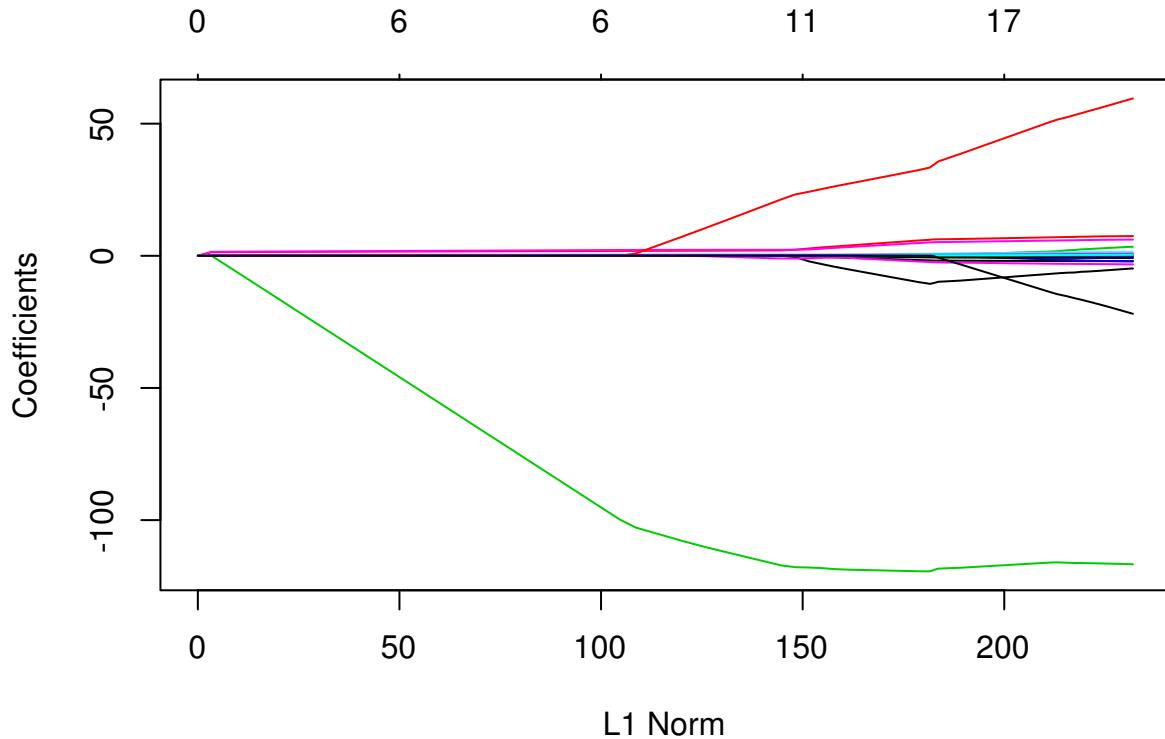
We now illustrate **lasso**, which can be fit using `glmnet()` with `alpha = 1` and seeks to minimize

$$\sum_{i=1}^n \left( y_i - \beta_0 - \sum_{j=1}^p \beta_j x_{ij} \right)^2 + \lambda \sum_{j=1}^p |\beta_j|.$$

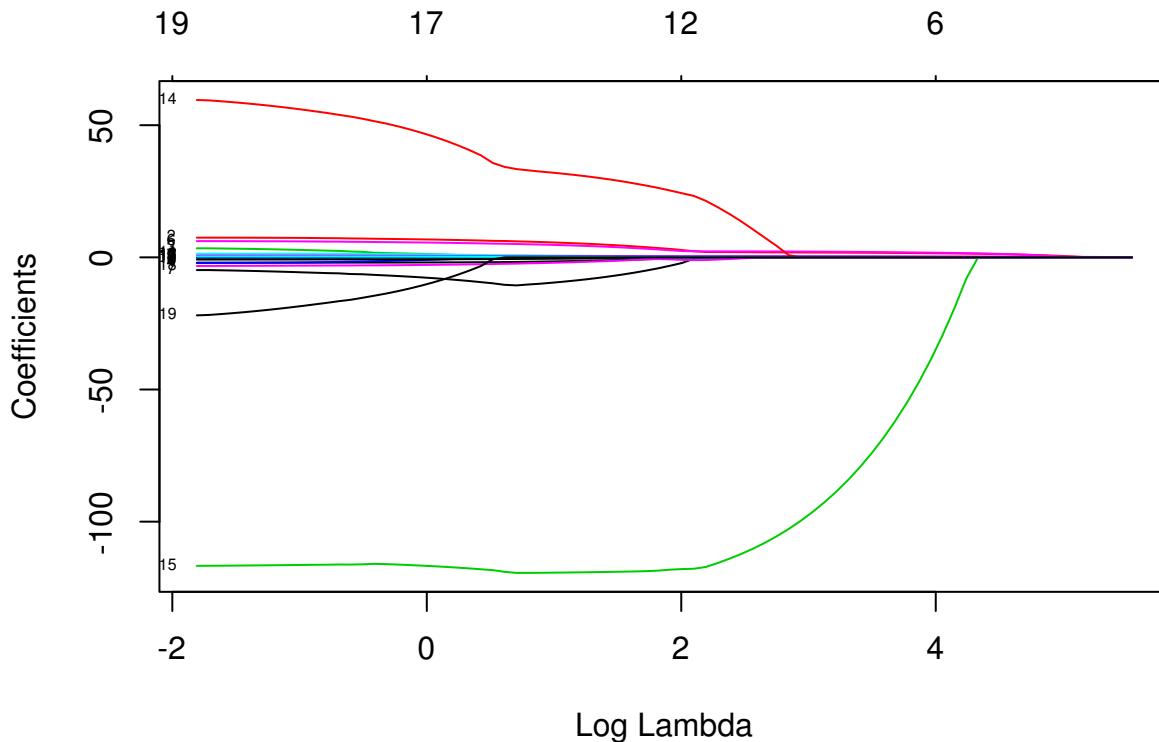
Like ridge, lasso is not scale invariant.

The two plots illustrate how much the coefficients are penalized for different values of  $\lambda$ . Notice some of the coefficients are forced to be zero.

```
fit_lasso = glmnet(X, y, alpha = 1)
plot(fit_lasso)
```



```
plot(fit_lasso, xvar = "lambda", label = TRUE)
```

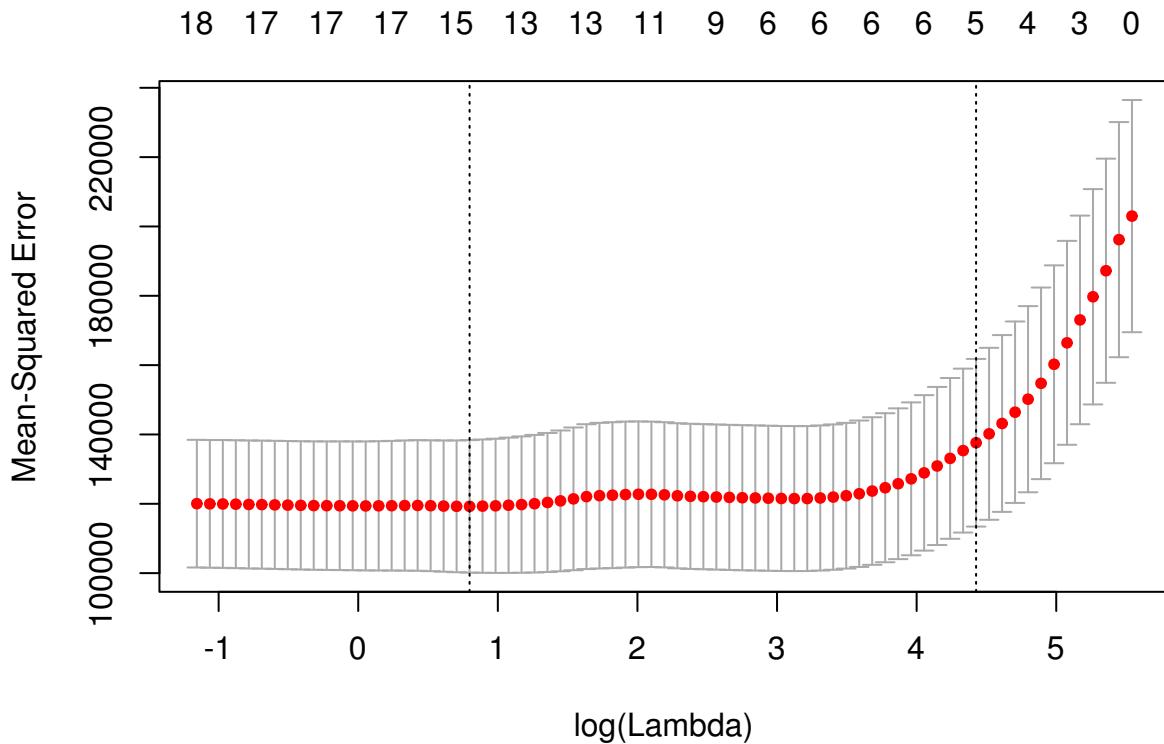


```
dim(coef(fit_lasso))
```

```
## [1] 20 80
```

Again, to actually pick a  $\lambda$ , we will use cross-validation. The plot is similar to the ridge plot. Notice along the top is the number of features in the model. (Which changed in this plot.)

```
fit_lasso_cv = cv.glmnet(X, y, alpha = 1)
plot(fit_lasso_cv)
```



`cv.glmnet()` returns several details of the fit for both  $\lambda$  values in the plot. Notice the penalty terms are again smaller than the full linear regression. (As we would expect.) Some coefficients are 0.

```
coef(fit_lasso_cv)
```

```
## 20 x 1 sparse Matrix of class "dgCMatrix"
##                               1
## (Intercept) 167.91202818
## AtBat          .
## Hits           1.29269756
## HmRun          .
## Runs           .
## RBI            .
## Walks          1.39817511
## Years          .
## CAtBat         .
## CHits          .
## CHmRun         .
## CRuns          0.14167760
## CRBI           0.32192558
## CWalks         .
## LeagueN        .
## DivisionW      .
## PutOuts        0.04675463
## Assists        .
## Errors         .
## NewLeagueN    .
```

```

coef(fit_lasso_cv, s = "lambda.min")

## 20 x 1 sparse Matrix of class "dgCMatrix"
##                               1
## (Intercept) 134.48030406
## AtBat        -1.67572220
## Hits         5.94122316
## HmRun        0.04746835
## Runs          .
## RBI          .
## Walks        4.95676182
## Years       -10.26657309
## CAtBat       .
## CHits        .
## CHmRun       0.56236426
## CRuns        0.70135135
## CRBI         0.38727139
## CWalks       -0.58111548
## LeagueN      32.92255640
## DivisionW   -119.37941356
## PutOuts      0.27580087
## Assists      0.19782326
## Errors       -2.26242857
## NewLeagueN  .

sum(abs(coef(fit_lasso_cv, s = "lambda.min")[-1])) # penalty term for lambda minimum

## [1] 180.1579

coef(fit_lasso_cv, s = "lambda.1se")

## 20 x 1 sparse Matrix of class "dgCMatrix"
##                               1
## (Intercept) 167.91202818
## AtBat        .
## Hits         1.29269756
## HmRun        .
## Runs          .
## RBI          .
## Walks        1.39817511
## Years        .
## CAtBat       .
## CHits        .
## CHmRun       .
## CRuns        0.14167760
## CRBI         0.32192558
## CWalks       .
## LeagueN      .
## DivisionW   .
## PutOuts      0.04675463
## Assists      .
## Errors       .
## NewLeagueN  .

```

```

sum(abs(coef(fit_lasso_cv, s = "lambda.1se")[-1])) # penalty term for lambda one SE

## [1] 3.20123

#predict(fit_lasso_cv, X, s = "lambda.min")
#predict(fit_lasso_cv, X)
mean((y - predict(fit_lasso_cv, X)) ^ 2) # "train error"

## [1] 123931.3

sqrt(fit_lasso_cv$cvm)

## [1] 450.5414 442.9439 432.7014 423.9339 415.9849 407.9633 400.3000
## [8] 393.3836 387.5208 382.6497 378.3763 374.4214 370.9577 367.8914
## [15] 364.8262 361.8138 359.0494 356.6500 354.6664 353.0280 351.6780
## [22] 350.5755 349.7565 349.1940 348.8177 348.5852 348.5694 348.6216
## [29] 348.7203 348.8324 348.9307 349.0659 349.2086 349.3564 349.4943
## [36] 349.7319 350.1319 350.3310 350.3492 350.2292 349.9839 349.7880
## [43] 349.3788 348.4578 347.6262 346.9568 346.4479 346.0841 345.8029
## [50] 345.5679 345.4333 345.3442 345.3514 345.4564 345.6046 345.7161
## [57] 345.6743 345.6086 345.5594 345.5233 345.5655 345.5972 345.6288
## [64] 345.6711 345.7517 345.8519 345.9576 346.0658 346.1287 346.2474
## [71] 346.3415 346.3809 346.4730

sqrt(fit_lasso_cv$cvm[fit_lasso_cv$lambda == fit_lasso_cv$lambda.min]) # CV-RMSE minimum

## [1] 345.3442

sqrt(fit_lasso_cv$cvm[fit_lasso_cv$lambda == fit_lasso_cv$lambda.1se]) # CV-RMSE one SE

## [1] 370.9577

```

## 21.3 broom

Sometimes, the output from `glmnet()` can be overwhelming. The `broom` package can help with that.

```

library(broom)
#fit_lasso_cv
tidy(fit_lasso_cv)

## #> #>   lambda estimate std.error conf.high conf.low nzero
## #> 1  255.2820965 202987.6  33487.70  236475.3 169499.9    0
## #> 2  232.6035386 196199.3  33916.49  230115.8 162282.8    1
## #> 3  211.9396813 187230.5  32329.34  219559.9 154901.2    2
## #> 4  193.1115442 179720.0  31057.85  210777.8 148662.1    2
## #> 5  175.9560468 173043.5  30091.50  203135.0 142952.0    3
## #> 6  160.3245966 166434.0  29409.46  195843.5 137024.6    4
## #> 7  146.0818013 160240.1  28539.89  188779.9 131700.2    4

```

```

## 8 133.1042967 154750.6 27636.91 182387.5 127113.7 4
## 9 121.2796778 150172.3 26849.91 177022.2 123322.4 4
## 10 110.5055255 146420.8 26168.99 172589.8 120251.8 4
## 11 100.6885192 143168.6 25501.92 168670.5 117666.7 5
## 12 91.7436287 140191.4 24803.59 164995.0 115387.8 5
## 13 83.5933775 137609.6 24181.21 161790.8 113428.4 5
## 14 76.1671723 135344.1 23642.14 158986.2 111701.9 5
## 15 69.4006906 133098.1 23190.35 156288.5 109907.8 6
## 16 63.2353245 130909.2 22801.80 153711.0 108107.4 6
## 17 57.6176726 128916.4 22421.45 151337.9 106495.0 6
## 18 52.4990774 127199.3 22050.38 149249.6 105148.9 6
## 19 47.8352040 125788.2 21745.74 147534.0 104042.5 6
## 20 43.5856563 124628.8 21495.05 146123.8 103133.7 6
## 21 39.7136268 123677.4 21287.35 144964.8 102390.1 6
## 22 36.1855776 122903.2 21117.25 144020.4 101785.9 6
## 23 32.9709506 122329.6 21010.59 143340.2 101319.0 6
## 24 30.0419022 121936.4 20960.16 142896.6 100976.3 6
## 25 27.3730624 121673.8 20926.98 142600.7 100746.8 6
## 26 24.9413150 121511.6 20905.10 142416.7 100606.5 6
## 27 22.7255973 121500.6 20910.13 142410.8 100590.5 6
## 28 20.7067179 121537.0 20917.72 142454.7 100619.3 6
## 29 18.8671902 121605.8 20925.72 142531.6 100680.1 6
## 30 17.1910810 121684.0 20934.03 142618.1 100750.0 7
## 31 15.6638727 121752.7 20931.37 142684.0 100821.3 7
## 32 14.2723374 121847.0 20930.02 142777.0 100917.0 7
## 33 13.0044223 121946.6 20930.20 142876.8 101016.4 9
## 34 11.8491453 122049.9 20930.56 142980.4 101119.3 9
## 35 10.7964999 122146.3 20929.67 143075.9 101216.6 9
## 36 9.8373686 122312.4 20928.00 143240.4 101384.4 9
## 37 8.9634439 122592.3 20941.04 143533.4 101651.3 9
## 38 8.1671562 122731.8 20967.18 143699.0 101764.6 11
## 39 7.4416086 122744.6 21019.91 143764.5 101724.7 11
## 40 6.7805166 122660.5 21060.20 143720.7 101600.3 12
## 41 6.1781542 122488.7 21040.36 143529.1 101448.4 12
## 42 5.6293040 122351.7 20999.86 143351.5 101351.8 13
## 43 5.1292121 122065.5 20889.69 142955.2 101175.8 13
## 44 4.6735471 121422.9 20586.52 142009.4 100836.3 13
## 45 4.2583620 120844.0 20305.49 141149.5 100538.5 13
## 46 3.8800609 120379.0 20061.23 140440.3 100317.8 13
## 47 3.5353670 120026.2 19844.13 139870.3 100182.0 13
## 48 3.2212947 119774.2 19664.36 139438.6 100109.8 13
## 49 2.9351238 119579.7 19507.30 139087.0 100072.4 13
## 50 2.6743755 119417.2 19352.36 138769.5 100064.8 13
## 51 2.4367913 119324.1 19223.25 138547.4 100100.9 13
## 52 2.2203135 119262.6 19109.85 138372.5 100152.8 14
## 53 2.0230670 119267.6 19005.00 138272.6 100262.6 15
## 54 1.8433433 119340.1 18926.00 138266.1 100414.1 15
## 55 1.6795857 119442.5 18870.79 138313.3 100571.7 17
## 56 1.5303760 119519.6 18839.70 138359.3 100680.0 17
## 57 1.3944216 119490.7 18772.77 138263.5 100717.9 17
## 58 1.2705450 119445.3 18701.29 138146.6 100744.0 17
## 59 1.1576733 119411.3 18646.56 138057.9 100764.8 17
## 60 1.0548288 119386.4 18603.46 137989.8 100782.9 17
## 61 0.9611207 119415.5 18583.82 137999.3 100831.7 17

```

```

## 62  0.8757374 119437.5 18558.22 137995.7 100879.2    17
## 63  0.7979393 119459.3 18535.76 137995.0 100923.5    17
## 64  0.7270526 119488.5 18515.88 138004.4 100972.6    17
## 65  0.6624632 119544.2 18501.16 138045.4 101043.0    18
## 66  0.6036118 119613.6 18489.14 138102.7 101124.4    18
## 67  0.5499886 119686.6 18478.49 138165.1 101208.2    18
## 68  0.5011291 119761.5 18467.03 138228.6 101294.5    17
## 69  0.4566102 119805.0 18460.15 138265.2 101344.9    18
## 70  0.4160462 119887.2 18443.37 138330.6 101443.9    18
## 71  0.3790858 119952.4 18438.98 138391.4 101513.4    18
## 72  0.3454089 119979.7 18409.67 138389.4 101570.1    18
## 73  0.3147237 120043.5 18410.07 138453.6 101633.5    18

```

```
glance(fit_lasso_cv) # the two lambda values of interest
```

```

##   lambda.min lambda.1se
## 1  2.220313  83.59338

```

## 21.4 Simulation Study, $p > n$

Aside from simply shrinking coefficients (ridge) and setting some coefficients to 0 (lasso), penalized regression also has the advantage of being able to handle the  $p > n$  case.

```

set.seed(1234)
n = 1000
p = 5500
X = replicate(p, rnorm(n = n))
beta = c(1, 1, 1, rep(0, 5497))
z = X %*% beta
prob = exp(z) / (1 + exp(z))
y = as.factor(rbinom(length(z), size = 1, prob))

```

We first simulate a classification example where  $p > n$ .

```

# glm(y ~ X, family = "binomial")
# will not converge

```

We then use a lasso penalty to fit penalized logistic regression. This minimizes

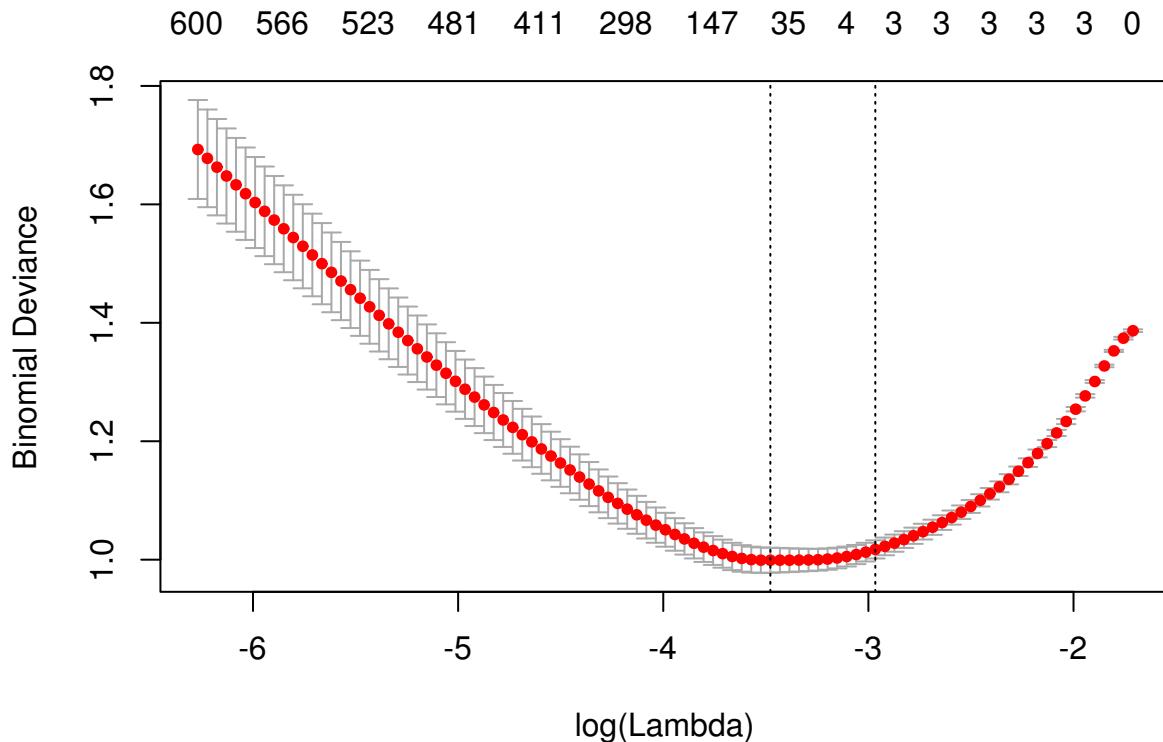
$$\sum_{i=1}^n L \left( y_i, \beta_0 + \sum_{j=1}^p \beta_j x_{ij} \right) + \lambda \sum_{j=1}^p |\beta_j|$$

where  $L$  is the appropriate *negative log*-likelihood.

```

library(glmnet)
fit_cv = cv.glmnet(X, y, family = "binomial", alpha = 1)
plot(fit_cv)

```



```
head(coef(fit_cv), n = 10)
```

```
## 10 x 1 sparse Matrix of class "dgCMatrix"
##           1
## (Intercept) 0.02397452
## V1          0.59674958
## V2          0.56251761
## V3          0.60065105
## V4          .
## V5          .
## V6          .
## V7          .
## V8          .
## V9          .

fit_cv$ nonzero
```

```
##   s0   s1   s2   s3   s4   s5   s6   s7   s8   s9   s10  s11  s12  s13  s14  s15  s16  s17
##   0    2    3    3    3    3    3    3    3    3    3    3    3    3    3    3    3    3    3
##   s18  s19  s20  s21  s22  s23  s24  s25  s26  s27  s28  s29  s30  s31  s32  s33  s34  s35
##   3    3    3    3    3    3    3    3    3    3    3    3    3    3    4    6    7    10   18   24
##   s36  s37  s38  s39  s40  s41  s42  s43  s44  s45  s46  s47  s48  s49  s50  s51  s52  s53
##   35   54   65   75   86   100  110  129  147  168  187  202  221  241  254  269  283  298
##   s54  s55  s56  s57  s58  s59  s60  s61  s62  s63  s64  s65  s66  s67  s68  s69  s70  s71
##   310  324  333  350  364  375  387  400  411  429  435  445  453  455  462  466  475  481
##   s72  s73  s74  s75  s76  s77  s78  s79  s80  s81  s82  s83  s84  s85  s86  s87  s88  s89
##   487  491  496  498  502  504  512  518  523  526  528  536  543  550  559  561  563  566
##   s90  s91  s92  s93  s94  s95  s96  s97  s98
##   570  571  576  582  586  590  596  596  600
```

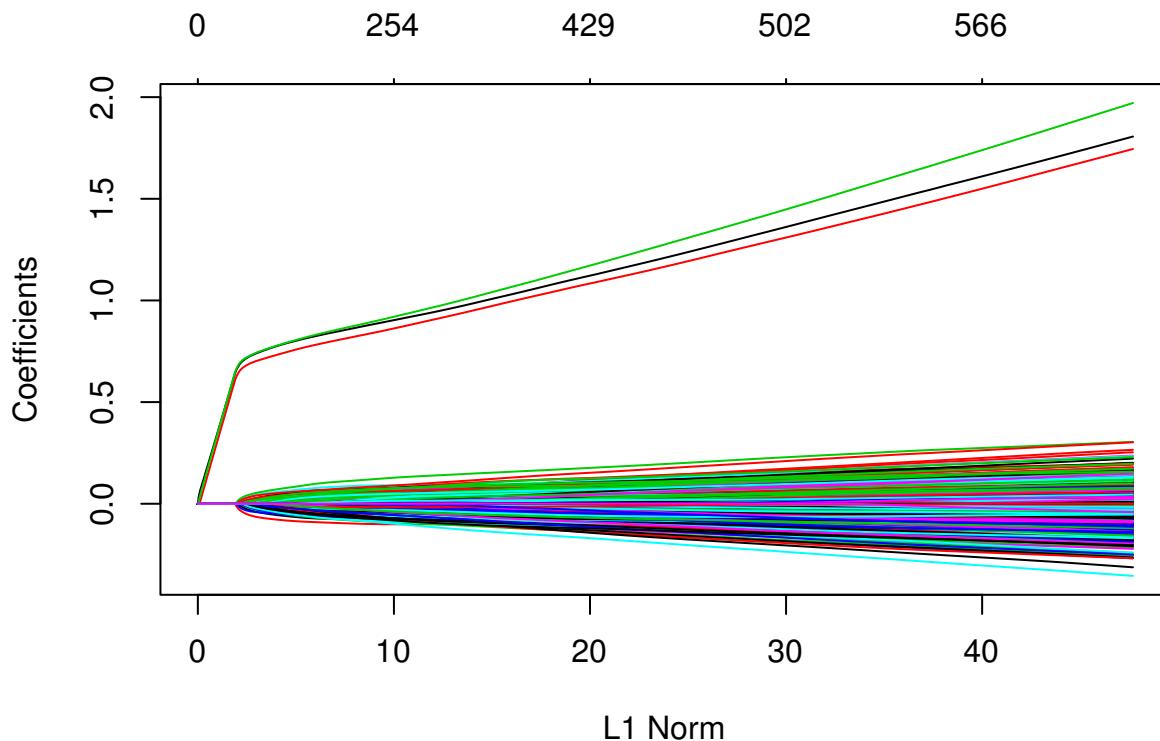
Notice, only the first three predictors generated are truly significant, and that is exactly what the suggested model finds.

```
fit_1se = glmnet(X, y, family = "binomial", lambda = fit_cv$lambda.1se)
which(as.vector(as.matrix(fit_1se$beta)) != 0)

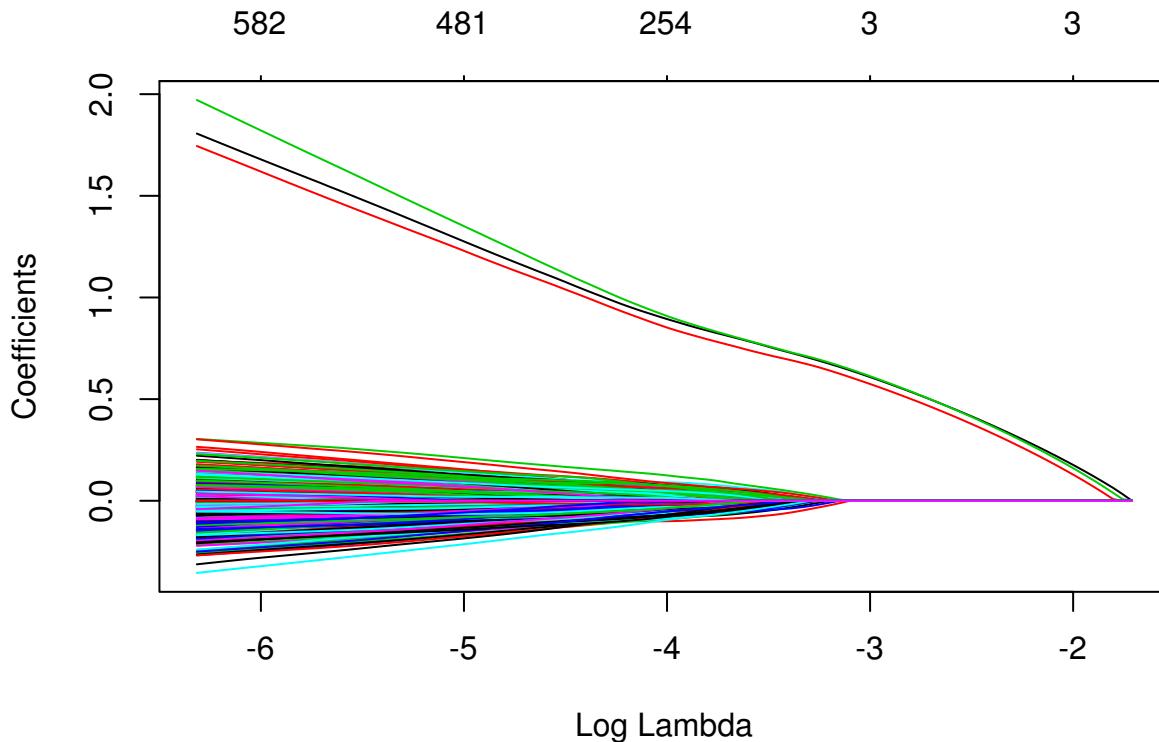
## [1] 1 2 3
```

We can also see in the following plots, the three features entering the model well ahead of the irrelevant features.

```
plot(glmnet(X, y, family = "binomial"))
```



```
plot(glmnet(X, y, family = "binomial"), xvar = "lambda")
```



We can extract the two relevant  $\lambda$  values.

```
fit_cv$lambda.min
```

```
## [1] 0.03087158
```

```
fit_cv$lambda.1se
```

```
## [1] 0.0514969
```

Since `cv.glmnet()` does not calculate prediction accuracy for classification, we take the  $\lambda$  values and create a grid for `caret` to search in order to obtain prediction accuracy with `train()`. We set  $\alpha = 1$  in this grid, as `glmnet` can actually tune over the  $\alpha = 1$  parameter. (More on that later.)

Note that we have to force `y` to be a factor, so that `train()` recognizes we want to have a binomial response. The `train()` function in `caret` use the type of variable in `y` to determine if you want to use `family = "binomial"` or `family = "gaussian"`.

```
library(caret)
cv_5 = trainControl(method = "cv", number = 5)
lasso_grid = expand.grid(alpha = 1,
                         lambda = c(fit_cv$lambda.min, fit_cv$lambda.1se))
lasso_grid

##   alpha      lambda
## 1     1 0.03087158
## 2     1 0.05149690
```

```

fit_lasso = train(
  x = X,
  y = y,
  method = "glmnet",
  trControl = cv_5,
  tuneGrid = lasso_grid
)
fit_lasso$results

##   alpha      lambda Accuracy      Kappa AccuracySD      KappaSD
## 1     1 0.03087158 0.7609903 0.5218887 0.01486223 0.03000986
## 2     1 0.05149690 0.7659604 0.5319189 0.01807380 0.03594319

```

## 21.5 External Links

- `glmnet` Web Vingette - Details from the package developers.

## 21.6 RMarkdown

The RMarkdown file for this chapter can be found [here](#). The file was created using R version 3.3.2 and the following packages:

- Base Packages, Attached

```

## [1] "methods"    "stats"       "graphics"    "grDevices"   "utils"       "datasets"
## [7] "base"

```

- Additional Packages, Attached

```

## [1] "caret"      "ggplot2"    "lattice"    "broom"      "glmnet"     "foreach"    "Matrix"

```

- Additional Packages, Not Attached

```

##  [1] "Rcpp"        "compiler"    "nloptr"      "plyr"
##  [5] "class"       " iterators"   "tools"       "lme4"
##  [9] "digest"      " evaluate"   "tibble"      "nlme"
## [13] "gtable"      "mgcv"       "psych"      "DBI"
## [17] "yaml"        "parallel"   "SparseM"    "e1071"
## [21] "dplyr"       "stringr"    "knitr"      "MatrixModels"
## [25] "stats4"      "nnet"       "rprojroot"  "grid"
## [29] "R6"          "foreign"    "rmarkdown"   "bookdown"
## [33] "minqa"       "car"        "reshape2"   "tidyverse"
## [37] "magrittr"    "splines"    "MASS"       "ModelMetrics"
## [41] "backports"   "scales"     "codetools"   "htmltools"
## [45] "pbkrtest"    "assertthat" "mnormt"     "colorspace"
## [49] "quantreg"    "stringi"    "lazyeval"   "munsell"

```



# Chapter 22

## Elastic Net

We again use the `Hitters` dataset from the `ISLR` package to explore another shrinkage method, **elastic net**, which combines the *ridge* and *lasso* methods from the previous chapter.

### 22.1 Hitters Data

```
data(Hitters, package = "ISLR")
Hitters = na.omit(Hitters)
```

We again remove the missing data, which was all in the response variable, `Salary`.

```
tibble::as_tibble(Hitters)

## # A tibble: 263 × 20
##   AtBat  Hits HmRun  Runs   RBI Walks Years CAtBat CHits CHmRun CRuns
## * <int> <int>
## 1   315    81     7    24    38    39    14   3449    835     69    321
## 2   479   130    18    66    72    76     3   1624    457     63    224
## 3   496   141    20    65    78    37    11   5628   1575    225    828
## 4   321    87    10    39    42    30     2    396    101     12     48
## 5   594   169     4    74    51    35    11   4408   1133     19    501
## 6   185    37     1    23     8    21     2    214     42      1     30
## 7   298    73     0    24    24     7     3    509    108      0     41
## 8   323    81     6    26    32     8     2    341     86      6     32
## 9   401    92    17    49    66    65    13   5206   1332    253    784
## 10  574   159    21   107    75    59    10   4631   1300     90    702
## # ... with 253 more rows, and 9 more variables: CRBI <int>, CWalks <int>,
## #   League <fctr>, Division <fctr>, PutOuts <int>, Assists <int>,
## #   Errors <int>, Salary <dbl>, NewLeague <fctr>
```

```
dim(Hitters)
```

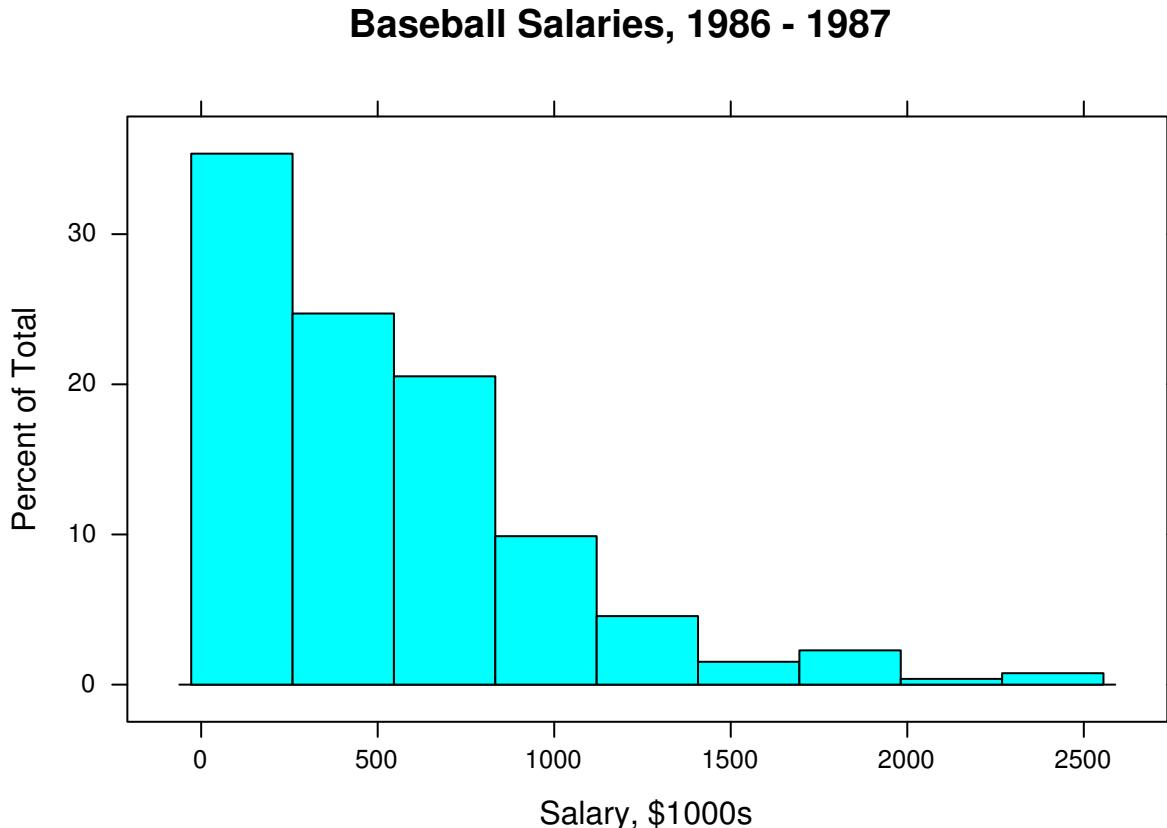
```
## [1] 263 20
```

Because this dataset isn't particularly large, we will forego a test-train split, and simply use all of the data as training data.

```
library(caret)
library(glmnet)
```

Since he have loaded `caret`, we also have access to the `lattice` package which has a nice histogram function.

```
histogram(Hitters$Salary, xlab = "Salary, $1000s", main = "Baseball Salaries, 1986 - 1987")
```



## 22.2 Elastic Net for Regression

Like ridge and lasso, we again attempt to minimize the residual sum of squares plus some penalty term.

$$\sum_{i=1}^n \left( y_i - \beta_0 - \sum_{j=1}^p \beta_j x_{ij} \right)^2 + \lambda \left[ (1-\alpha) \|\beta\|_2^2 / 2 + \alpha \|\beta\|_1 \right]$$

Here,  $\|\beta\|_1$  is called the  $l_1$  norm.

$$\|\beta\|_1 = \sum_{j=1}^p |\beta_j|$$

Similarly,  $\|\beta\|_2$  is called the  $l_2$ , or Euclidean norm.

$$\|\beta\|_2 = \sqrt{\sum_{j=1}^p \beta_j^2}$$

These both quantify how “large” the coefficients are. Like lasso and ridge, the intercept is not penalized and `glmnet` takes care of standardization internally. Also reported coefficients are on the original scale.

The new penalty is  $\frac{\lambda \cdot (1-\alpha)}{2}$  times the ridge penalty plus  $\lambda \cdot \alpha$  times the lasso lasso penalty. (Dividing the ridge penalty by 2 is a mathematical convenience for optimization.) Essentially, with the correct choice of  $\lambda$  and  $\alpha$  these two “penalty coefficients” can be any positive numbers.

