Using R for Introduction to Econometrics

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Chapter 1

Preface

What this book is (and what it is not)

This book is an interactive script aiming to provide students of economic sciences with a platform-independent E-learning arrangement that seamlessly intertwines both, teaching of theoretical core knowledge and empirical skills in undergraduate econometrics. Thereby, the focus clearly lays on empirical applications with the freely available statistical software package R and omitts tedious derivations and formal proof. The script is aligned on *Introduction to Econometrics* (Stock and Watson, 2014), a standard textbook in introductory econometrics. While the book does well in motivating theory by real-world applications, we want to take it a step further and intend to enable students not only to learn how to reproduce results of case studies with R but also to strengthen their ability to use the newly acquired skills in other empirical applications. Therefore, this book is neither an introduction to R, nor is it indended to be a replacement for the textbook let alone a full course in econometrics.

Chapter 2

Probability Theory

This chapter reviews some basic concepts of probability theory and demonstrates how they can be applied in R.

Most of the statistical functionalities in R's standard version are collected in the stats package. It provides simple functions which compute descriptive measures and faciliate calculus involving a variety of probability distributions but also holds more sophisticated routines that e.g. enable the user to estimate a large number of models based on the same data or help to conduct extensive simulation studies. Execute `library(help = "stats")` in the console to view the documentation and a complete list of all functions gathered in `stats`.

In what follows, we lay our focus on (some of) the probability distributions that are handled by R and show how to use the relevant functions to solve simple problems. Thereby we will repeat some core concepts of probability theory. Among other things, You will learn how to draw random numbers, how to compute densities, probabilities, quantiles and alike. As we shall see, it is very convenient to rely on these routines, especially when writing Your own functions.

2.1 Random Variables and Probability Distributions

For a start, let us briefly review some basic concepts in probability.

- The mutually exclusive results of a random process are called the *outcomes*. 'Mutually exclusive' means that only one of the possible outcomes is observed.
- We refer to the *probability* of an outcome as the proportion of the time that the outcome occurs in the long run, that is if the experiment is repeated very often.
- The set of all possible outcomes of a random variable is called the *sample space*.
- An *event* is a subset of the sample space and consists of one or more outcomes.

These indeas are unified in the concept of a *random variable* which is a numerical summary of random outcomes. Random variables can be *discrete* or *continuous*.

- Discrete random variables have discrete outcomes, e.g. 0 and 1.
- A continuous random variable takes on a continuum of possible values.

Probability Distributions of Discrete Random Variables

A typical example for a discrete random variable D is the result of a die roll: in terms of a random experiment this is nothing but randomly selecting a sample of size 1 from a set of numbers which are mutually exclusive outcomes. Here, the sample space is $\{1, 2, 3, 4, 5, 6\}$ and we can think of many different events, e.g. 'the observed outcome lies between 2 and 5'.

A basic function to draw random samples from a specified set of elements is the the function `sample()`, see `?sample`. We can use it to simulate the random outcome of a die roll. Let's role the dice!

```r
sample(1:6, 1)
```

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

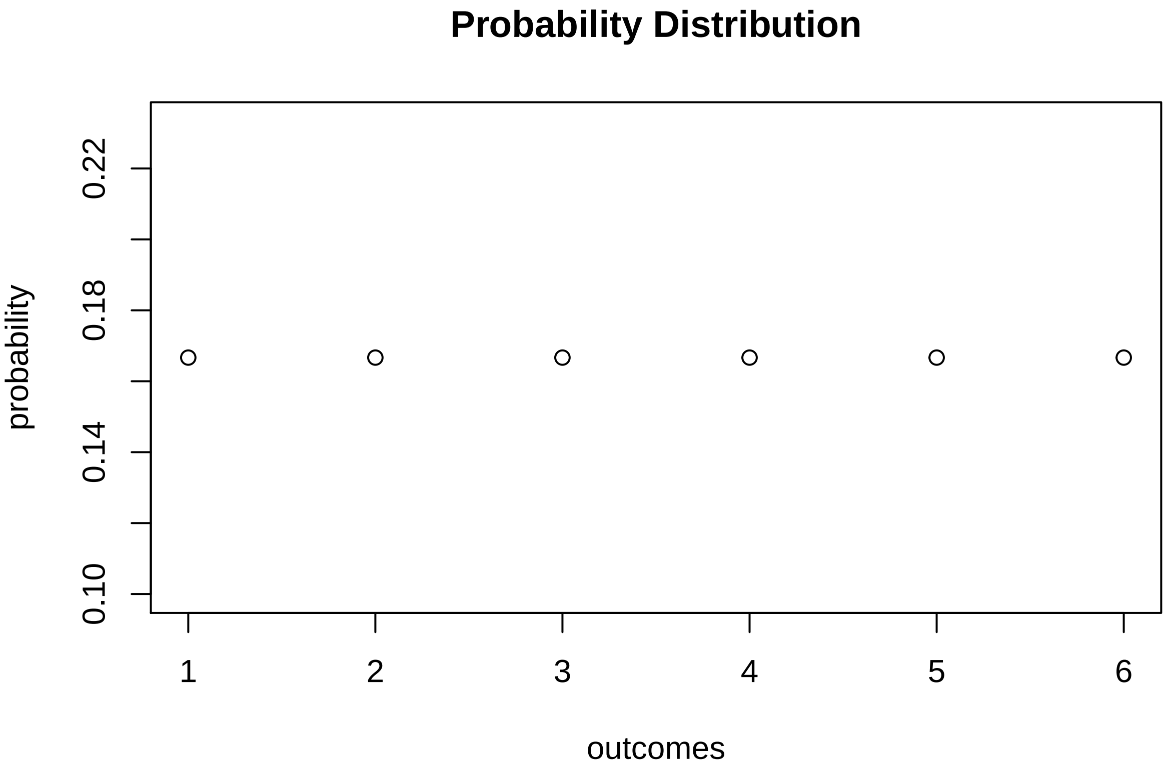
The probability distribution of a discrete random variable is the list of all possible values of the variable and thier probabilities which sum to 1. The cumulative probability distribution function states the probability that the random variable is less than or equal to a particular value.

For the die roll, this is straightforward to set up

Outcome	1	2	3	4	5	6
Probability distribution	1/6	1/6	1/6	1/6	1/6	1/6
Cumulative probability distribution	1/6	2/6	3/6	4/6	5/6	1