Often it is more useful to simply think of  $\alpha$  as controlling the mixing between the two penalties and  $\lambda$  controlling the amount of penalization.  $\alpha$  takes values between 0 and 1. Using  $\alpha = 1$  gives the lasso that we have seen before. Similarly,  $\alpha = 0$  gives ridge. We used these two before with `glmnet()` to specify which method we wanted. Now we also allow for  $\alpha$  values in between.

```
set.seed(430)
cv_5 = trainControl(method = "cv", number = 5)
```

We first setup our cross-validation strategy, which will be 5 fold. We then use `train()` with `method = "glmnet"` which is actually fitting the elastic net.

```
hit_elnet = train(
  Salary ~ ., data = Hitters,
  method = "glmnet",
  trControl = cv_5
)
```

First, note that since we are using `caret()` directly, it is taking care of dummy variable creation. So unlike before when we used `glmnet()`, we do not need to manually create a model matrix.

Also note that we have allowed `caret` to choose the tuning parameters for us.

```
hit_elnet

## glmnet
##
## 263 samples
## 19 predictor
##
## No pre-processing
## Resampling: Cross-Validated (5 fold)
## Summary of sample sizes: 211, 211, 210, 210, 210
## Resampling results across tuning parameters:
##
##   alpha  lambda    RMSE   Rsquared
##   0.10    0.5106  346.2  0.4628
##   0.10    5.1056  342.6  0.4709
##   0.10   51.0564  339.2  0.4767
##   0.55    0.5106  346.7  0.4617
##   0.55    5.1056  342.5  0.4697
##   0.55   51.0564  338.2  0.4831
##   1.00    0.5106  347.1  0.4606
```

```

##   1.00    5.1056  342.6  0.4677
##   1.00   51.0564  344.9  0.4703
##
## RMSE was used to select the optimal model using  the smallest value.
## The final values used for the model were alpha = 0.55 and lambda = 51.06.

```

Notice a few things with these results. First, we have tried three  $\alpha$  values, 0.1, 0.55, and 1. It is not entirely clear why `caret` doesn't use 0. It likely uses 0.1 to fit a model close to ridge, but with some potential for sparsity.

Here, the best result uses  $\alpha = 0.55$ , so this result is somewhere between ridge and lasso.

```

hit_elnet_int = train(
  Salary ~ . ^ 2, data = Hitters,
  method = "glmnet",
  trControl = cv_5,
  tuneLength = 10
)

```

Now we try a much larger model search. First, we're expanding the feature space to include all interactions. Since we are using penalized regression, we don't have to worry as much about overfitting. If many of the added variables are not useful, we will likely use a model close to lasso which makes many of them 0.

We're also using a larger tuning grid. By setting `tuneLength = 10`, we will search 10  $\alpha$  values and 10  $\lambda$  values for each. Because of this larger tuning grid, the results will be very large.

To deal with this, we write a quick helper function to extract the row with the best tuning parameters.

```

get_best_result = function(caret_fit) {
  best_result = caret_fit$results[as.numeric(rownames(caret_fit$bestTune)), ]
  rownames(best_result) = NULL
  best_result
}

```

We then call this function on the trained object.

```

get_best_result(hit_elnet_int)

##   alpha lambda  RMSE Rsquared RMSESD RsquaredSD
## 1      1  4.135 313.9    0.5476  29.05     0.1232

```

We see that the best result uses  $\alpha = 1$ , which makes since. With  $\alpha = 1$ , many of the added interaction coefficients are likely set to zero. (Unfortunately, obtaining this information after using `caret` with `glmnet` isn't easy. The two don't actually play very nice together. We'll use `cv.glmnet()` with the expanded feature space to explore this.)

Also, this CV-RMSE is better than the lasso and ridge from the previous chapter that did not use the expanded feature space.

We also perform a quick analysis using `cv.glmnet()` instead. Due in part to randomness in cross validation, and differences in how `cv.glmnet()` and `train()` search for  $\lambda$ , the results are slightly different.

```

set.seed(430)
X = model.matrix(Salary ~ . ^ 2, Hitters)[, -1]
y = Hitters$Salary

fit_lasso_cv = cv.glmnet(X, y, alpha = 1)
sqrt(fit_lasso_cv$cvm[fit_lasso_cv$lambda == fit_lasso_cv$lambda.min]) # CV-RMSE minimum

## [1] 304.1

```

The commented line is not run, since it produces a lot of output, but if run, it will show that the fast majority of the coefficients are zero! (Also, you'll notice that `cv.glmnet()` does not respect the usual predictor hierarchy. Not a problem for prediction, but a massive interpretation issue!)

```
#coef(fit_lasso_cv)
```

## 22.3 Elastic Net for Classification

Above, we have performed a regression task. But like lasso and ridge, elastic net can also be used for classification by using the deviance instead of the residual sum of squares. This essentially happens automatically in `caret` if the response variable is a factor.

We'll test this using the familiar `Default` dataset, which we first test-train split.

```
data(Default, package = "ISLR")
```

```

set.seed(430)
default_idx = createDataPartition(Default$default, p = 0.75, list = FALSE)
default_trn = Default[default_idx, ]
default_tst = Default[-default_idx, ]

```

We then fit an elastic net with a default tuning grid.

```

def_elnet = train(
  default ~ ., data = default_trn,
  method = "glmnet",
  trControl = cv_5
)
def_elnet

## glmnet
##
## 7501 samples
##      3 predictor
##      2 classes: 'No', 'Yes'
##
## No pre-processing
## Resampling: Cross-Validated (5 fold)
## Summary of sample sizes: 6000, 6001, 6001, 6001, 6001
## Resampling results across tuning parameters:
##

```

```

##   alpha lambda Accuracy Kappa
## 0.10 0.0001242 0.9725 0.39713
## 0.10 0.0012424 0.9725 0.36692
## 0.10 0.0124239 0.9679 0.09249
## 0.55 0.0001242 0.9727 0.40200
## 0.55 0.0012424 0.9724 0.37378
## 0.55 0.0124239 0.9685 0.12567
## 1.00 0.0001242 0.9728 0.40289
## 1.00 0.0012424 0.9724 0.38125
## 1.00 0.0124239 0.9689 0.15106
##
## Accuracy was used to select the optimal model using the largest value.
## The final values used for the model were alpha = 1 and lambda = 0.0001242.

```

Since the best model used  $\alpha = 1$ , this is a lasso model.

We also try an expanded feature space, and a larger tuning grid.

```

def_elnet_int = train(
  default ~ . ^ 2, data = default_trn,
  method = "glmnet",
  trControl = cv_5,
  tuneLength = 10
)

```

Since the result here will return 100 models, we again use are helper function to simply extract the best result.

```

get_best_result(def_elnet_int)

##   alpha lambda Accuracy Kappa AccuracySD KappaSD
## 1 0.3 0.0008174 0.9732 0.4 0.001275 0.01547

```

Here we see  $\alpha = 0.3$ , which is a mix between ridge and lasso.

```

accuracy = function(actual, predicted) {
  mean(actual == predicted)
}

```

Evaluating the test accuracy of this model, we obtain one of the highest accuracies for this dataset of all methods we have tried.

```

# test acc
accuracy(actual = default_tst$default,
          predicted = predict(def_elnet_int, newdata = default_tst))

## [1] 0.9752

```

## 22.4 External Links

- [glmnet Web Vinette](#) - Details from the package developers.
- [glmnet with caret](#) - Some details on Elastic Net tuning in the `caret` package.

## 22.5 RMarkdown

The RMarkdown file for this chapter can be found [here](#). The file was created using R version 3.3.2 and the following packages:

- Base Packages, Attached

```
## [1] "methods"    "stats"       "graphics"   "grDevices"  "utils"      "datasets"  
## [7] "base"
```

- Additional Packages, Attached

```
## [1] "glmnet"     "foreach"    "Matrix"    "caret"      "ggplot2"    "lattice"
```

- Additional Packages, Not Attached

```
## [1] "Rcpp"        "compiler"    "nloptr"     "plyr"  
## [5] "class"       " iterators"   "tools"      "digest"  
## [9] "lme4"        "evaluate"    "tibble"     "gttable"  
## [13] "nlme"        "mgcv"       "yaml"      "parallel"  
## [17] "SparseM"     "e1071"      "stringr"    "knitr"  
## [21] "MatrixModels" "stats4"     "rprojroot"  "grid"  
## [25] "nnet"        "rmarkdown"   "bookdown"   "minqa"  
## [29] "reshape2"    "car"        "magrittr"   "backports"  
## [33] "scales"      "codetools"   "ModelMetrics" "htmltools"  
## [37] "MASS"        "splines"    "assertthat"  "pbkrtest"  
## [41] "colorspace"  "quantreg"   "stringi"    "lazyeval"  
## [45] "munsell"
```



# Chapter 23

## Regularized Discriminant Analysis

We now use the `Sonar` dataset from the `mlbench` package to explore a new regularization method, **regularized discriminant analysis** (RDA), which combines the LDA and QDA. This is similar to how elastic net combines the ridge and lasso.

### 23.1 Sonar Data

```
library(mlbench)
library(caret)
library(glmnet)
library(klaR)

data(Sonar)

#View(Sonar)

table(Sonar$Class) / nrow(Sonar)

##
##          M          R
## 0.5336538 0.4663462

ncol(Sonar) - 1

## [1] 60
```

### 23.2 RDA

Regularized discriminant analysis uses the same general setup as LDA and QDA but estimates the covariance in a new way, which combines the covariance of QDA ( $\hat{\Sigma}_k$ ) with the covariance of LDA ( $\hat{\Sigma}$ ) using a tuning parameter  $\lambda$ .

$$\hat{\Sigma}_k(\lambda) = (1 - \lambda)\hat{\Sigma}_k + \lambda\hat{\Sigma}$$

Using the `rda()` function from the `klaR` package, which `caret` utilizes, makes an additional modification to the covariance matrix, which also has a tuning parameter  $\gamma$ .

$$\hat{\Sigma}_k(\lambda, \gamma) = (1 - \gamma)\hat{\Sigma}_k(\lambda) + \gamma \frac{1}{p} \text{tr}(\hat{\Sigma}_k(\lambda))I$$

Both  $\gamma$  and  $\lambda$  can be thought of as mixing parameters, as they both take values between 0 and 1. For the four extremes of  $\gamma$  and  $\lambda$ , the covariance structure reduces to special cases:

- ( $\gamma = 0, \lambda = 0$ ): QDA - individual covariance for each group.
- ( $\gamma = 0, \lambda = 1$ ): LDA - a common covariance matrix.
- ( $\gamma = 1, \lambda = 0$ ): Conditional independent variables - similar to Naive Bayes, but variable variances within group (main diagonal elements) are all equal.
- ( $\gamma = 1, \lambda = 1$ ): Classification using euclidean distance - as in previous case, but variances are the same for all groups. Objects are assigned to group with nearest mean.

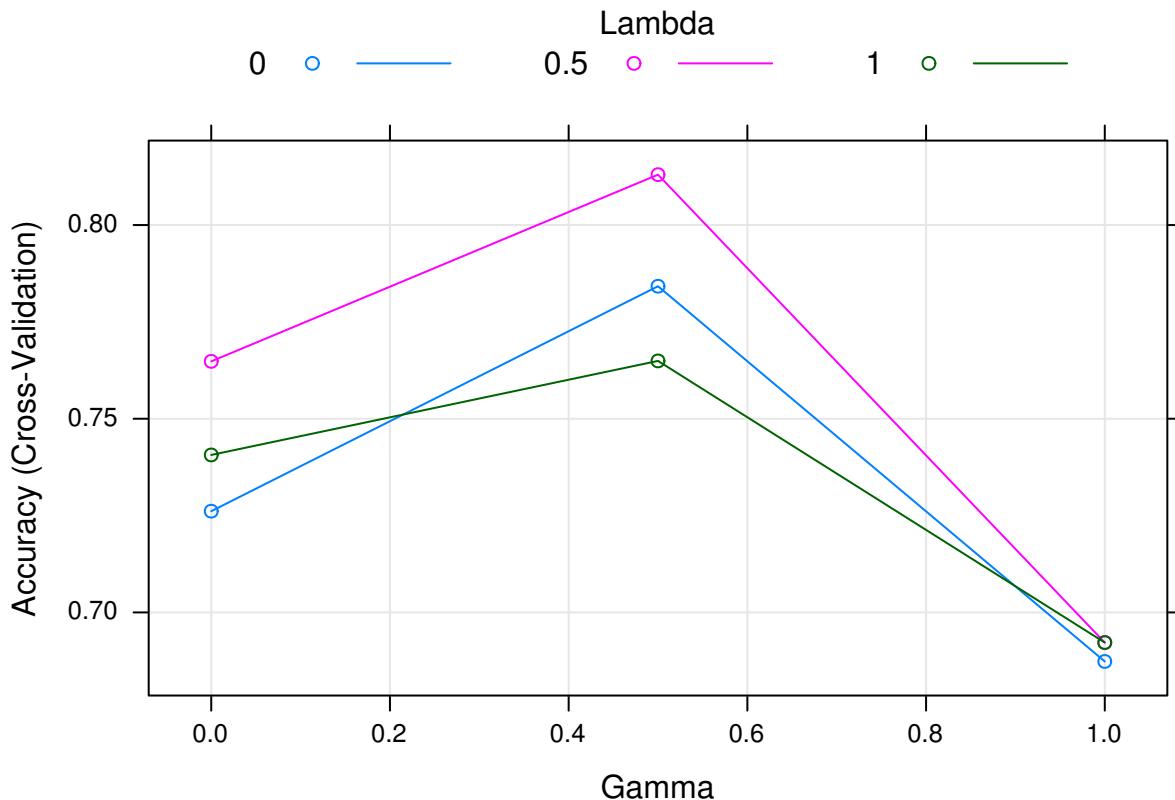
### 23.3 RDA with Grid Search

```
set.seed(1337)
cv_5_grid = trainControl(method = "cv", number = 5)

set.seed(1337)
fit_rda_grid = train(Class ~ ., data = Sonar, method = "rda", trControl = cv_5_grid)
fit_rda_grid

## Regularized Discriminant Analysis
##
## 208 samples
## 60 predictor
## 2 classes: 'M', 'R'
##
## No pre-processing
## Resampling: Cross-Validated (5 fold)
## Summary of sample sizes: 166, 167, 166, 167, 166
## Resampling results across tuning parameters:
##
##     gamma  lambda  Accuracy  Kappa
##     0.0    0.0     0.7261324 0.4397685
##     0.0    0.5     0.7648084 0.5279282
##     0.0    1.0     0.7406504 0.4796821
##     0.5    0.0     0.7842044 0.5641761
##     0.5    0.5     0.8130081 0.6226443
##     0.5    1.0     0.7649245 0.5284504
##     1.0    0.0     0.6873403 0.3728292
##     1.0    0.5     0.6922184 0.3830140
##     1.0    1.0     0.6922184 0.3829488
##
## Accuracy was used to select the optimal model using the largest value.
## The final values used for the model were gamma = 0.5 and lambda = 0.5.
```

```
plot(fit_rda_grid)
```



## 23.4 RDA with Random Search Search

```
set.seed(1337)
cv_5_rand = trainControl(method = "cv", number = 5, search = "random")
```

```
fit_rda_rand = train(Class ~ ., data = Sonar, method = "rda",
                      trControl = cv_5_rand, tuneLength = 9)
fit_rda_rand
```

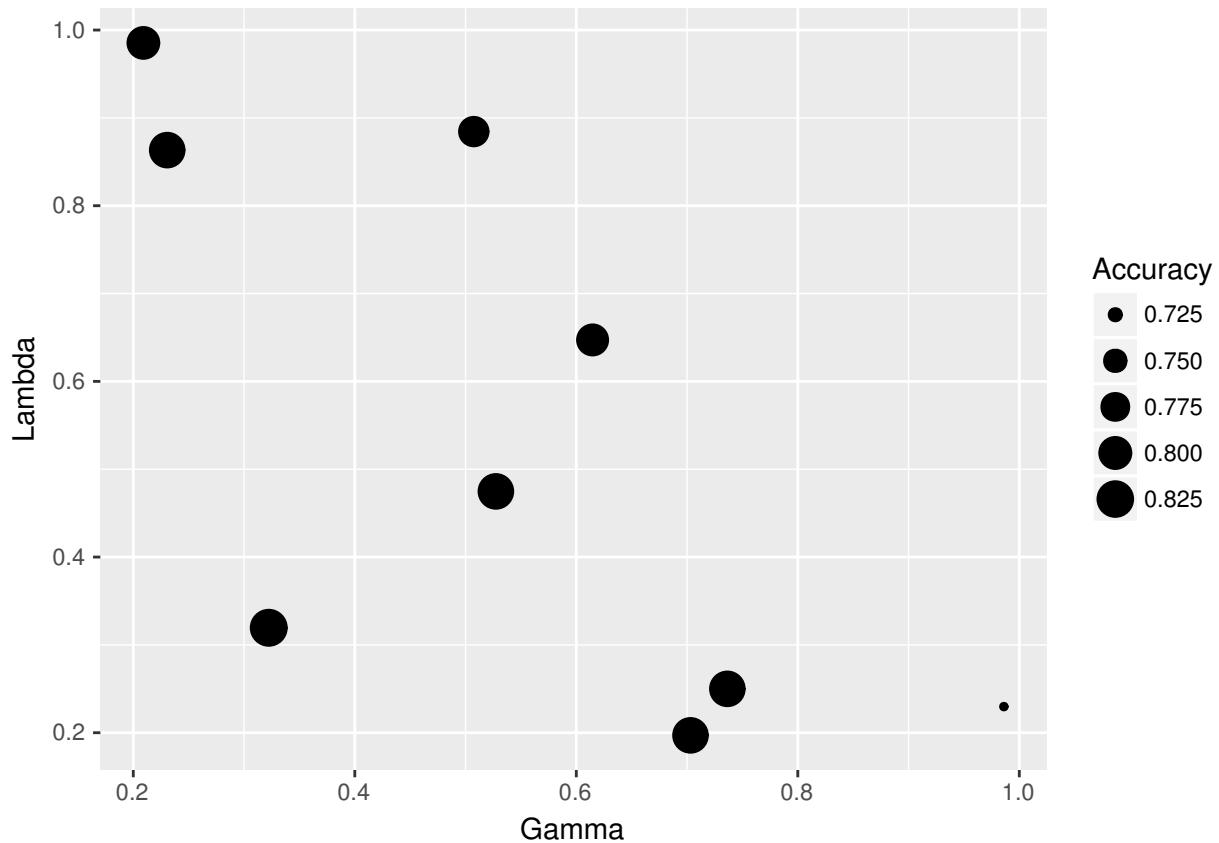
```
## Regularized Discriminant Analysis
##
## 208 samples
## 60 predictor
## 2 classes: 'M', 'R'
##
## No pre-processing
## Resampling: Cross-Validated (5 fold)
## Summary of sample sizes: 166, 167, 166, 167, 166
## Resampling results across tuning parameters:
##
##     gamma      lambda      Accuracy      Kappa
##     0.2091218  0.9853343  0.7986063  0.5944959
```

```

##  0.2306276  0.8632831  0.8177700  0.6328588
##  0.3223120  0.3194769  0.8275261  0.6509822
##  0.5074480  0.8843909  0.7842044  0.5654024
##  0.5274011  0.4747535  0.8178862  0.6323459
##  0.6146998  0.6471883  0.7937282  0.5828269
##  0.7031213  0.1969985  0.8178862  0.6304034
##  0.7363932  0.2499440  0.8177700  0.6295909
##  0.9860836  0.2297174  0.7207898  0.4384828
##
## Accuracy was used to select the optimal model using the largest value.
## The final values used for the model were gamma = 0.322312 and lambda
## = 0.3194769.

```

```
ggplot(fit_rda_rand)
```



## 23.5 Comparison to Elastic Net

```

set.seed(1337)
fit_elnet_grid = train(Class ~ ., data = Sonar, method = "glmnet",
trControl = cv_5_grid, tuneLength = 10)

```

```

set.seed(1337)
fit_elnet_int_grid = train(Class ~ . ^ 2, data = Sonar, method = "glmnet",
trControl = cv_5_grid, tuneLength = 10)

```

## 23.6 Results

```
get_best_result = function(caret_fit) {
  best_result = caret_fit$results[as.numeric(rownames(caret_fit$bestTune)), ]
  rownames(best_result) = NULL
  best_result
}
```

```
knitr::kable(rbind(
  get_best_result(fit_rda_grid),
  get_best_result(fit_rda_rand)))
```

gamma	lambda	Accuracy	Kappa	AccuracySD	KappaSD
0.500000	0.5000000	0.8130081	0.6226443	0.0553439	0.1099849
0.322312	0.3194769	0.8275261	0.6509822	0.0650432	0.1322546

```
knitr::kable(rbind(
  get_best_result(fit_elnet_grid),
  get_best_result(fit_elnet_int_grid)))
```

alpha	lambda	Accuracy	Kappa	AccuracySD	KappaSD
1.0	0.0350306	0.7984901	0.5953995	0.0652593	0.1311529
0.1	0.0243225	0.8321719	0.6617794	0.0744795	0.1480774

## 23.7 External Links

- Random Search for Hyper-Parameter Optimization - Paper justifying random tuning parameter search.
- Random Hyperparameter Search - Details on random tuning parameter search in `caret`.

## 23.8 RMarkdown

The RMarkdown file for this chapter can be found [here](#). The file was created using R version 3.3.2 and the following packages:

- Base Packages, Attached

```
## [1] "methods"     "stats"        "graphics"    "grDevices"   "utils"       "datasets"
## [7] "base"
```

- Additional Packages, Attached

```
## [1] "klaR"        "MASS"        "glmnet"      "foreach"     "Matrix"      "caret"       "ggplot2"
## [8] "lattice"     "mlbench"
```

- Additional Packages, Not Attached

```
## [1] "Rcpp"          "compiler"      "nloptr"        "plyr"
## [5] "class"         " iterators"    "tools"         "digest"
## [9] "lme4"          " evaluate"     "tibble"        "gtable"
## [13] "nlme"          "mgcv"         "parallel"     "yaml"
## [17] "SparseM"       "e1071"        "stringr"      "knitr"
## [21] "MatrixModels"  "combinat"     "stats4"       "rprojroot"
## [25] "grid"          "nnet"         "rmarkdown"    "bookdown"
## [29] "minqa"         "reshape2"     "car"          "magrittr"
## [33] "backports"     "scales"       "codetools"    "ModelMetrics"
## [37] "htmltools"     "splines"      "assertthat"   "pbkrtest"
## [41] "colorspace"    "labeling"     "quantreg"     "stringi"
## [45] "lazyeval"      "munsell"
```

# Chapter 24

## Non-Linear Models

Some notes:

- Currently, most of this code is similar to that of the non-linear chapter of ISLR. It will likely change in the future.
- GAMs and `caret` have some issues working together!
- These are currently notes without narrative.

```
library(ISLR)
```

### 24.1 Polynomial Regression

```
fit_poly_4 = lm(wage ~ poly(age, 4), data = Wage)
summary(fit_poly_4)

##
## Call:
## lm(formula = wage ~ poly(age, 4), data = Wage)
##
## Residuals:
##      Min      1Q      Median      3Q      Max 
## -98.707 -24.626   -4.993   15.217  203.693 
## 
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)    
## (Intercept) 111.7036    0.7287 153.283 < 2e-16 ***
## poly(age, 4)1 447.0679   39.9148 11.201 < 2e-16 ***
## poly(age, 4)2 -478.3158   39.9148 -11.983 < 2e-16 ***
## poly(age, 4)3 125.5217   39.9148   3.145  0.00168 ** 
## poly(age, 4)4 -77.9112   39.9148  -1.952  0.05104 .  
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 
## Residual standard error: 39.91 on 2995 degrees of freedom
## Multiple R-squared:  0.08626,    Adjusted R-squared:  0.08504 
## F-statistic: 70.69 on 4 and 2995 DF,  p-value: < 2.2e-16
```

```
fit_poly_4_raw = lm(wage ~ poly(age, 4, raw = TRUE), data = Wage)
summary(fit_poly_4_raw)
```

```
##
## Call:
## lm(formula = wage ~ poly(age, 4, raw = TRUE), data = Wage)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -98.707 -24.626  -4.993  15.217 203.693
##
## Coefficients:
##                               Estimate Std. Error t value Pr(>|t|)
## (Intercept)             -1.842e+02  6.004e+01 -3.067 0.002180 **
## poly(age, 4, raw = TRUE)1 2.125e+01  5.887e+00  3.609 0.000312 ***
## poly(age, 4, raw = TRUE)2 -5.639e-01  2.061e-01 -2.736 0.006261 **
## poly(age, 4, raw = TRUE)3  6.811e-03  3.066e-03  2.221 0.026398 *
## poly(age, 4, raw = TRUE)4 -3.204e-05  1.641e-05 -1.952 0.051039 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 39.91 on 2995 degrees of freedom
## Multiple R-squared:  0.08626,    Adjusted R-squared:  0.08504
## F-statistic: 70.69 on 4 and 2995 DF,  p-value: < 2.2e-16
```

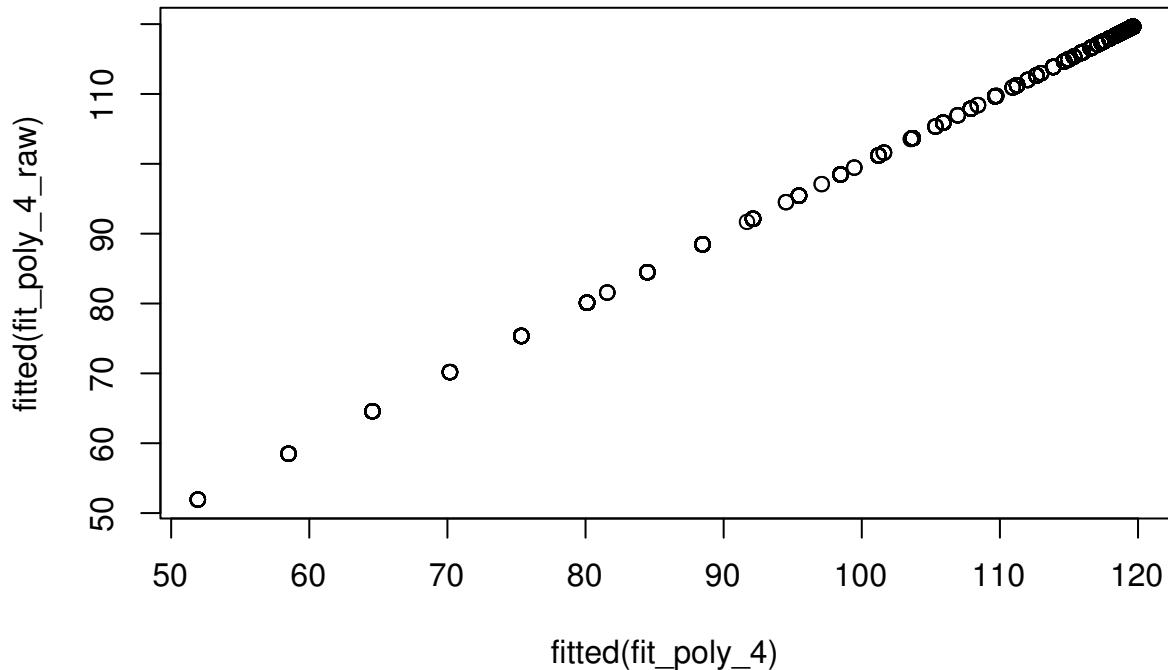
```
coef(fit_poly_4)
```

```
## (Intercept) poly(age, 4)1 poly(age, 4)2 poly(age, 4)3 poly(age, 4)4
## 111.70361     447.06785    -478.31581     125.52169    -77.91118
```

```
coef(fit_poly_4_raw)
```

```
##                               (Intercept) poly(age, 4, raw = TRUE)1
## -1.841542e+02                 2.124552e+01
## poly(age, 4, raw = TRUE)2 poly(age, 4, raw = TRUE)3
## -5.638593e-01                  6.810688e-03
## poly(age, 4, raw = TRUE)4
## -3.203830e-05
```

```
plot(fitted(fit_poly_4), fitted(fit_poly_4_raw))
```



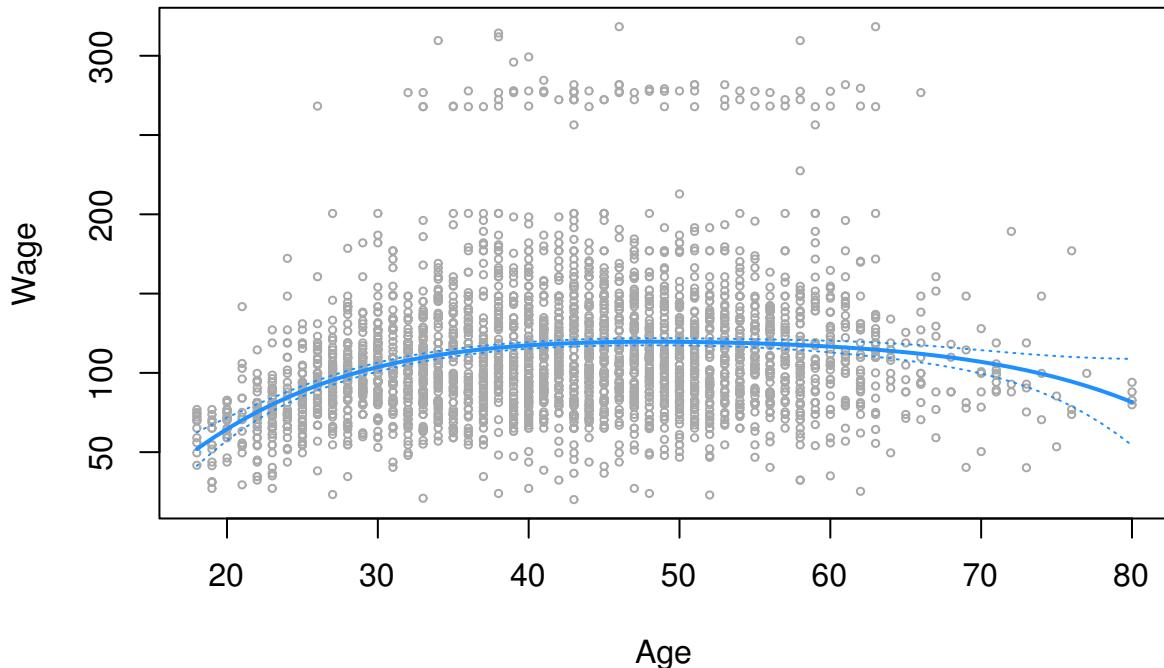
```

age_lower = range(Wage$age)[1]
age_upper = range(Wage$age)[2]
age_grid = seq(from = age_lower, to = age_upper, by = 1)

age_pred = predict(fit_poly_4, newdata = data.frame(age = age_grid), se = TRUE)
age_se_bands = cbind(age_pred$fit + 2 * age_pred$se.fit, age_pred$fit - 2 * age_pred$se.fit)

plot(wage ~ age, data = Wage,
      cex = .5, col = "darkgrey",
      xlab = "Age", ylab = "Wage"
)
lines(age_grid, age_pred$fit, lwd = 2, col = "dodgerblue")
matlines(age_grid, age_se_bands, lwd = 1, col = "dodgerblue", lty = 3)

```



### 24.1.1 ANOVA

```

fit_a = lm(wage ~ education, data = Wage)
fit_b = lm(wage ~ education + age, data = Wage)
fit_c = lm(wage ~ education + poly(age, 2), data = Wage)
fit_d = lm(wage ~ education + poly(age, 3), data = Wage)
anova(fit_a, fit_b, fit_c, fit_d)

## Analysis of Variance Table
##
## Model 1: wage ~ education
## Model 2: wage ~ education + age
## Model 3: wage ~ education + poly(age, 2)
## Model 4: wage ~ education + poly(age, 3)
##   Res.Df   RSS Df Sum of Sq    F Pr(>F)
## 1   2995 3995721
## 2   2994 3867992  1   127729 102.7378 <2e-16 ***
## 3   2993 3725395  1   142597 114.6969 <2e-16 ***
## 4   2992 3719809  1      5587  4.4936 0.0341 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```

## 24.2 Logistic Regression, Polynomial Terms

```

glm_poly_4 = glm(I(wage > 250) ~ poly(age, 4), data = Wage, family = binomial)
summary(glm_poly_4)

```

```

## 
## Call:
## glm(formula = I(wage > 250) ~ poly(age, 4), family = binomial,
##      data = Wage)
## 
## Deviance Residuals:
##    Min      1Q  Median      3Q     Max 
## -0.3110 -0.2607 -0.2488 -0.1791  3.7859 
## 
## Coefficients:
##             Estimate Std. Error z value Pr(>|z|)    
## (Intercept) -4.3012    0.3451 -12.465 < 2e-16 ***
## poly(age, 4)1 71.9642   26.1176   2.755  0.00586 ** 
## poly(age, 4)2 -85.7729   35.9043  -2.389  0.01690 *  
## poly(age, 4)3  34.1626   19.6890   1.735  0.08272 .  
## poly(age, 4)4 -47.4008   24.0909  -1.968  0.04912 *  
## --- 
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1 
## 
## (Dispersion parameter for binomial family taken to be 1)
## 
## Null deviance: 730.53  on 2999  degrees of freedom
## Residual deviance: 701.22  on 2995  degrees of freedom
## AIC: 711.22
## 
## Number of Fisher Scoring iterations: 9

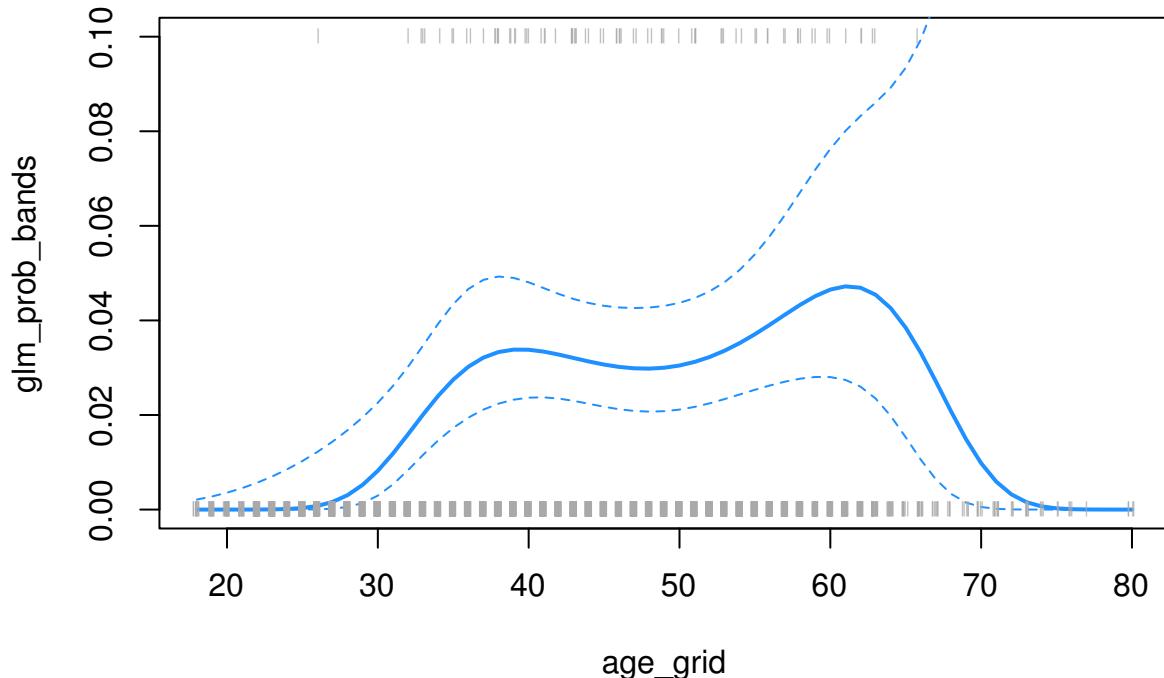
```

```

glm_pred = predict(glm_poly_4, newdata = data.frame(age = age_grid), se = TRUE)
glm_se_bands = cbind(fit = glm_pred$fit,
                      lower = glm_pred$fit - 2 * glm_pred$se.fit,
                      upper = glm_pred$fit + 2 * glm_pred$se.fit)

glm_prob_bands = exp(glm_se_bands) / (1 + exp(glm_se_bands))
matplot(age_grid, glm_prob_bands,
        lwd = c(2, 1, 1), lty = c(1, 2, 2),
        type = "l", col = "dodgerblue",
        ylim = c(0, 0.1))
points(jitter(Wage$age), I((Wage$wage > 250) / 10),
       cex = .5, pch = "|", col = "darkgrey")
)

```



### 24.3 Step Functions

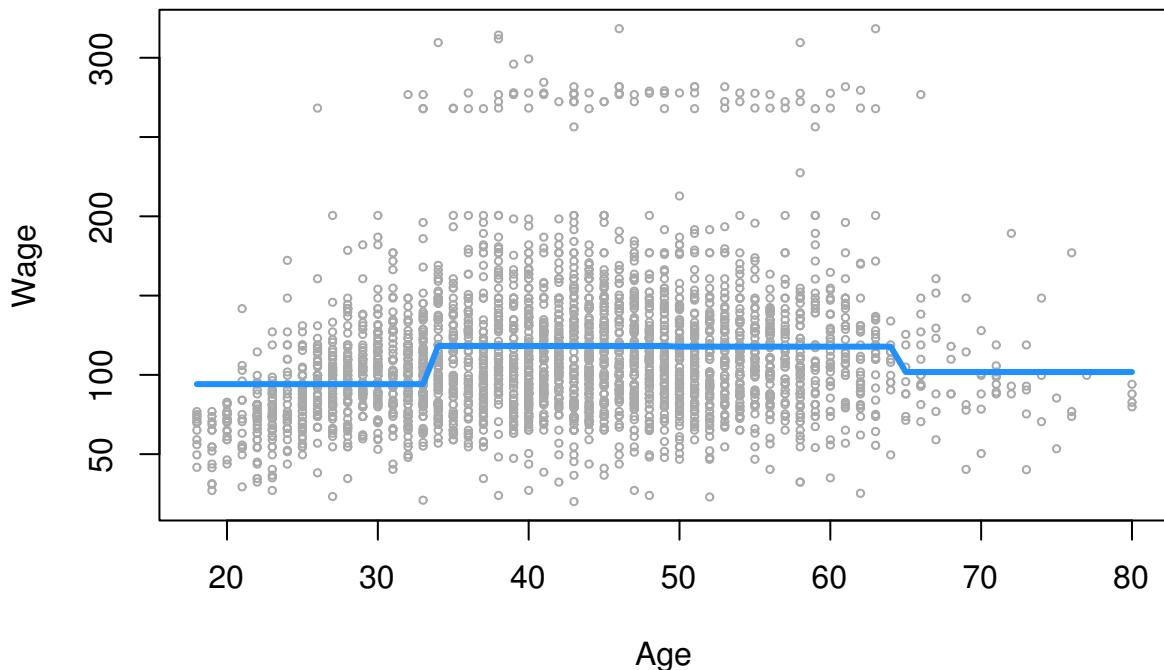
```
table(cut(Wage$age, 4))
```

```
##  
## (17.9,33.5] (33.5,49] (49,64.5] (64.5,80.1]  
##      750      1399      779      72
```

```
step_fit = lm(wage ~ cut(age, 4), data = Wage)
age_pred = predict(step_fit, newdata = data.frame(age = age_grid), se = TRUE)
coef(summary(step_fit))
```

	Estimate	Std. Error	t value	Pr(> t )
## (Intercept)	94.158392	1.476069	63.789970	0.000000e+00
## cut(age, 4)(33.5,49]	24.053491	1.829431	13.148074	1.982315e-38
## cut(age, 4)(49,64.5]	23.664559	2.067958	11.443444	1.040750e-29
## cut(age, 4)(64.5,80.1]	7.640592	4.987424	1.531972	1.256350e-01

```
plot(wage ~ age, data = Wage,
      cex = .5, col = "darkgrey",
      xlab = "Age", ylab = "Wage"
)
lines(age_grid, age_pred$fit, col = "dodgerblue", lwd = 3)
```



### 24.3.1 Smoothing Splines

```

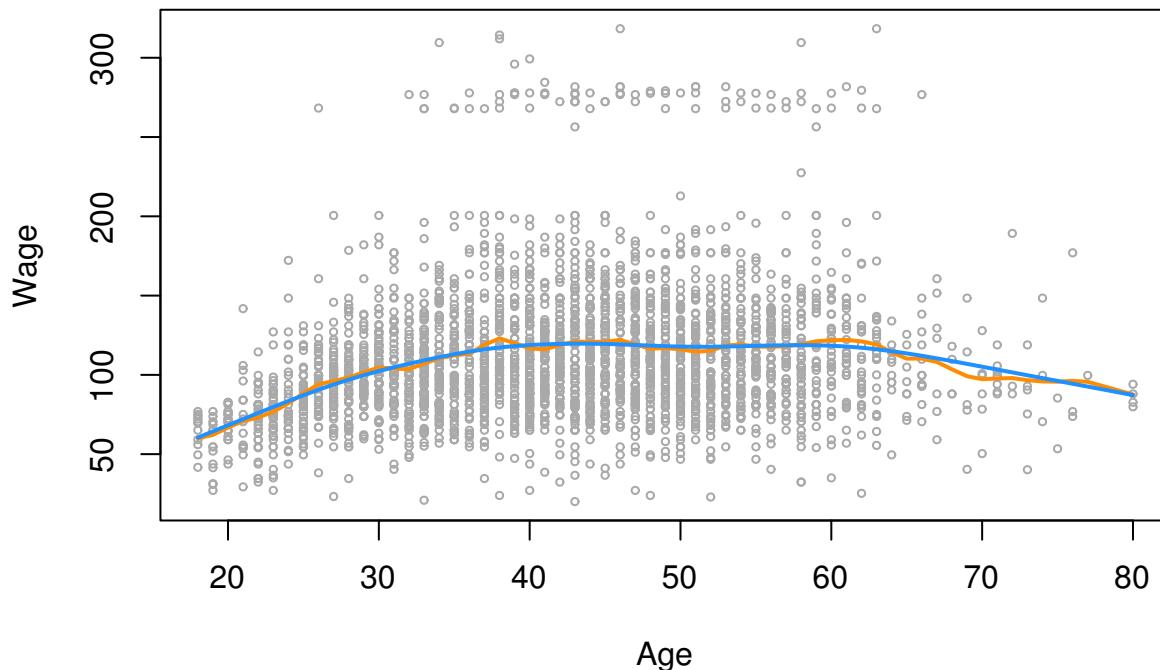
library(splines)
ss_age = smooth.spline(Wage$age, Wage$wage, df = 28)
plot(wage ~ age, data = Wage,
      cex = .5, col = "darkgrey",
      xlab = "Age", ylab = "Wage"
)
lines(ss_age, col = "darkorange", lwd = 2)

ss_age_cv = smooth.spline(Wage$age, Wage$wage, cv = TRUE)
ss_age_cv

## Call:
## smooth.spline(x = Wage$age, y = Wage$wage, cv = TRUE)
##
## Smoothing Parameter  spar= 0.6988943  lambda= 0.02792303 (12 iterations)
## Equivalent Degrees of Freedom (Df): 6.794596
## Penalized Criterion: 75215.9
## PRESS: 1593.383

lines(ss_age_cv, col = "dodgerblue", lwd = 2)

```



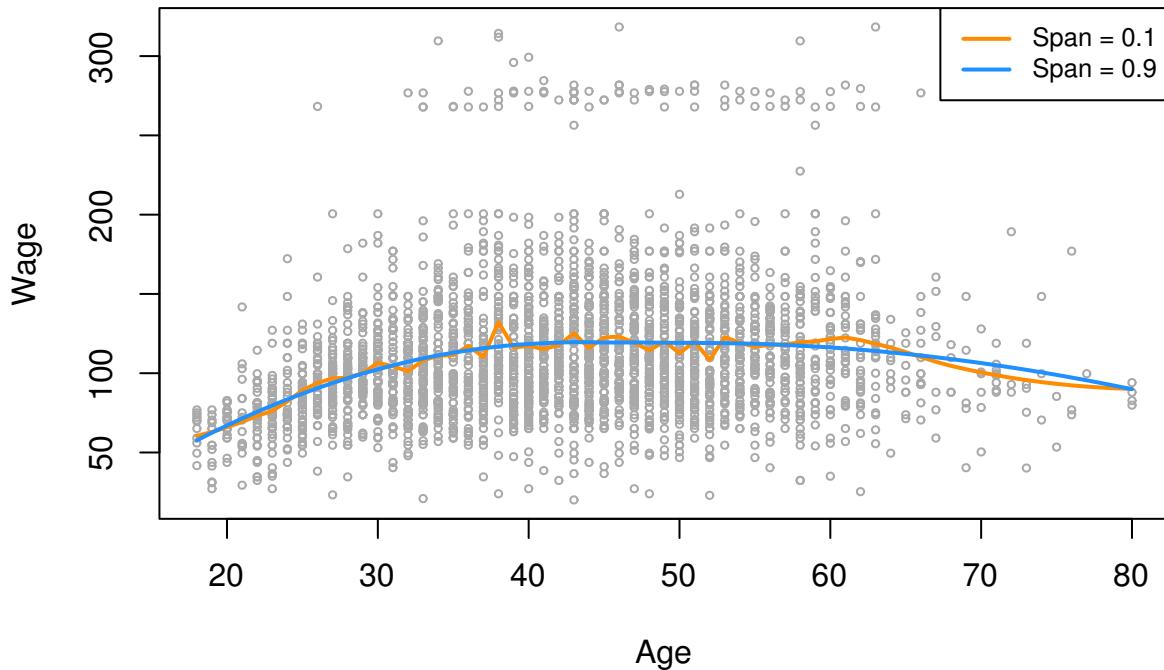
## 24.4 Local Regression

```

plot(wage ~ age, data = Wage,
      cex = .5, col = "darkgrey",
      xlab = "Age", ylab = "Wage"
)
title("Local Regression")
local_span_01 = loess(wage ~ age, span = .1, data = Wage)
local_span_09 = loess(wage ~ age, span = .9, data = Wage)
lines(age_grid, predict(local_span_01, data.frame(age = age_grid)),
      col = "darkorange", lwd = 2)
lines(age_grid, predict(local_span_09, data.frame(age = age_grid)),
      col = "dodgerblue", lwd = 2)
legend("topright", legend = c("Span = 0.1", "Span = 0.9"),
      col = c("darkorange", "dodgerblue"), lty = 1, lwd = 2, cex = .8)

```

## Local Regression



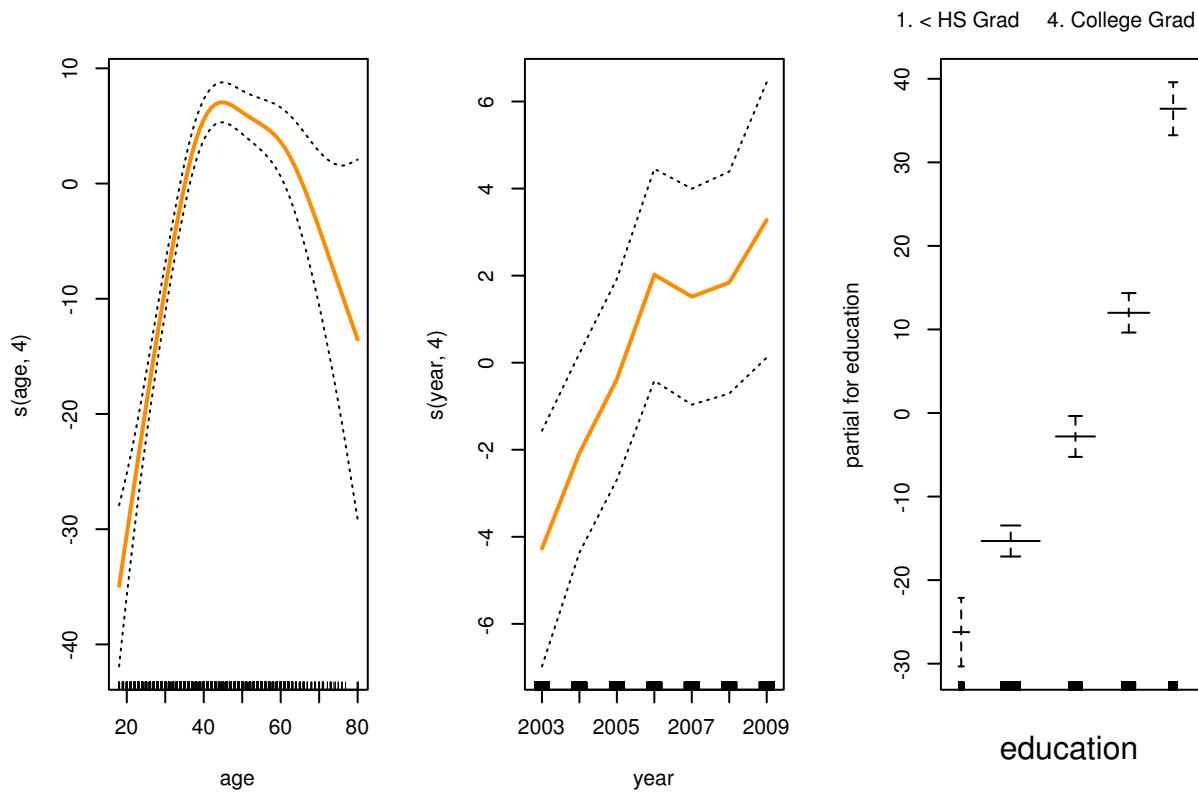
## 24.5 Generalized Additive Models (GAMs)

```
library(gam)
```

```
## Loading required package: foreach
```

```
## Loaded gam 1.14
```

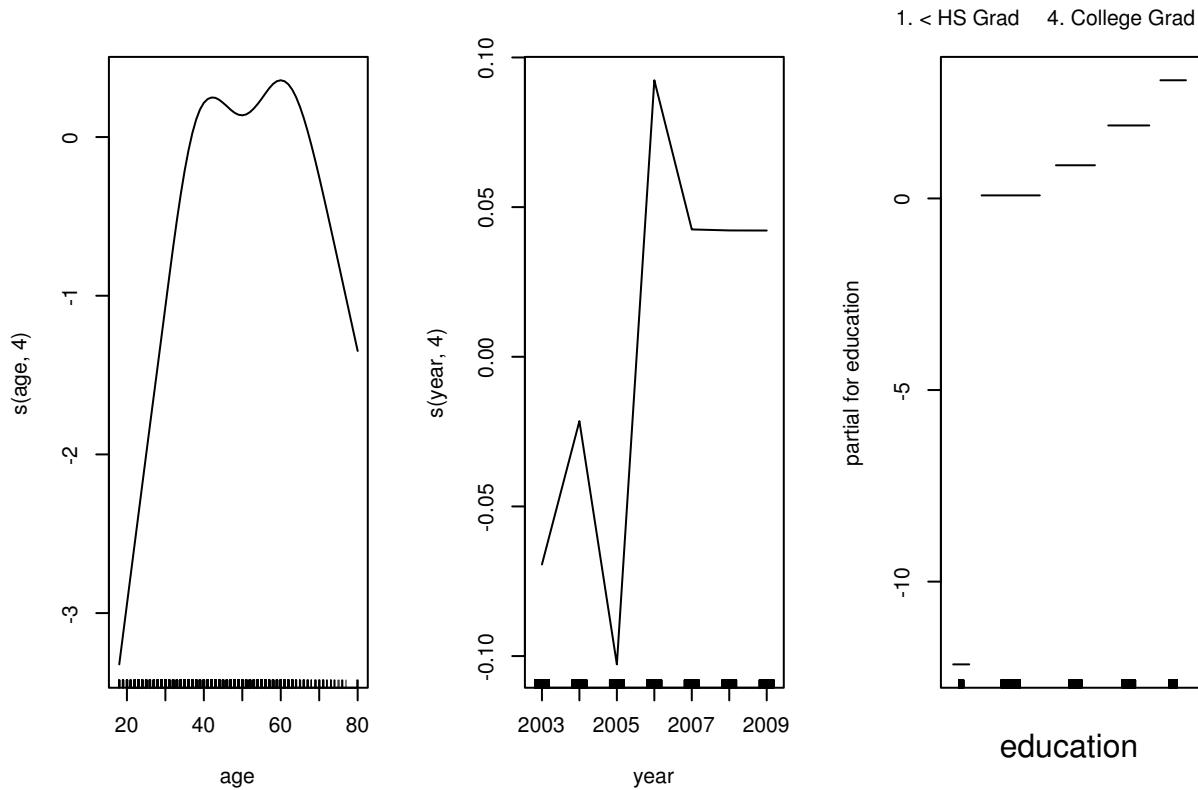
```
gam_fit = gam(wage ~ s(age, 4) + s(year, 4) + education, data = Wage)
par(mfrow = c(1, 3))
plot(gam_fit, se = TRUE, col = "darkorange", lwd = 2)
```



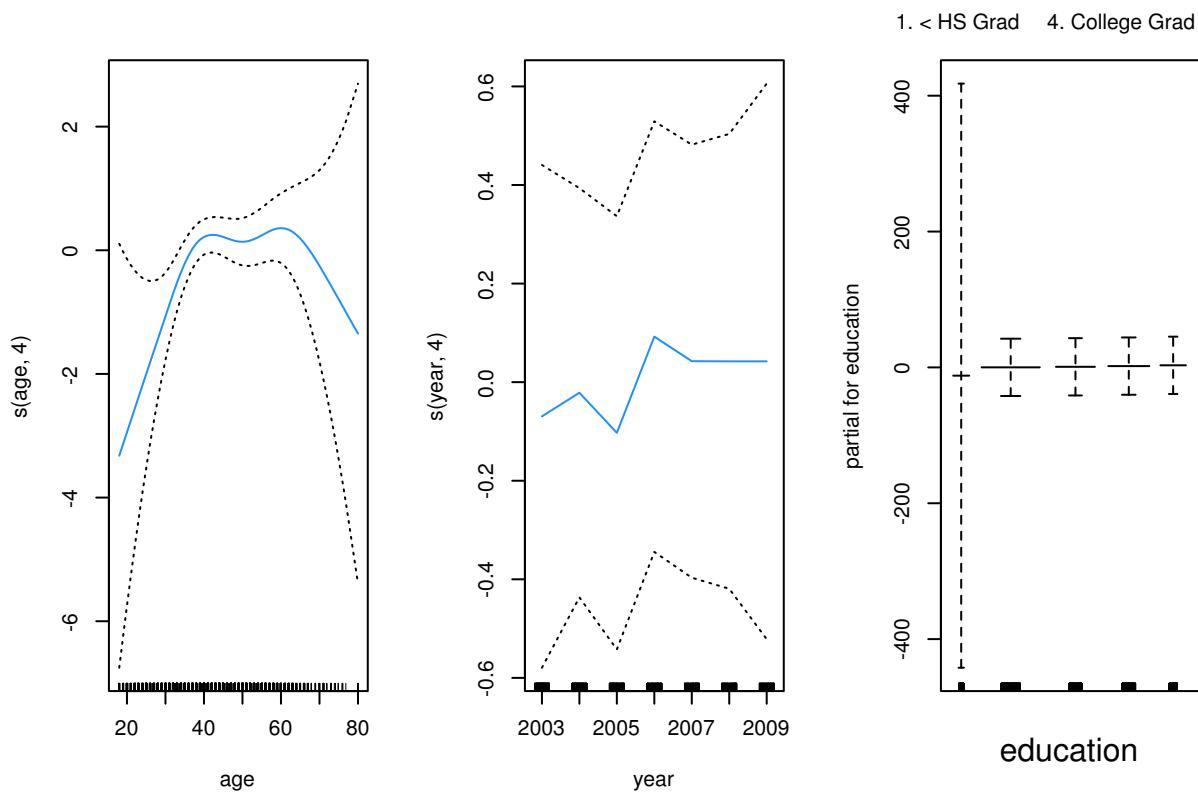
```
gam_fit_small = gam(wage ~ s(age, 4) + education, data = Wage)
anova(gam_fit_small, gam_fit, test = "F")
```

```
## Analysis of Deviance Table
##
## Model 1: wage ~ s(age, 4) + education
## Model 2: wage ~ s(age, 4) + s(year, 4) + education
##   Resid. Df Resid. Dev Df Deviance      F    Pr(>F)
## 1     2991    3714465
## 2     2987    3692824  4     21641 4.3761 0.001573 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
gam_log = gam(I(wage > 250) ~ s(age, 4) + s(year, 4) + education,
              family = binomial, data = Wage)
par(mfrow = c(1, 3))
plot(gam_log)
```



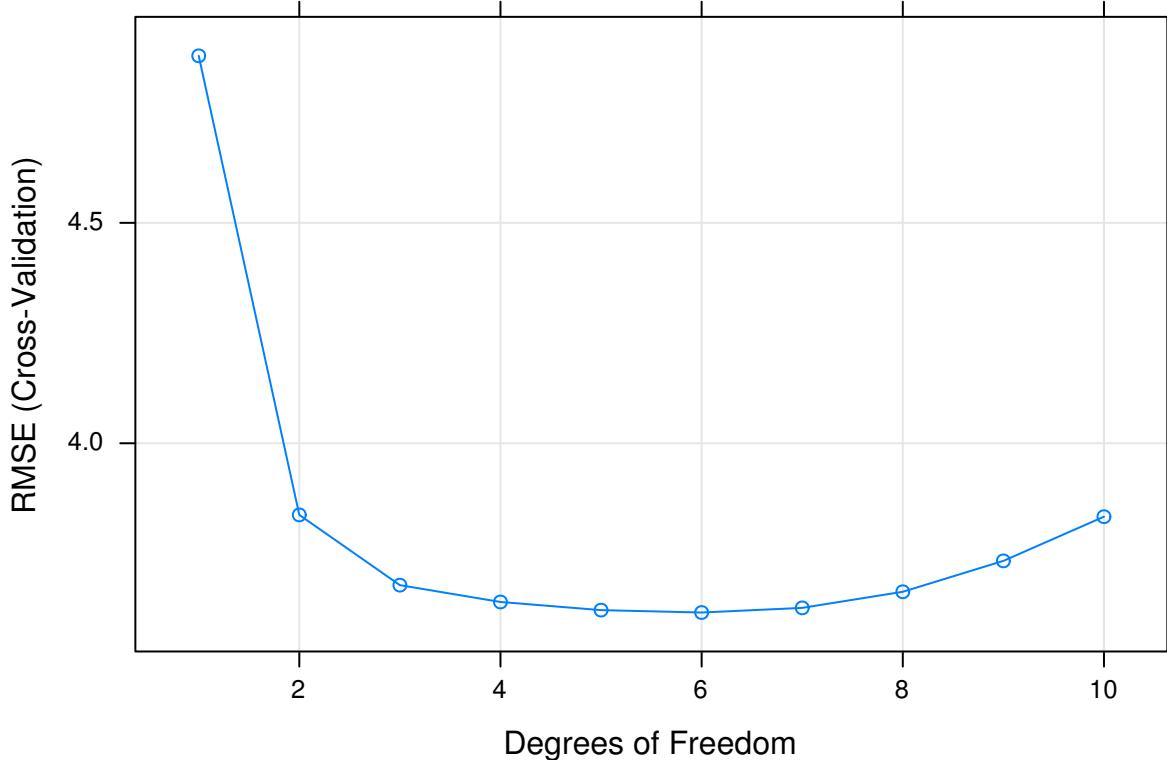
```
par(mfrow = c(1, 3))
plot(gam_log, se = TRUE, col = "dodgerblue")
```



### 24.5.1 GAMs in caret

```
set.seed(430)
library(caret)
library(MASS)
bos_idx = createDataPartition(Boston$medv, p = 0.75, list = FALSE)
bos_trn = Boston[bos_idx, ]
bos_tst = Boston[-bos_idx, ]

cv_5 = trainControl(method = "cv", number = 5)
gam_grid = expand.grid(df = 1:10)
gam_train = train(medv ~ ., data = bos_trn, trControl = cv_5,
                  method = "gamSpline", tuneGrid = gam_grid)
plot(gam_train)
```



```
gam_train

## Generalized Additive Model using Splines
##
## 381 samples
## 13 predictor
##
## No pre-processing
## Resampling: Cross-Validated (5 fold)
## Summary of sample sizes: 305, 305, 304, 305, 305
## Resampling results across tuning parameters:
##
```

```

##   df   RMSE      Rsquared
##   1  4.878874  0.7351130
##   2  3.837483  0.8331653
##   3  3.678147  0.8465347
##   4  3.640002  0.8497681
##   5  3.621525  0.8513187
##   6  3.616083  0.8519814
##   7  3.626592  0.8515926
##   8  3.663142  0.8493004
##   9  3.733215  0.8444341
##  10 3.833477  0.8372057
##
## RMSE was used to select the optimal model using the smallest value.
## The final value used for the model was df = 6.

```

## 24.6 External Links

- GAM: The Predictive Modeling Silver Bullet

## 24.7 RMarkdown

The RMarkdown file for this chapter can be found [here](#). The file was created using R version 3.3.2 and the following packages:

- Base Packages, Attached

```

## [1] "methods"     "splines"      "stats"       "graphics"    "grDevices"   "utils"
## [7] "datasets"    "base"

```

- Additional Packages, Attached

```

## [1] "MASS"        "caret"        "ggplot2"      "lattice"      "gam"         "foreach"     "ISLR"

```

- Additional Packages, Not Attached

```

##  [1] "Rcpp"          "compiler"      "nloptr"        "plyr"
##  [5] " iterators"    "tools"        "digest"        "lme4"
##  [9] " evaluate"     "tibble"       "gttable"       "nlme"
## [13] "mgcv"          "Matrix"       "parallel"      "yaml"
## [17] "SparseM"       "stringr"      "knitr"         "MatrixModels"
## [21] "stats4"        "rprojroot"    "grid"          "nnet"
## [25] "rmarkdown"     "bookdown"     "minqa"         "reshape2"
## [29] "car"           "magrittr"     "backports"     "scales"
## [33] "codetools"     "ModelMetrics" "htmltools"     "assertthat"
## [37] "pbkrtest"      "colorspace"   "quantreg"      "stringi"
## [41] "lazyeval"      "munsell"

```



# Chapter 25

## Trees

```
library(tree)
```

In this document, we will use the package `tree` for both classification and regression trees. Note that there are many packages to do this in R. `rpart` may be the most common, however, we will use `tree` for simplicity.

### 25.1 Classification Trees

```
library(ISLR)
```

To understand classification trees, we will use the `Carseats` dataset from the `ISLR` package. We will first modify the response variable `Sales` from its original use as a numerical variable, to a categorical variable with `High` for high sales, and `Low` for low sales.

```
data(Carseats)
#?Carseats
str(Carseats)

## 'data.frame': 400 obs. of 11 variables:
## $ Sales      : num  9.5 11.22 10.06 7.4 4.15 ...
## $ CompPrice   : num  138 111 113 117 141 124 115 136 132 132 ...
## $ Income      : num  73 48 35 100 64 113 105 81 110 113 ...
## $ Advertising: num  11 16 10 4 3 13 0 15 0 0 ...
## $ Population  : num  276 260 269 466 340 501 45 425 108 131 ...
## $ Price       : num  120 83 80 97 128 72 108 120 124 124 ...
## $ ShelveLoc   : Factor w/ 3 levels "Bad","Good","Medium": 1 2 3 3 1 1 3 2 3 3 ...
## $ Age         : num  42 65 59 55 38 78 71 67 76 76 ...
## $ Education   : num  17 10 12 14 13 16 15 10 10 17 ...
## $ Urban       : Factor w/ 2 levels "No","Yes": 2 2 2 2 2 1 2 2 1 1 ...
## $ US          : Factor w/ 2 levels "No","Yes": 2 2 2 2 1 2 1 2 1 2 ...
```

```
Carseats$Sales = as.factor(ifelse(Carseats$Sales <= 8, "Low", "High"))
str(Carseats)
```

```
## 'data.frame':   400 obs. of  11 variables:
## $ Sales      : Factor w/ 2 levels "High","Low": 1 1 1 2 2 1 2 1 2 2 ...
## $ CompPrice  : num  138 111 113 117 141 124 115 136 132 132 ...
## $ Income     : num  73 48 35 100 64 113 105 81 110 113 ...
## $ Advertising: num  11 16 10 4 3 13 0 15 0 0 ...
## $ Population : num  276 260 269 466 340 501 45 425 108 131 ...
## $ Price      : num  120 83 80 97 128 72 108 120 124 124 ...
## $ ShelveLoc  : Factor w/ 3 levels "Bad","Good","Medium": 1 2 3 3 1 1 3 2 3 3 ...
## $ Age        : num  42 65 59 55 38 78 71 67 76 76 ...
## $ Education  : num  17 10 12 14 13 16 15 10 10 17 ...
## $ Urban      : Factor w/ 2 levels "No","Yes": 2 2 2 2 2 1 2 2 1 1 ...
## $ US         : Factor w/ 2 levels "No","Yes": 2 2 2 2 1 2 1 2 1 2 ...
```

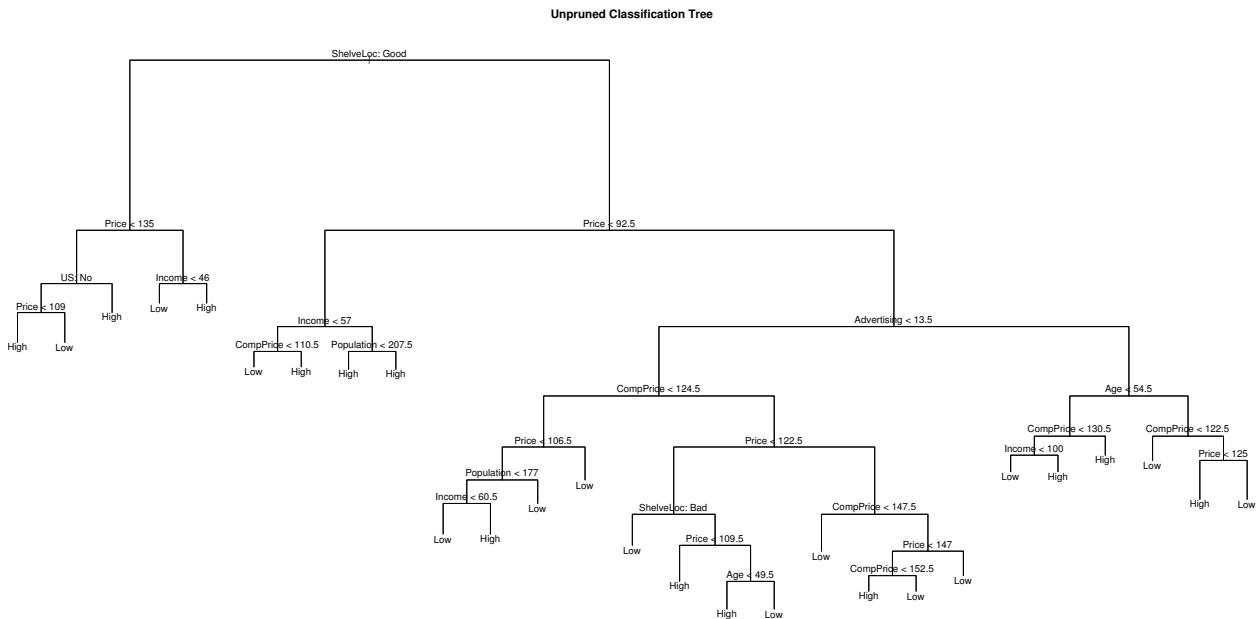
We first fit an unpruned classification tree using all of the predictors. Details of this process can be found using `?tree` and `?tree.control`

```
seat_tree = tree(Sales ~ ., data = Carseats)
# seat_tree = tree(Sales ~ ., data = Carseats,
#                  control = tree.control(nobs = nrow(Carseats), minsize = 10))
summary(seat_tree)
```

```
##
## Classification tree:
## tree(formula = Sales ~ ., data = Carseats)
## Variables actually used in tree construction:
## [1] "ShelveLoc"    "Price"        "US"          "Income"       "CompPrice"
## [6] "Population"   "Advertising"  "Age"
## Number of terminal nodes:  27
## Residual mean deviance:  0.4575 = 170.7 / 373
## Misclassification error rate: 0.09 = 36 / 400
```

We see this tree has 27 terminal nodes and a misclassification rate of 0.09.

```
plot(seat_tree)
text(seat_tree, pretty = 0)
title(main = "Unpruned Classification Tree")
```



Above we plot the tree. Below we output the details of the splits.

```
seat_tree
```

```
## node), split, n, deviance, yval, (yprob)
##      * denotes terminal node
##
## 1) root 400 541.500 Low ( 0.41000 0.59000 )
## 2) ShelveLoc: Good 85  90.330 High ( 0.77647 0.22353 )
## 4) Price < 135 68  49.260 High ( 0.88235 0.11765 )
##     8) US: No 17  22.070 High ( 0.64706 0.35294 )
##        16) Price < 109 8  0.000 High ( 1.00000 0.00000 ) *
##        17) Price > 109 9  11.460 Low ( 0.33333 0.66667 ) *
##        9) US: Yes 51  16.880 High ( 0.96078 0.03922 ) *
## 5) Price > 135 17  22.070 Low ( 0.35294 0.64706 )
## 10) Income < 46 6  0.000 Low ( 0.00000 1.00000 ) *
## 11) Income > 46 11  15.160 High ( 0.54545 0.45455 ) *
## 3) ShelveLoc: Bad,Medium 315 390.600 Low ( 0.31111 0.68889 )
## 6) Price < 92.5 46  56.530 High ( 0.69565 0.30435 )
## 12) Income < 57 10  12.220 Low ( 0.30000 0.70000 )
##        24) CompPrice < 110.5 5  0.000 Low ( 0.00000 1.00000 ) *
##        25) CompPrice > 110.5 5  6.730 High ( 0.60000 0.40000 ) *
##        13) Income > 57 36  35.470 High ( 0.80556 0.19444 )
##        26) Population < 207.5 16  21.170 High ( 0.62500 0.37500 ) *
##        27) Population > 207.5 20  7.941 High ( 0.95000 0.05000 ) *
## 7) Price > 92.5 269 299.800 Low ( 0.24535 0.75465 )
## 14) Advertising < 13.5 224 213.200 Low ( 0.18304 0.81696 )
## 28) CompPrice < 124.5 96  44.890 Low ( 0.06250 0.93750 )
##        56) Price < 106.5 38  33.150 Low ( 0.15789 0.84211 )
##        112) Population < 177 12  16.300 Low ( 0.41667 0.58333 )
##        224) Income < 60.5 6  0.000 Low ( 0.00000 1.00000 ) *
##        225) Income > 60.5 6  5.407 High ( 0.83333 0.16667 ) *
##        113) Population > 177 26  8.477 Low ( 0.03846 0.96154 ) *
## 57) Price > 106.5 58  0.000 Low ( 0.00000 1.00000 ) *
```

```

##      29) CompPrice > 124.5 128 150.200 Low ( 0.27344 0.72656 )
##      58) Price < 122.5 51 70.680 High ( 0.50980 0.49020 )
##      116) ShelveLoc: Bad 11 6.702 Low ( 0.09091 0.90909 ) *
##      117) ShelveLoc: Medium 40 52.930 High ( 0.62500 0.37500 )
##      234) Price < 109.5 16 7.481 High ( 0.93750 0.06250 ) *
##      235) Price > 109.5 24 32.600 Low ( 0.41667 0.58333 )
##          470) Age < 49.5 13 16.050 High ( 0.69231 0.30769 ) *
##          471) Age > 49.5 11 6.702 Low ( 0.09091 0.90909 ) *
##      59) Price > 122.5 77 55.540 Low ( 0.11688 0.88312 )
##      118) CompPrice < 147.5 58 17.400 Low ( 0.03448 0.96552 ) *
##      119) CompPrice > 147.5 19 25.010 Low ( 0.36842 0.63158 )
##          238) Price < 147 12 16.300 High ( 0.58333 0.41667 )
##              476) CompPrice < 152.5 7 5.742 High ( 0.85714 0.14286 ) *
##              477) CompPrice > 152.5 5 5.004 Low ( 0.20000 0.80000 ) *
##          239) Price > 147 7 0.000 Low ( 0.00000 1.00000 ) *
##      15) Advertising > 13.5 45 61.830 High ( 0.55556 0.44444 )
##      30) Age < 54.5 25 25.020 High ( 0.80000 0.20000 )
##          60) CompPrice < 130.5 14 18.250 High ( 0.64286 0.35714 )
##          120) Income < 100 9 12.370 Low ( 0.44444 0.55556 ) *
##          121) Income > 100 5 0.000 High ( 1.00000 0.00000 ) *
##          61) CompPrice > 130.5 11 0.000 High ( 1.00000 0.00000 ) *
##      31) Age > 54.5 20 22.490 Low ( 0.25000 0.75000 )
##          62) CompPrice < 122.5 10 0.000 Low ( 0.00000 1.00000 ) *
##          63) CompPrice > 122.5 10 13.860 Low ( 0.50000 0.50000 )
##          126) Price < 125 5 0.000 High ( 1.00000 0.00000 ) *
##          127) Price > 125 5 0.000 Low ( 0.00000 1.00000 ) *

```

We now test-train split the data so we can evaluate how well our tree is working. We use 200 observations for each.

```

dim(Carseats)

## [1] 400 11

set.seed(2)
seat_idx = sample(1:nrow(Carseats), 200)
seat_trn = Carseats[seat_idx,]
seat_tst = Carseats[-seat_idx,]

seat_tree = tree(Sales ~ ., data = seat_trn)

summary(seat_tree)

##
## Classification tree:
## tree(formula = Sales ~ ., data = seat_trn)
## Variables actually used in tree construction:
## [1] "ShelveLoc"    "Price"        "Population"   "Advertising" "Income"
## [6] "Age"           "CompPrice"
## Number of terminal nodes: 19
## Residual mean deviance: 0.4282 = 77.51 / 181
## Misclassification error rate: 0.105 = 21 / 200

```

Note that, the tree is not using all of the available variables.

```
summary(seat_tree)$used

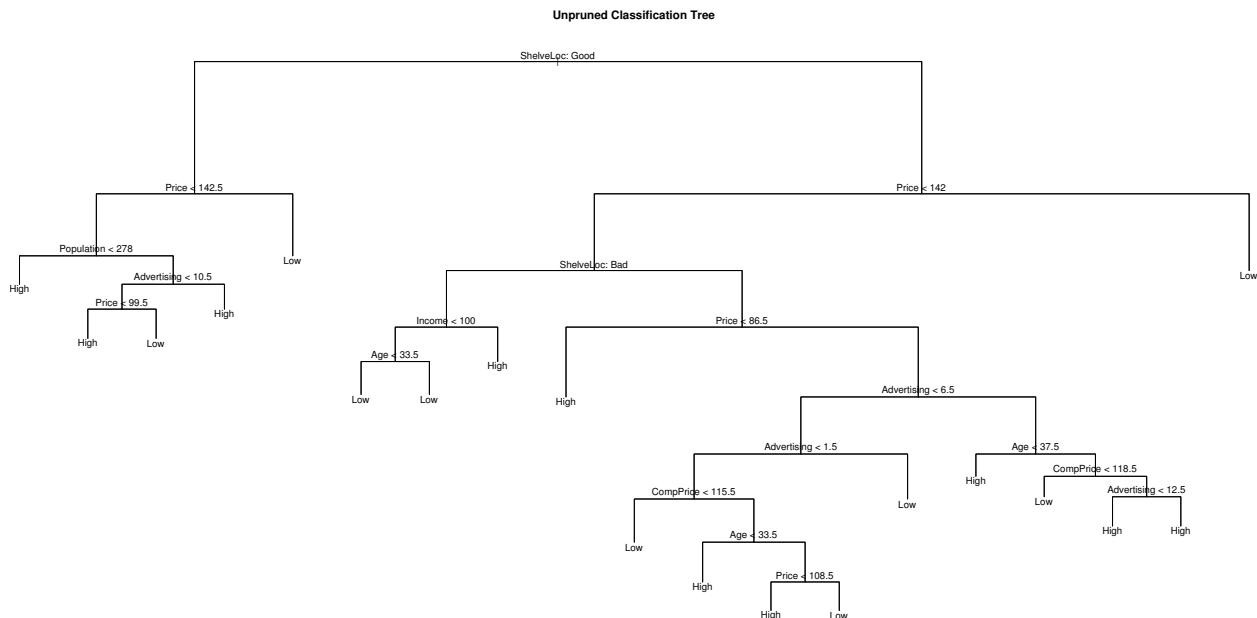
## [1] ShelveLoc    Price        Population   Advertising Income      Age
## [7] CompPrice
## 11 Levels: <leaf> CompPrice Income Advertising Population ... US

names(Carseats)[which(!(names(Carseats) %in% summary(seat_tree)$used))]

## [1] "Sales"      "Education"   "Urban"       "US"
```

Also notice that, this new tree is slightly different than the tree fit to all of the data.

```
plot(seat_tree)
text(seat_tree, pretty = 0)
title(main = "Unpruned Classification Tree")
```



When using the `predict()` function on a tree, the default `type` is `vector` which gives predicted probabilities for both classes. We will use `type = class` to directly obtain classes. We first fit the tree using the training data (above), then obtain predictions on both the train and test set, then view the confusion matrix for both.

```
seat_trn_pred = predict(seat_tree, seat_trn, type = "class")
seat_tst_pred = predict(seat_tree, seat_tst, type = "class")
#predict(seat_tree, seat_trn, type = "vector")
#predict(seat_tree, seat_tst, type = "vector")
```

```
# train confusion
table(predicted = seat_trn_pred, actual = seat_trn$Sales)
```

```

##           actual
## predicted High Low
##      High    66  10
##      Low     14 110

# test confusion
table(predicted = seat_tst$pred, actual = seat_tst$Sales)

##           actual
## predicted High Low
##      High    57  29
##      Low     27  87

accuracy = function(actual, predicted) {
  mean(actual == predicted)
}

# train acc
accuracy(predicted = seat_trn$pred, actual = seat_trn$Sales)

## [1] 0.88

# test acc
accuracy(predicted = seat_tst$pred, actual = seat_tst$Sales)

## [1] 0.72

```

Here it is easy to see that the tree has been over-fit. The train set performs much better than the test set. We will now use cross-validation to find a tree by considering trees of different sizes which have been pruned from our original tree.