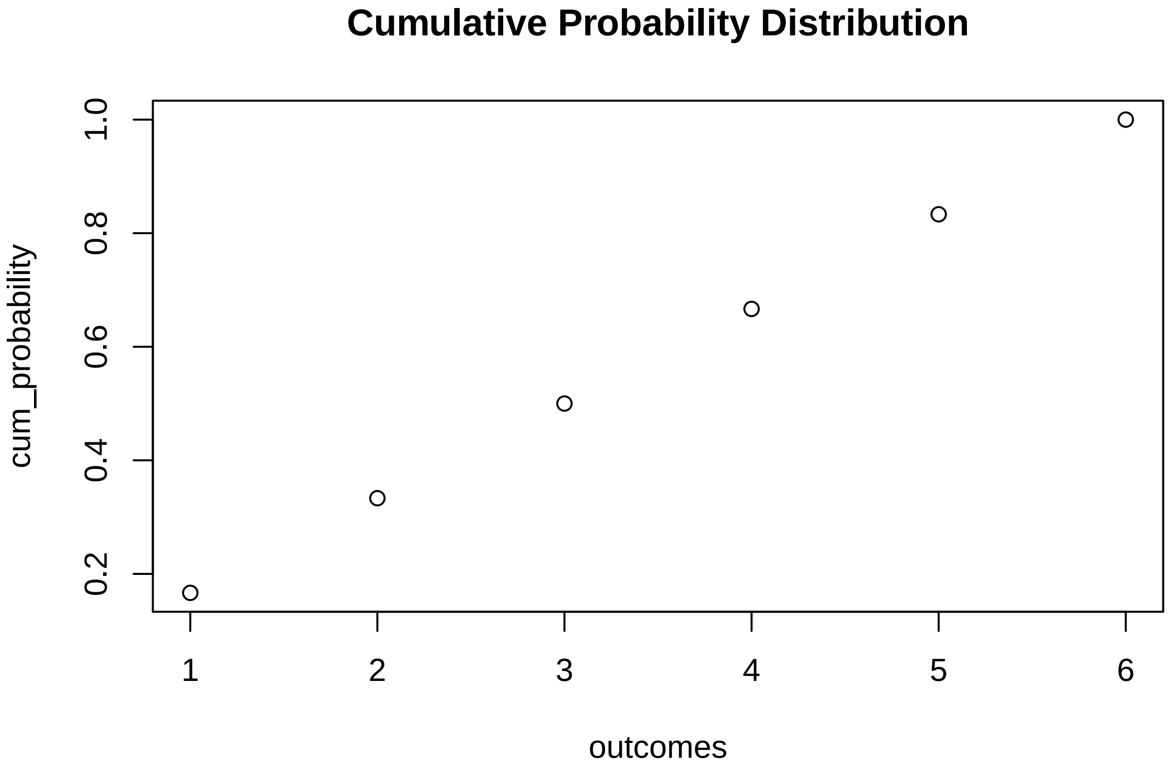
We can easily plot both functions using R. Since the probability equals 1/6 for each outcome, we set up the vector `probability` by using the `rep()` function which replicates a given value a specified number of times.

```r
# generate the vector of probabilities
probability <- rep(1/6,6)

# plot the probabilites
plot(probability, xlab = "outcomes",
     main = "Probability Distribution"
     )
```



For the cumulative probability distribution we need the cumulative probabilities i.e. we need the cumulative sums of the vector `probability`. These sums can be computed using `cumsum()`.

```
#generate the vector of cumulative probabilities
cum_probability <- cumsum(probability)

# plot the probabilites
plot(cum_probability,
     xlab = "outcomes",
     main = "Cumulative Probability Distribution"
     )
```



Bernoulli Trials

The set of elements `sample()` draws from does not have to consist of numbers only. We might as well simulate coin tossing with outcomes H (head) and T (tail).

```
sample(c("H","T"),1)
```

```
## [1] "H"
```

The result of a coin toss is a Bernoulli distributed random variable i.e. a variable with to possible distinct outcomes.

Imagine you are about to toss a coin 10 times in a row and wonder how likely it is to end up with a sequence of outcomes like

$$H\,H\,T\,T\,T\,H\,T\,T\,H\,H.$$

This is a typical example of a Bernoulli experiment as it consists of $n = 10$ Bernoulli trials that are independent of each other and we are interested in the likelihood of observing $k = 5$ successes H that occur with probability $p = 0.5$ (assuming a fair coin) in each trial.

It is a well known result that the number of successes k follows a binomial distribution

$$k \sim B(n, p).$$

The probability of observing k successes in the experiment $B(n, p)$ is hence given by

$$f(k) = P(k) = \binom{n}{k} \cdot p^k \cdot q^{n-k} = \frac{n!}{k!(n-k)!} \cdot p^k \cdot q^{n-k}$$

where $\binom{n}{k}$ is a binomial coefficient.

In R, we can solve the problem stated above by means of the function `dbinom()` which calculates the probability of the binomial distribution for parameters `x`, `size`, and `prob`, see `?binom`.

```
dbinom(x = 5,
       size = 10,
       prob = 0.5
       )
```

```
## [1] 0.2460938
```

We conclude that the probability of observing Head $k = 5$ times when tossing the coin $n = 10$ times is about 24.6%.

Now assume we are interested in $P(4 \leq k \leq 7)$ i.e. the probability of observing 4, 5, 6 or 7 successes for $B(10, 0.5)$. This is easily computed by providing a vector as the `x` argument in our call of `dbinom()` and summing up using `sum()`.

```
sum(
  dbinom(x = 4:7,
         size = 10,
         prob = 0.5
         )
  )
```

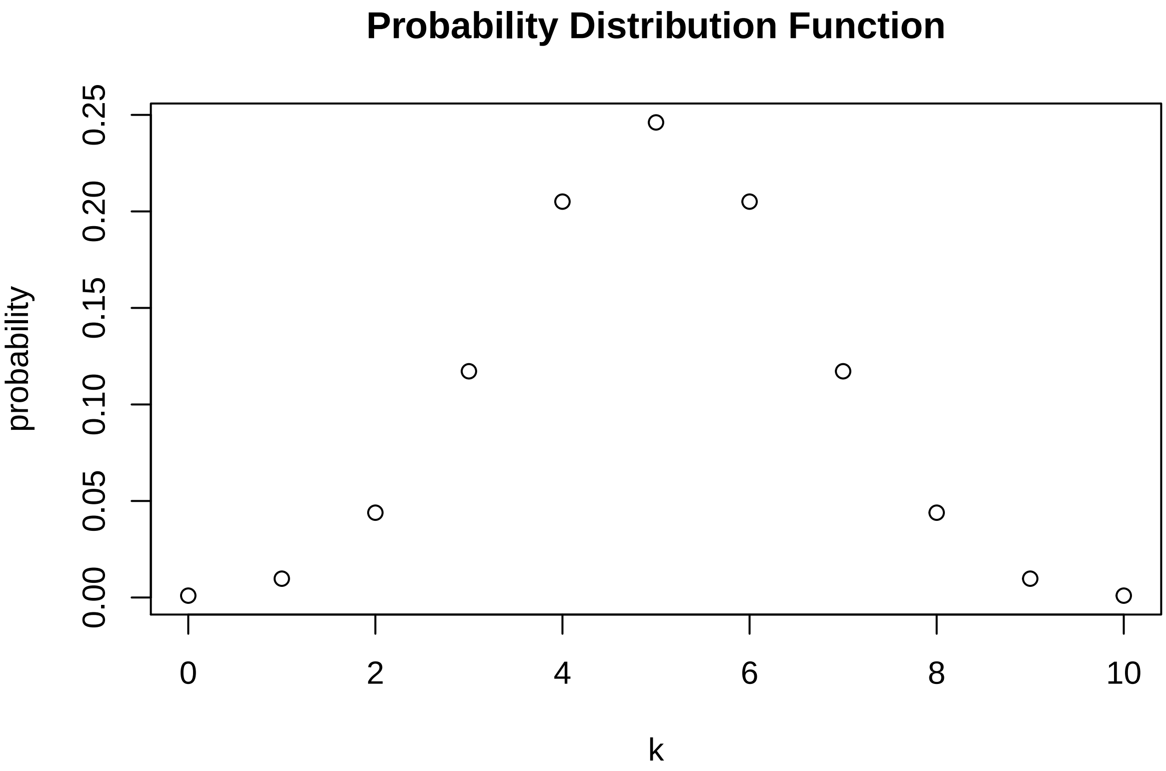
```
## [1] 0.7734375
```

The Probability distribution of a discrete random variable is nothing but a list of all possible outcomes that can occur and their respective probabilities. In our coin tossing example, we face 11 possible outcomes for k

```
# set up vector of possible outcomes
k <- 0:10
```