```

set.seed(3)
seat_tree_cv = cv.tree(seat_tree, FUN = prune.misclass)

# index of tree with minimum error
min_idx = which.min(seat_tree_cv$dev)
min_idx

## [1] 5

# number of terminal nodes in that tree
seat_tree_cv$size[min_idx]

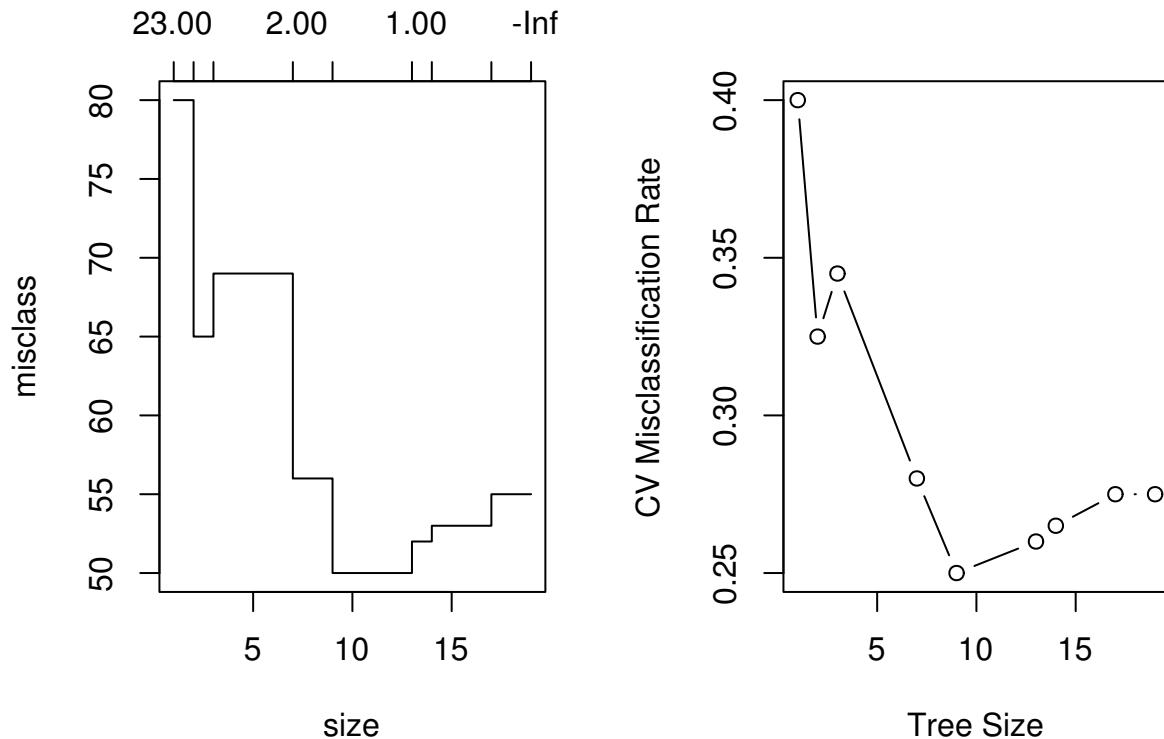
## [1] 9

# misclassification rate of each tree
seat_tree_cv$dev / length(seat_idx)

## [1] 0.275 0.275 0.265 0.260 0.250 0.280 0.345 0.325 0.400

```

```
par(mfrow = c(1, 2))
# default plot
plot(seat_tree_cv)
# better plot
plot(seat_tree_cv$size, seat_tree_cv$dev / nrow(seat_trn), type = "b",
     xlab = "Tree Size", ylab = "CV Misclassification Rate")
```



It appears that a tree of size 9 has the fewest misclassifications of the considered trees, via cross-validation.

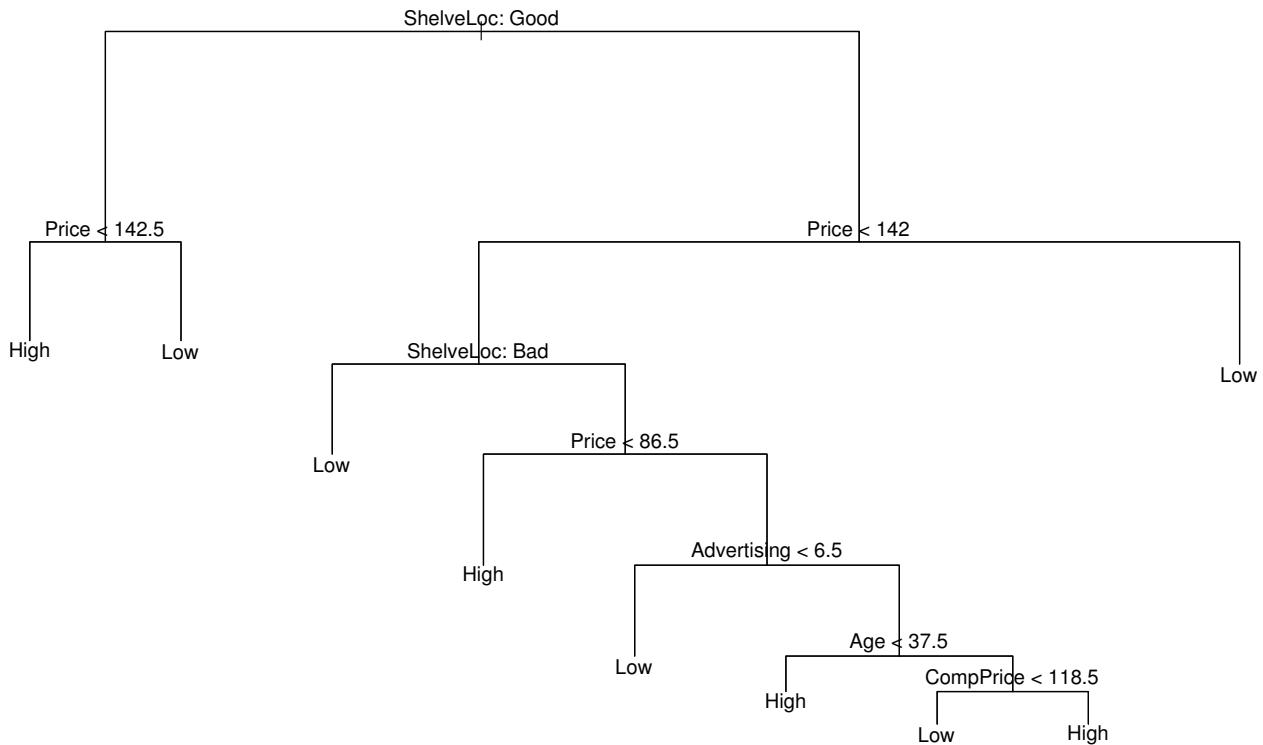
We use `prune.misclass()` to obtain that tree from our original tree, and plot this smaller tree.

```
seat_tree_prune = prune.misclass(seat_tree, best = 9)
summary(seat_tree_prune)
```

```
##
## Classification tree:
## snip.tree(tree = seat_tree, nodes = c(223L, 4L, 12L, 54L))
## Variables actually used in tree construction:
## [1] "ShelveLoc"    "Price"        "Advertising"   "Age"          "CompPrice"
## Number of terminal nodes:  9
## Residual mean deviance:  0.8103 = 154.8 / 191
## Misclassification error rate: 0.155 = 31 / 200
```

```
plot(seat_tree_prune)
text(seat_tree_prune, pretty = 0)
title(main = "Pruned Classification Tree")
```

### Pruned Classification Tree



We again obtain predictions using this smaller tree, and evaluate on the test and train sets.

```
# train
seat_prune_trn_pred = predict(seat_tree_prune, seat_trn, type = "class")
table(predicted = seat_prune_trn_pred, actual = seat_trn$Sales)
```

```
##           actual
## predicted High Low
##       High   59  10
##       Low    21 110
```

```
accuracy(predicted = seat_prune_trn_pred, actual = seat_trn$Sales)
```

```
## [1] 0.845
```

```
# test
seat_prune_tst_pred = predict(seat_tree_prune, seat_tst, type = "class")
table(predicted = seat_prune_tst_pred, actual = seat_tst$Sales)
```

```
##           actual
## predicted High Low
##       High   60  22
##       Low    24  94
```

```
accuracy(predicted = seat_prune_tst$pred, actual = seat_tst$Sales)
```

```
## [1] 0.77
```

The train set has performed almost as well as before, and there was a **small** improvement in the test set, but it is still obvious that we have over-fit. Trees tend to do this. We will look at several ways to fix this, including: bagging, boosting and random forests.

## 25.2 Regression Trees

To demonstrate regression trees, we will use the **Boston** data. Recall **medv** is the response. We first split the data in half.

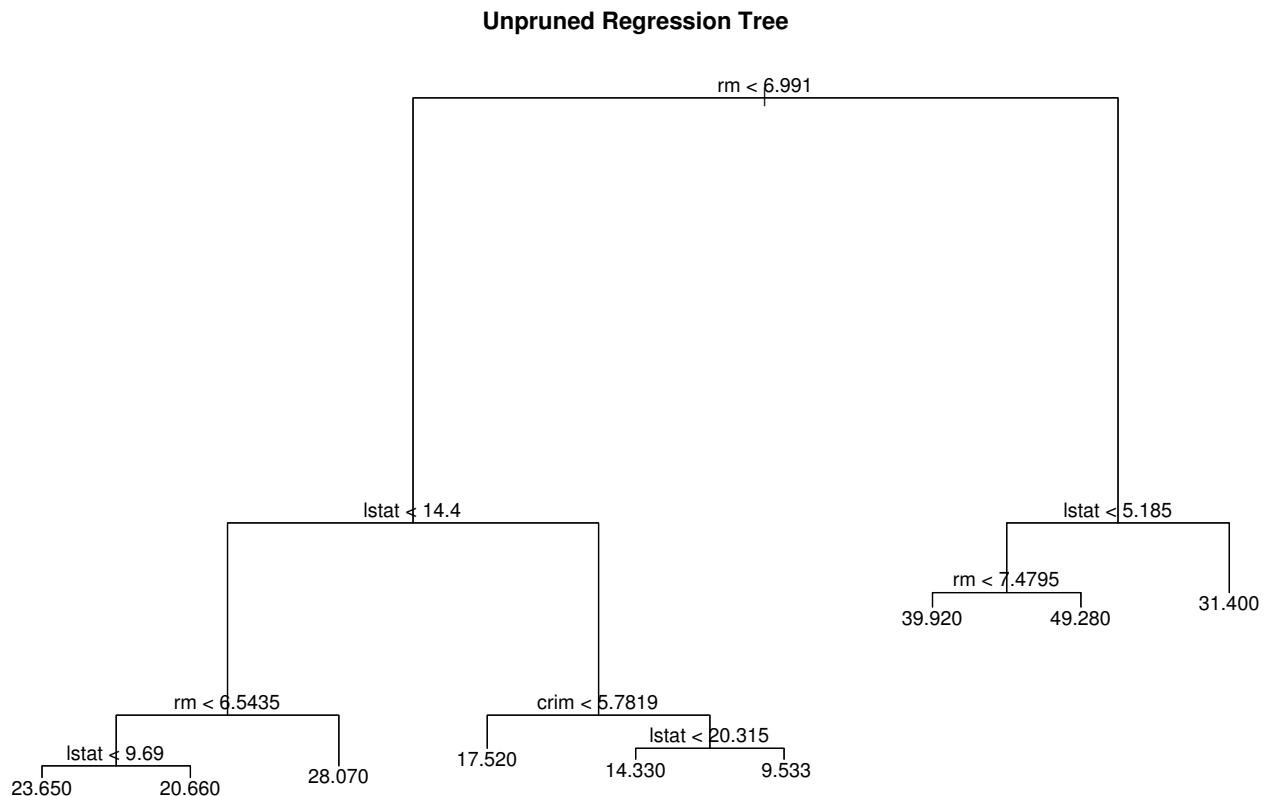
```
library(MASS)
set.seed(18)
boston_idx = sample(1:nrow(Boston), nrow(Boston) / 2)
boston_trn = Boston[boston_idx,]
boston_tst = Boston[-boston_idx,]
```

Then fit an unpruned regression tree to the training data.

```
boston_tree = tree(medv ~ ., data = boston_trn)
summary(boston_tree)
```

```
##
## Regression tree:
## tree(formula = medv ~ ., data = boston_trn)
## Variables actually used in tree construction:
## [1] "rm"      "lstat"   "crim"
## Number of terminal nodes:  9
## Residual mean deviance:  12.35 = 3013 / 244
## Distribution of residuals:
##    Min. 1st Qu. Median  Mean 3rd Qu. Max.
## -13.600 -1.832 -0.120  0.000  1.348  26.350
```

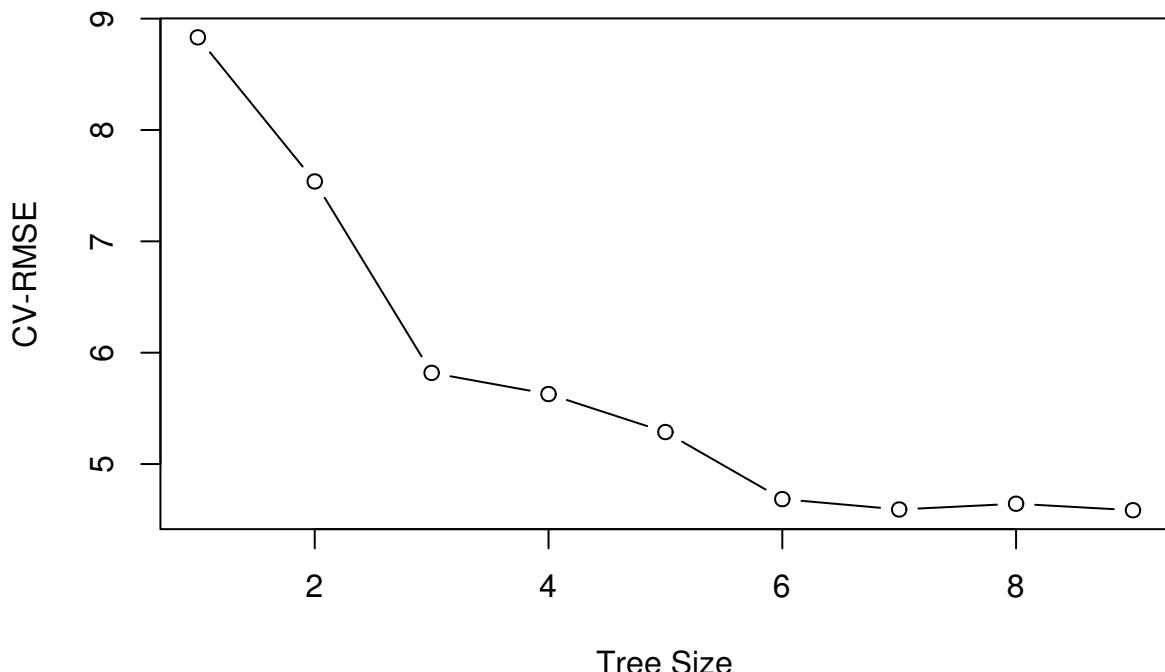
```
plot(boston_tree)
text(boston_tree, pretty = 0)
title(main = "Unpruned Regression Tree")
```



As with classification trees, we can use cross-validation to select a good pruning of the tree.

```

set.seed(18)
boston_tree_cv = cv.tree(boston_tree)
plot(boston_tree_cv$size, sqrt(boston_tree_cv$dev / nrow(boston_trn)), type = "b",
     xlab = "Tree Size", ylab = "CV-RMSE")
  
```



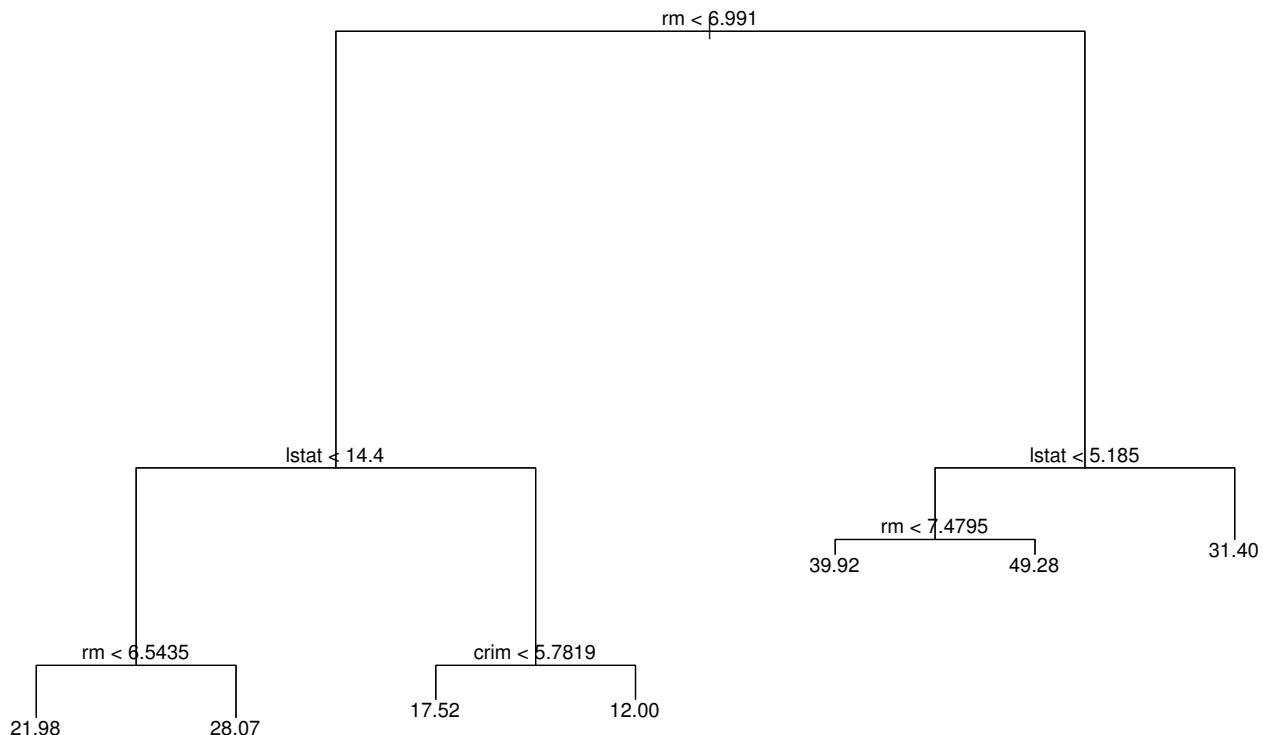
While the tree of size 9 does have the lowest RMSE, we'll prune to a size of 7 as it seems to perform just as well. (Otherwise we would not be pruning.) The pruned tree is, as expected, smaller and easier to interpret.

```
boston_tree_prune = prune.tree(boston_tree, best = 7)
summary(boston_tree_prune)
```

```
##
## Regression tree:
## snip.tree(tree = boston_tree, nodes = c(11L, 8L))
## Variables actually used in tree construction:
## [1] "rm"      "lstat"   "crim"
## Number of terminal nodes: 7
## Residual mean deviance: 14.05 = 3455 / 246
## Distribution of residuals:
##      Min.   1st Qu.    Median     Mean   3rd Qu.   Max.
## -13.60000 -2.12000  0.01731  0.00000  1.88000  28.02000
```

```
plot(boston_tree_prune)
text(boston_tree_prune, pretty = 0)
title(main = "Pruned Regression Tree")
```

**Pruned Regression Tree**



Let's compare this regression tree to an additive linear model and use RMSE as our metric.

```
rmse = function(actual, predicted) {
  sqrt(mean((actual - predicted) ^ 2))
}
```

We obtain predictions on the train and test sets from the pruned tree. We also plot actual vs predicted. This plot may look odd. We'll compare it to a plot for linear regression below.

```
# training RMSE two ways
sqrt(summary(boston_tree_prune)$dev / nrow(boston_trn))

## [1] 3.695598

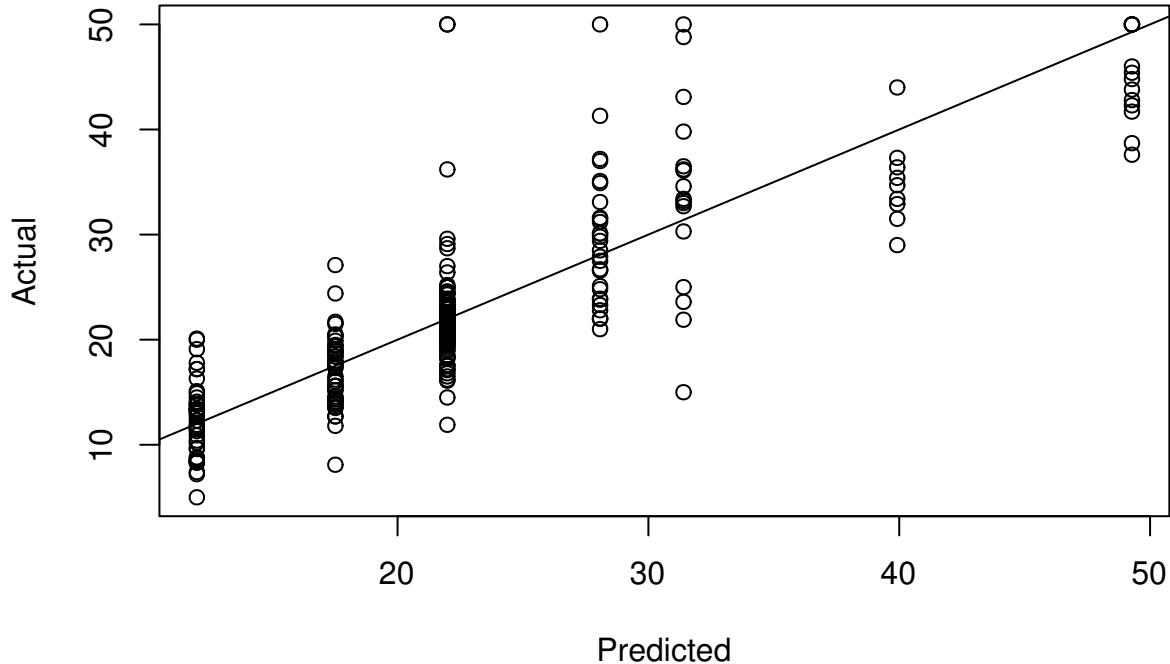
boston_prune_trn_pred = predict(boston_tree_prune, newdata = boston_trn)
rmse(boston_prune_trn_pred, boston_trn$medv)

## [1] 3.695598

# test RMSE
boston_prune_tst_pred = predict(boston_tree_prune, newdata = boston_tst)
rmse(boston_prune_tst_pred, boston_tst$medv)

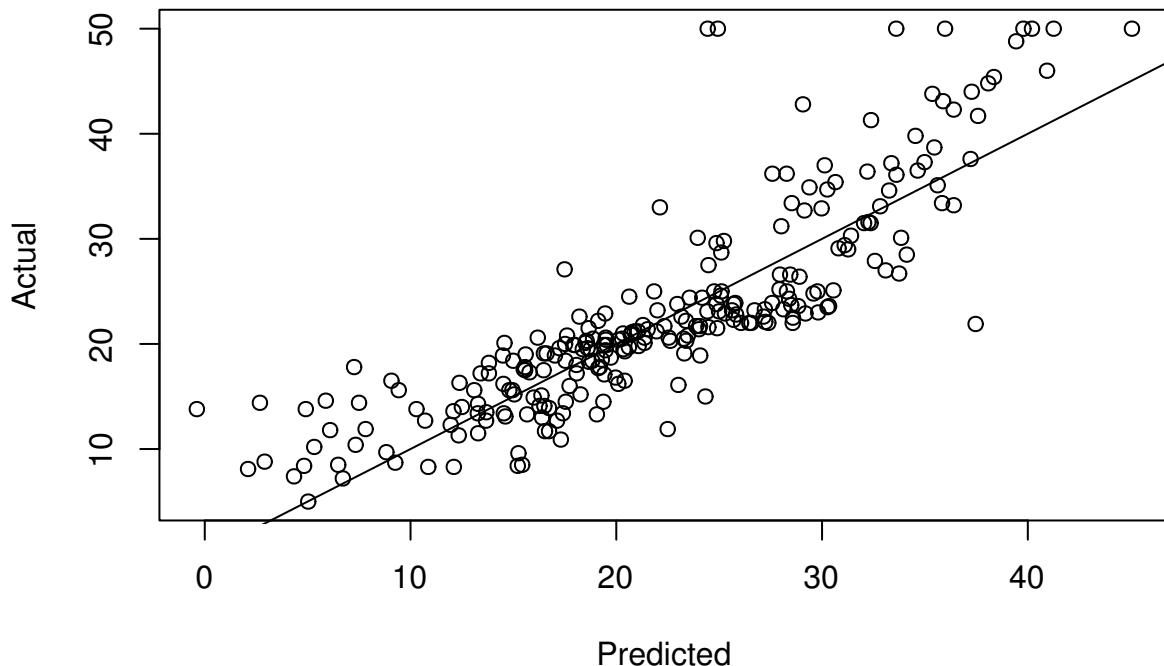
## [1] 5.331457

plot(boston_prune_tst_pred, boston_tst$medv, xlab = "Predicted", ylab = "Actual")
abline(0, 1)
```



Here, using an additive linear regression the actual vs predicted looks much more like what we are used to.

```
boston_lm = lm(medv ~ ., data = boston_trn)
boston_lm_pred = predict(boston_lm, newdata = boston_tst)
plot(boston_lm_pred, boston_tst$medv, xlab = "Predicted", ylab = "Actual")
abline(0, 1)
```



```
rmse(boston_lm_pred, boston_tst$medv)
```

```
## [1] 5.125877
```

We also see a lower test RMSE. The most obvious linear regression beats the tree! Again, we'll improve on this tree soon. Also note the summary of the additive linear regression below. Which is easier to interpret, that output, or the small tree above?

```
coef(boston_lm)
```

```
##   (Intercept)      crim       zn     indus      chas
## 43.340158284 -0.113490889  0.046881038  0.018046856 3.557944155
##      nox        rm       age      dis      rad
## -21.904534125  3.486780787 -0.010592511 -1.766227892  0.354167931
##      tax      ptratio     black    lstat
## -0.015036451 -0.830144898  0.003722857 -0.576134200
```

## 25.3 rpart Package

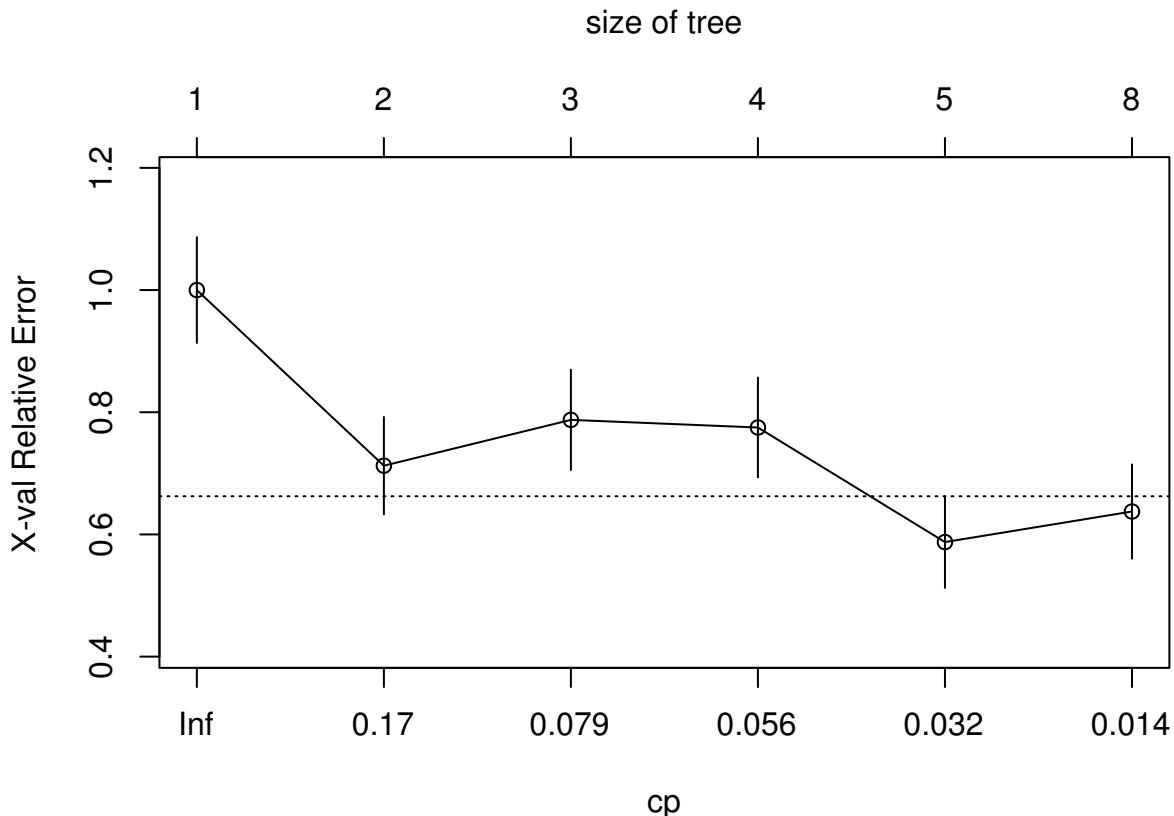
The `rpart` package is an alternative method for fitting trees in R. It is much more feature rich, including fitting multiple cost complexities and performing cross-validation by default. It also has the ability to produce much nicer trees. Based on its default settings, it will often result in smaller trees than using the `tree` package. See the references below for more information. `rpart` can also be tuned via `caret`.

```
library(rpart)
set.seed(430)
# Fit a decision tree using rpart
# Note: when you fit a tree using rpart, the fitting routine automatically
# performs 10-fold CV and stores the errors for later use
```

```
# (such as for pruning the tree)

# fit a tree using rpart
seat_rpart = rpart(Sales ~ ., data = seat_trn, method = "class")

# plot the cv error curve for the tree
# rpart tries different cost-complexities by default
# also stores cv results
plotcp(seat_rpart)
```

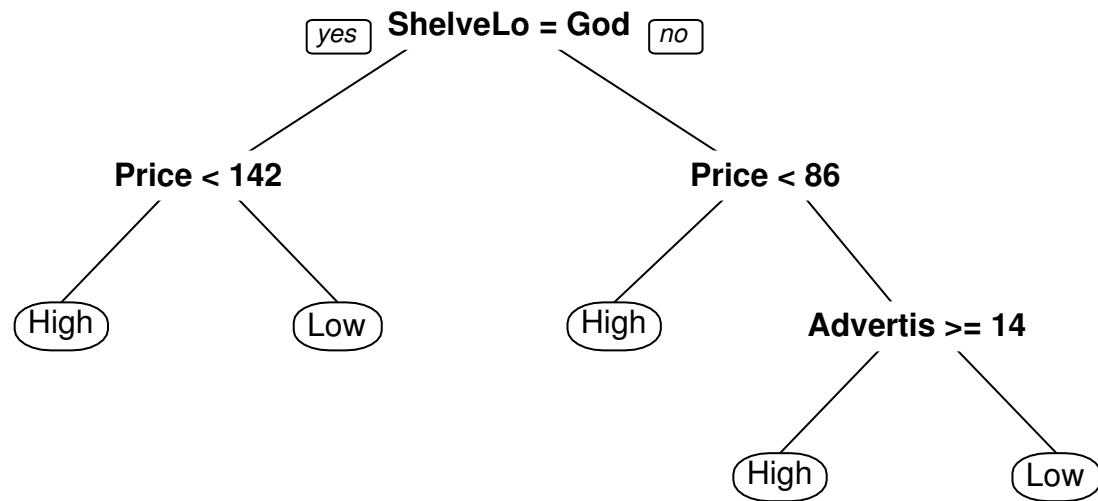


```
# find best value of cp
min_cp = seat_rpart$cptable[which.min(seat_rpart$cptable[, "xerror"]),"CP"]
min_cp
```

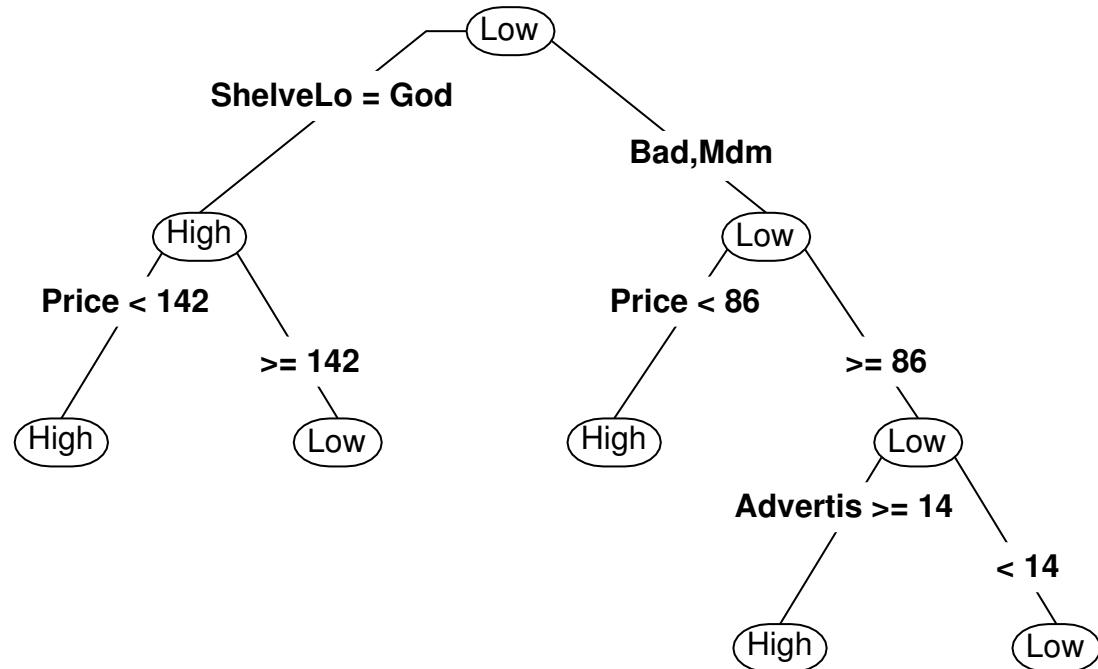
```
## [1] 0.02083333
```

```
# prune tree using best cp
seat_rpart_prune = prune(seat_rpart, cp = min_cp)

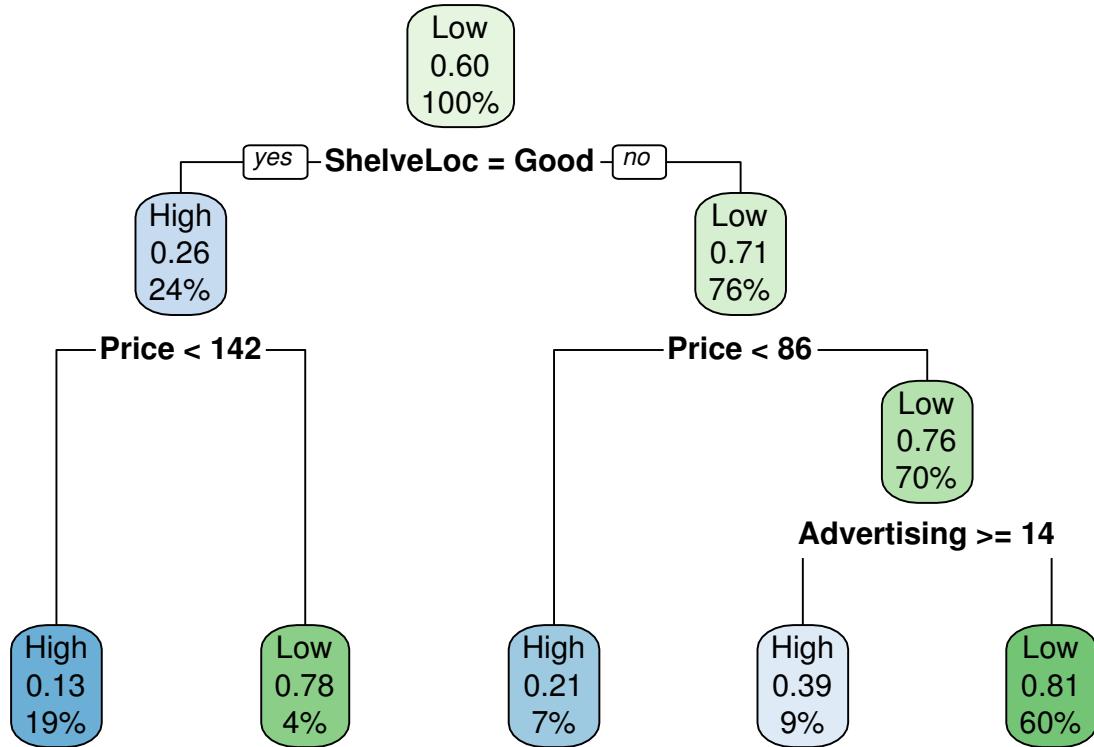
# nicer plots
library(rpart.plot)
prp(seat_rpart_prune)
```



```
prp(seat_rpart_prune, type = 4)
```



```
rpart.plot(seat_rpart_prune)
```



## 25.4 External Links

- An Introduction to Recursive Partitioning Using the `rpart` Routines - Details of the `rpart` package.
- `rpart.plot` Package - Detailed manual on plotting with `rpart` using the `rpart.plot` package.

## 25.5 RMarkdown

The RMarkdown file for this chapter can be found [here](#). The file was created using R version 3.3.2 and the following packages:

- Base Packages, Attached

```
## [1] "stats"      "graphics"    "grDevices"   "utils"       "datasets"    "base"
```

- Additional Packages, Attached

```
## [1] "rpart.plot"  "rpart"       "MASS"        "ISLR"        "tree"
```

- Additional Packages, Not Attached

```
## [1] "Rcpp"        "bookdown"    "digest"      "rprojroot"  "backports"
## [6] "magrittr"    "evaluate"    "stringi"    "rmarkdown"   "tools"
## [11] "stringr"     "yaml"        "htmltools"   "knitr"      "methods"
```

# Chapter 26

## Ensemble Methods

We'll now consider ensembles of trees.

### 26.1 Regression

We first consider the regression case, using the `Boston` data from the `MASS` package. We will use RMSE as our metric, so we write a function which will help us along the way.

```
rmse = function(actual, predicted) {  
  sqrt(mean((actual - predicted) ^ 2))  
}
```

We also load all of the packages that we will need.

```
library(tree)  
library(MASS)  
library(ISLR)  
library(randomForest)  
library(gbm)  
library(caret)
```

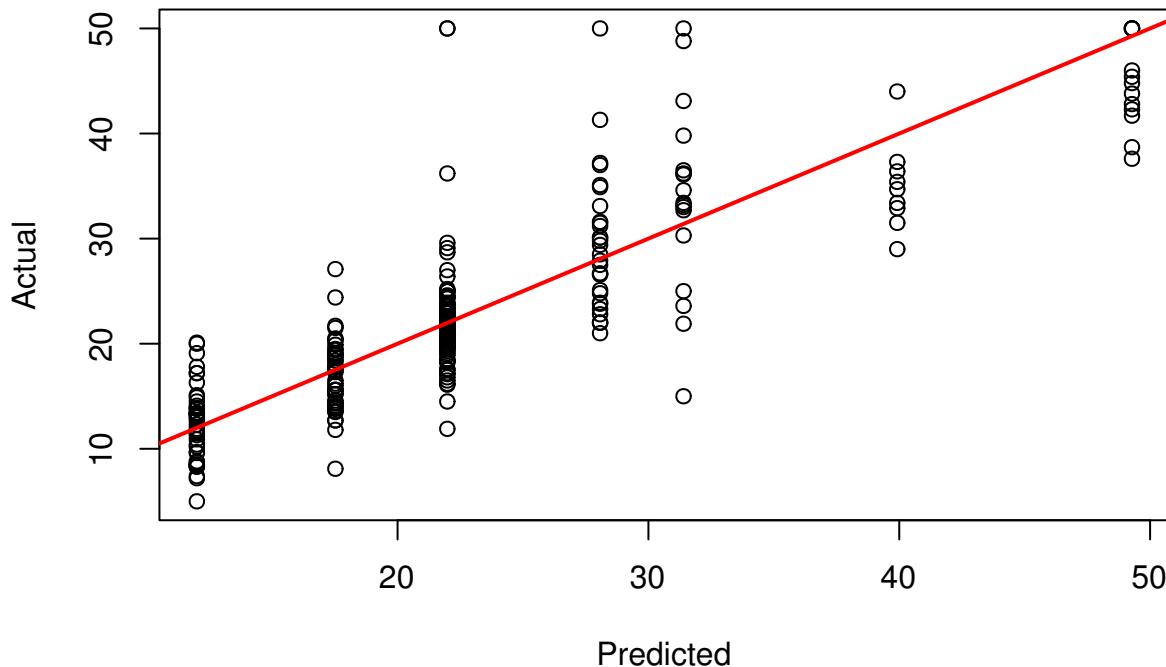
We first test-train split the data and fit the same pruned tree as before. (Note: When pruning the tree, the best tree is actually the unpruned tree. View the results of `cv.tree` to see this. However, we select the tree of size 7 as the best of the pruned trees.)