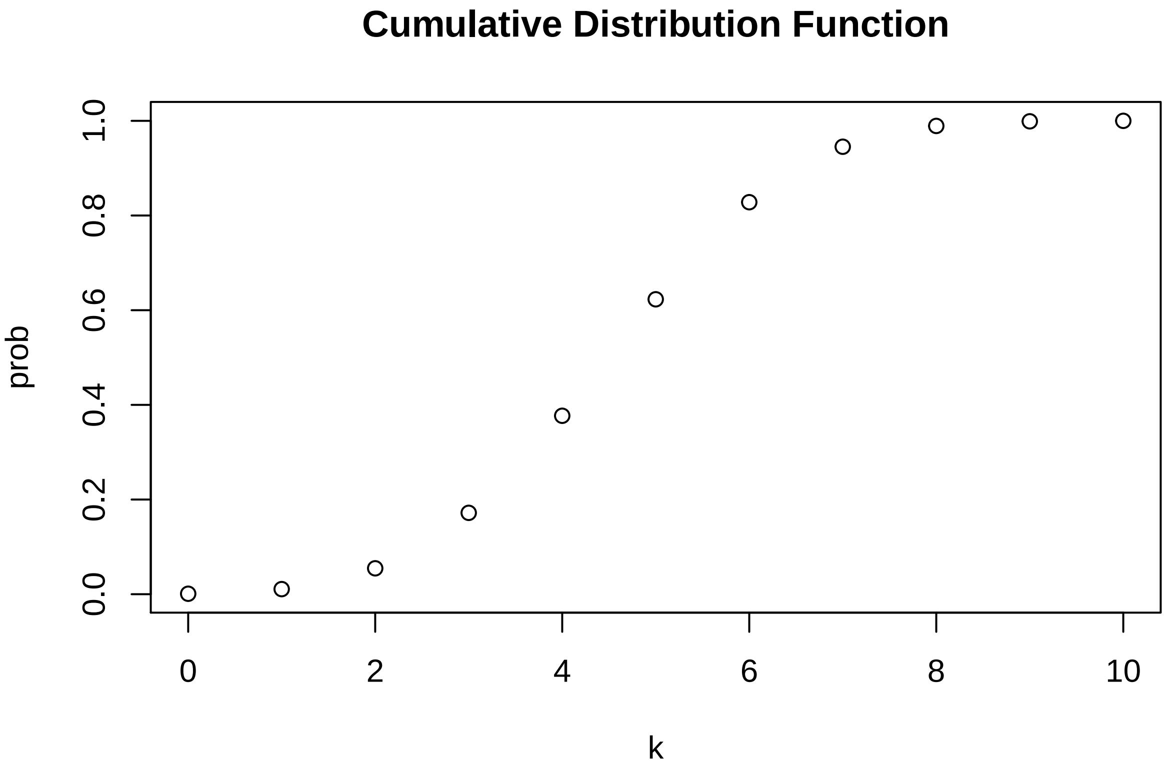
To visualize the probability distribution function of k we may therefore simply call

```
# assign probabilities
probability <- dbinom(x = k,
                      size = 10,
                      prob = 0.5
                      )

# plot outcomes against probabilities
plot(x = k,
     y = probability,
     main = "Probability Distribution Function")
```



In a similar fashion we may plot the cumulative distribution function of k by executing the following code chunk:

```
prob <- cumsum(
              dbinom(x =0:10,
                     size = 10,
                     prob = 0.5
                     )
              )

k <- 0:10
plot(x = k,
     y = prob,
     main = "Cumulative Distribution Function")
```



Expected Values, Mean and Variance

The expected value of a random variable is the long-run average value of the random variable over many repeated trials. For a discrete random variable, the expected value is computed as a weighted average of its possible outcomes whereby the weights are the related probabilities. This is formalized in Key Concept 2.1.

Key Concept 2.1

Expected Value and the Mean

Suppose the random variable Y takes on k possible values, $y_1, \dots, y_k$, where y_1 denotes the first value, y_2 denotes the second value, and so forth, and that the probability that Y takes on y_1 is p_1, the probability that Y takes on y_2 is p_2 and so forth. The expected value of Y, $E(Y)$ is defined as

$$E(Y) = y_1 p_1 + y_2 p_2 + \cdots + y_k p_k = \sum_{i=1}^{k} y_i p_i$$

where the notation $\sum_{i=1}^{k} y_i p_i$ means "the sum of y_i p_i for i running from 1 to k". The expected value of Y is also called the mean of Y or the expectation of Y and is denoted by μ_y.

In the dice example, the random variable, D say, takes on 6 possible values $d_1 = 1, d_2 = 2, \dots, d_6 = 6$. Assuming a fair dice, each of the 6 outcomes occurs with a probability of 1/6. It is therefore easy to calculate the exact value of $E(D)$ by hand:

$$E(D) = 1/6 \sum_{i=1}^{6} d_i = 3.5$$

Here, this is simply the average of the natural numbers from 1 to 6 since all wights p_i are 1/6. Convince Yourself that this can be easily calculated using the function `mean()` which computes the arithmetic mean of a numeric vector.

```
mean(1:6)
```

```
## [1] 3.5
```

An example of sampling with replacement is rolling a dice three times in a row.

```
# set random seed for reproducibility
set.seed(1)

# rolling a dice three times in a row
sample(1:6, 3, replace = T)
```

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

Of course we could also consider a much bigger number of trials, 10000 say. Doing so, it would be pointless to simply print the results to the console: by default R displays up to 1000 entries of large vectors and omitts the remainder (give it a go). Eyeballing the numbers does not reveal too much. Instead let us calculate the sample average of the outcomes using `mean()` and see if the result comes close to the expected value $E(D) = 3.5$.

```
# set random seed for reproducibility
set.seed(1)

# compute the sample mean of 10000 die rolls
mean(
    sample(1:6,
           10000,
           replace = T
           )
    )
```

```
## [1] 3.5039
```

We find the sample mean to be fairly close to the expected value. (ref to WLLN)

Other frequently encountered measures are the variance and the standard deviation. Both are measures of the *dispersion* of a random variable.

Key Concept 2.2

Variance and Standard Deviation

The Variance of the discrete *random variable* Y, denoted σ^2_Y, is

$$\sigma^2_Y = \text{Var}(Y) = E\left[(Y - \mu_y)^2\right] = \sum_{i=1}^{k} (y_i - \mu_y)^2 p_i$$

The standard deviation of Y is σ_Y, the square root of the variance. The units of the standard deviation are the same as the units of Y.

The variance as defined in Key Concept 2.2 *is not* implemented as a function in R. Instead we have the function `var()` which computes the *sample variance*

$$s^2_Y = \frac{1}{n-1} \sum_{i=1}^{n} (y_i - \overline{y})^2.$$

Remember that s_Y^2 is different from the so called *population variance* of Y,

$$\text{Var}(Y) = \frac{1}{N}\sum_{i=1}^{N}(y_i - \mu_Y)^2,$$

since it measures how the data is dispersed around the sample average $\overline{y}$ instead of the population mean μ_Y. This becomes clear when we look at our dice rolling example. For D we have

$$\text{Var}(D) = 1/6\sum_{i=1}^{6}(d_i - 3.5)^2 = 2.92$$

which is obviously different from the result of s^2 as computed by `var()`.

```r
var(1:6)
```

```
## [1] 3.5
```

2.2 Probability Distributions of Continuous Random Variables

Since a continuous random variable takes on a continuum of possible values, we cannot use the concept of a probability distribution as used for discrete random variables. Instead, the probability distribution of a continuous random variable is summarized by its *probability density function* (PDF).

The cumulative probability distribution function (CDF) for a continuous random variable is defined just as in the discrete case. Hence, the cumulative probability distribution of a continuous random variables states the probability that the random variable is less than or equal to a particular value.

For completeness, we present revisions of Key Concepts 2.1 and 2.2 for the continuous case.

Key Concept 2.3

Probabilities, Expected Value and Variance of a Continuous Random Variable

Let $f_Y(y)$ denote the probability density function of Y. Because probabilities cannot be negative, we have $f_Y \geq 0$ for all y. The Probability that Y falls between a and b, $a < b$ is

$$P(a \leq Y \leq b) = \int_a^b f_Y(y)\mathrm{d}y.$$

We further have that $P(-\infty \leq Y \leq \infty) = 1$ and therefore $\int_{-\infty}^{\infty} f_Y(y)\mathrm{d}y = 1$.

As for the discrete case, the expected value of Y is the probability weighted average of its values. Due to continuity, we use intergrals instead of sums.

The expected value of Y is

$$E(Y) = \mu_Y = \int y f_Y(y)\mathrm{d}y.$$

The variance is the expected value of $(Y - \mu_Y)^2$. We thus have

$$\text{Var}(Y) = \sigma_Y^2 = \int (y - \mu_Y)^2 f_Y(y)\mathrm{d}y.$$

Let us discuss an example:

Consider the continuous random variable X with propability density function

$$f_X(x) = \frac{3}{x^4}, x > 1.$$

- We can show analytically that the integral of $f_X(x)$ over the real line equals 1.

$$\begin{align}
\int f_X(x) \mathrm{d}x =& \int_1^\infty \frac{3}{x^4} \mathrm{d}x \tag{2.1}\\
=& \lim_{t \to \infty} \int_1^t \frac{3}{x^4} \mathrm{d}x \tag{2.2}\\
=& \lim_{t \to \infty} -x^{-3}\rvert_{x=1}^t \tag{2.3}\\
=& -\left(\lim_{t \to \infty} \frac{1}{t^3} - 1 \right) \tag{2.4}\\
=&1 \tag{2.5}
\end{align}$$

- The expectation of X can be computed as follows:

$$\begin{align}
E(X) = \int x \cdot f_X(x) \mathrm{d}x =& \int_1^\infty x \cdot \frac{3}{x^4} \mathrm{d}x \tag{2.6}\\
=& -\frac{3}{2} x^{-2}\rvert_{x=1}^\infty \tag{2.7}\\
=& -\frac{3}{2} \left(\lim_{t \to \infty} \frac{1}{t^2} - 1 \right) \tag{2.8}\\
=&\frac{3}{2} \tag{2.9}
\end{align}$$

- Note that the variance of X can be expressed as $\text{Var}(X) = E(X^2) - E(X)^2$. Since $E(X)$ has been computed in the previous step, we seek $E(X^2)$:

$$\begin{align}
E(X^2) = \int x^2 \cdot f_X(x) \mathrm{d}x =& \int_1^\infty x^2 \cdot \frac{3}{x^4} \mathrm{d}x \tag{2.10}\\
=& -3x^{-1}\rvert_{x=1}^\infty \tag{2.11}\\
=& -3 \left(\lim_{t \to \infty} \frac{1}{t} - 1 \right) \tag{2.12}\\
=&3 \tag{2.13}
\end{align}$$

So we have shown that the area under the curve equals one, that the expectation is $E(X) = \frac{3}{2}$ and we found the variance to be $\text{Var}(X) = \frac{3}{4}$. However, this was quite tedious and, as we shall see soon, an analytic approach is not applicable for some probability density functions e.g. if integrals have no closed form solutions.

Luckily, R enables us to find the results derived above in an instant. The tool we use for this is the function `integrate()`. First, we have to define the functions we want to calculate integrals for as R functions, i.e. the PDF $f_X(x)$ as well as the expressions $x \cdot f_X(x)$ and $x^2 \cdot f_X(x)$.

```r
# define functions
f <- function(x) 3/x^4
g <- function(x) x*f(x)
h <- function(x) x^2*f(x)
```

Next, we use `integrate()` and set lower and upper limits of integration to 1 and ∞ using arguments `lower` and `upper`. By default, `integrate()` prints the result along with an estimate of the calculation error to the console. However, the outcome is not a numeric value one can do further calculation with readily. In order to get only a numeric value of the integral, we need to use the `$` operator in conjunction with `value`.

```
# calculate area under curve
AUC <- integrate(f,
                 lower = 1,
                 upper = Inf
                 )
AUC
```

```
## 1 with absolute error < 1.1e-14
```

```
# calculate E(X)
EX <- integrate(g,
                lower = 1,
                upper = Inf)
EX
```

```
## 1.5 with absolute error < 1.7e-14
```

```
# calculate Var(X)
VarX <- integrate(h,
                  lower = 1,
                  upper = Inf
                  )$value - EX$value^2
VarX
```

```
## [1] 0.75
```

Although there is a wide variety of distributions, the ones most often encountered in econometrics are the normal, chi-squared, Student t and F distributions. Therefore we will discuss some core R functions that allow to do calculations involving densities, probabilities and quantiles of these distributions.

Every probability distribution that R handles has four basic functions whose names consist of a prefix followed by a root name. As an example, take the normal distribution. The root name of all four functions associated with the normal distribution is norm. The four prefixes are

- d for “density” - probability function / probability density function
- p for “probability” - cumulative distribution function
- q for “quantile” - quantile function (inverse cumulative distribution function)
- r for “random” - random number generator

Thus, for the normal distribution we have the R functions `dnorm()`, `pnorm()`, `qnorm()` and `rnorm()`.

The Normal Distribution

The probably most important probability distribution considered here is the normal distribution. This is not least due to the special role of the standard normal distribution and the Central Limit Theorem which is treated shortly during the course of this section. Distributions of the normal family have a familiar symmetric, bell-shaped probability density. A normal distribution is characterized by its mean μ and its standard deviation σ what is concisely expressed by $N(\mu, \sigma^2)$. The normal distribution has the PDF

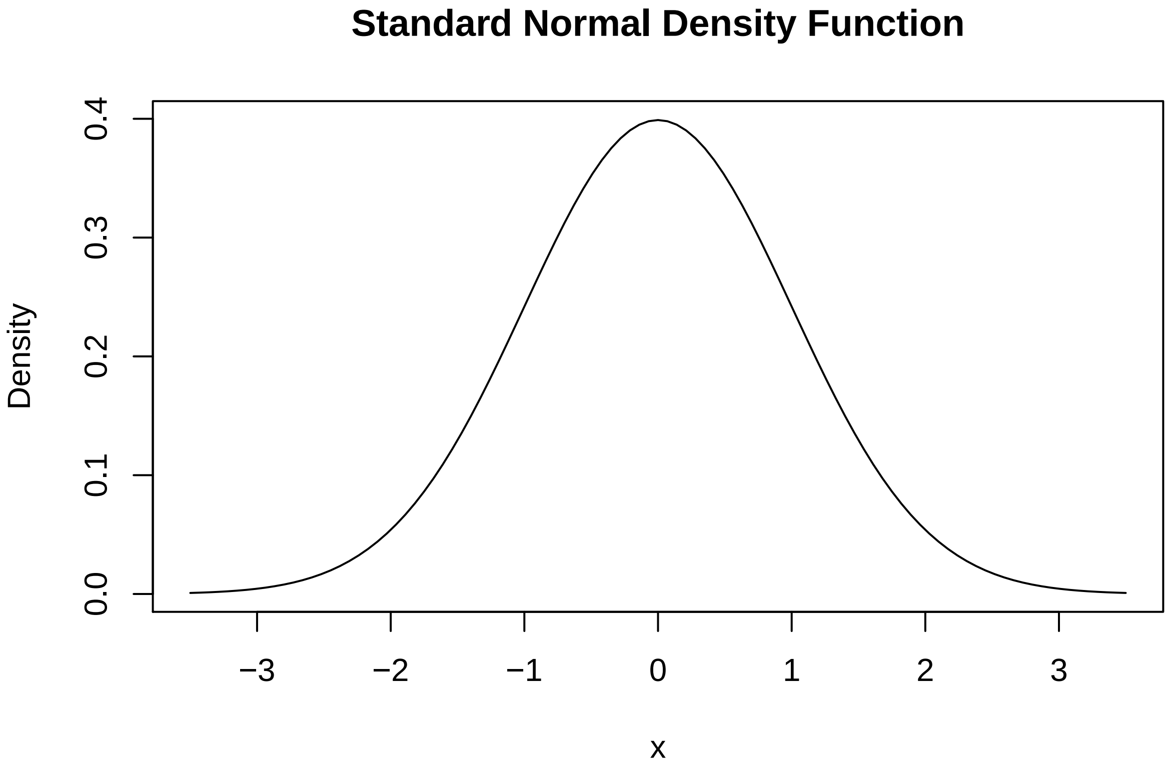
$$f(x) = \frac{1}{\sqrt{2\pi}\sigma} e^{-(x-)^2/(2^2)}.$$