```
set.seed(18)  
boston_idx = sample(1:nrow(Boston), nrow(Boston) / 2)  
boston_trn = Boston[boston_idx,]  
boston_tst = Boston[-boston_idx,]
```

#### 26.1.1 Tree Model

```
boston_tree = tree(medv ~ ., data = boston_trn)
set.seed(18)
boston_tree_cv = cv.tree(boston_tree)
boston_tree_prune = prune.tree(boston_tree, best = 7)
boston_prune_tst_pred = predict(boston_tree_prune, newdata = boston_tst)
plot(boston_prune_tst_pred, boston_tst$medv,
     xlab = "Predicted", ylab = "Actual",
     main = "Predicted vs Actual: Tree, Test Data")
abline(0, 1, col = "red", lwd = 2)
```

**Predicted vs Actual: Tree, Test Data**



```
(tree_tst_rmse = rmse(boston_prune_tst_pred, boston_tst$medv))
```

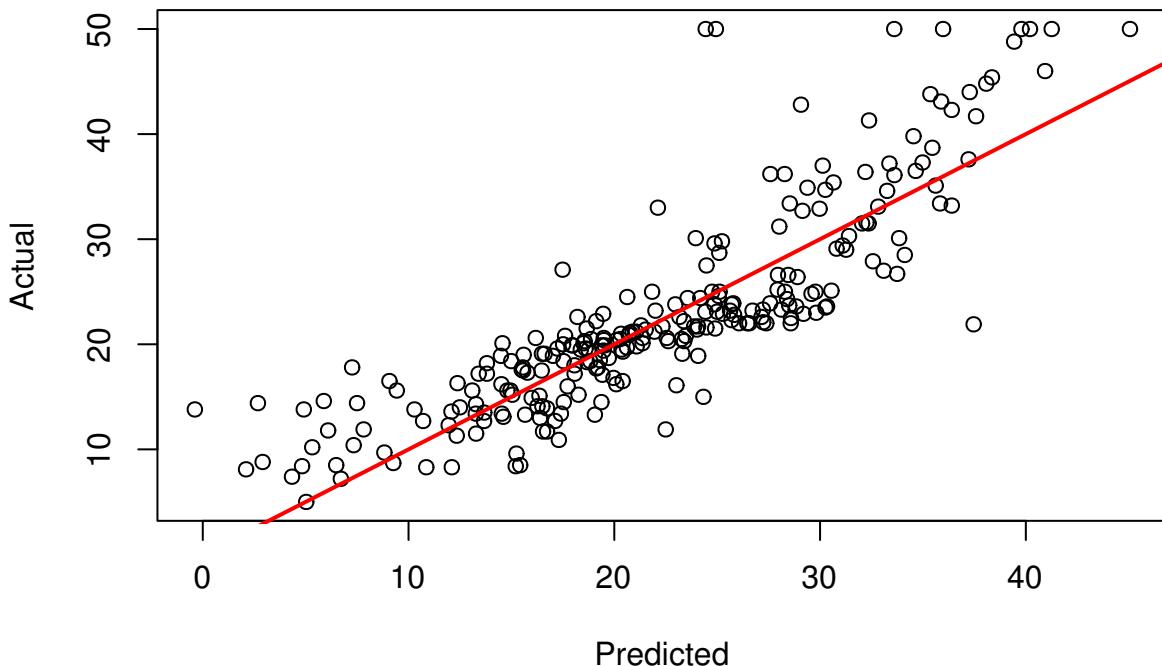
```
## [1] 5.331457
```

### 26.1.2 Linear Model

Last time, we also fit an additive linear model, which we found to work better than the tree. The test RMSE is lower, and the predicted vs actual plot looks much better.

```
boston_lm = lm(medv ~ ., data = boston_trn)
boston_lm_tst_pred = predict(boston_lm, newdata = boston_tst)
plot(boston_lm_tst_pred, boston_tst$medv,
     xlab = "Predicted", ylab = "Actual",
     main = "Predicted vs Actual: Linear Model, Test Data"
)
abline(0, 1, col = "red", lwd = 2)
```

### Predicted vs Actual: Linear Model, Test Data



```
(lm_tst_rmse = rmse(boston_lm_tst$pred, boston_tst$medv))
```

```
## [1] 5.125877
```

#### 26.1.3 Bagging

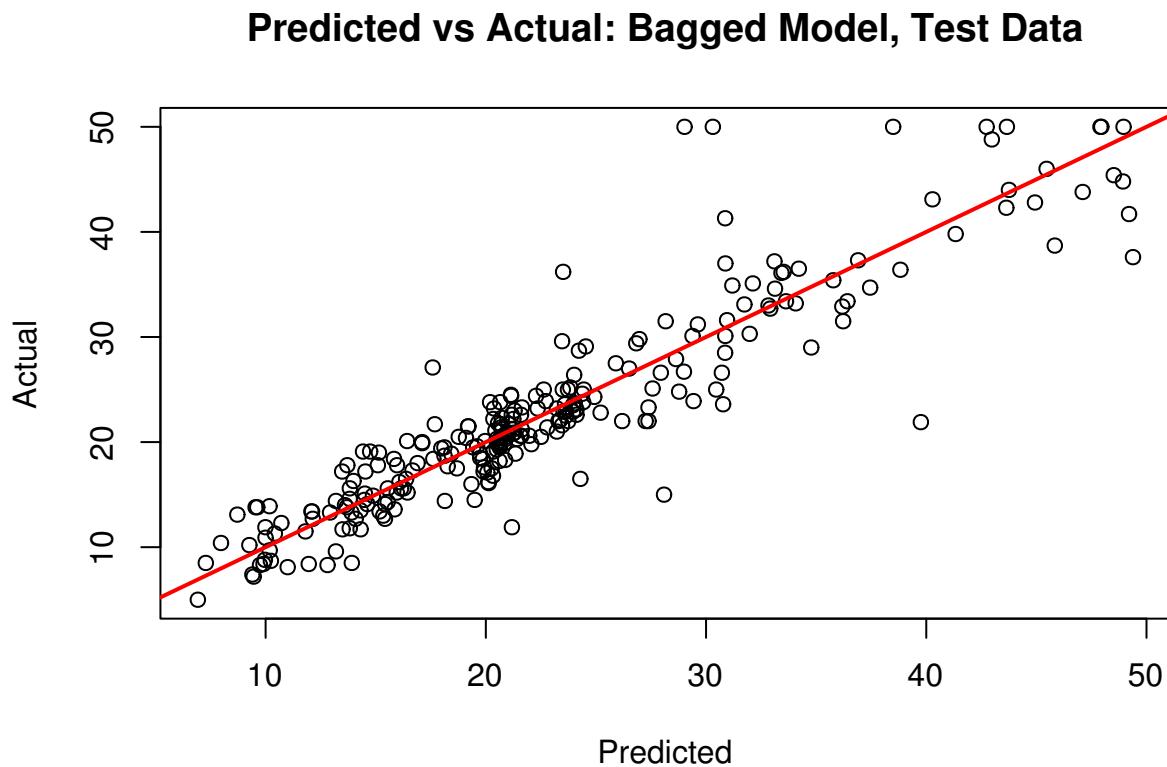
We now fit a bagged model, using the `randomForest` package. Bagging is actually a special case of a random forest where `mtry` is equal to  $p$ , the number of predictors.

```
boston_bag = randomForest(medv ~ ., data = boston_trn, mtry = 13,
                           importance = TRUE, ntrees = 500)
boston_bag
```

```
##
## Call:
## randomForest(formula = medv ~ ., data = boston_trn, mtry = 13,      importance = TRUE, ntrees = 500)
##           Type of random forest: regression
##                   Number of trees: 500
## No. of variables tried at each split: 13
##
##           Mean of squared residuals: 14.20299
##           % Var explained: 80.92
```

```
boston_bag_tst_pred = predict(boston_bag, newdata = boston_tst)
plot(boston_bag_tst_pred, boston_tst$medv,
     xlab = "Predicted", ylab = "Actual",
     main = "Predicted vs Actual: Bagged Model, Test Data")
```

```
)
abline(0, 1, col = "red", lwd = 2)
```



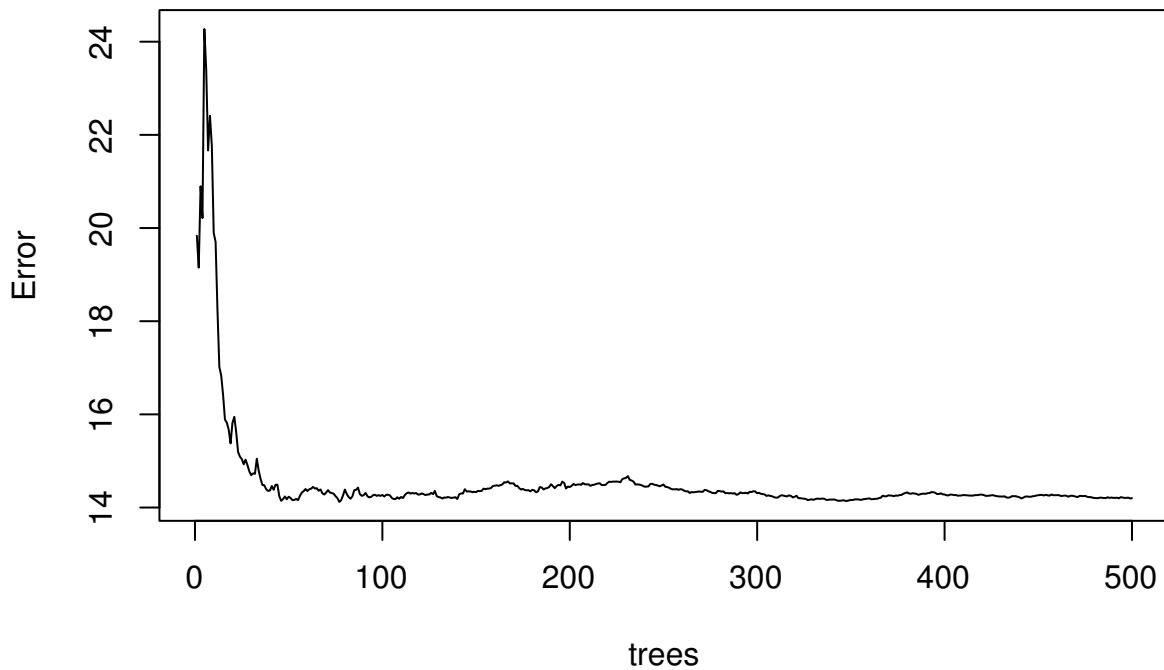
```
(bag_tst_rmse = rmse(boston_bag_tst$pred, boston_tst$medv))
```

```
## [1] 3.814368
```

Here we see two interesting results. First, the predicted versus actual plot no longer has a small number of predicted values. Second, our test error has dropped dramatically. Also note that the “Mean of squared residuals” which is output by `randomForest` is the **Out of Bag** estimate of the error.

```
plot(boston_bag)
```

### boston\_bag



#### 26.1.4 Random Forest

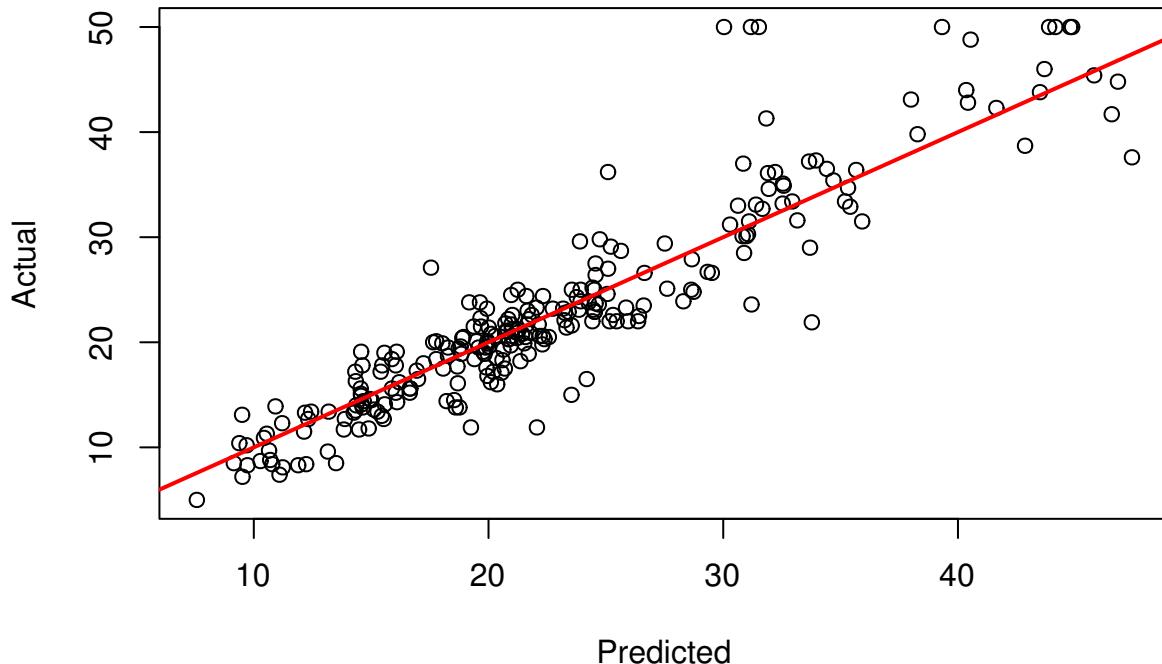
We now try a random forest. For regression, the suggestion is to use `mtry` equal to  $p/3$ .

```
boston_forest = randomForest(medv ~ ., data = boston_trn, mtry = 4,
                               importance = TRUE, ntrees = 500)
boston_forest

## 
## Call:
##  randomForest(formula = medv ~ ., data = boston_trn, mtry = 4,      importance = TRUE, ntrees = 500)
##              Type of random forest: regression
##                      Number of trees: 500
## No. of variables tried at each split: 4
##
##                  Mean of squared residuals: 12.80737
##                  % Var explained: 82.79

#importance(boston_forest)
#varImpPlot(boston_forest)
boston_forest_tst_pred = predict(boston_forest, newdata = boston_tst)
plot(boston_forest_tst_pred, boston_tst$medv,
     xlab = "Predicted", ylab = "Actual",
     main = "Predicted vs Actual: Random Forest, Test Data"
)
abline(0, 1, col = "red", lwd = 2)
```

## Predicted vs Actual: Random Forest, Test Data



```
(forest_tst_rmse = rmse(boston_forest_tst_pred, boston_tst$medv))
```

```
## [1] 3.73447
```

```
boston_forest_trn_pred = predict(boston_forest, newdata = boston_trn)
forest_trn_rmse = rmse(boston_forest_trn_pred, boston_trn$medv)
forest_oob_rmse = rmse(boston_forest$predicted, boston_trn$medv)
```

Here we note three RMSEs. The training RMSE (which is optimistic), the OOB RMSE (which is a good estimate of the test error) and the test RMSE. Also note that variables importance was calculated, however, the results are not shown here. (The code to view the results is commented out.)

```
##      Data    Error
## 1 Training 1.563253
## 2      OOB 3.578738
## 3      Test 3.734470
```

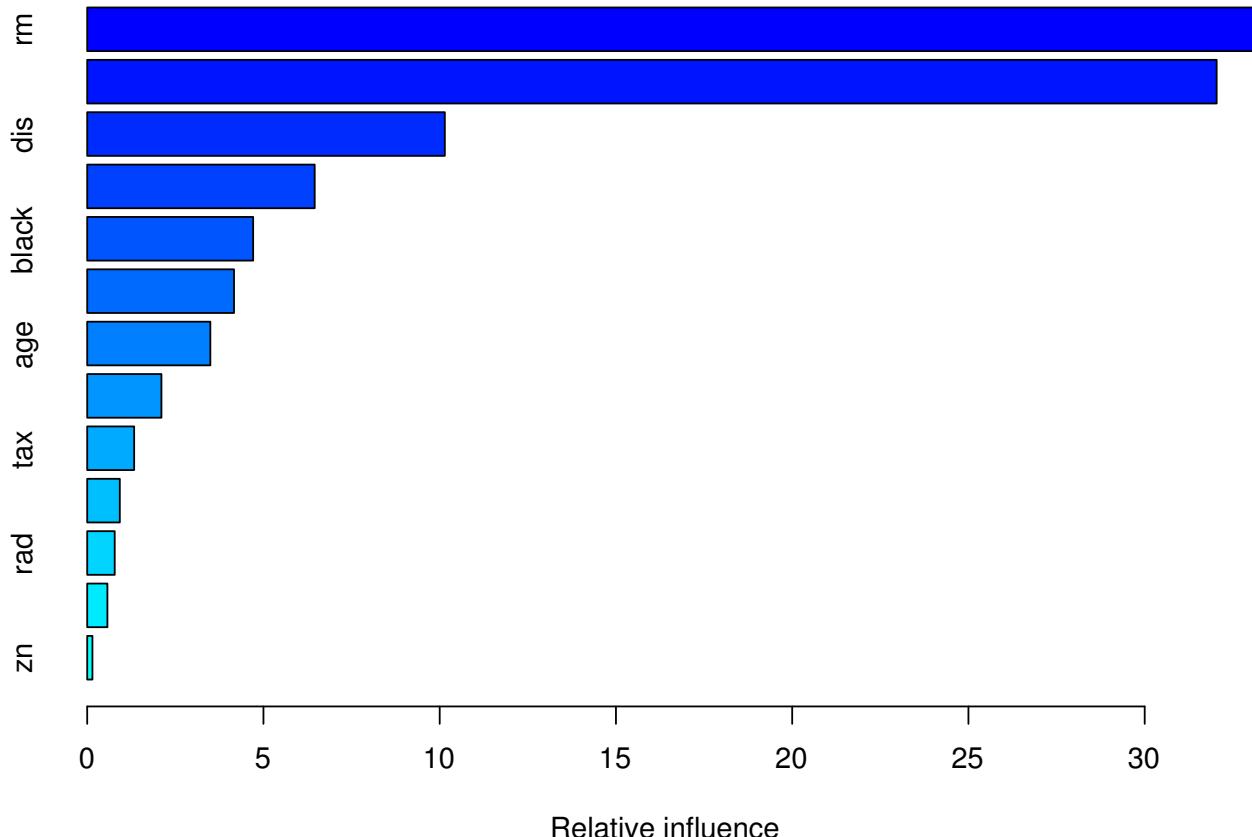
### 26.1.5 Boosting

Lastly, we try a boosted model, which by default will produce a nice **variable importance** plot as well as plots of the marginal effects of the predictors. We use the **gbm** package.

```
booston_boost = gbm(medv ~ ., data = boston_trn, distribution = "gaussian",
                     n.trees = 5000, interaction.depth = 4, shrinkage = 0.01)
booston_boost
```

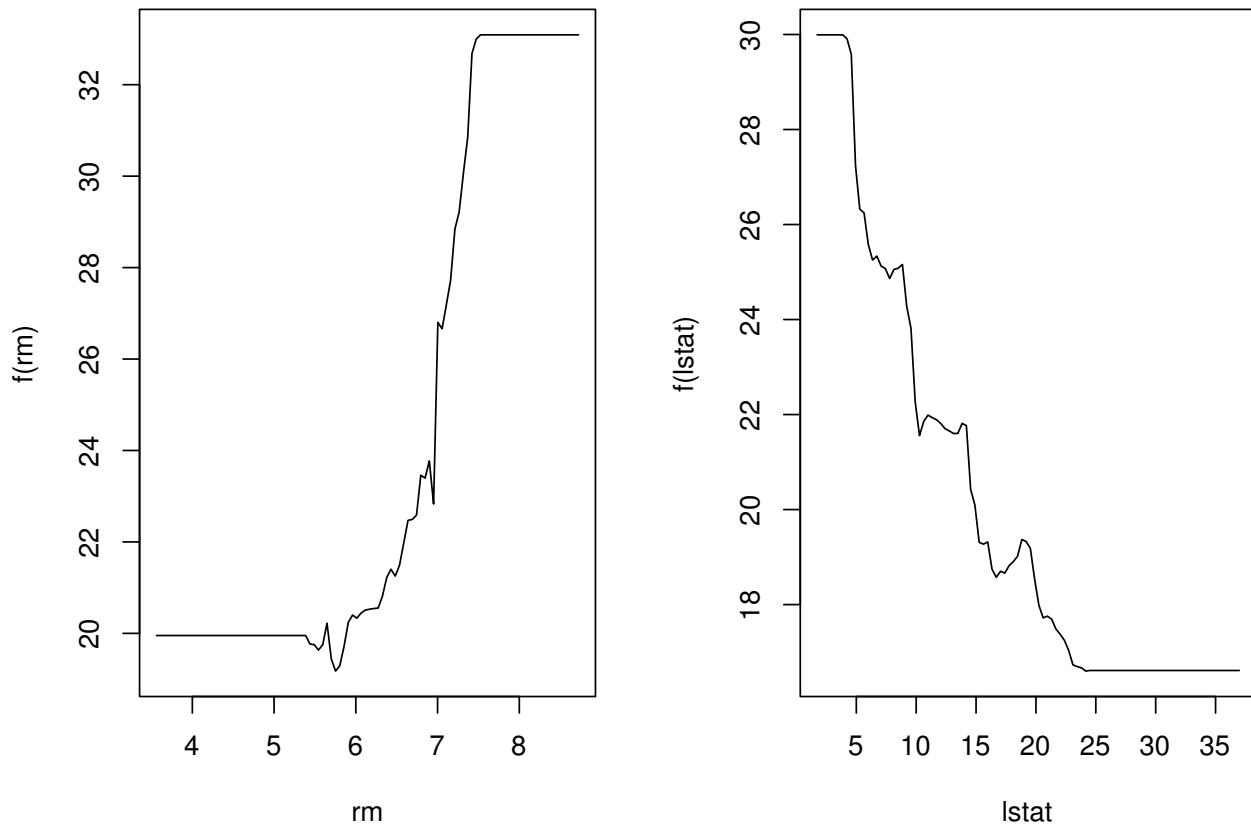
```
## gbm(formula = medv ~ ., distribution = "gaussian", data = boston_trn,
##       n.trees = 5000, interaction.depth = 4, shrinkage = 0.01)
## A gradient boosted model with gaussian loss function.
## 5000 iterations were performed.
## There were 13 predictors of which 13 had non-zero influence.
```

```
summary(booston_boost)
```



```
##          var      rel.inf
## rm        rm 33.1305117
## lstat    lstat 32.0413077
## dis      dis 10.1450348
## crim    crim  6.4535978
## black   black  4.7076459
## nox     nox  4.1647148
## age     age  3.4933055
## ptratio ptratio 2.1056374
## tax     tax  1.3320146
## indus   indus  0.9248479
## rad     rad  0.7800278
## chas   chas  0.5731764
## zn      zn  0.1481777
```

```
par(mfrow = c(1, 2))
plot(booston_boost, i = "rm")
plot(booston_boost, i = "lstat")
```

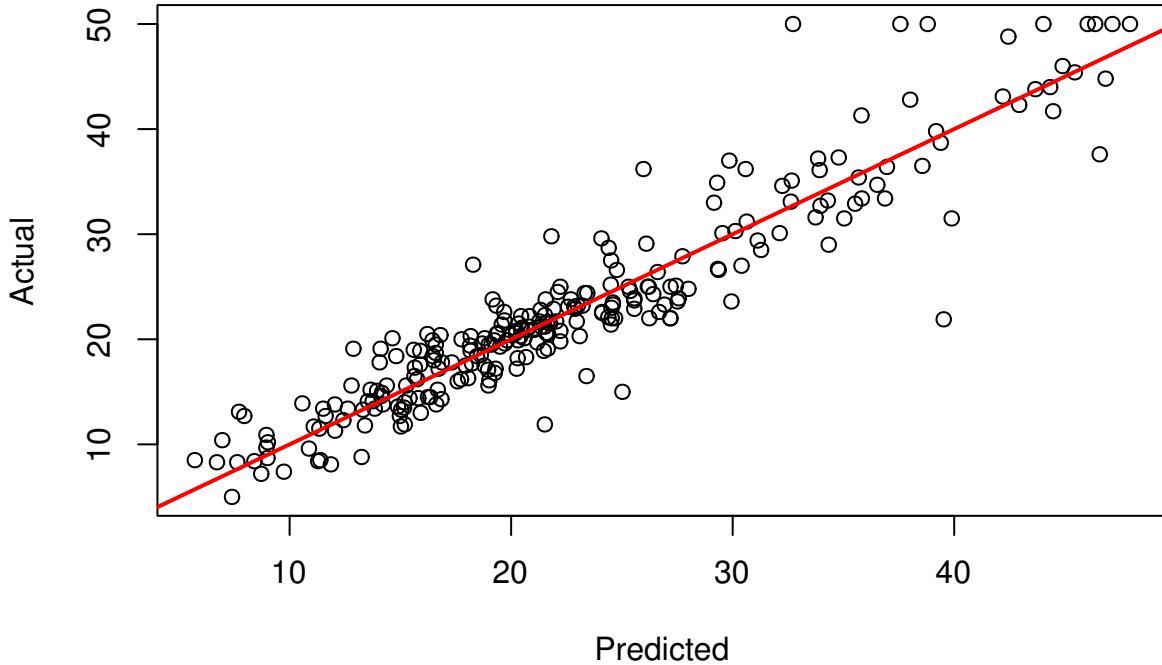


```
boston_boost_tst_pred = predict(boston_boost, newdata = boston_tst, n.trees = 5000)
(boost_tst_rmse = rmse(boston_boost_tst_pred, boston_tst$medv))
```

```
## [1] 3.437024
```

```
plot(boston_boost_tst_pred, boston_tst$medv,
     xlab = "Predicted", ylab = "Actual",
     main = "Predicted vs Actual: Boosted Model, Test Data"
)
abline(0, 1, col = "red", lwd = 2)
```

### Predicted vs Actual: Boosted Model, Test Data



#### 26.1.6 Results

```
(boston_rmse = data.frame(
  Model = c("Single Tree", "Linear Model", "Bagging", "Random Forest", "Boosting"),
  TestError = c(tree_tst_rmse, lm_tst_rmse, bag_tst_rmse, forest_tst_rmse, boost_tst_rmse)
)
)

##           Model TestError
## 1   Single Tree  5.331457
## 2  Linear Model  5.125877
## 3      Bagging  3.814368
## 4 Random Forest  3.734470
## 5     Boosting  3.437024
```

While a single tree does not beat linear regression, each of the ensemble methods perform much better!

## 26.2 Classification

We now return to the `Carseats` dataset and the classification setting. We see that an additive logistic regression performs much better than a single tree, but we expect ensemble methods to bring trees closer to the logistic regression. Can they do better?

We now use prediction accuracy as our metric:

```

accuracy = function(actual, predicted) {
  mean(actual == predicted)
}

data(Carseats)
Carseats$Sales = as.factor(ifelse(Carseats$Sales <= 8, "Low", "High"))
set.seed(2)
seat_idx = sample(1:nrow(Carseats), 200)
seat_trn = Carseats[seat_idx,]
seat_tst = Carseats[-seat_idx,]

```

### 26.2.1 Tree Model

```

seat_tree = tree(Sales ~ ., data = seat_trn)
set.seed(3)
seat_tree_cv = cv.tree(seat_tree, FUN = prune.misclass)

seat_tree_prune = prune.misclass(seat_tree, best = 9)
seat_prune_tst_pred = predict(seat_tree_prune, seat_tst, type = "class")

table(predicted = seat_prune_tst_pred, actual = seat_tst$Sales)

##           actual
## predicted High Low
##       High   60  22
##       Low    24  94

(tree_tst_acc = accuracy(predicted = seat_prune_tst_pred, actual = seat_tst$Sales))

## [1] 0.77

```

### 26.2.2 Logistic Regression

```

seat_glm = glm(Sales ~ ., data = seat_trn, family = "binomial")
seat_glm_tst_pred = ifelse(predict(seat_glm, seat_tst, "response") > 0.5,
                           "Low", "High")
table(predicted = seat_glm_tst_pred, actual = seat_tst$Sales)

##           actual
## predicted High Low
##       High   75   9
##       Low    9 107

(glm_tst_acc = accuracy(predicted = seat_glm_tst_pred, actual = seat_tst$Sales))

## [1] 0.91

```

### 26.2.3 Bagging

```

seat_bag = randomForest(Sales ~ ., data = seat_trn, mtry = 10,
                        importance = TRUE, ntrees = 500)
seat_bag

## 
## Call:
## randomForest(formula = Sales ~ ., data = seat_trn, mtry = 10,      importance = TRUE, ntrees = 500)
##           Type of random forest: classification
##                   Number of trees: 500
## No. of variables tried at each split: 10
##
##           OOB estimate of  error rate: 21.5%
## Confusion matrix:
##       High Low class.error
## High   51  29   0.3625000
## Low    14 106   0.1166667

seat_bag_tst_pred = predict(seat_bag, newdata = seat_tst)
table(predicted = seat_bag_tst_pred, actual = seat_tst$Sales)

##           actual
## predicted High Low
##       High   68  21
##       Low    16  95

(bag_tst_acc = accuracy(predicted = seat_bag_tst_pred, actual = seat_tst$Sales))

## [1] 0.815

```

### 26.2.4 Random Forest

For classification, the suggested `mtry` for a random forest is  $\sqrt{p}$ .

```

seat_forest = randomForest(Sales ~ ., data = seat_trn, mtry = 3, importance = TRUE, ntrees = 500)
seat_forest

## 
## Call:
## randomForest(formula = Sales ~ ., data = seat_trn, mtry = 3,      importance = TRUE, ntrees = 500)
##           Type of random forest: classification
##                   Number of trees: 500
## No. of variables tried at each split: 3
##
##           OOB estimate of  error rate: 22%
## Confusion matrix:
##       High Low class.error
## High   49  31   0.3875000
## Low    13 107   0.1083333

```

```

seat_forest_tst_perd = predict(seat_forest, newdata = seat_tst)
table(predicted = seat_forest_tst_perd, actual = seat_tst$Sales)

##           actual
## predicted High Low
##       High   63  16
##       Low    21 100

(forest_tst_acc = accuracy(predicted = seat_forest_tst_perd, actual = seat_tst$Sales))

## [1] 0.815

```

### 26.2.5 Boosting

To perform boosting, we modify the response to be 0 and 1 to work with `gbm`. Later we will use `caret` to fit `gbm` models, which will avoid this annoyance.

```

seat_trn_mod = seat_trn
seat_trn_mod$Sales = as.numeric(ifelse(seat_trn_mod$Sales == "Low", "0", "1"))

seat_boost = gbm(Sales ~ ., data = seat_trn_mod, distribution = "bernoulli",
                  n.trees = 5000, interaction.depth = 4, shrinkage = 0.01)
seat_boost

## gbm(formula = Sales ~ ., distribution = "bernoulli", data = seat_trn_mod,
##      n.trees = 5000, interaction.depth = 4, shrinkage = 0.01)
## A gradient boosted model with bernoulli loss function.
## 5000 iterations were performed.
## There were 10 predictors of which 10 had non-zero influence.

seat_boost_tst_pred = ifelse(predict(seat_boost, seat_tst, n.trees = 5000, "response") > 0.5,
                             "High", "Low")
table(predicted = seat_boost_tst_pred, actual = seat_tst$Sales)

##           actual
## predicted High Low
##       High   70  17
##       Low    14  99

(boost_tst_acc = accuracy(predicted = seat_boost_tst_pred, actual = seat_tst$Sales))

## [1] 0.845

```

### 26.2.6 Results

```

(seat_acc = data.frame(
  Model = c("Single Tree", "Logistic Regression", "Bagging", "Random Forest", "Boosting"),
  TestAccuracy = c(tree_tst_acc, glm_tst_acc, bag_tst_acc, forest_tst_acc, boost_tst_acc)
)
)
```

```

##          Model TestAccuracy
## 1      Single Tree      0.770
## 2 Logistic Regression   0.910
## 3      Bagging          0.815
## 4      Random Forest    0.815
## 5      Boosting         0.845

```

Here we see each of the ensemble methods performing better than a single tree, however, they still fall behind logistic regression. Sometimes a simple linear model will beat more complicated models! This is why you should always try a logistic regression for classification.

## 26.3 Tuning

So far we fit bagging, boosting and random forest models, but did not tune any of them, we simply used certain, somewhat arbitrary, parameters. Now we will see how to modify the tuning parameters to make these models better.

- Bagging: Actually just a subset of Random Forest with `mtry = p`.
- Random Forest: `mtry`
- Boosting: `n.trees`, `interaction.depth`, `shrinkage`, `n.minobsinnode`

We will use the `caret` package to accomplish this. Technically `ntrees` is a tuning parameter for both bagging and random forest, but `caret` will use 500 by default and there is no easy way to tune it. This will not make a big difference since for both we simply need “enough” and 500 seems to do the trick.

While `mtry` is a tuning parameter, there are suggested values for classification and regression:

- Regression:  $mtry = p/3$ .
- Classification:  $mtry = \sqrt{p}$ .

Also note that with these tree-based ensemble methods there are two resampling solutions for tuning the model:

- Out of Bag
- Cross-Validation

Using Out of Bag samples is advantageous with these methods as compared to Cross-Validation since it removes the need to refit the model and is thus much more computationally efficient. Unfortunately OOB methods cannot be used with `gbm` models. See the `caret` documentation for details.

### 26.3.1 Random Forest and Bagging

Here we setup training control for both OOB and cross-validation methods. Note we specify `verbose = FALSE` which suppresses output related to progress. You may wish to set this to TRUE when first tuning a model since it will give you an idea of how long the tuning process will take. (Which can sometimes be a long time.)

```

oob = trainControl(method = "oob")
cv_5 = trainControl(method = "cv", number = 5)

```

To tune a Random Forest in `caret` we will use `method = "rf"` which uses the `randomForest` function in the background. Here we elect to use the OOB training control that we created. We could also use Cross-Validation, however it will likely select a similar model, but requiring more time.

We setup a grid of `mtry` values which include all possible values since there are 10 predictors in the dataset. An `mtry` of 10 is actually bagging.

```
dim(seat_trn)

## [1] 200 11

rf_grid = expand.grid(mtry = 1:10)
set.seed(825)
seat_rf_tune = train(Sales ~ ., data = seat_trn,
                      method = "rf",
                      trControl = oob,
                      verbose = FALSE,
                      tuneGrid = rf_grid)
seat_rf_tune

## Random Forest
##
## 200 samples
## 10 predictor
## 2 classes: 'High', 'Low'
##
## No pre-processing
## Resampling results across tuning parameters:
##
##   mtry  Accuracy  Kappa
##   1    0.750    0.4318182
##   2    0.785    0.5295405
##   3    0.785    0.5315904
##   4    0.805    0.5824411
##   5    0.785    0.5356371
##   6    0.810    0.5957447
##   7    0.810    0.5922747
##   8    0.805    0.5842217
##   9    0.785    0.5396146
##  10   0.795    0.5591398
##
## Accuracy was used to select the optimal model using the largest value.
## The final value used for the model was mtry = 6.

accuracy(predict(seat_rf_tune, seat_tst), seat_tst$Sales)

## [1] 0.81
```

The results returned are based on the OOB samples. (Coincidentally, the test accuracy is the same as the best accuracy found using OOB samples.) Note that when using OOB, for some reason the default plot is not what you would expect and is not at all useful. (Which is why it is omitted here.)

```
seat_rf_tune$bestTune
```

```
##   mtry
## 6    6
```

Based on these results, we would select the random forest model with an `mtry` of 6. Note that based on the OOB estimates, the bagging model is expected to perform worse than this select model, however, based on our results above, that is not what we find to be true in our test set.

Also note that `method = "ranger"` would also fit a random forest model. Ranger is a newer R package for random forests that has been shown to be much faster, especially when there are a larger number of predictors.

### 26.3.2 Boosting

We now tune a boosted tree model. We will use the cross-validation tune control setup above. We will fit the model using `gbm` with `caret`.

To setup the tuning grid, we must specify four parameters to tune:

- `interaction.depth`: How many splits to use with each tree.
- `n.trees`: The number of trees to use.
- `shrinkage`: The shrinkage parameters, which controls how fast the method learns.
- `n.minobsinnode`: The minimum number of observations in a node of the tree. (`caret` requires us to specify this. This is actually a tuning parameter of the trees, not boosting, and we would normally just accept the default.)

Finally, `expand.grid` comes in handy, as we can specify a vector of values for each parameter, then we get back a matrix of all possible combinations.

```
gbm_grid = expand.grid(interaction.depth = 1:5,
                      n.trees = (1:6) * 500,
                      shrinkage = c(0.001, 0.01, 0.1),
                      n.minobsinnode = 10)
```

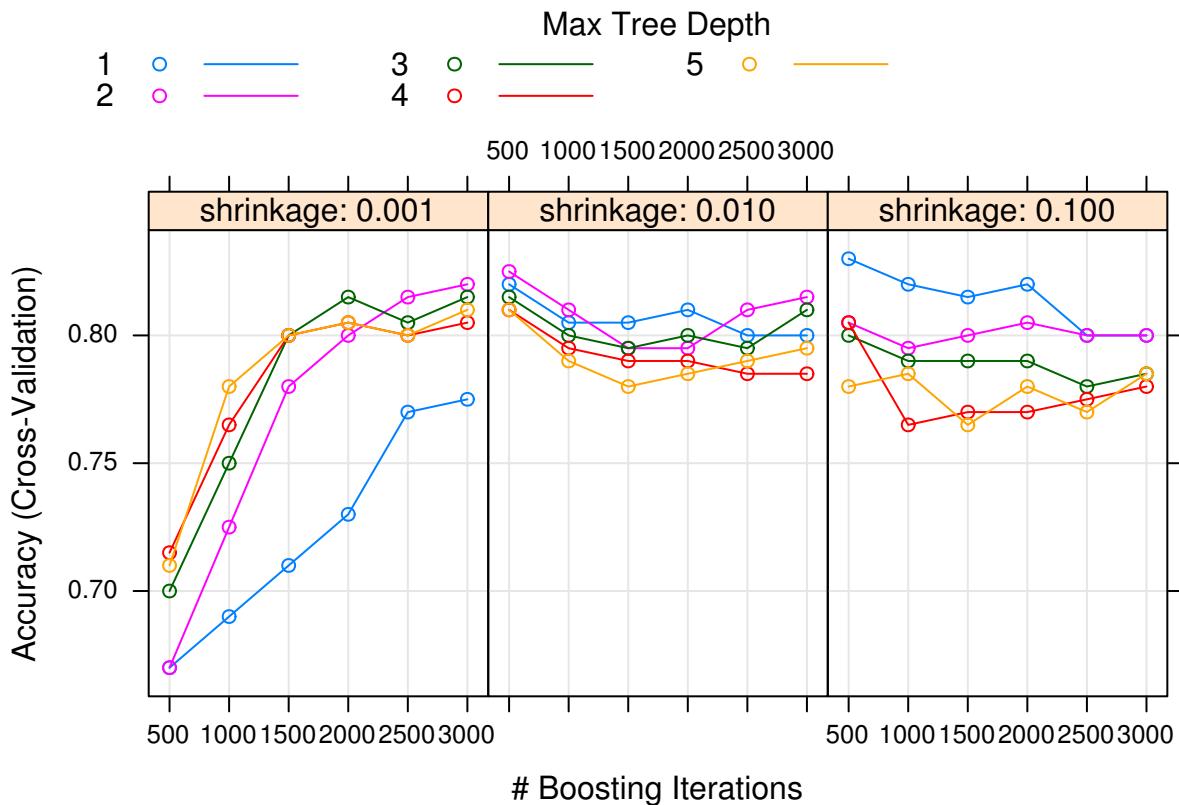
We now train the model using all possible combinations of the tuning parameters we just specified.

```
seat_gbm_tune = train(Sales ~ ., data = seat_trn,
                      method = "gbm",
                      trControl = cv_5,
                      verbose = FALSE,
                      tuneGrid = gbm_grid)
```

The additional `verbose = FALSE` in the `train` call suppresses additional output from each `gbm` call.

By default, calling `plot` here will produce a nice graphic of the results.