For the standard normal distribution we have $\mu = 0$ and $\sigma = 1$. Standard normal variates are often denoted Z. Usually, the standard normal PDF is denoted by ϕ and the standard normal CDF is denoted by Φ. Hence,

$$\phi(c) = \Phi'(c) \ \ , \ \ \Phi(c) = P(Z \leq c) \ \ , \ \ Z \sim N(0,1).$$

In R, we can conveniently obtain density values of normal distributions using the function `dnorm()`. Let us draw a plot of the standard normal density function using `curve()` and `dnorm()`.

```
# draw a plot of the N(0,1) pdf
curve(dnorm(x),
      xlim=c(-3.5, 3.5),
      ylab = "Density",
      main = "Standard Normal Density Function"
      )
```



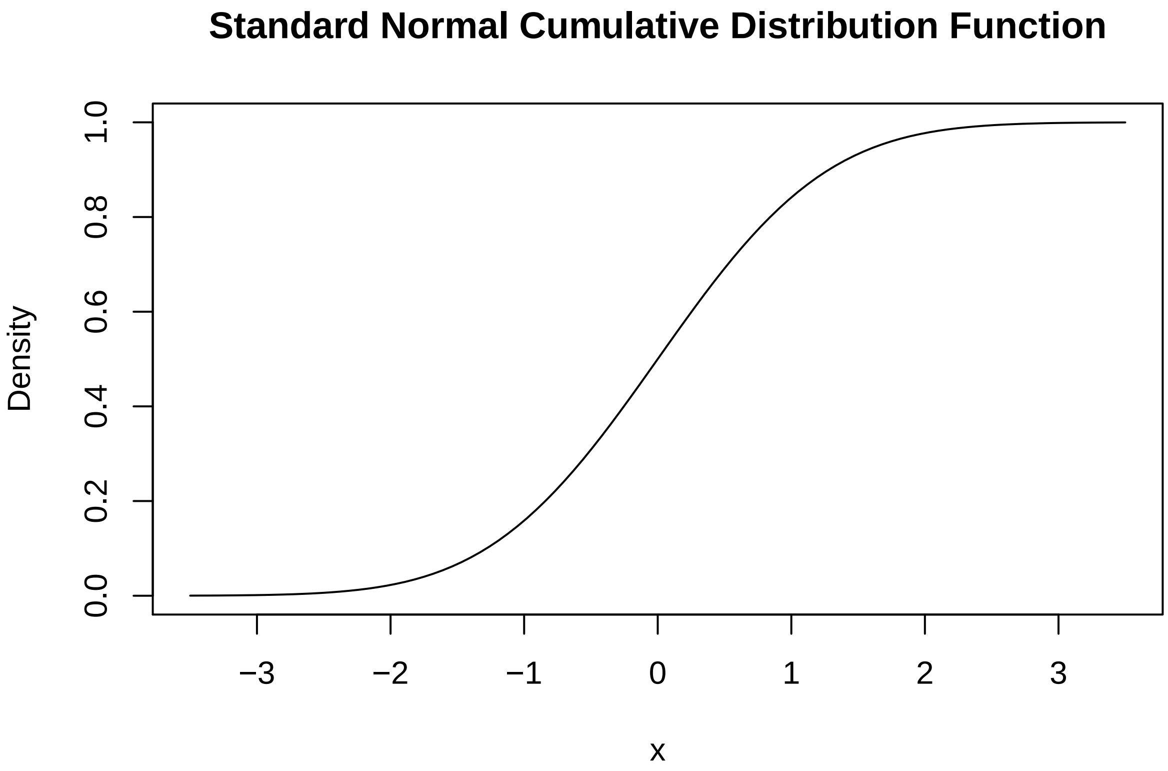
We can obtain the density at different positions by passing a vector of quantiles to `dnorm()`.

```
# compute denstiy at x=-1.96, x=0 and x=1.96
dnorm(x = c(-1.96, 0, 1.96))
```

```
## [1] 0.05844094 0.39894228 0.05844094
```

Similary as for the PDF, we can plot the standard normal CDF using `curve()` and `pnorm()`.

```
# plot the standard normal CDF
curve(pnorm(x),
      xlim=c(-3.5, 3.5),
      ylab = "Density",
      main = "Standard Normal Cumulative Distribution Function"
      )
```



We can also use R to calculate the probability of events associated with a standard normal random variate.

Let us say we are interested in $P(Z \leq 1.337)$. For some general continuous random variable Z on $[-\infty, \infty]$ with density function $g(x)$ we would have to determine $G(x)$, the antiderivative of $g(x)$ since

$$P(Z \leq 1,337) = G(1,337) = \int_{-\infty}^{1,337} g(x)\mathrm{d}x.$$

However, if $Z \sim N(0,1)$, we have $g(x) = \phi(x)$ so there is no analytic solution to the integral above and it is cumbersome to come up with an approximation. However, we may circumvent this using R in different ways. The first approach makes use of the function `integrate()` which allows to solve one-dimensional integration problems using a numerical method. For this, we first define the function we want to compute the integral of as a R function `f`. In our example, `f` needs to be the standard normal density function and hence takes a single argument `x`. Following the definition of $\phi(x)$ we define `f` as

```r
# define the standard normal PDF as a R function
f <- function(x) {
  1/(sqrt(2 * pi)) * exp(-0.5 * x^2)
}
```

Let us check if this function enables us to compute standard normal density values by passing it a vector of quantiles.

```r
# define vector of quantiles
quants <- c(-1.96,0,1.96)

# compute density values
f(quants)
```

```
## [1] 0.05844094 0.39894228 0.05844094
```

```
# compare to results produced by dnorm()
f(quants) == dnorm(quants)
```

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

Notice that the results produces by `f()` are indeed equivalent to those given by `dnorm()`.

Next, we call `integrate()` on `f()` and further specify the arguments `lower` and `upper`, the lower and upper limits of integration.

```
# integrate f()
integrate(f,
          lower = -Inf,
          upper = 1.337
          )
```

```
## 0.9093887 with absolute error < 1.7e-07
```

We find that the probability of observing $Z \leq 1,337$ is about 0.9094%.

A second and much more convenient way is to use the function `pnorm()` which also allows calculus involving the standard normal cumulative distribution function.

```
# compute a probability using pnorm()
pnorm(1.337)
```

```
## [1] 0.9093887
```

The result matches the outcome of the approach using `integrate()`.

Let us discuss some further examples:

A commonly known result is that 95% probability mass of a standard normal lies in the intervall $[-1.96, 1.96]$, that is in a distance of about 2 standard deviations to the mean. We can easily confirm this by calculating

$$P(-1.96 \leq Z \leq 1.96) = 1 - 2 \times P(Z \leq -1.96)$$

due to symmetry of the standard normal PDF. Thanks to R, we can abondon the table of the standard normal CDF again and instead solve this by means of the function `pnorm()`.

```
# compute the probability
1 - 2 * (pnorm(-1.96))
```

```
## [1] 0.9500042
```

Now consider a random variable Y with $Y \sim N(5, 25)$. As You should already know from Your statistics courses it is not possible to make any statement of probability without prior standardizing as shown in Key Concept 2.4.

Key Concept 2.4

Computing Probabilities Involving Normal Random Variables

Suppose Y is normally distributed with mean μ and variance σ^2:

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

Then Y is standardized by substracting its mean and dividing by its standard deviation:

$$Z = \frac{Y - \mu}{\sigma}$$

Let c_1 and c_2 denote two numbers whereby $c_1 < c_2$ and further $d_1 = (c_1 - \mu)/\sigma$ and $d_2 = (c_2 - \mu)/\sigma$. Then

$$
\begin{aligned}
P(Y \leq c_2) &= P(Z \leq d_2) = \Phi(d_2) && (2.14)\\
P(Y \geq c_1) &= P(Z \geq d_1) = 1 - \Phi(d_1) && (2.15)\\
P(c_1 \leq Y \leq c_2) &= P(d_1 \leq Z \leq d_2) = \Phi(d_2) - \Phi(d_1) && (2.16)
\end{aligned}
$$

R functions that handle the normal distribution can perform this standardization. If we are interested in $P(3 \leq Y \leq 4)$ we can use `pnorm()` and adjust for a mean and/or a standard deviation that deviate from $\mu = 0$ and $\sigma = 1$ by specifying the arguments `mean` and `sd` accordingly. **Attention**: `pnorm()` requires the argument `sd` which is the standard deviation, not the variance!

```
pnorm(4, mean = 5, sd = 5) - pnorm(3, mean = 5, sd = 5)
```

```
## [1] 0.07616203
```

An extension of the normal distribution in a univariate setting is the multivariate normal distribution. The PDF of two random normal variables X and Y is given by

$$
\begin{aligned}
g_{X,Y}(x,y) = &\frac{1}{2\pi\sigma_X\sigma_Y\sqrt{1-\rho_{XY}^2}} && (2.17)\\
&\cdot \exp\left\{\frac{1}{-2(1-\rho_{XY}^2)}\left[\left(\frac{x-\mu_x}{\sigma_x}\right)^2 - 2\rho_{XY}\left(\frac{x-\mu_X}{\sigma_X}\right)\left(\frac{y-\mu_Y}{\sigma_Y}\right) + \left(\frac{y-\mu_Y}{\sigma_Y}\right)^2\right]\right\}. && (2.18)
\end{aligned}
$$

Equation (2.18) contains the bivariate normal PDF. Admittedly, it is hard to gain insights from this complicated expression. Instead, let us consider the special case where X and Y are uncorrelated standard normal random variables with density functions $f_X(x)$ and $f_Y(y)$ and we assume that they have a joint normal distribution. We then have the parameters $\sigma_X = \sigma_Y = 1$, $\mu_X = \mu_Y = 0$ (due to marginal standard normality) and $\rho_{XY} = 0$ (due to uncorrelatedness). The joint probability density function of X and Y then becomes

$$
g_{X,Y}(x,y) = f_X(x)f_Y(y) = \frac{1}{2\pi} \cdot \exp\left\{-\frac{1}{2}\left[x^2 + y^2\right]\right\}, \tag{2.2}
$$

the PDF of the bivariate standard normal distribution. The next plot provides an interactive three dimensional plot of (2.2). By moving the mouse curser over the plot You can see that the density is rotationally invariant.

The Chi-Squared Distribution

Another distribution relevant in econometric day-to-day work is the chi-squared distribution. It is often needed when testing special types of hypotheses frequently ecountered when dealing with regression models.

The sum of M squared independent standard normal distributed random variables follows a chi-squared distribution with M degrees of freedom.

$$
Z_1^2 + \cdots + Z_M^2 = \sum_{m=1}^{M} Z_m^2 \sim \chi_M^2 \ \text{ with } \ Z_m \overset{i.i.d.}{\sim} N(0,1)
$$

A χ^2 distributed random variable with M degrees of freedom has expectation M, mode at $M-2$ for $n \geq 2$ and variance $2 \cdot M$.

For example, if we have

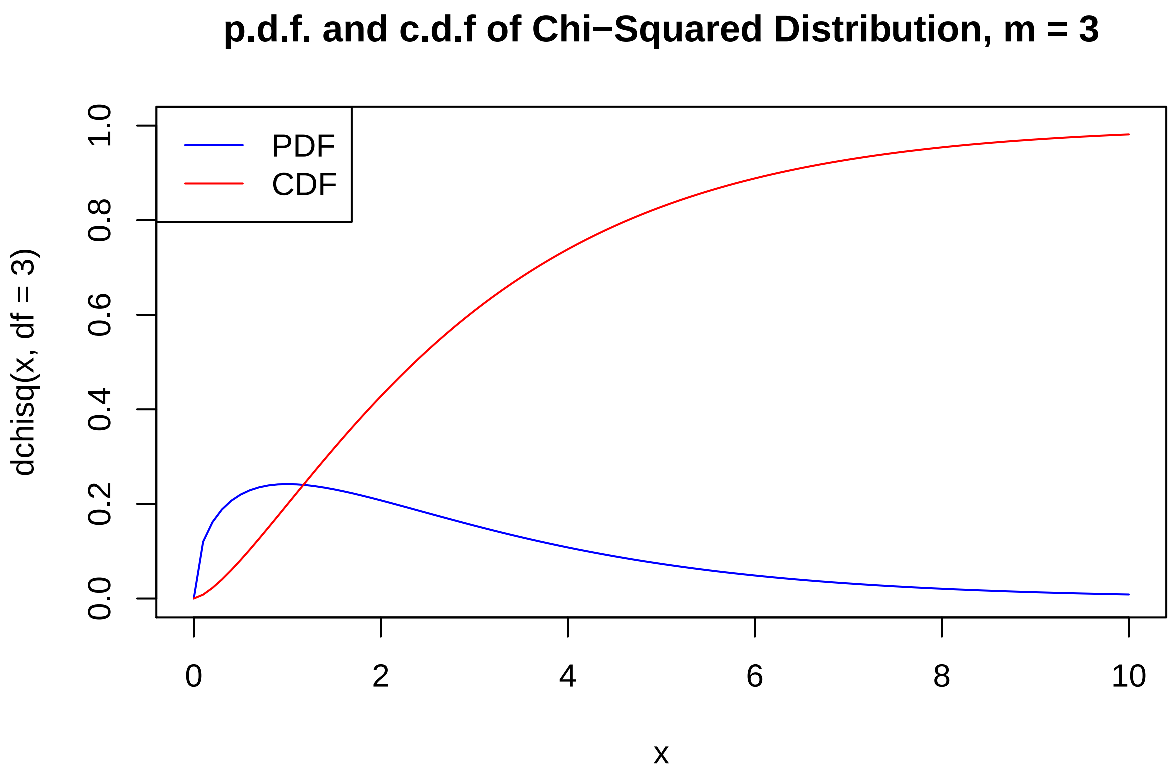
$$Z_1, Z_2, Z_3 \overset{i.i.d.}{\sim} N(0,1)$$

it holds that

$$Z_1^2 + Z_2^2 + Z_3^3 \sim \chi^2_3. \tag{2.3}$$

By means of the code below, we can display the PDF and the CDF of a χ^2_3 random variable in a single plot. This is achieved by setting the argument `add = TRUE` in the second call of `curve()`. Further we adjust limits of both axes using `xlim` and `ylim` and choose different colors to make both functions better distinguishable. The plot is completed by adding a legend with help of the function `legend()`.

```r
# plot the PDF
curve(dchisq(x, df=3),
      xlim=c(0,10),
      ylim = c(0,1),
      col="blue",
      main="p.d.f. and c.d.f of Chi-Squared Distribution, m = 3"
      )

# add the CDF to the plot
curve(pchisq(x, df=3),
      xlim=c(0,10),
      add = TRUE,
      col="red"
      )

# add a legend to the plot
legend("topleft",
       c("PDF","CDF"),
       col = c("blue","red"),
       lty = c(1,1)
       )
```