```
#seat_gbm_tune
plot(seat_gbm_tune)
```



```
accuracy(predict(seat_gbm_tune, seat_tst), seat_tst$Sales)
```

```
## [1] 0.845
```

We see our tuned model does no better on the test set than the arbitrary boosted model we had fit above, with the slightly different parameters seen below. We could perhaps try a larger tuning grid, but at this point it seems unlikely that we could find a much better model. There seems to be no way to get a tree method to out-perform logistic regression in this dataset.

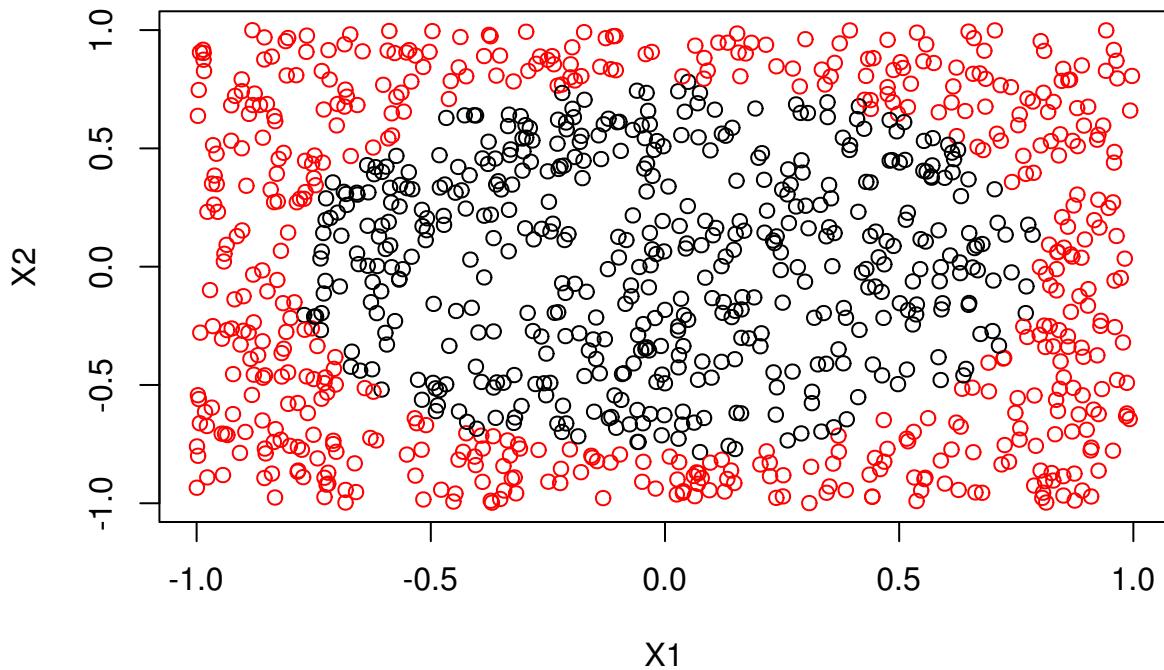
```
seat_gbm_tune$bestTune
```

```
##      n.trees interaction.depth shrinkage n.minobsinnode
## 61      500                  1       0.1              10
```

## 26.4 Tree versus Ensemble Boundaries

```
library(mlbench)
set.seed(42)
sim_trn = mlbench.circle(n = 1000, d = 2)
sim_trn = data.frame(sim_trn$x, class = as.factor(sim_trn$classes))
sim_tst = mlbench.circle(n = 1000, d = 2)
sim_tst = data.frame(sim_tst$x, class = as.factor(sim_tst$classes))
```

```
plot(sim_trn$X1, sim_trn$X2, col = sim_trn$class,
     xlab = "X1", ylab = "X2")
```

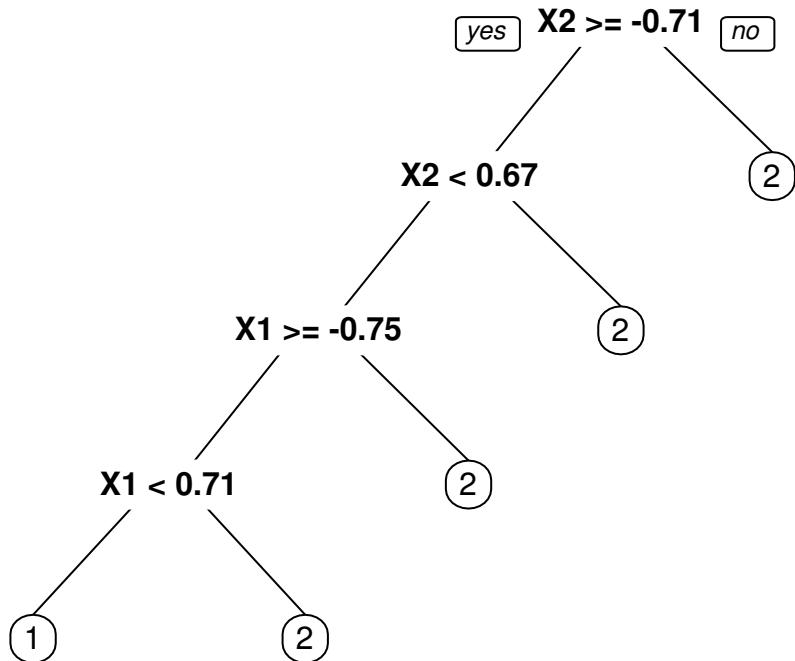


```
cv_5 = trainControl(method = "cv", number = 5)
oob  = trainControl(method = "oob")
```

```
sim_tree_cv = train(class ~ .,
                     data = sim_trn,
                     trControl = cv_5,
                     method = "rpart")
```

```
## Loading required package: rpart
```

```
library(rpart.plot)
prp(sim_tree_cv$finalModel)
```



```
rf_grid = expand.grid(mtry = c(1, 2))
sim_rf_oob = train(class ~ .,
                    data = sim_trn,
                    trControl = oob,
                    tuneGrid = rf_grid)
```

```
gbm_grid = expand.grid(interaction.depth = 1:5,  
                      n.trees = (1:6) * 500,  
                      shrinkage = c(0.001, 0.01, 0.1),  
                      n.minobsinnode = 10)
```

```
sim_gbm_cv = train(class ~ .,  
                    data = sim_trn,  
                    method = "gbm",  
                    trControl = cv_5,  
                    verbose = FALSE,  
                    tuneGrid = gbm_grid)
```

```

plot_grid = expand.grid(
  X1 = seq(min(sim_tst$X1), max(sim_tst$X1), by = 0.01),
  X2 = seq(min(sim_tst$X2), max(sim_tst$X2), by = 0.01)
)

```

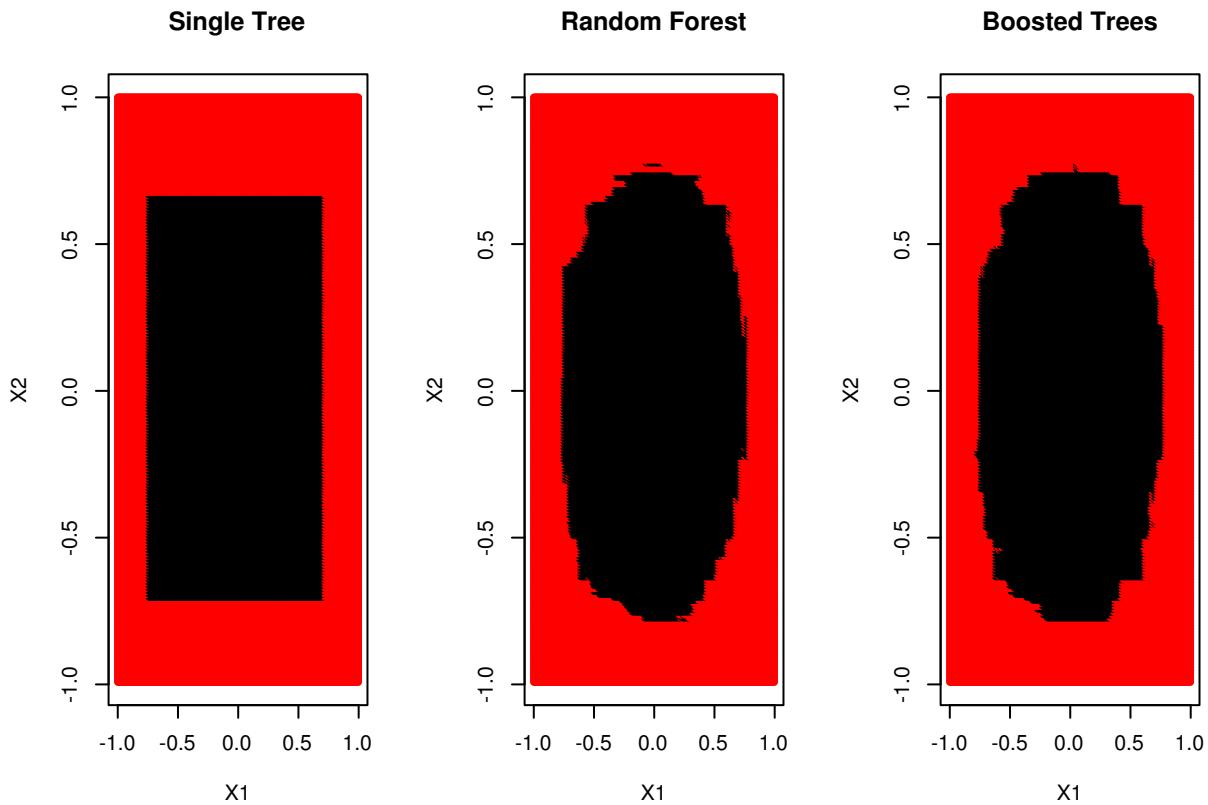
```
tree_pred = predict(sim_tree_cv, plot_grid)
rf_pred   = predict(sim_rf_oob, plot_grid)
gbm_pred  = predict(sim_gbm_cv, plot_grid)
```

```
par(mfrow = c(1, 3))
plot(plot_grid$X1, plot_grid$X2, col = tree_pred,
      xlab = "X1", ylab = "X2", pch = 20, main = "Single Tree")
plot(plot_grid$X1, plot_grid$X2, col = rf_pred,
```

```

  xlab = "X1", ylab = "X2", pch = 20, main = "Random Forest")
plot(plot_grid$X1, plot_grid$X2, col = gbm_pred,
  xlab = "X1", ylab = "X2", pch = 20, main = "Boosted Trees")

```



## 26.5 External Links

- Classification and Regression by `randomForest` - Introduction to the `randomForest` package in R news.
- `ranger`: A Fast Implementation of Random Forests - Alternative package for fitting random forests with potentially better speed.
- On `ranger`'s `respect.unordered.factors` Argument - A note on handling of categorical variables with random forests.
- Extremely Randomized Trees
- `extraTrees` Method for Classificationand Regression
- XGBoost - Scalable and Flexible Gradient Boosting
- XGBoost R Tutorial

## 26.6 RMarkdown

The RMarkdown file for this chapter can be found [here](#). The file was created using R version 3.3.2 and the following packages:

- Base Packages, Attached

```

## [1] "methods"    "parallel"    "splines"     "stats"       "graphics"   "grDevices"
## [7] "utils"      "datasets"    "base"

```

- Additional Packages, Attached

```
## [1] "rpart.plot"     "rpart"          "mlbench"        "plyr"  
## [5] "caret"          "ggplot2"         "gbm"            "lattice"  
## [9] "survival"        "randomForest"    "ISLR"           "MASS"  
## [13] "tree"
```

- Additional Packages, Not Attached

```
## [1] "Rcpp"           "compiler"       "nloptr"         "class"  
## [5] "iterators"      "tools"          "lme4"           "digest"  
## [9] "evaluate"       "tibble"         "gtable"         "nlme"  
## [13] "mgcv"           "Matrix"         "foreach"        "yaml"  
## [17] "SparseM"        "e1071"          "stringr"        "knitr"  
## [21] "MatrixModels"   "stats4"         "nnet"           "rprojroot"  
## [25] "grid"           "rmarkdown"      "bookdown"       "minqa"  
## [29] "car"             "reshape2"       "magrittr"       "backports"  
## [33] "scales"          "codetools"      "ModelMetrics"   "htmltools"  
## [37] "pbkrtest"        "assertthat"     "colorspace"     "quantreg"  
## [41] "stringi"         "lazyeval"       "munsell"
```

# Chapter 27

# Support Vector Machines

## 27.1 R Packages

```
library(randomForest)
library(caret)
library(kernlab)
```

For working with SVMs in R we will use the kernlab package instead of e1071. For examples of e1071 see the relevant chapter in ISL. We do not discuss the details of the method, however show how the method can be tuned.

## 27.2 Classification

SVMs are mostly used for classification. Note that they can be modified for regression but we will not do that here. Since we are performing classification, we will use accuracy as our metric.

```
accuracy = function(actual, predicted) {
  mean(actual == predicted)
}
```

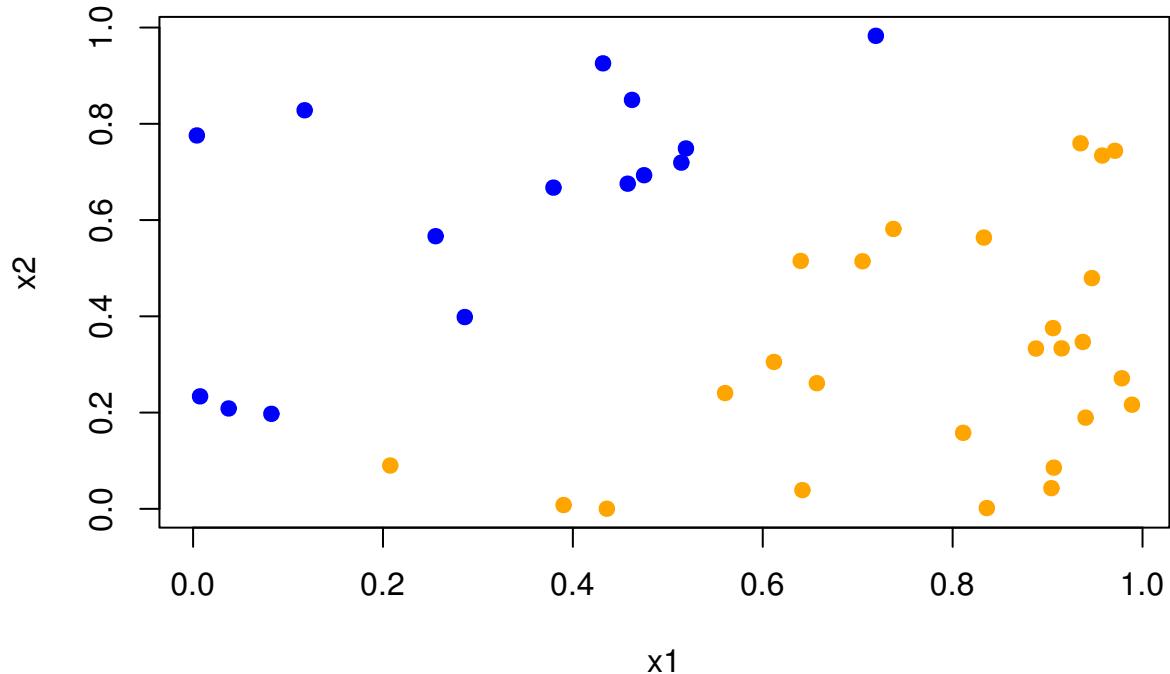
## 27.3 Linear, Separable Example

### 27.3.1 Data Simulation

```
sim_sep = function(n = 1000) {
  x1 = runif(n)
  x2 = runif(n)
  keep = x1 + 0.1 < x2 | x1 - 0.1 > x2
  x1 = x1[keep]
  x2 = x2[keep]
  y = 1 * (x1 - x2 > 0)
  y = ifelse(y == 1, "Orange", "Blue")
```

```
  data.frame(y = as.factor(y), x1 = x1, x2 = x2)
}
```

```
set.seed(42)
train_data = sim_sep(n = 50)
plot(x2 ~ x1, data = train_data, col = as.character(y), pch = 19)
```



```
test_data = sim_sep(n = 500)
str(train_data)
```

```
## 'data.frame':    41 obs. of  3 variables:
## $ y : Factor w/ 2 levels "Blue","Orange": 2 2 1 2 1 2 2 1 1 2 ...
## $ x1: num  0.915 0.937 0.286 0.642 0.519 ...
## $ x2: num  0.3334 0.3467 0.3985 0.0389 0.7488 ...
```

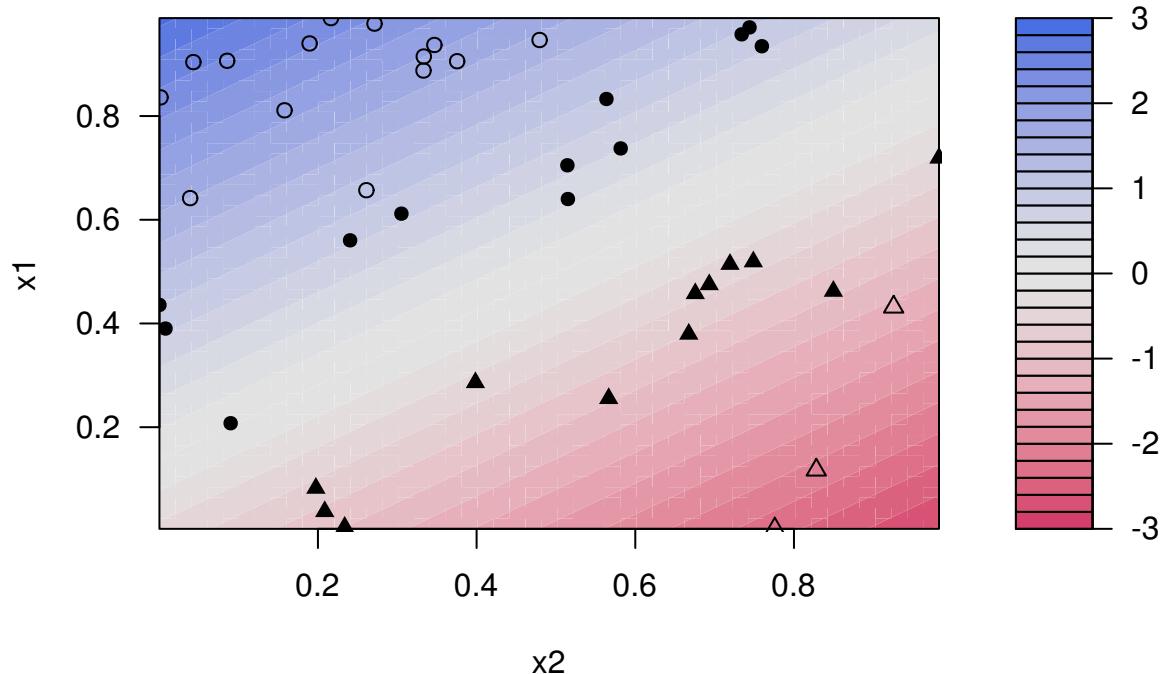
### 27.3.2 Linear Kernel, Parameter C

```
lin_svm_fit = ksvm(y ~ ., data = train_data, kernel = 'vanilladot', C = 0.1)
```

```
## Setting default kernel parameters
```

```
plot(lin_svm_fit, data = train_data)
```

### SVM classification plot



```
# train accuracy
accuracy(actual = train_data$y,
         predicted = predict(lin_svm_fit, train_data))
```

```
## [1] 1
```

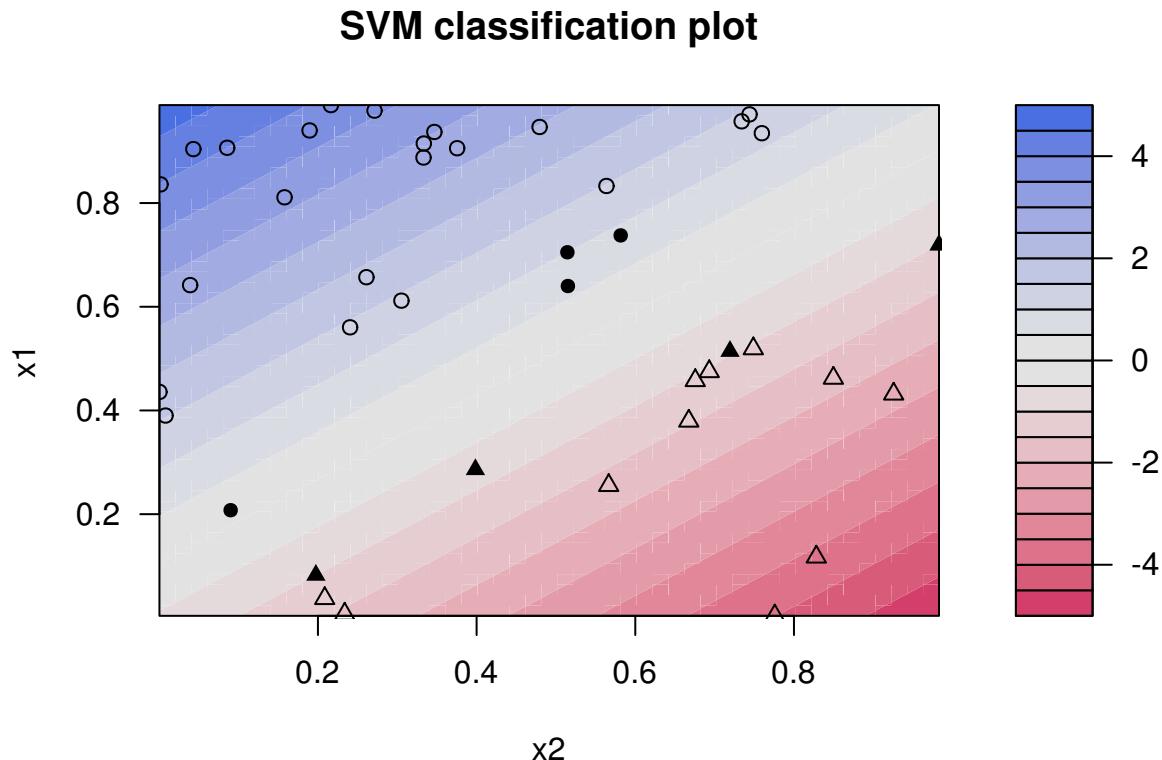
```
# test accuracy
accuracy(actual = test_data$y,
         predicted = predict(lin_svm_fit, test_data))
```

```
## [1] 0.9872449
```

```
lin_svm_fit = ksvm(y ~ ., data = train_data, kernel = 'vanilladot', C = 1)
```

```
## Setting default kernel parameters
```

```
plot(lin_svm_fit, data = train_data)
```



```
# train accuracy
accuracy(actual = train_data$y,
         predicted = predict(lin_svm_fit, train_data))
```

```
## [1] 1
```

```
# test accuracy
accuracy(actual = test_data$y,
         predicted = predict(lin_svm_fit, test_data))
```

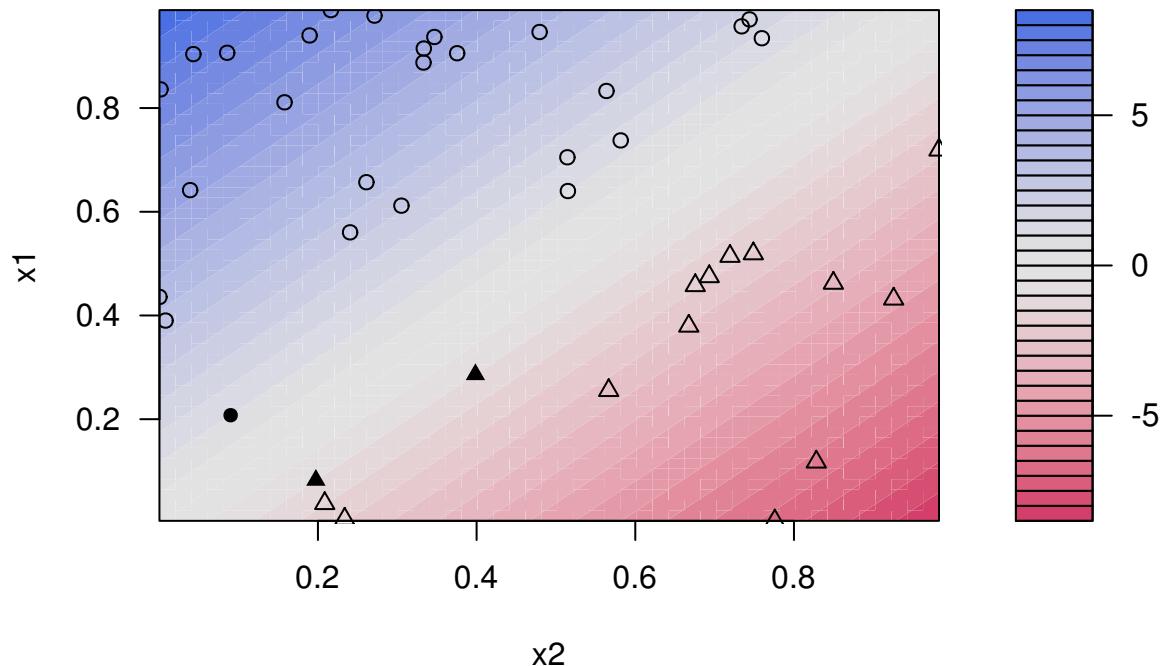
```
## [1] 1
```

```
lin_svm_fit = ksvm(y ~ ., data = train_data, kernel = 'vanilladot', C = 10)
```

```
## Setting default kernel parameters
```

```
plot(lin_svm_fit, data = train_data)
```

### SVM classification plot



```
# train accuracy
accuracy(actual = train_data$y,
         predicted = predict(lin_svm_fit, train_data))
```

```
## [1] 1
```

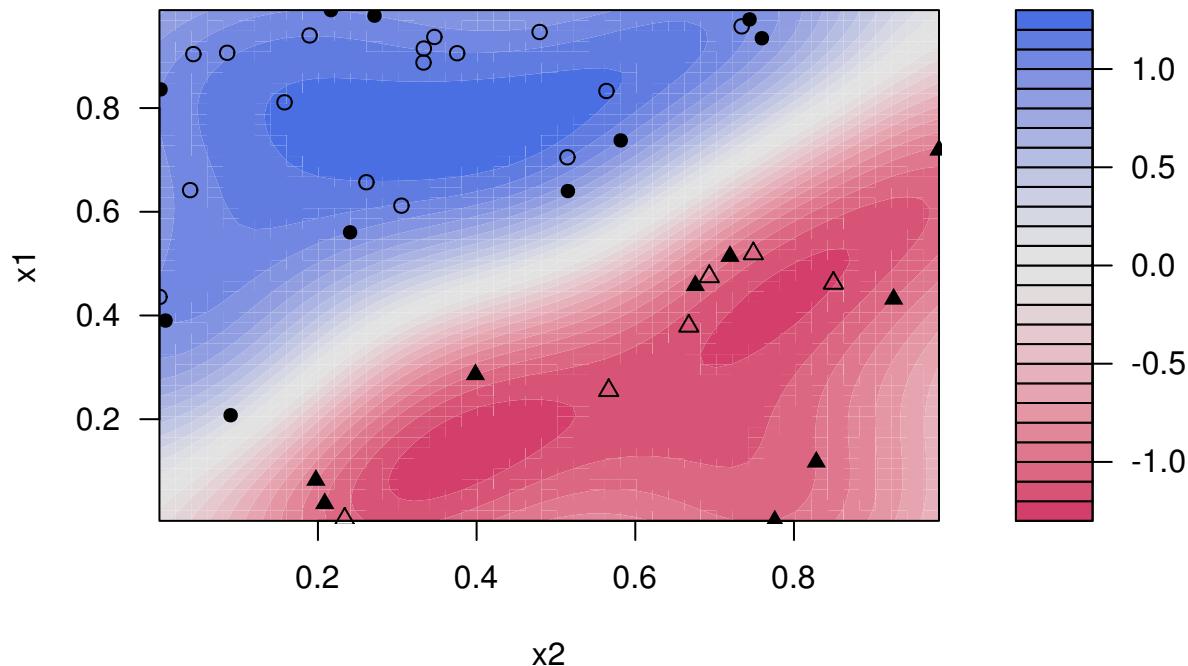
```
# test accuracy
accuracy(actual = test_data$y,
         predicted = predict(lin_svm_fit, test_data))
```

```
## [1] 1
```

#### 27.3.3 Radial Kernel

```
set.seed(42)
rad_svm_fit = ksvm(y ~ ., data = train_data, kernel = 'rbfdot', C = 1)
plot(rad_svm_fit, data = train_data)
```

## SVM classification plot



```
# train accuracy
accuracy(actual = train_data$y,
         predicted = predict(rad_svm_fit, train_data))
```

```
## [1] 1
```

```
# test accuracy
accuracy(actual = test_data$y,
         predicted = predict(rad_svm_fit, test_data))
```

```
## [1] 1
```

### 27.3.4 Tuning with caret

```
svm_grid = expand.grid(C = c(2 ^ (-5:5)))
svm_control = trainControl(method = "cv", number = 5,
                           returnResamp = "all", verbose = FALSE)

set.seed(42)
lin_svm_fit = train(y ~ ., data = train_data, method = "svmLinear",
                     trControl = svm_control, tuneGrid = svm_grid)

lin_svm_fit
```

```
## Support Vector Machines with Linear Kernel
##
```

```

## 41 samples
## 2 predictor
## 2 classes: 'Blue', 'Orange'
##
## No pre-processing
## Resampling: Cross-Validated (5 fold)
## Summary of sample sizes: 33, 33, 33, 33, 32
## Resampling results across tuning parameters:
##
##     C      Accuracy   Kappa
## 0.03125  0.850    0.6197802
## 0.06250  0.950    0.8928571
## 0.12500  0.975    0.9500000
## 0.25000  0.975    0.9500000
## 0.50000  0.975    0.9500000
## 1.00000  1.000    1.0000000
## 2.00000  0.975    0.9500000
## 4.00000  1.000    1.0000000
## 8.00000  1.000    1.0000000
## 16.00000 1.000    1.0000000
## 32.00000 1.000    1.0000000
##
## Accuracy was used to select the optimal model using the largest value.
## The final value used for the model was C = 1.

```

```
lin_svm_fit$bestTune
```

```

##     C
## 6 1

# train accuracy
accuracy(actual = train_data$y,
         predicted = predict(lin_svm_fit, train_data))

## [1] 1

# test accuracy
accuracy(actual = test_data$y,
         predicted = predict(lin_svm_fit, test_data))

## [1] 1

```

### 27.3.5 Compare: Random Forest

```

set.seed(42)
rf_grid = expand.grid(mtry = 1:2)
rf_fit = train(y ~ ., data = train_data, method = "rf",
               trControl = svm_control, tuneGrid = rf_grid)
rf_fit$bestTune

```

```

##     mtry
## 1      1

# train accuracy
accuracy(actual = train_data$y,
          predicted = predict(rf_fit, train_data))

## [1] 1

# test accuracy
accuracy(actual = test_data$y,
          predicted = predict(rf_fit, test_data))

## [1] 0.9591837

```

## 27.4 Non-Linear, Non-Separable Example

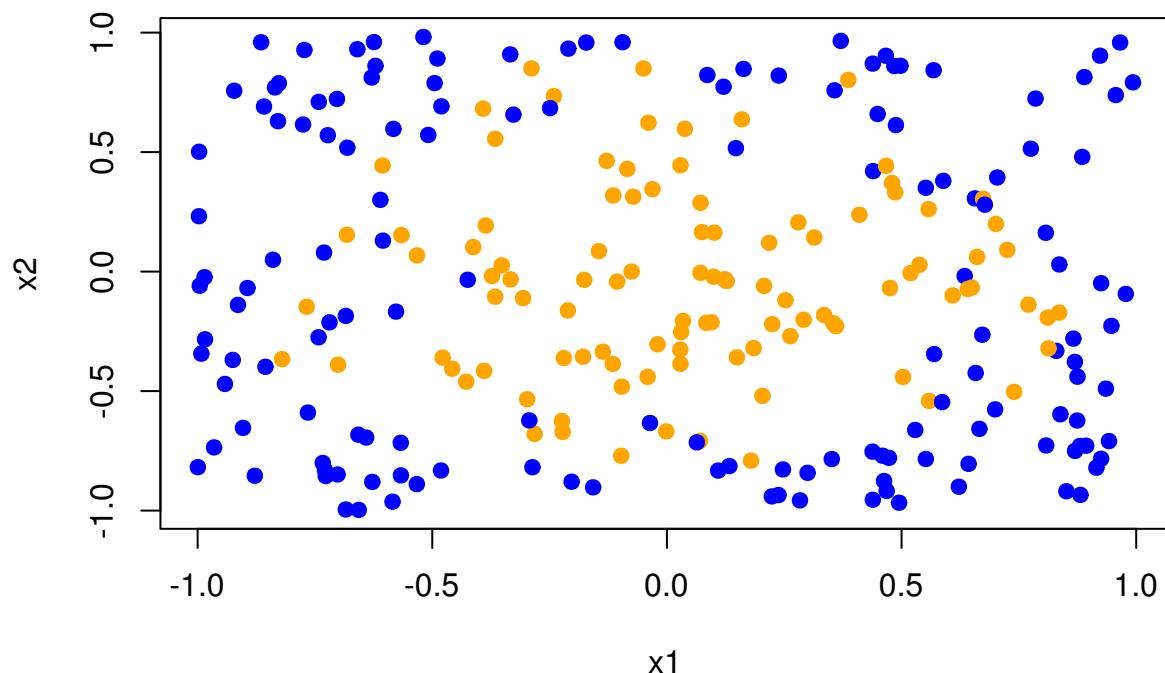
### 27.4.1 Data Simulation

```

sim_rad = function(n = 1000) {
  x1 = runif(n, -1, 1)
  x2 = runif(n, -1, 1)
  y = 1 * (x1 ^ 2 + x2 ^ 2 + rnorm(n, 0, 0.25) < 0.5)
  y = ifelse(y == 1, "Orange", "Blue")
  data.frame(y = as.factor(y), x1 = x1, x2 = x2)
}

set.seed(42)
train_data = sim_rad(n = 250)
plot(x2 ~ x1, data = train_data, col = as.character(y), pch = 19)

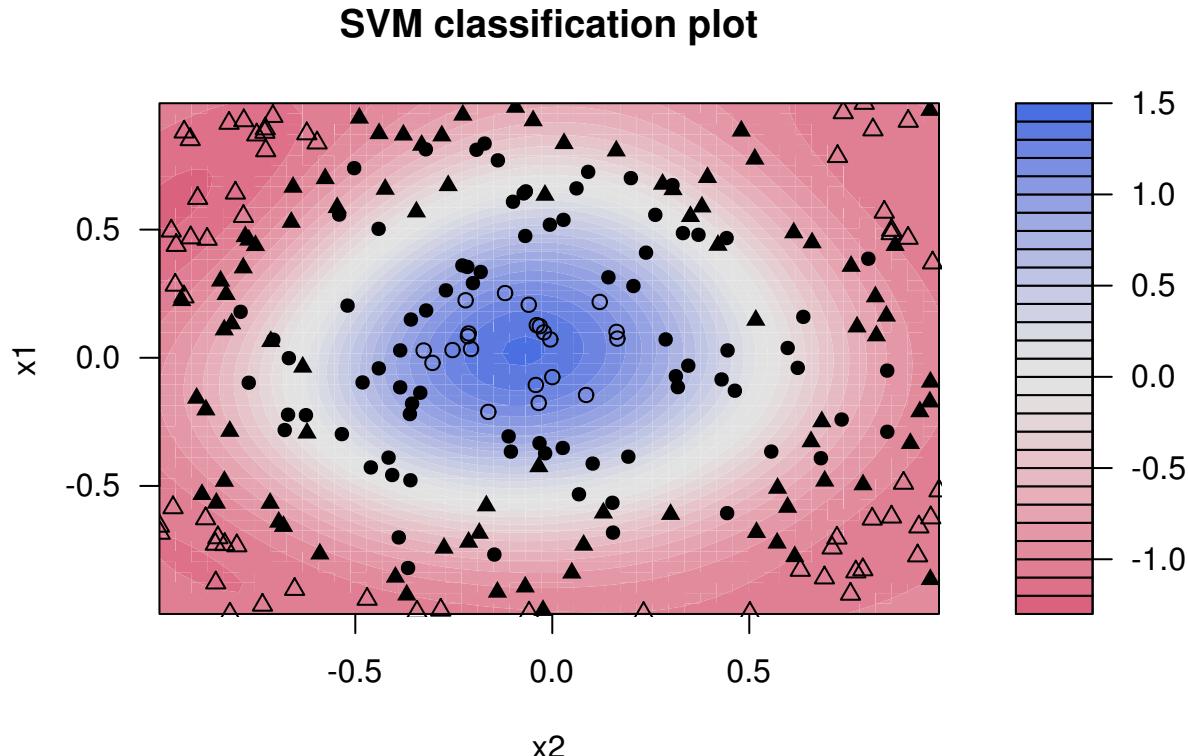
```



```
test_data = sim_rad(n = 2000)
```

#### 27.4.2 Radial Kernel, Parameter C

```
rad_svm_fit = ksvm(y ~ ., data = train_data, kernel = 'rbfdot',
                    C = 0.1, kpar = list(sigma = 1))
plot(rad_svm_fit, data = train_data)
```



```
# train accuracy
accuracy(actual = train_data$y,
         predicted = predict(rad_svm_fit, train_data))
```

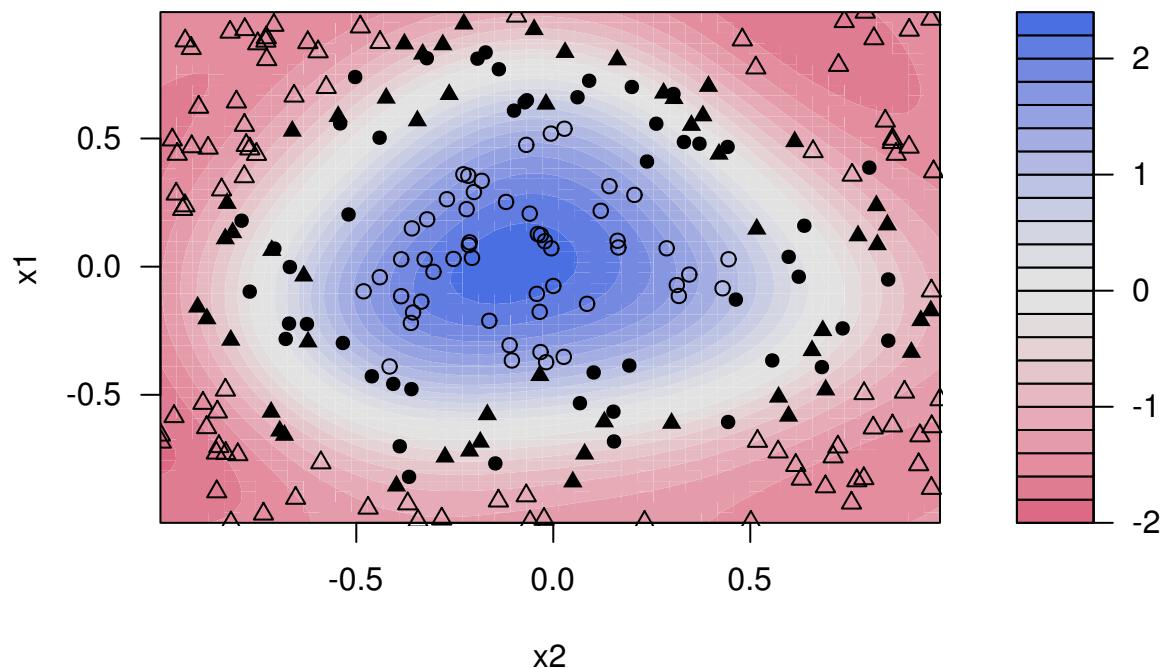
```
## [1] 0.852
```

```
# test accuracy
accuracy(actual = test_data$y,
         predicted = predict(rad_svm_fit, test_data))
```

```
## [1] 0.812
```

```
rad_svm_fit = ksvm(y ~ ., data = train_data, kernel = 'rbfdot',
                    C = 1, kpar = list(sigma = 1))
plot(rad_svm_fit, data = train_data)
```

## SVM classification plot



```
# train accuracy
accuracy(actual = train_data$y,
         predicted = predict(rad_svm_fit, train_data))
```

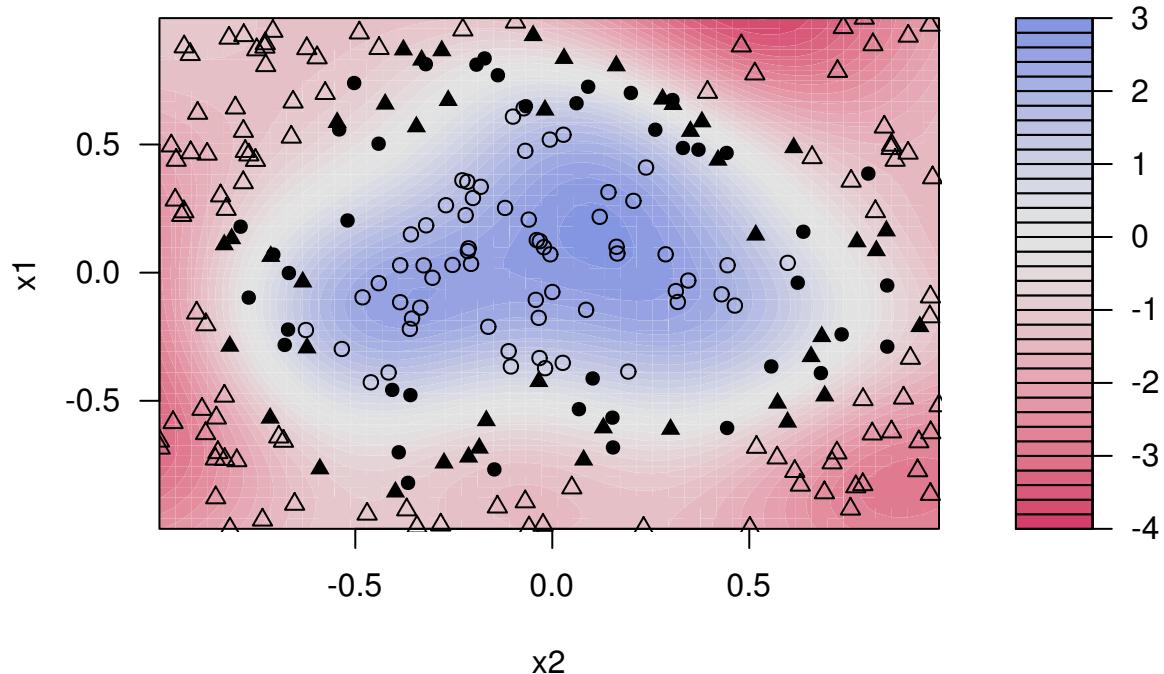
```
## [1] 0.876
```

```
# test accuracy
accuracy(actual = test_data$y,
         predicted = predict(rad_svm_fit, test_data))
```

```
## [1] 0.833
```

```
rad_svm_fit = ksvm(y ~ ., data = train_data, kernel = 'rbfdot',
                    C = 10, kpar = list(sigma = 1))
plot(rad_svm_fit, data = train_data)
```

### SVM classification plot



```
# train accuracy
accuracy(actual = train_data$y,
         predicted = predict(rad_svm_fit, train_data))
```

```
## [1] 0.884
```

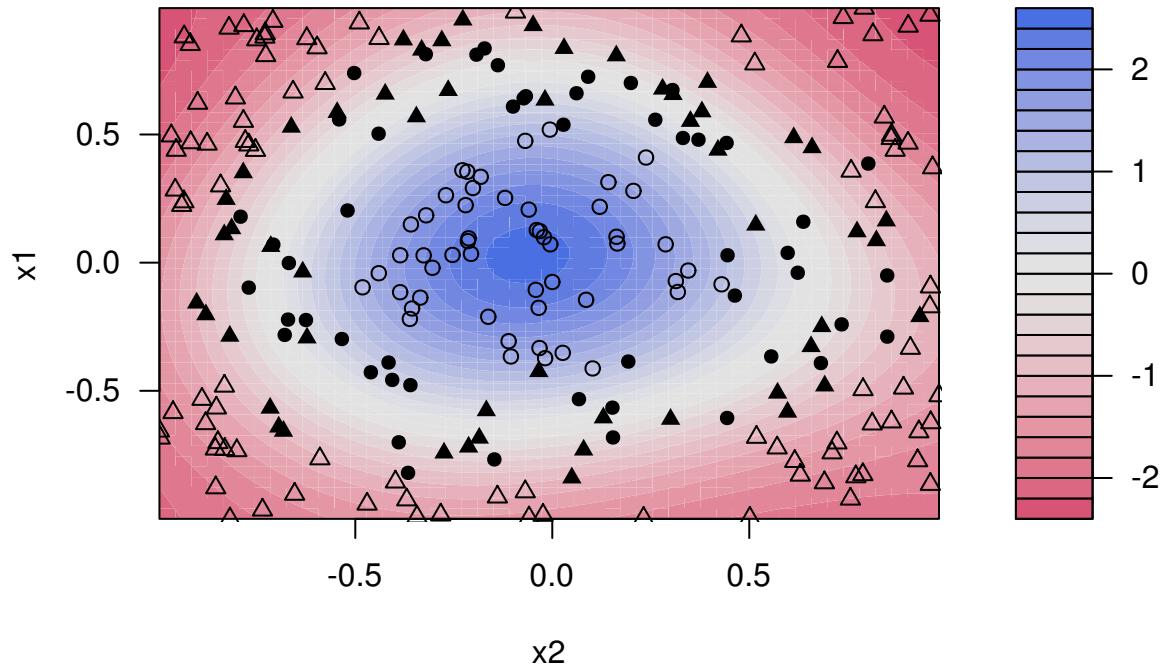
```
# test accuracy
accuracy(actual = test_data$y,
         predicted = predict(rad_svm_fit, test_data))
```

```
## [1] 0.8285
```

#### 27.4.3 Radial Kernel, Parameter sigma

```
rad_svm_fit = ksvm(y ~ ., data = train_data, kernel = 'rbfdot',
                     C = 1, kpar = list(sigma = 0.5))
plot(rad_svm_fit, data = train_data)
```

## SVM classification plot



```
# train accuracy
accuracy(actual = train_data$y,
         predicted = predict(rad_svm_fit, train_data))
```

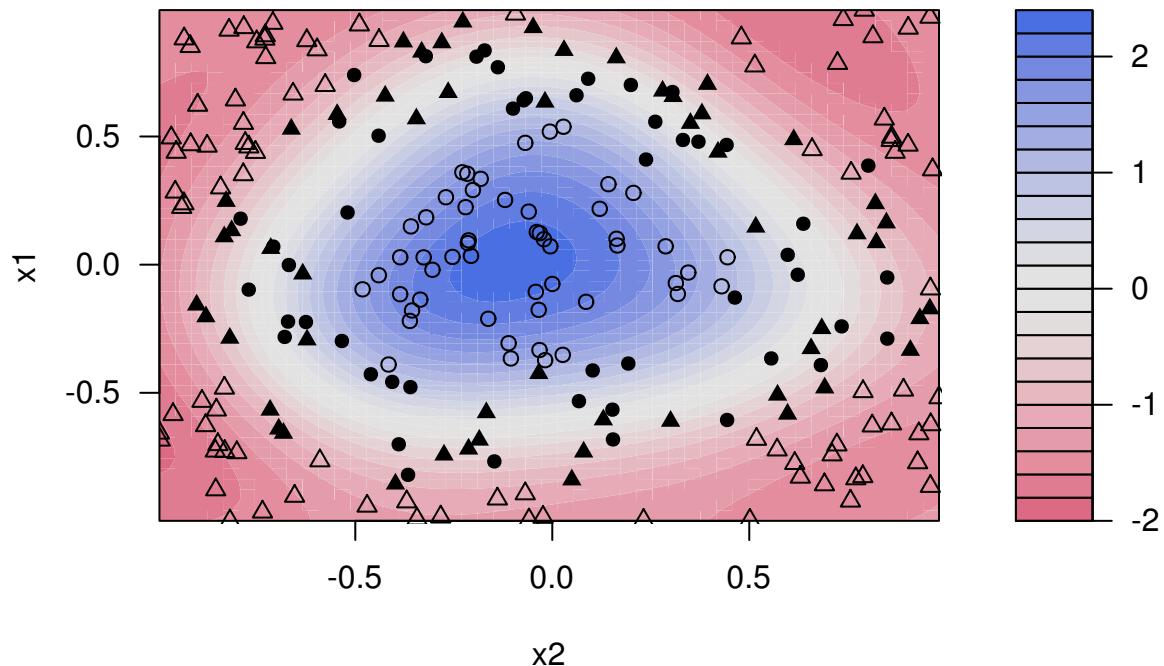
```
## [1] 0.864
```

```
# test accuracy
accuracy(actual = test_data$y,
         predicted = predict(rad_svm_fit, test_data))
```

```
## [1] 0.8365
```

```
rad_svm_fit = ksvm(y ~ ., data = train_data, kernel = 'rbfdot',
                    C = 1, kpar = list(sigma = 1))
plot(rad_svm_fit, data = train_data)
```

### SVM classification plot



```
# train accuracy
accuracy(actual = train_data$y,
         predicted = predict(rad_svm_fit, train_data))
```

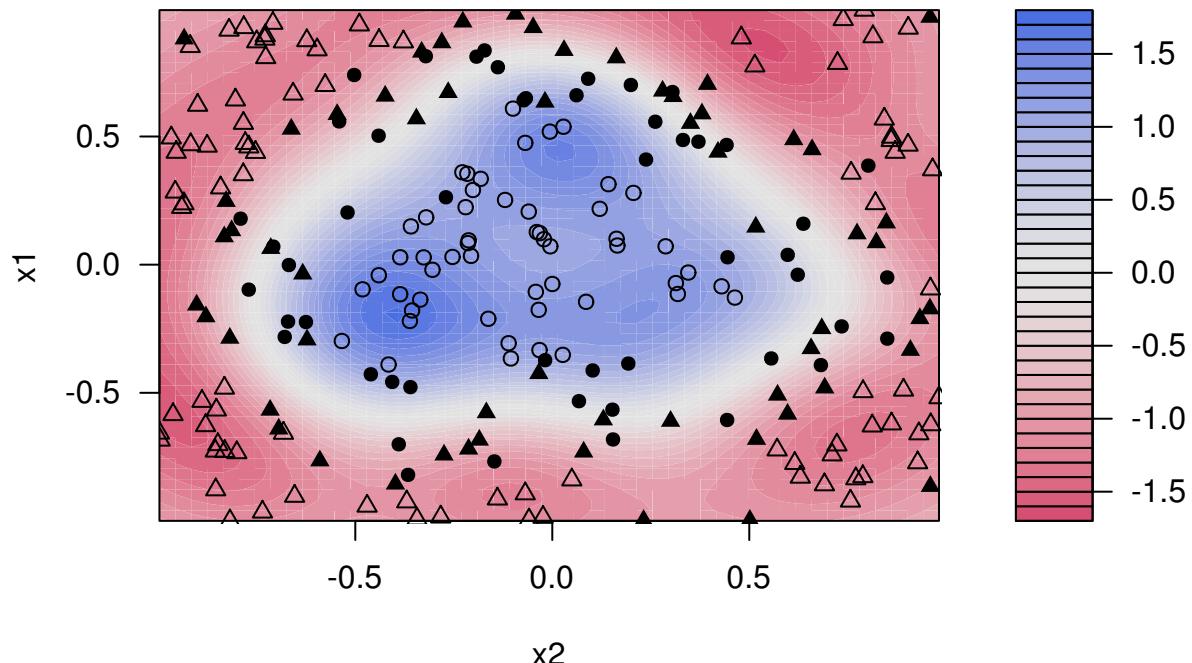
```
## [1] 0.876
```

```
# test accuracy
accuracy(actual = test_data$y,
         predicted = predict(rad_svm_fit, test_data))
```

```
## [1] 0.833
```

```
rad_svm_fit = ksvm(y ~ ., data = train_data, kernel = 'rbfdot',
                    C = 1, kpar = list(sigma = 2))
plot(rad_svm_fit, data = train_data)
```

## SVM classification plot



```
# train accuracy
accuracy(actual = train_data$y,
         predicted = predict(rad_svm_fit, train_data))
```

```
## [1] 0.884
```

```
# test accuracy
accuracy(actual = test_data$y,
         predicted = predict(rad_svm_fit, test_data))
```

```
## [1] 0.828
```

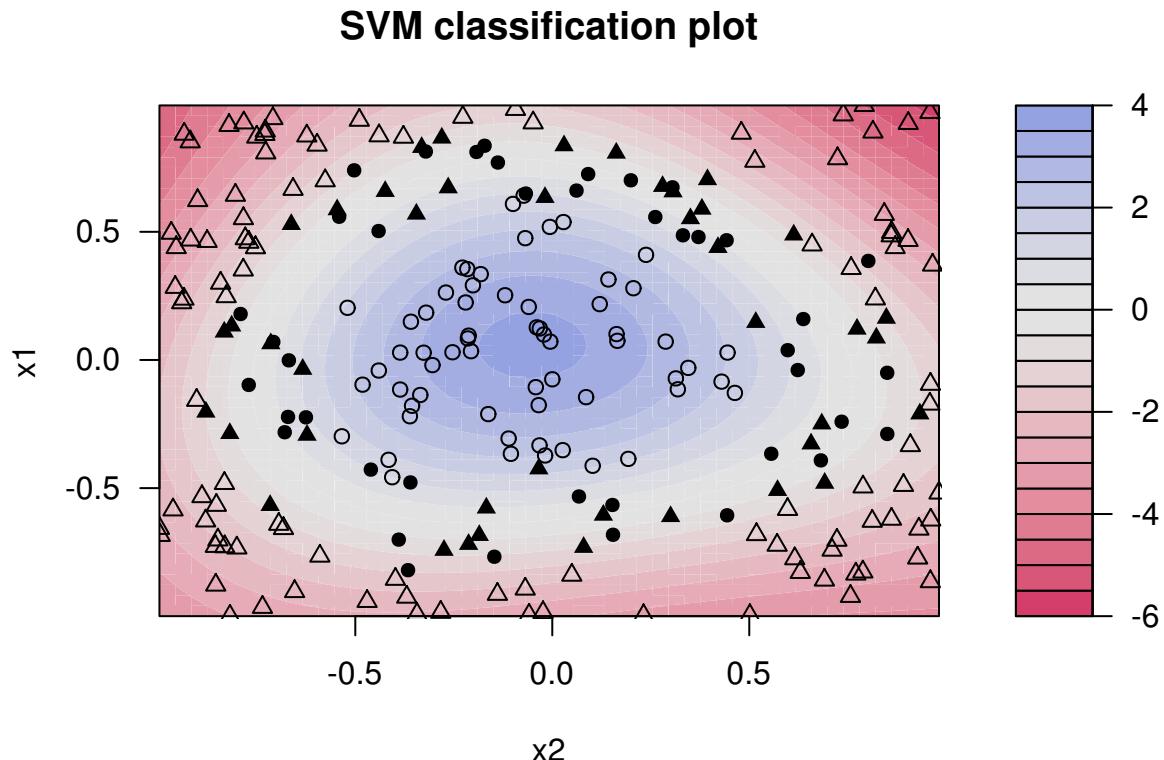
### 27.4.4 Radial Kernel, Tuning

```
svm_grid = expand.grid( C = c(2 ^ (-5:5)),
                        sigma = c(2 ^ (-3:3)))

set.seed(42)
rad_svm_fit = train(y ~ ., data = train_data, method = "svmRadial",
                     trControl = svm_control, tuneGrid = svm_grid)
#rad_svm_fit
rad_svm_fit$bestTune

##      sigma   C
## 65  0.25 16
```

```
rad_svm_fit = ksvm(y ~ ., data = train_data, kernel = 'rbfdot',
                    C = 16, kpar = list(sigma = 0.25))
plot(rad_svm_fit, data = train_data)
```



```
# train accuracy
accuracy(actual = train_data$y,
         predicted = predict(rad_svm_fit, train_data))
```

```
## [1] 0.876
```

```
# test accuracy
accuracy(actual = test_data$y,
         predicted = predict(rad_svm_fit, test_data))
```

```
## [1] 0.838
```

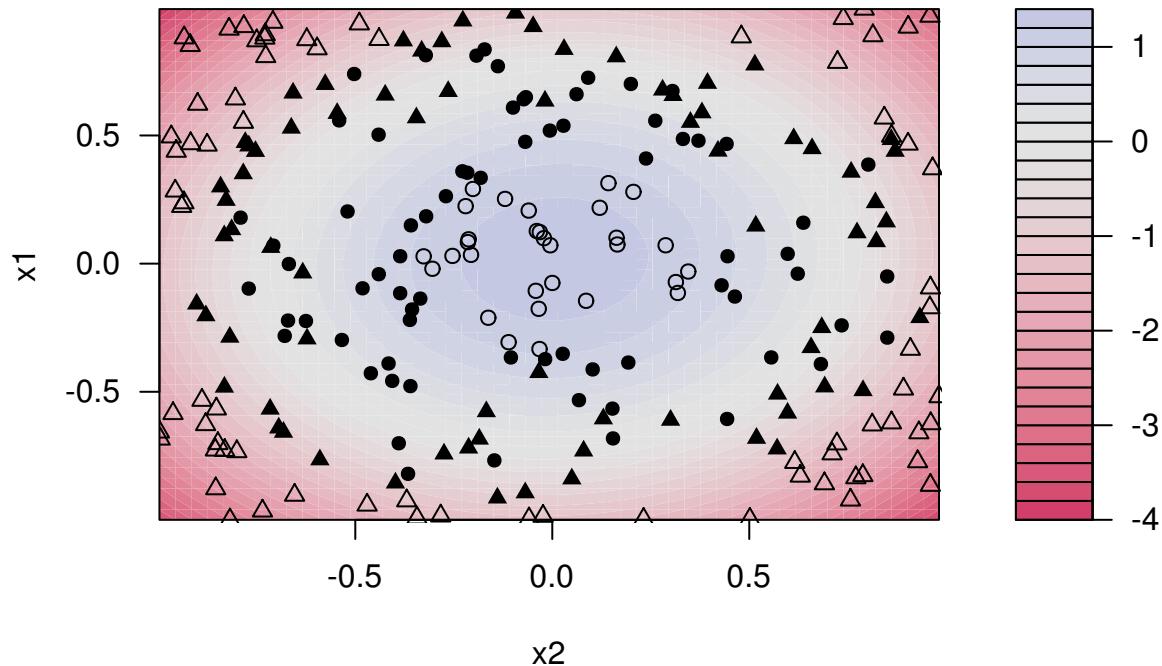
#### 27.4.5 Polynomial Kernel, Tuning

```
set.seed(42)
poly_svm_fit = train(y ~ ., data = train_data, method = "svmPoly",
                      trControl = svm_control)
#poly_svm_fit
poly_svm_fit$bestTune
```

```
##      degree scale C
## 27          3   0.1 1
```

```
poly_svm_fit = ksvm(y ~ ., data = train_data, kernel = 'polydot',
                     C = 1, kpar = list(scale = 0.1, degree = 3))
plot(poly_svm_fit, data = train_data)
```

## SVM classification plot



```
# train accuracy
accuracy(actual = train_data$y,
         predicted = predict(poly_svm_fit, train_data))
```

```
## [1] 0.864
```

```
# test accuracy
accuracy(actual = test_data$y,
         predicted = predict(poly_svm_fit, test_data))
```

```
## [1] 0.8425
```

### 27.4.6 Linear Kernel, Tuning

```
svm_grid = expand.grid(C = c(2 ^ (-5:5)))
set.seed(42)
lin_svm_fit = train(y ~ ., data = train_data, method = "svmLinear",
                     trControl = svm_control, tuneGrid = svm_grid)
lin_svm_fit
```

```
## Support Vector Machines with Linear Kernel
```

```
##  
## 250 samples  
##   2 predictor  
##   2 classes: 'Blue', 'Orange'  
##  
## No pre-processing  
## Resampling: Cross-Validated (5 fold)  
## Summary of sample sizes: 200, 200, 201, 199, 200  
## Resampling results across tuning parameters:  
##  
##   C      Accuracy   Kappa  
##   0.03125  0.5920144  0  
##   0.06250  0.5920144  0  
##   0.12500  0.5920144  0  
##   0.25000  0.5920144  0  
##   0.50000  0.5920144  0  
##   1.00000  0.5920144  0  
##   2.00000  0.5920144  0  
##   4.00000  0.5920144  0  
##   8.00000  0.5920144  0  
##  16.00000 0.5920144  0  
##  32.00000 0.5920144  0  
##  
## Accuracy was used to select the optimal model using the largest value.  
## The final value used for the model was C = 0.03125.
```

```
lin_svm_fit$bestTune
```

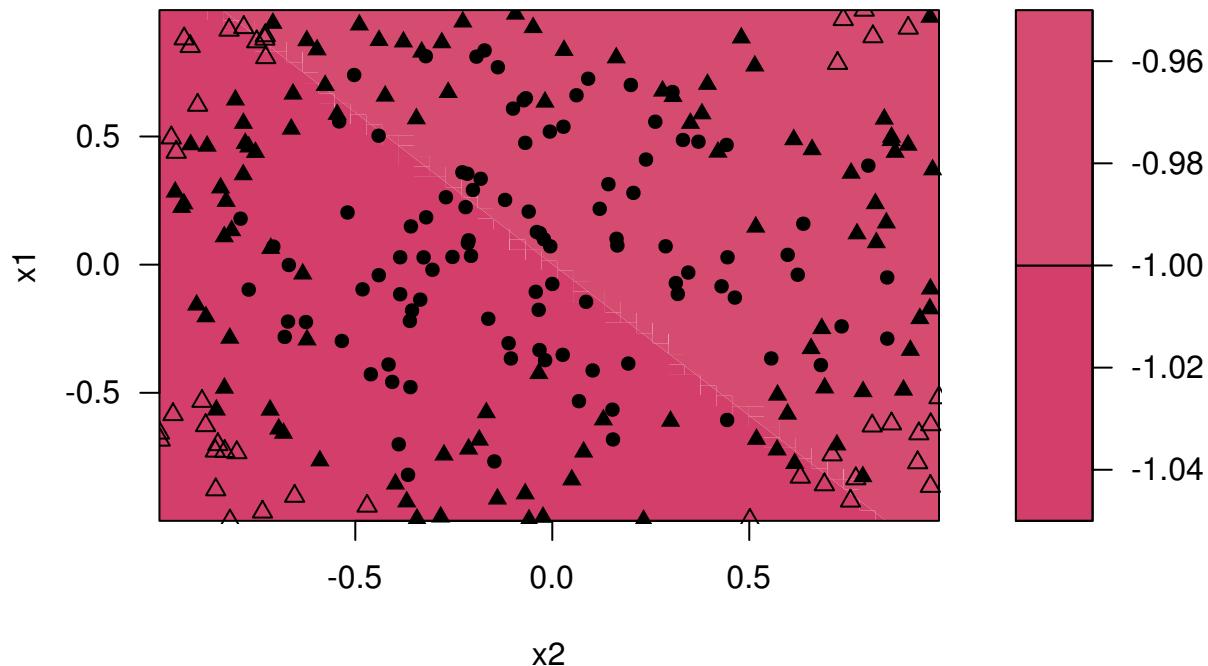
```
##      C  
## 1 0.03125
```

```
lin_svm_fit = ksvm(y ~., data = train_data, kernel = 'vanilladot',  
                    C = lin_svm_fit$bestTune)
```

```
## Setting default kernel parameters
```

```
plot(lin_svm_fit, data = train_data)
```

## SVM classification plot



```
# train accuracy
accuracy(actual = train_data$y,
         predicted = predict(lin_svm_fit, train_data))
```

```
## [1] 0.592
```

```
# test accuracy
accuracy(actual = test_data$y,
         predicted = predict(lin_svm_fit, test_data))
```

```
## [1] 0.6005
```

### 27.4.7 Compare: Random Forest

```
set.seed(42)
rf_grid = expand.grid(mtry = 1:2)
rf_fit = train(y ~ ., data = train_data, method = "rf",
               trControl = svm_control, tuneGrid = rf_grid)
rf_fit$bestTune
```

```
##   mtry
## 2     2

# train accuracy
accuracy(actual = train_data$y,
         predicted = predict(rf_fit, train_data))
```

```
## [1] 1

# test accuracy
accuracy(actual = test_data$y,
          predicted = predict(rf_fit, test_data))

## [1] 0.809
```



# Chapter 28

## Unsupervised Learning

### 28.1 Methods

#### 28.1.1 Principal Component Analysis

To perform PCA in R we will use `prcomp()`. See `?prcomp()` for details.

#### 28.1.2 *k*-Means Clustering

To perform *k*-means in R we will use `kmeans()`. See `?kmeans()` for details.

#### 28.1.3 Hierarchical Clustering

To perform hierarchical clustering in R we will use `hclust()`. See `?hclust()` for details.

### 28.2 Examples

#### 28.2.1 US Arrests

```
library(ISLR)
data(USArrests)
apply(USArrests, 2, mean)

##   Murder Assault UrbanPop      Rape
##   7.788  170.760   65.540   21.232

apply(USArrests, 2, sd)

##   Murder Assault UrbanPop      Rape
##   4.355510 83.337661 14.474763  9.366385
```

“Before” performing PCA, we will scale the data. (This will actually happen inside the `prcomp()` function.)

```
USArrests_pca = prcomp(USArrests, scale = TRUE)
```

A large amount of information is stored in the output of `prcomp()`, some of which can neatly be displayed with `summary()`.

```
names(USArrests_pca)
```

```
## [1] "sdev"      "rotation"   "center"    "scale"     "x"
```

```
summary(USArrests_pca)
```

```
## Importance of components:
```

	PC1	PC2	PC3	PC4
## Standard deviation	1.5749	0.9949	0.59713	0.41645
## Proportion of Variance	0.6201	0.2474	0.08914	0.04336
## Cumulative Proportion	0.6201	0.8675	0.95664	1.00000

```
USArrests_pca$center
```

Murder	Assault	UrbanPop	Rape
7.788	170.760	65.540	21.232

```
USArrests_pca$scale
```

Murder	Assault	UrbanPop	Rape
4.355510	83.337661	14.474763	9.366385

```
USArrests_pca$rotation
```

	PC1	PC2	PC3	PC4
## Murder	-0.5358995	0.4181809	-0.3412327	0.64922780
## Assault	-0.5831836	0.1879856	-0.2681484	-0.74340748
## UrbanPop	-0.2781909	-0.8728062	-0.3780158	0.13387773
## Rape	-0.5434321	-0.1673186	0.8177779	0.08902432

We see that `$center` and `$scale` give the mean and standard deviations for the original variables. `$rotation` gives the loading vectors that are used to rotate the original data to obtain the principal components.

```
dim(USArrests_pca$x)
```

```
## [1] 50  4
```

```
dim(USArrests)
```

```
## [1] 50  4
```

```
head(USArrests_pca$x)

##           PC1         PC2         PC3         PC4
## Alabama -0.9756604  1.1220012 -0.43980366  0.154696581
## Alaska   -1.9305379  1.0624269  2.01950027 -0.434175454
## Arizona  -1.7454429 -0.7384595  0.05423025 -0.826264240
## Arkansas  0.1399989  1.1085423  0.11342217 -0.180973554
## California -2.4986128 -1.5274267  0.59254100 -0.338559240
## Colorado   -1.4993407 -0.9776297  1.08400162  0.001450164
```

The dimension of the principal components is the same as the original data. The principal components are stored in `$x`.

```
scale(as.matrix(USArrests))[1, ] %*% USArrests_pca$rotation[, 1]
```

```
##           [,1]
## [1,] -0.9756604
```

```
scale(as.matrix(USArrests))[1, ] %*% USArrests_pca$rotation[, 2]
```

```
##           [,1]
## [1,] 1.122001
```

```
scale(as.matrix(USArrests))[1, ] %*% USArrests_pca$rotation[, 3]
```

```
##           [,1]
## [1,] -0.4398037
```

```
scale(as.matrix(USArrests))[1, ] %*% USArrests_pca$rotation[, 4]
```

```
##           [,1]
## [1,] 0.1546966
```

```
head(scale(as.matrix(USArrests)) %*% USArrests_pca$rotation[,1])
```

```
##           [,1]
## Alabama -0.9756604
## Alaska   -1.9305379
## Arizona  -1.7454429
## Arkansas  0.1399989
## California -2.4986128
## Colorado   -1.4993407
```

```
head(USArrests_pca$x[, 1])
```

```
##      Alabama      Alaska      Arizona      Arkansas      California      Colorado
## -0.9756604 -1.9305379 -1.7454429  0.1399989 -2.4986128 -1.4993407
```

```

sum(USArrests_pca$rotation[, 1] ^ 2)

## [1] 1

USArrests_pca$rotation[, 1] %*% USArrests_pca$rotation[, 2]

## [,1]
## [1,] -1.387779e-16

USArrests_pca$rotation[, 1] %*% USArrests_pca$rotation[, 3]

## [,1]
## [1,] -5.551115e-17

USArrests_pca$x[, 1] %*% USArrests_pca$x[, 2]

## [,1]
## [1,] -2.062239e-14

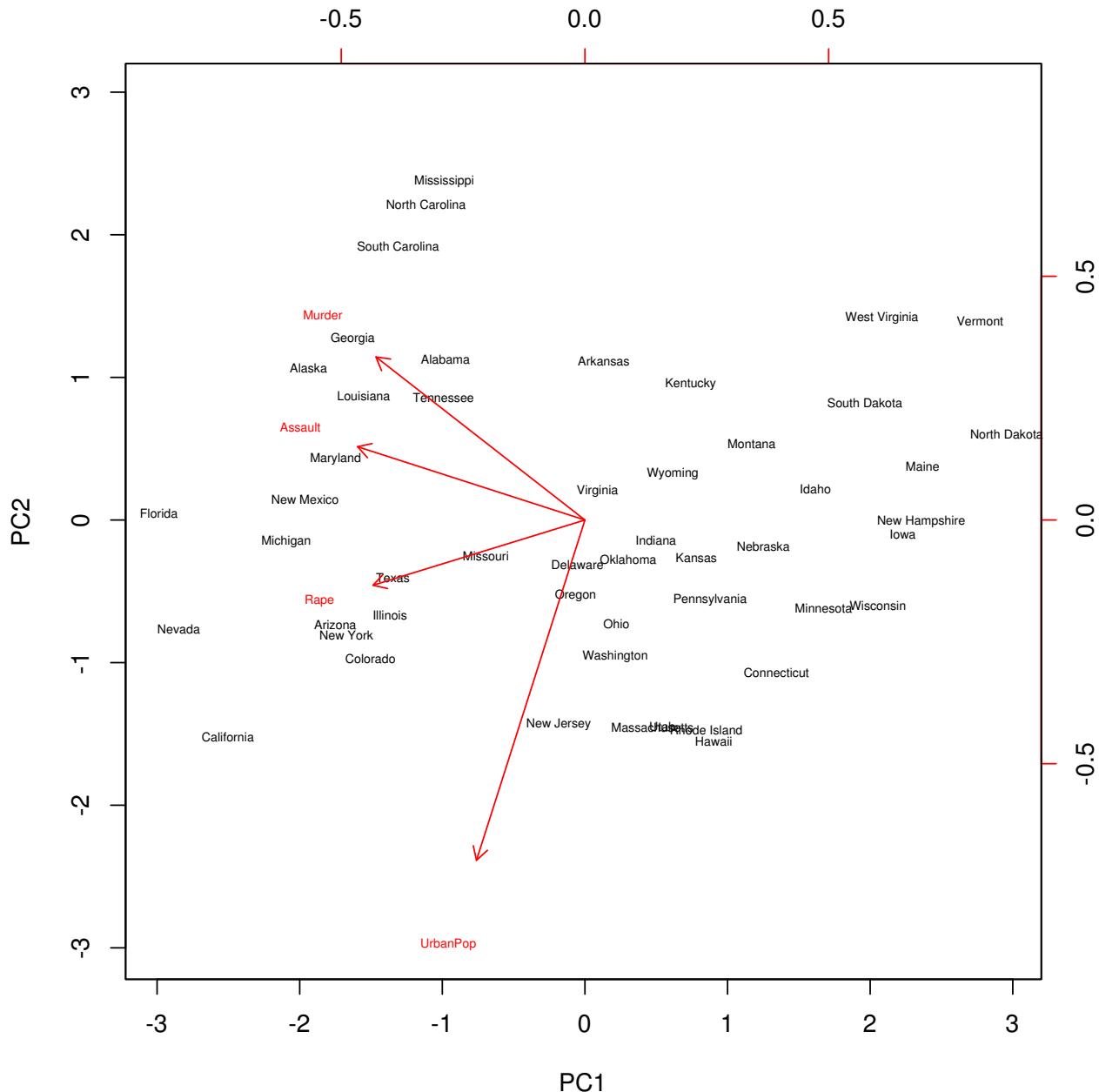
USArrests_pca$x[, 1] %*% USArrests_pca$x[, 3]

## [,1]
## [1,] 5.384582e-15

```

The above verifies some of the “math” of PCA. We see how the loadings obtain the principal components from the original data. We check that the loading vectors are normalized. We also check for orthogonality of both the loading vectors and the principal components. (Note the above inner products aren’t exactly 0, but that is simply a numerical issue.)

```
biplot(USArrests_pca, scale = 0, cex = 0.5)
```



A biplot can be used to visualize both the principal component scores and the principal component loadings. (Note the two scales for each axis.)

```
USArrests_pca$sdev
```

```
## [1] 1.5748783 0.9948694 0.5971291 0.4164494
```

```
USArrests_pca$sdev ^ 2 / sum(USArrests_pca$sdev ^ 2)
```

```
## [1] 0.62006039 0.24744129 0.08914080 0.04335752
```

Frequently we will be interested in the proportion of variance explained by a principal component.

```
get_PVE = function(pca_out) {
  pca_out$sdev ^ 2 / sum(pca_out$sdev ^ 2)
}
```

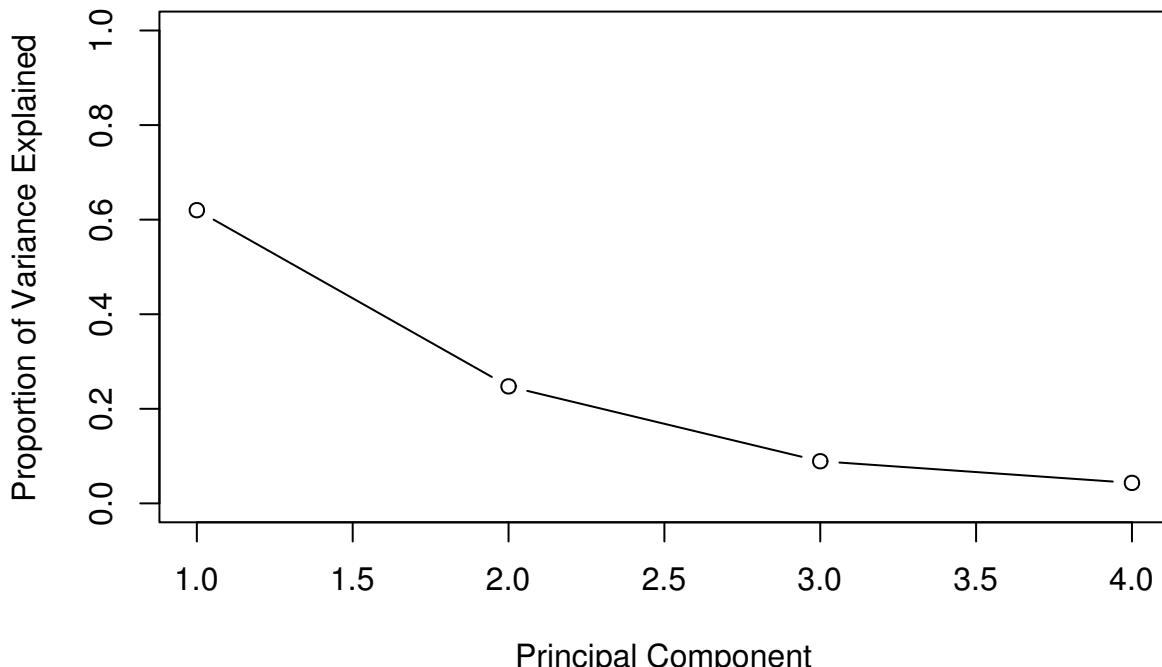
So frequently, we would be smart to write a function to do so.

```
pve = get_PVE(USArrests_pca)

pve
```

## [1] 0.62006039 0.24744129 0.08914080 0.04335752

```
plot(
  pve,
  xlab = "Principal Component",
  ylab = "Proportion of Variance Explained",
  ylim = c(0, 1),
  type = 'b'
)
```



We can then plot the proportion of variance explained for each PC. As expected, we see the PVE decrease.

```
cumsum(pve)

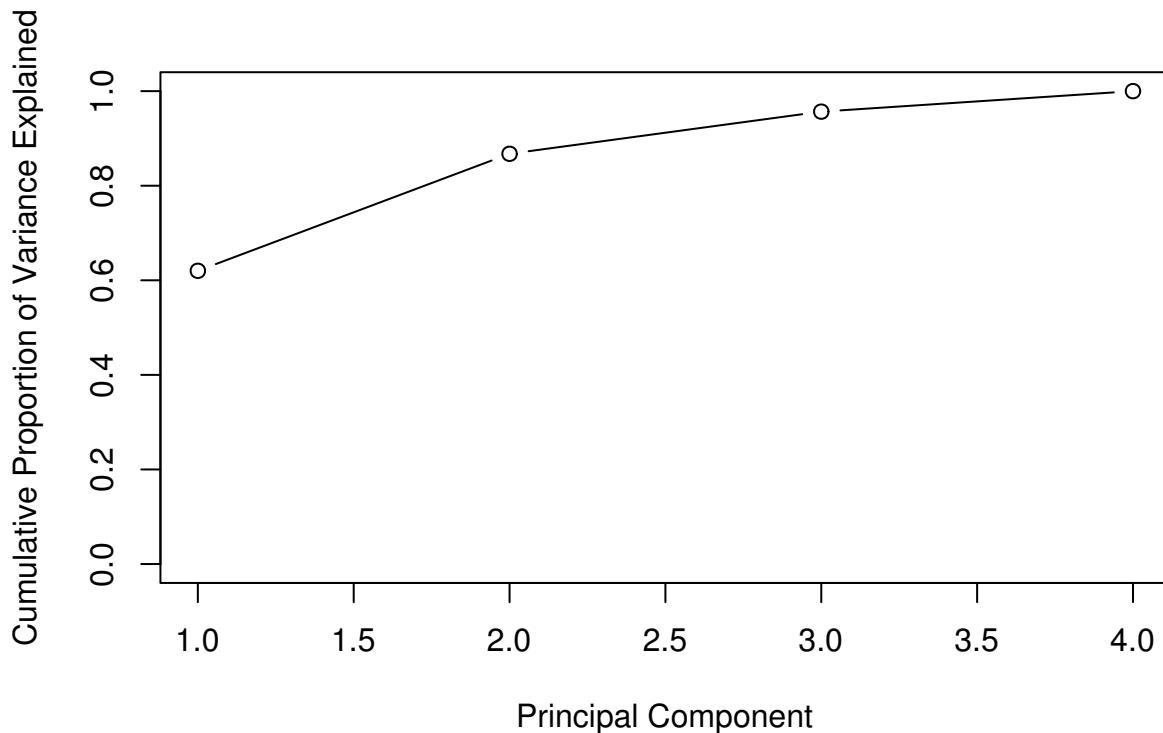
## [1] 0.6200604 0.8675017 0.9566425 1.0000000
```

```
plot(
  cumsum(pve),
  xlab = "Principal Component",
```

```

ylab = "Cumulative Proportion of Variance Explained",
ylim = c(0, 1),
type = 'b'
)

```



Often we are interested in the cumulative proportion. A common use of PCA outside of visualization is dimension reduction for modeling. If  $p$  is large, PCA is performed, and the principal components that account for a large proportion of variation, say 95%, are used for further analysis. In certain situations that can reduce the dimensionality of data significantly. This can be done almost automatically using `caret`:

```

library(caret)

## Loading required package: lattice

## Loading required package: ggplot2

library(mlbench)
data(Sonar)
set.seed(18)
using_pca = train(Class ~ ., data = Sonar, method = "knn",
                  trControl = trainControl(method = "cv", number = 5),
                  preProcess = "pca",
                  tuneGrid = expand.grid(k = c(1, 3, 5, 7, 9)))
regular_scaling = train(Class ~ ., data = Sonar, method = "knn",
                        trControl = trainControl(method = "cv", number = 5),
                        preProcess = c("center", "scale"),
                        tuneGrid = expand.grid(k = c(1, 3, 5, 7, 9)))
max(using_pca$results$Accuracy)

```

```

## [1] 0.8652729

max(regular_scaling$results$Accuracy)

## [1] 0.8558653

using_pca$preProcess

## Created from 208 samples and 60 variables
##
## Pre-processing:
##   - centered (60)
##   - ignored (0)
##   - principal component signal extraction (60)
##   - scaled (60)
##
## PCA needed 30 components to capture 95 percent of the variance

```

It won't always outperform simply using the original predictors, but here using 30 of 60 principal components shows a slight advantage over using all 60 predictors. In other situation, it may result in a large performance gain.

### 28.2.2 Simulated Data

```

library(MASS)
set.seed(42)
n = 180
p = 10
clust_data = rbind(
  mvtnorm(n = n / 3, sample(c(1, 2, 3, 4), p, replace = TRUE), diag(p)),
  mvtnorm(n = n / 3, sample(c(1, 2, 3, 4), p, replace = TRUE), diag(p)),
  mvtnorm(n = n / 3, sample(c(1, 2, 3, 4), p, replace = TRUE), diag(p))
)

```

Above we simulate data for clustering. Note that, we did this in a way that will result in three clusters.