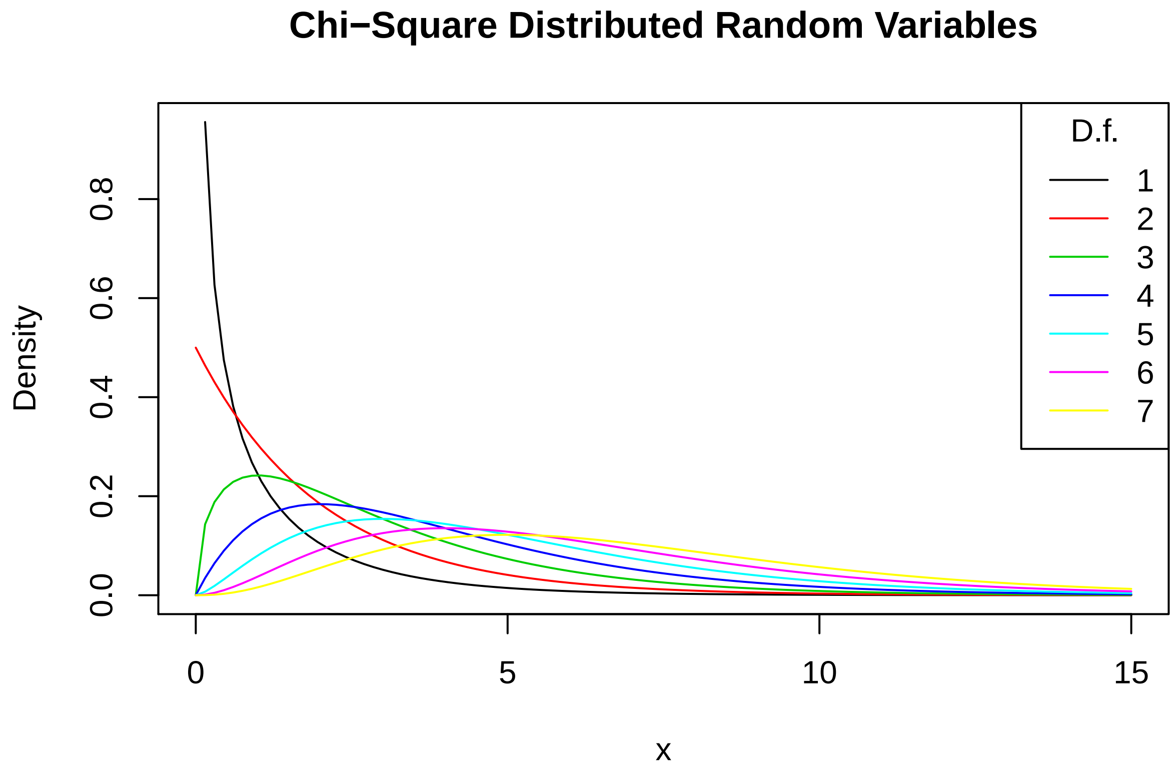
Notice that, since the outcomes of a χ^2_M distributed random variable are always positive, the domain of the related PDF and CDF is $\mathbb{R}_{\geq 0}$.

As expectation and variance depend (solely) on the degrees of freedom, the distribution's shape changes drastically if we vary the number of squared standard normals that are summed up. This relation is often depicted by overlaying densities for different M, see e.g. the Wikipedia Article.

Of course, one can easily reproduce such a plot using R. Again we start by plotting the density of the χ_1^2 distribution on the intervall $[0, 15]$ with `curve()`. In the next step, we loop over degrees of freedom $m = 2, ..., 7$ and add a density curve for each m to the plot. We also adjust the line color for each iteration of the loop by setting `col = m`. At last, we add a legend that displays degrees of freedom and the associated colors.

```
# plot the density for m=1
curve(dchisq(x, df=1),
      xlim=c(0,15),
      xlab = "x",
      ylab = "Density",
      main="Chi-Square Distributed Random Variables"
      )

# add densities for m=2,...,7 to the plot using a for loop
for (m in 2:7) {
  curve(dchisq(x, df = m),
        xlim = c(0,15),
        add = T,
        col = m
        )
}

# add a legend
```

```r
legend("topright",
       as.character(1:7),
       col = 1:7 ,
       lty = 1,
       title = "D.f."
       )
```



It is evident that increasing the degrees of freedom shifts the distribution to the right (the modus becomes larger) and increases its dispersion (the distribution's variance grows).

The Student t Distribution

Let Z be a standard normal variate, W a random variable that follows a χ^2_M distribution with M degrees of freedom and further assume that Z and W are independently distributed. Then it holds that

$$\frac{Z}{\sqrt{W/M}} =: X \sim t_M$$

and we say that X follows a student t distribution (or simple t distribution) with M degrees of freedom.

As for the χ^2_M distribution, a t distribution depends on the degrees of freedom M. t distributions are symmetric, bell-shaped and look very similar to a normal distribution, especially when M is large. This is not a coincidence: for a sufficient large M, a t_M distribution can be approximated by the standard normal distribution. This approximation works reasonably well for $M \geq 30$. As we will show later by means of a small simulation study, the t_∞ distribution *is* the standard normal distribution.

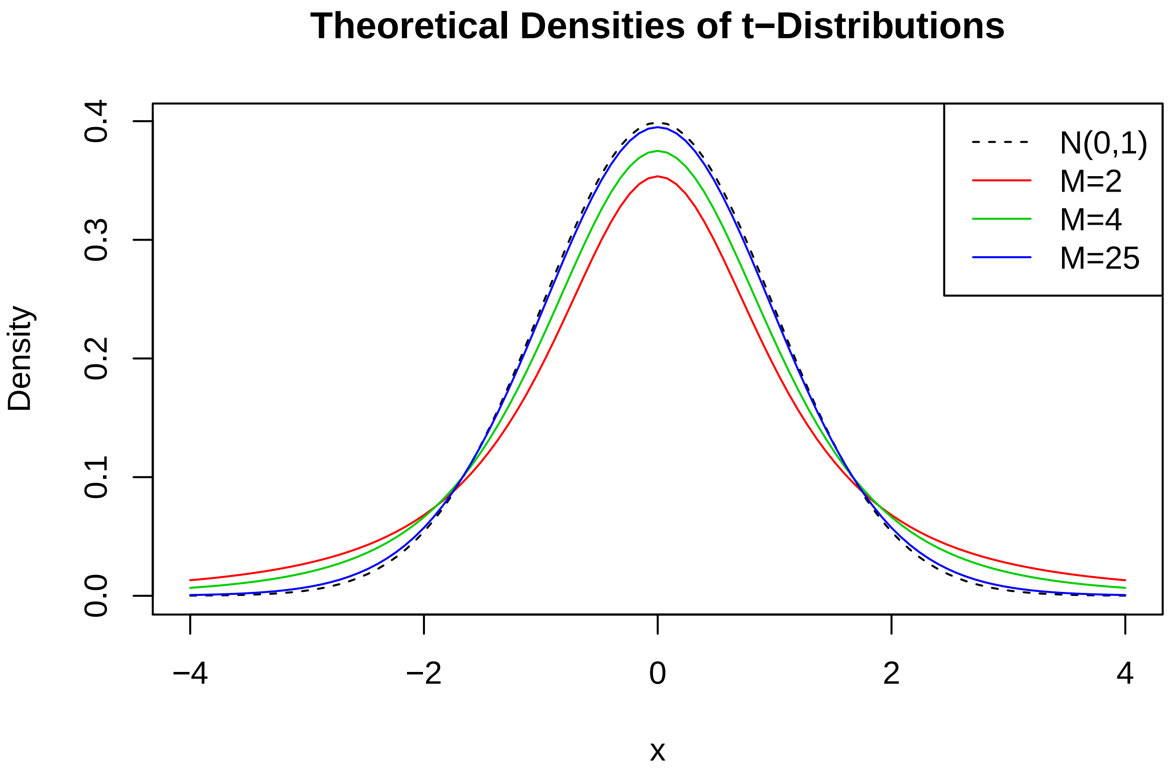
A t_M distributed random variable has an expectation value if $M > 1$ and a variance if $n > 2$.

$$E(X) = 0 \ , \ \ M > 1 \tag{2.19}$$

$$\text{Var}(X) = \frac{M}{M-2} \ , \ \ M > 2 \tag{2.20}$$

Let us graph some t distributions with different M and compare them with the standard normal distribution.

```
# plot the standard normal density
curve(dnorm(x),
      xlim=c(-4,4),
      xlab = "x",
      lty=2,
      ylab = "Density",
      main="Theoretical Densities of t-Distributions"
      )

# plot the t density for m=2
curve(dt(x, df=2),
      xlim=c(-4,4),
      col=2,
      add = T
      )

# plot the t density for m=4
curve(dt(x, df=4),
      xlim=c(-4,4),
      col=3,
      add=T
      )

# plot the t density for m=25
curve(dt(x, df=25),
      xlim=c(-4,4),
      col=4,
      add=T
      )

# add a legend
legend("topright",
       c("N(0,1)","M=2","M=4","M=25"),
       col = 1:4,
       lty = c(2,1,1,1)
       )
```



The plot indicates what has been claimed in the previous paragraph: as the degrees of freedom increase, the shape of the t distribution comes closer to that of a standard normal bell. Already for $M = 25$ we find little difference to the dashed line which belongs to the standard normal density curve. If M is small, we find the distribution to have slightly havier tails than a standard normal, i.e. it has a "fatter" bell shape.