```
true_clusters = c(rep(3, n / 3), rep(1, n / 3), rep(2, n / 3))
```

We label the true clusters 1, 2, and 3 in a way that will "match" output from  $k$ -means. (Which is somewhat arbitrary.)

```

kmean_out = kmeans(clust_data, 3, nstart = 10)
names(kmean_out)

## [1] "cluster"      "centers"       "totss"        "withinss"
## [5] "tot.withinss" "betweenss"     "size"         "iter"
## [9] "ifault"

```

Notice that we used `nstart = 10` which will give us a more stable solution by attempting 10 random starting positions for the means. Also notice we chose to use `centers = 3`. (The  $k$  in  $k$ -mean). How did we know to do this? We'll find out on the homework. (It will involve looking at `tot.withinss`)

```
kmean_out
```

```
## K-means clustering with 3 clusters of sizes 61, 60, 59
##
## Cluster means:
##      [,1]      [,2]      [,3]      [,4]      [,5]      [,6]      [,7]
## 1 3.997352 4.085592 0.7846534 2.136643 4.059886 3.2490887 1.747697
## 2 1.008138 2.881229 4.3102354 4.094867 3.022989 0.8878413 4.002270
## 3 3.993468 4.049505 1.9553560 4.037748 2.825907 2.9960855 3.026397
##      [,8]      [,9]      [,10]
## 1 1.8341976 0.8193371 4.043725
## 2 3.8085492 2.0905060 0.977065
## 3 0.8992179 3.0041820 2.931030
##
## Clustering vector:
## [1] 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3
## [36] 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3
## [71] 1 1 3 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
## [106] 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
## [141] 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2
## [176] 2 2 2 2 2
##
## Within cluster sum of squares by cluster:
## [1] 609.2674 581.8780 568.3845
##   (between_SS / total_SS =  54.0 %)
##
## Available components:
##
## [1] "cluster"      "centers"       "totss"        "withinss"
## [5] "tot.withinss" "betweenss"    "size"         "iter"
## [9] "ifault"
```

```
kmeans_clusters = kmean_out$cluster
```

```
table(true_clusters, kmeans_clusters)
```

```
##          kmeans_clusters
## true_clusters 1 2 3
##                1 58 0 2
##                2 0 60 0
##                3 3 0 57
```

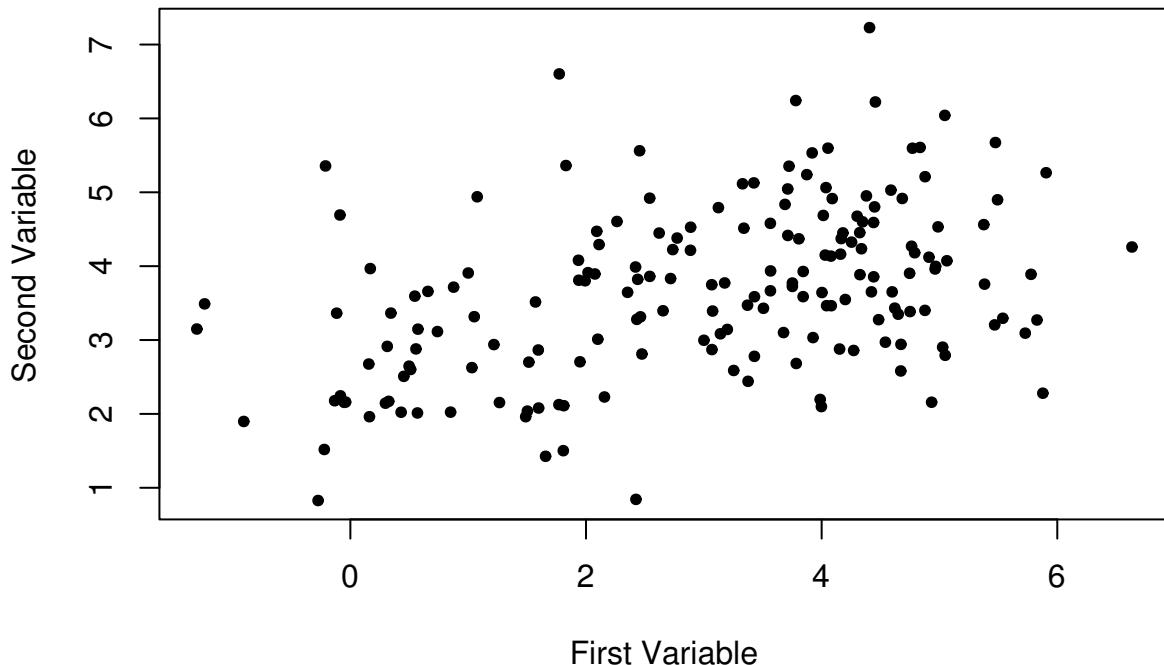
We check how well the clustering is working.

```
dim(clust_data)
```

```
## [1] 180 10
```

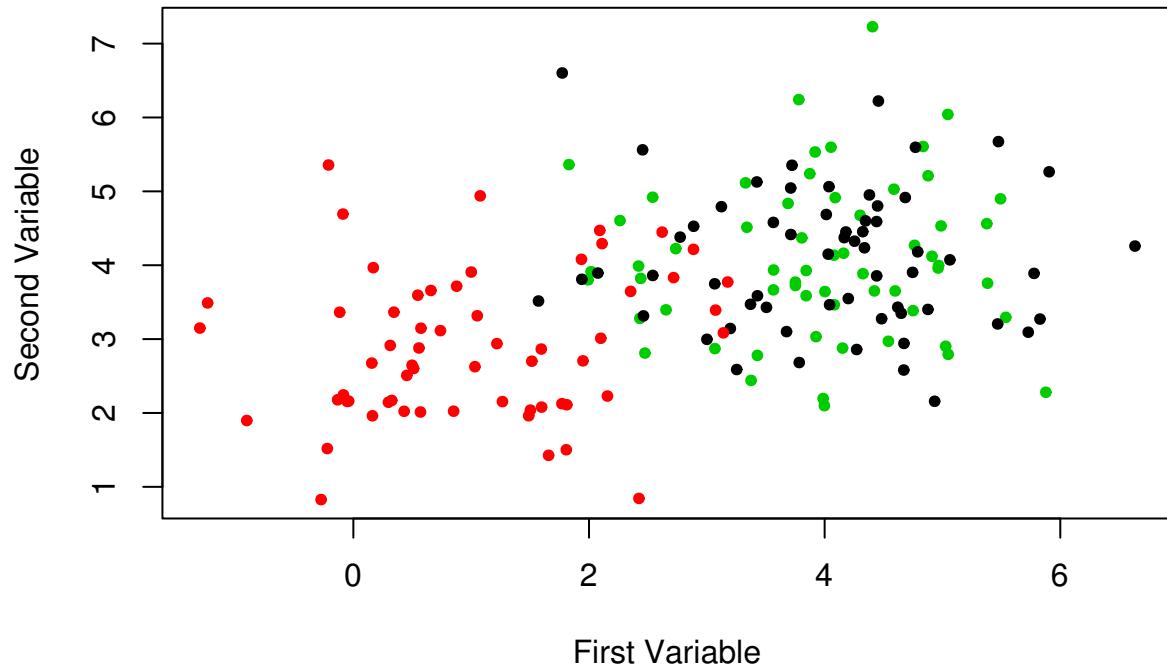
This data is “high dimensional” so it is difficult to visualize. (Anything more than 2 is hard to visualize.)

```
plot(  
  clust_data[, 1],  
  clust_data[, 2],  
  pch = 20,  
  xlab = "First Variable",  
  ylab = "Second Variable"  
)
```



Plotting the first and second variables simply results in a blob.

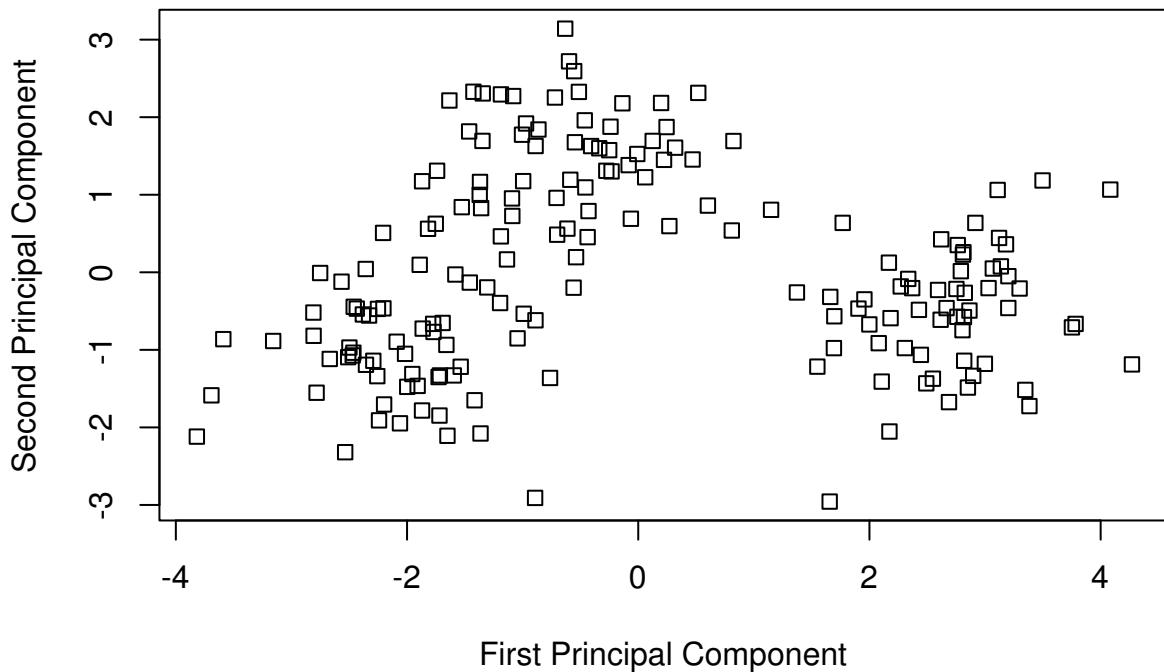
```
plot(  
  clust_data[, 1],  
  clust_data[, 2],  
  col = true_clusters,  
  pch = 20,  
  xlab = "First Variable",  
  ylab = "Second Variable"  
)
```



Even when using their true clusters for coloring, this plot isn't very helpful.

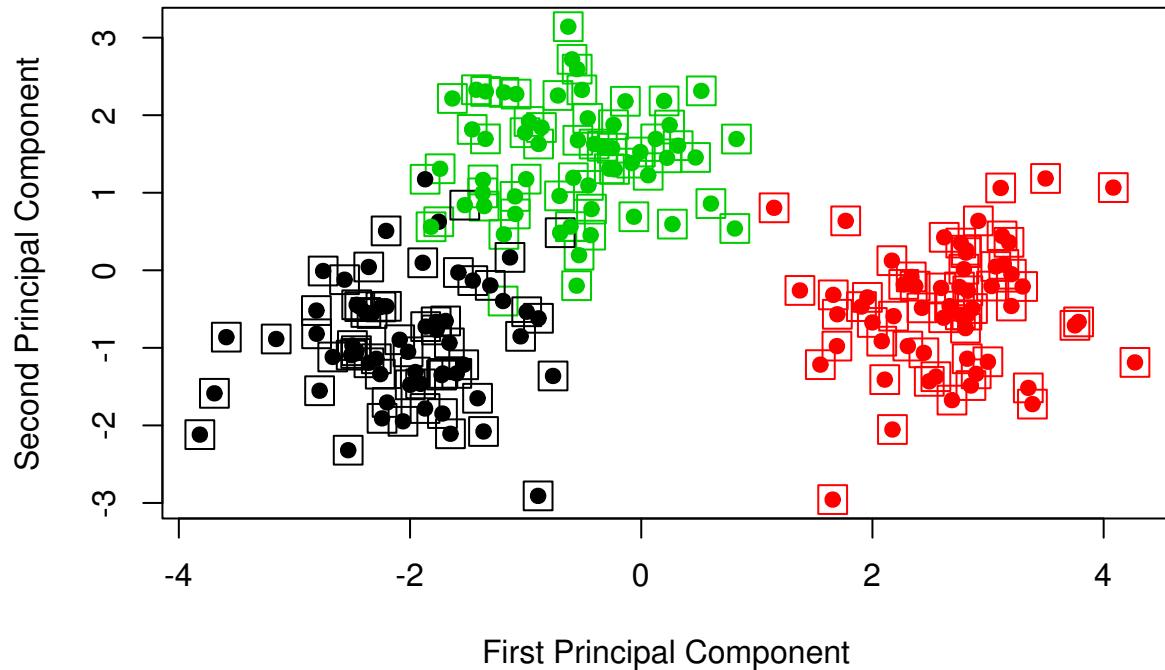
```
clust_data_pca = prcomp(clust_data, scale = TRUE)

plot(
  clust_data_pca$x[, 1],
  clust_data_pca$x[, 2],
  pch = 0,
  xlab = "First Principal Component",
  ylab = "Second Principal Component"
)
```



If we instead plot the first two principal components, we see, even without coloring, once blob that is clearly separate from the rest.

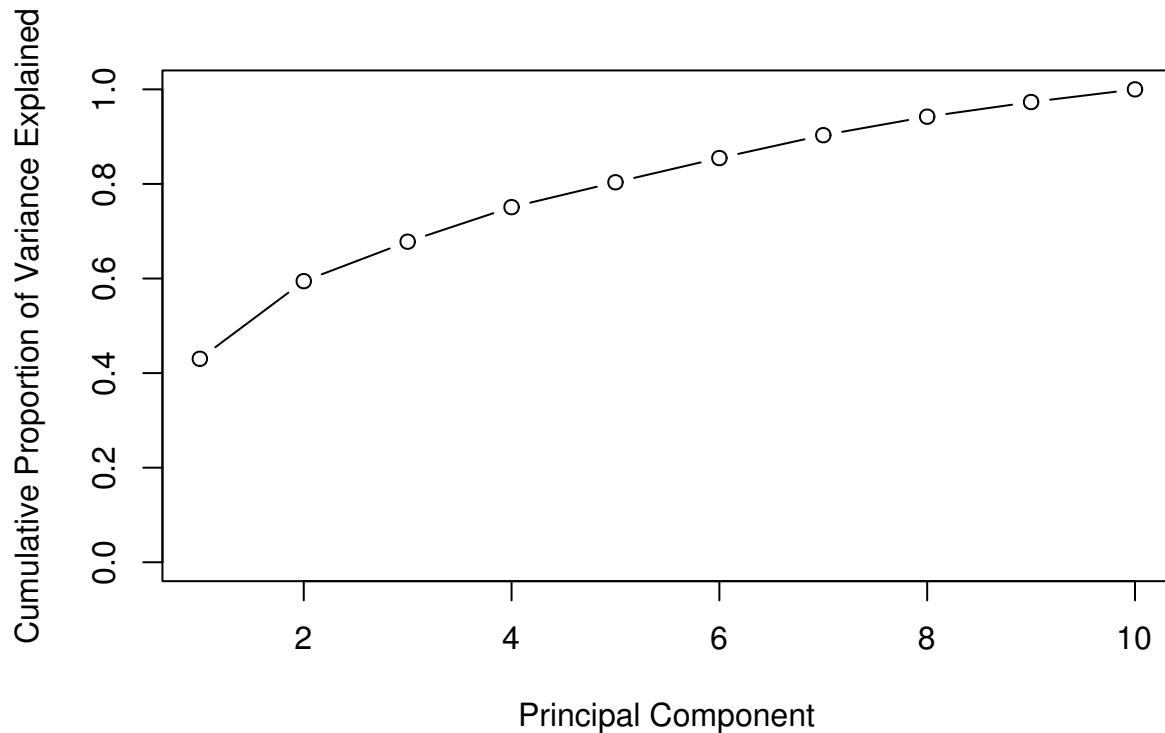
```
plot(  
  clust_data_pca[, 1],  
  clust_data_pca[, 2],  
  col = true_clusters,  
  pch = 0,  
  xlab = "First Principal Component",  
  ylab = "Second Principal Component",  
  cex = 2  
)  
points(clust_data_pca[, 1], clust_data_pca[, 2], col = kmeans_clusters, pch = 20, cex = 1.5)
```



Now adding the true colors (boxes) and the  $k$ -means results (circles), we obtain a nice visualization.

```
clust_data_pve = get_PVE(clust_data_pca)

plot(
  cumsum(clust_data_pve),
  xlab = "Principal Component",
  ylab = "Cumulative Proportion of Variance Explained",
  ylim = c(0, 1),
  type = 'b'
)
```



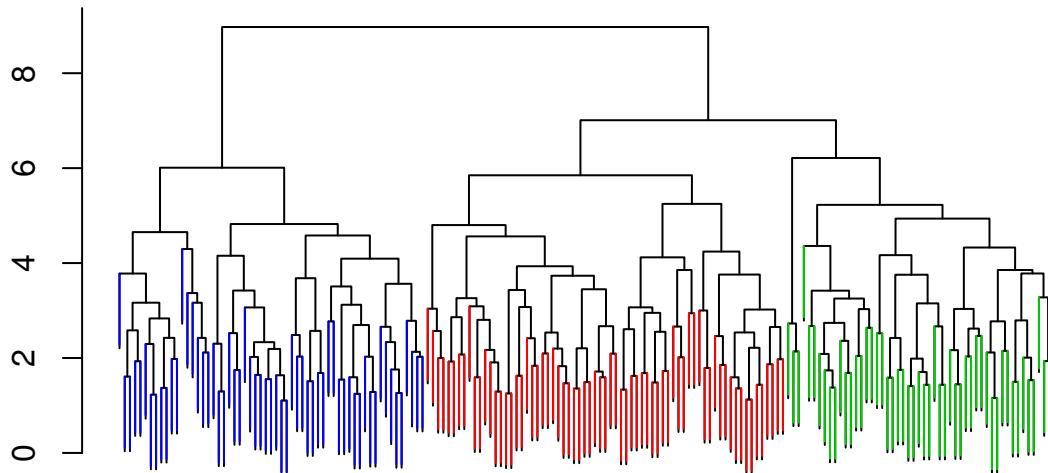
The above visualization works well because the first two PCs explain a large proportion of the variance.

```
#install.packages('sparcl')
library(sparcl)
```

To create colored dendograms we will use `ColorDendrogram()` in the `sparcl` package.

```
clust_data_hc = hclust(dist(scale(clust_data)), method = "complete")
clust_data_cut = cutree(clust_data_hc , 3)
ColorDendrogram(clust_data_hc, y = clust_data_cut,
                labels = names(clust_data_cut),
                main = "Simulated Data, Complete Linkage",
                branchlength = 1.5)
```

## Simulated Data, Complete Linkage



```
dist(scale(clust_data))
hclust (*, "complete")
```

Here we apply hierarchical clustering to the `scaled` data. The `dist()` function is used to calculate pairwise distances between the (scaled in this case) observations. We use complete linkage. We then use the `cutree()` function to cluster the data into 3 clusters. The `ColorDendrogram()` function is then used to plot the dendrogram. Note that the `branchlength` argument is somewhat arbitrary (the length of the colored bar) and will need to be modified for each dendrogram.

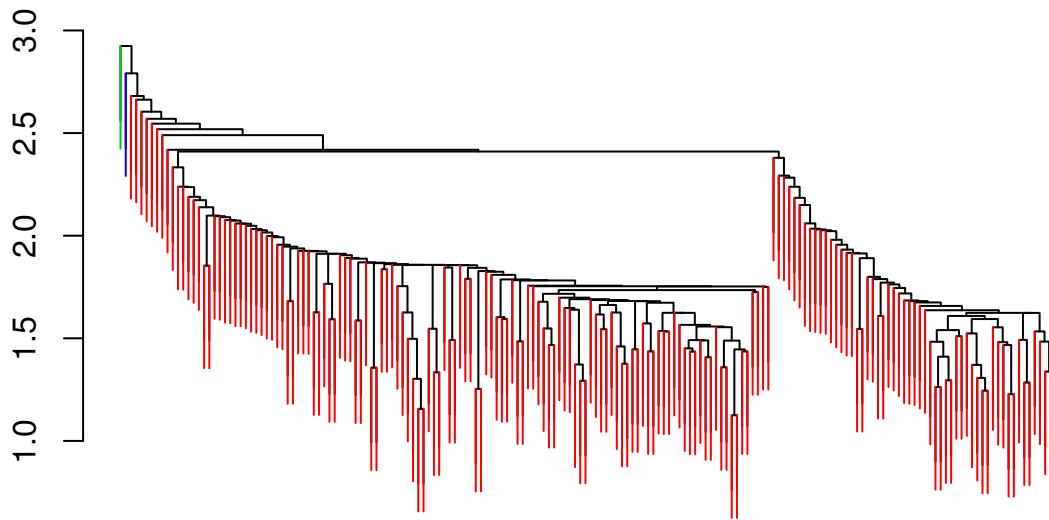
```
table(true_clusters, clust_data_cut)
```

```
##                  clust_data_cut
## true_clusters  1   2   3
##                 1   9  51  0
##                 2   1   0  59
##                 3  59   1   0
```

We see in this case hierarchical clustering doesn't "work" as well as  $k$ -means.

```
clust_data_hc = hclust(dist(scale(clust_data)), method = "single")
clust_data_cut = cutree(clust_data_hc , 3)
ColorDendrogram(clust_data_hc, y = clust_data_cut,
                labels = names(clust_data_cut),
                main = "Simulated Data, Single Linkage",
                branchlength = 0.5)
```

## Simulated Data, Single Linkage



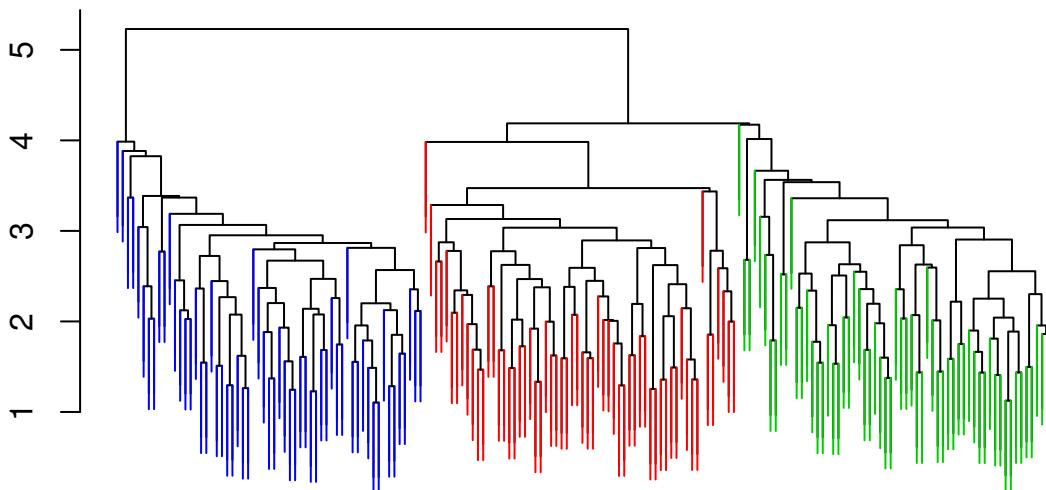
```
dist(scale(clust_data))
hclust (*, "single")
```

```
table(true_clusters, clust_data_cut)
```

```
##                  clust_data_cut
## true_clusters  1   2   3
##               1 59  1  0
##               2 59  0  1
##               3 60  0  0
```

```
clust_data_hc = hclust(dist(scale(clust_data)), method = "average")
clust_data_cut = cutree(clust_data_hc , 3)
ColorDendrogram(clust_data_hc, y = clust_data_cut,
                 labels = names(clust_data_cut),
                 main = "Simulated Data, Average Linkage",
                 branchlength = 1)
```

## Simulated Data, Average Linkage



```
dist(scale(clust_data))
hclust (*, "average")
```

```
table(true_clusters, clust_data_cut)
```

```
##           clust_data_cut
## true_clusters 1 2 3
##       1 1 59 0
##       2 1 0 59
##       3 58 2 0
```

We also try single and average linkage. Single linkage seems to perform poorly here, while average linkage seems to be working well.

### 28.2.3 Iris Data

```
str(iris)
```

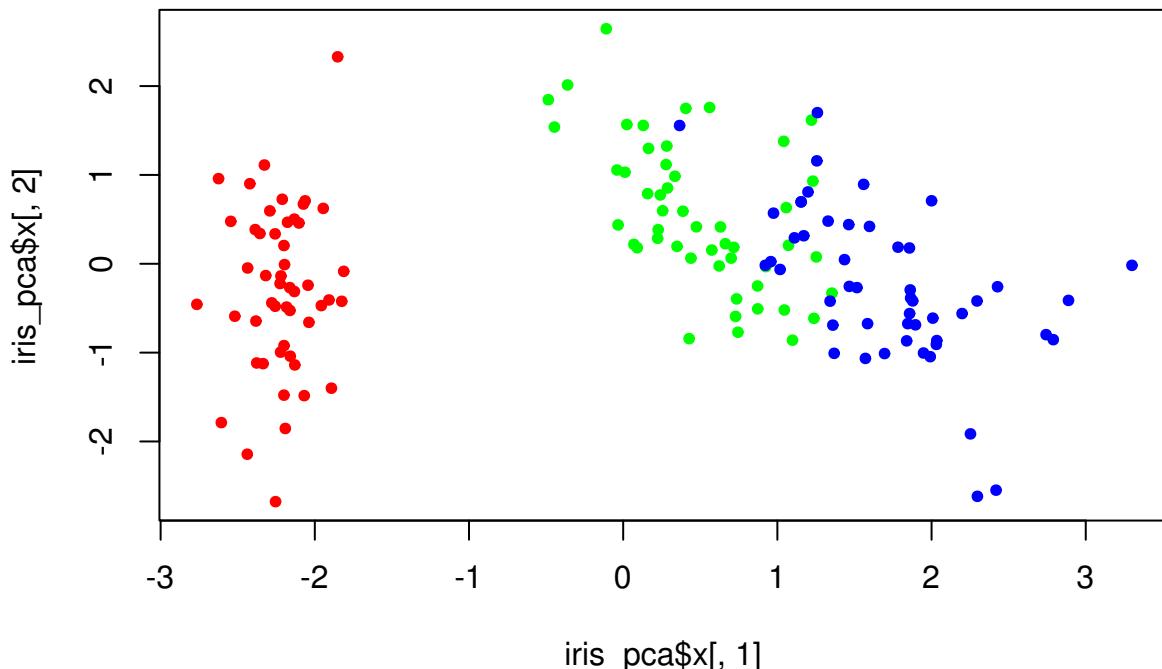
```
## 'data.frame': 150 obs. of 5 variables:
## $ Sepal.Length: num 5.1 4.9 4.7 4.6 5 5.4 4.6 5 4.4 4.9 ...
## $ Sepal.Width : num 3.5 3 3.2 3.1 3.6 3.9 3.4 3.4 2.9 3.1 ...
## $ Petal.Length: num 1.4 1.4 1.3 1.5 1.4 1.7 1.4 1.5 1.4 1.5 ...
## $ Petal.Width : num 0.2 0.2 0.2 0.2 0.2 0.4 0.3 0.2 0.2 0.1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

```
iris_pca = prcomp(iris[,-5], scale = TRUE)
iris_pca$rotation
```

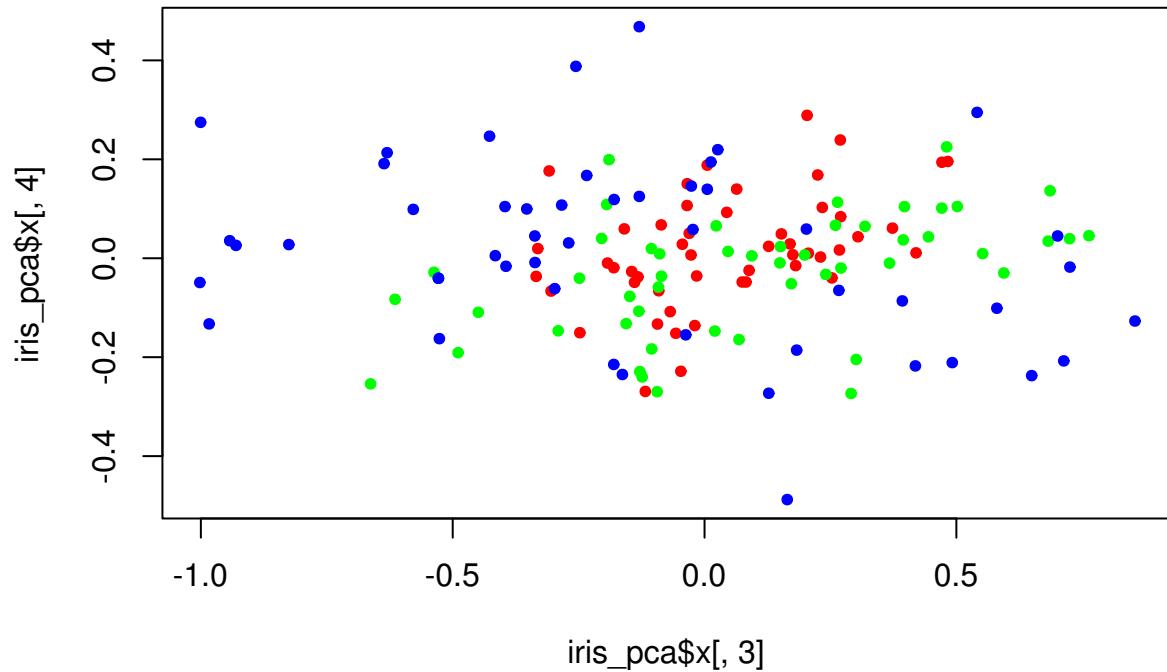
```
##          PC1         PC2         PC3         PC4
## Sepal.Length  0.5210659 -0.37741762  0.7195664  0.2612863
## Sepal.Width   -0.2693474 -0.92329566 -0.2443818 -0.1235096
## Petal.Length   0.5804131 -0.02449161 -0.1421264 -0.8014492
## Petal.Width    0.5648565 -0.06694199 -0.6342727  0.5235971
```

```
lab_to_col = function (labels){
  cols = rainbow (length(unique(labels)))
  cols[as.numeric (as.factor(labels))]
}

plot(iris_pca$x[,1], iris_pca$x[,2], col = lab_to_col(iris$Species), pch = 20)
```

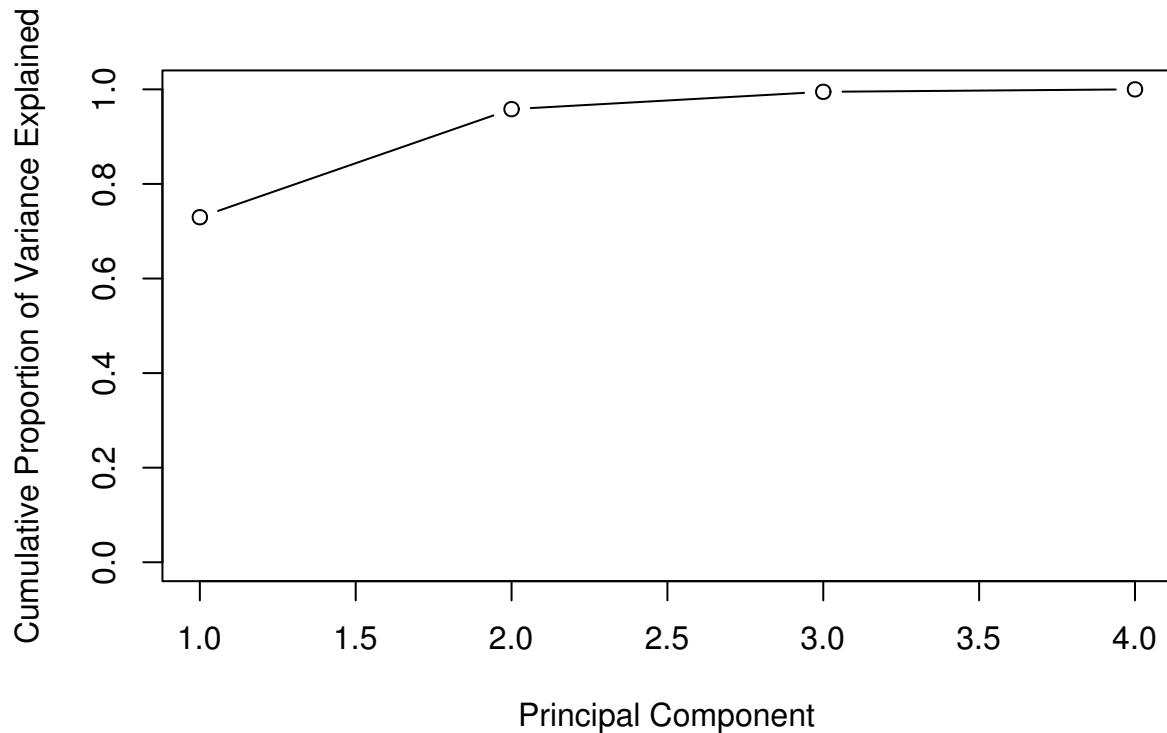


```
plot(iris_pca$x[,3], iris_pca$x[,4], col = lab_to_col(iris$Species), pch = 20)
```



```
iris_pve = get_PVE(iris_pca)

plot(
  cumsum(iris_pve),
  xlab = "Principal Component",
  ylab = "Cumulative Proportion of Variance Explained",
  ylim = c(0, 1),
  type = 'b'
)
```

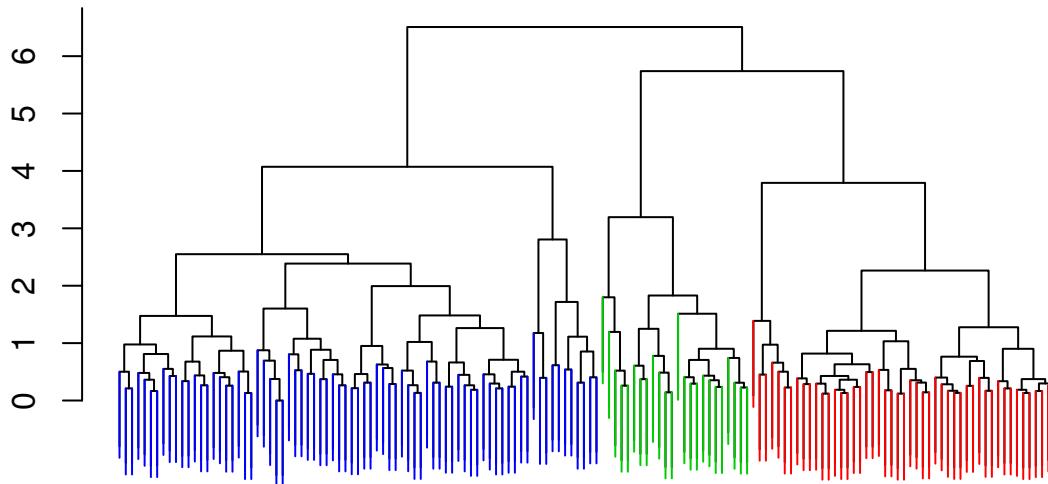


```
iris_kmeans = kmeans(iris[,-5], centers = 3, nstart = 10)
table(iris_kmeans$clust, iris[,5])
```

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

```
iris_hc = hclust(dist(scale(iris[,-5])), method = "complete")
iris_cut = cutree(iris_hc , 3)
ColorDendrogram(iris_hc, y = iris_cut,
                 labels = names(iris_cut),
                 main = "Iris, Complete Linkage",
                 branchlength = 1.5)
```

## Iris, Complete Linkage



```
dist(scale(iris[, -5]))
hclust (*, "complete")
```

```
table(iris_cut, iris[,5])
```

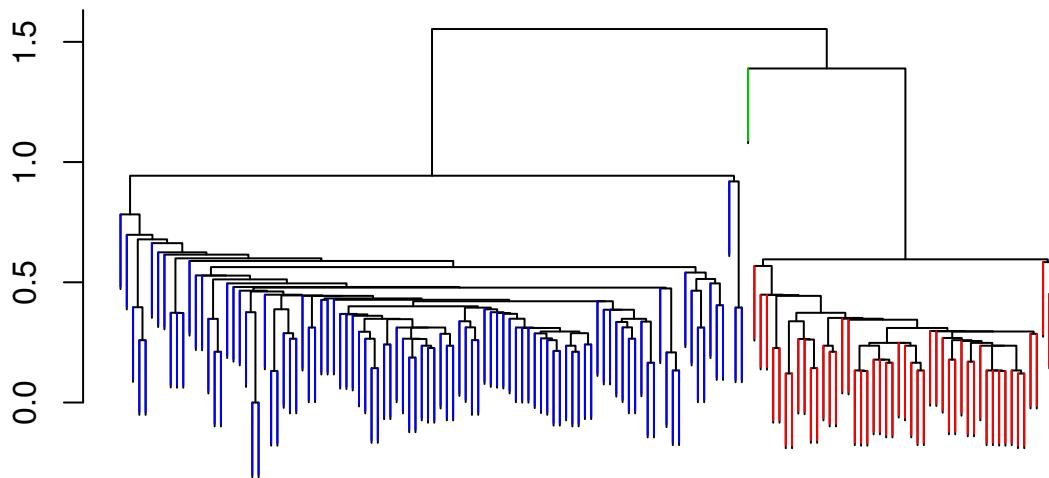
```
##
## iris_cut setosa versicolor virginica
##      1     49          0          0
##      2      1         21          2
##      3      0         29         48
```

```
table(iris_cut, iris_kmeans$clust)
```

```
##
## iris_cut 1 2 3
##      1 0 0 49
##      2 23 0 1
##      3 39 38 0
```

```
iris_hc = hclust(dist(scale(iris[,-5])), method = "single")
iris_cut = cutree(iris_hc , 3)
ColorDendrogram(iris_hc, y = iris_cut,
                labels = names(iris_cut),
                main = "Iris, Single Linkage",
                branchlength = 0.3)
```

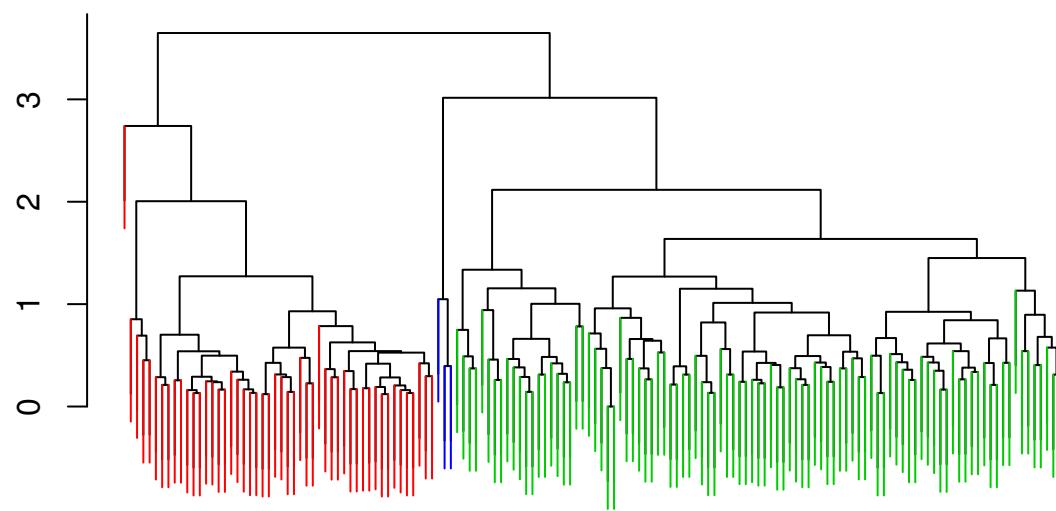
## Iris, Single Linkage



```
dist(scale(iris[, -5]))  
hclust (*, "single")
```

```
iris_hc = hclust(dist(scale(iris[,-5])), method = "average")  
iris_cut = cutree(iris_hc , 3)  
ColorDendrogram(iris_hc, y = iris_cut,  
                labels = names(iris_cut),  
                main = "Iris, Average Linkage",  
                branchlength = 1)
```

## Iris, Average Linkage



```
dist(scale(iris[, -5]))  
hclust (*, "average")
```



# Bibliography