The F Distribution

Another ratio of random variables important to econometricians is the ratio of two indpendently χ^2 distributed random variables that are divided by their degrees of freedom. Such a quantity follows a F distribution with numerator degrees of freedom M and denominator degrees of freedom n, denoted $F_{M,n}$. The distribution was first derived by George Snedecor but was named in honor of Sir Ronald Fisher.

$$\frac{W/M}{V/n} \sim F_{M,n} \ \text{ with } \ W \sim \chi^2_M \ \ , \ \ V \sim \chi^2_n$$

By definition, the domain of both PDF and CDF of a $F_{M,n}$ distributed random variable is $\mathbb{R}_{\geq 0}$.

Say we have a F distributed random variable Y with numerator degrees of freedom 3 and denominator degrees of freedom 14 and are interested in $P(Y \geq 2)$. This can be computed with help of the function `pf()`. By setting the argument `lower.tail` to `TRUE` we ensure that R computes $1 - P(Y \leq 2)$, i.e. the probability mass in the tail right of 2.

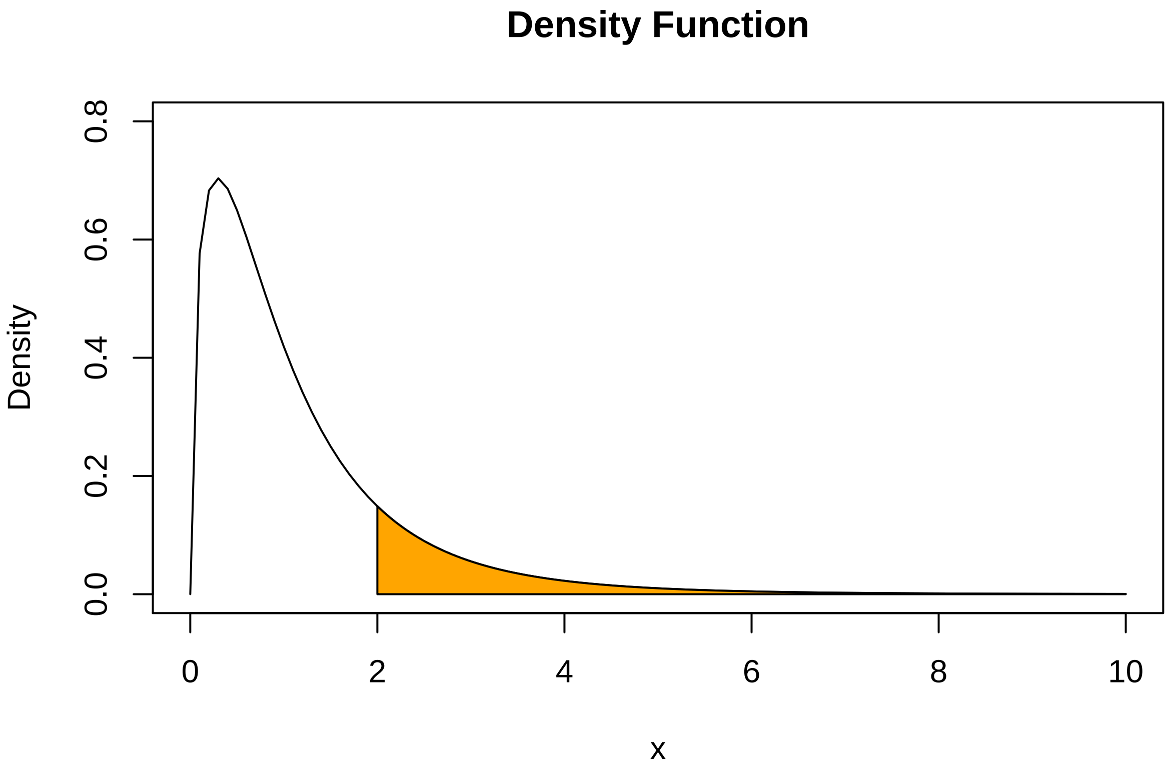
```
pf(2, 3, 13, lower.tail = F)
```

```
## [1] 0.1638271
```

We can visualize this probability by drawing a line plot of the related density function and adding a color shading with `polygon()`.

```
# define coordinate vectors for vertices of the polygon
x <- c(2, seq(2, 10, 0.01), 10)
```

```
y <- c(0, df(seq(2, 10, 0.01), 3, 14), 0)

# draw density of F_{3, 14}
curve(df(x ,3 ,14),
      ylim = c(0, 0.8),
      xlim = c(0, 10),
      ylab = "Density",
      main = "Density Function"
      )

# draw the polygon
polygon(x, y, col="orange")
```



The F distribution is related to many other distributions. An important special case encountered in econometrics arises if the denominator degrees of freedom are large such that the $F_{M,n}$ distribution can be approximated by the $F_{M,\infty}$ distribution which turns out to be simply the distribution of a χ^2_M random variable divided by its degrees of freedom M.

$$W/M \sim F_{M,\infty} \quad , \quad W \sim \chi^2_M$$

2.3 Random Sampling and the Distribution of Sample Averages

To clarify the basic idea of random sampling, let us jump back to the die rolling example:

Suppose we are rolling the dice n times. This means we are interested in the outcomes of n random processes $Y_i, \ i = 1, ..., n$ which are characterized by the same distribution. Since these outcomes are selected randomly, they are *random variables* themselves and their realisations will differ each time we draw a sample, i.e. each time we roll the dice n times. Furthermore, each observation is randomly drawn from the same population, that is the numbers from 1 to 6, and their individual distribution is the same. Hence we say that $Y_1, \dots, Y_n$ are identically distributed. Moreover, we know that the value of any of the Y_i does not provide any information on the remainder of the sample. In our example, rolling a six as the first observation in our sample does not alter the distributions of $Y_2, \dots, Y_n$: all numbers are equally likely to occur. This means that all Y_i are also independently distributed. Thus, we say that $Y_1, \dots, Y_n$ are independently and identically distributed ($i.i.d$). The dice example is the simplest sampling scheme used in statistics. That is why it is called *simple random sampling*. This concept is condensed in Key Concept 2.5.

Key Concept 2.5

Simple Random Sampling and i.i.d. Random Variables

In simple random sampling, n objects are drawn at random from a population. Each object is equally likely to end up in the sample. We denote the value of the random variable Y for the i^{th} randomly drawn object as Y_i. Since all objects are equally likely to be drawn and the distribution of Y_i is the same for all i, the $Y_i, \dots, Y_n$ are independently and identically distributed (i.i.d.). This means the distribution of Y_i is the same for all $i = 1, \dots, n$ and Y_1 is distributed independently of $Y_2, \dots, Y_n$ Y_2 is distributed independently of $Y_1, Y_3, \dots, Y_n$ and so forth.

What happens if we consider functions of the sample data? Consider the example of rolling a dice two times in a row once again. A sample now consists of two independent random draws from the set $\{1, 2, 3, 4, 5, 6\}$. In view of the aforementioned, it is apparent that any function of these two random variables is also random, e.g. their sum. Convince Yourself by executing the code below several times.

```r
sum(sample(1:6, 2, replace = T))
```

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

Clearly this sum, let us call it S, is a random variable as it depends on randomly drawn summands. For this example, we can completely enumerate all outcomes and hence write down the theoretical probability distribution of our function of the sample data, S:

We face $6^2 = 36$ possible pairs. Those pairs are

$$
\begin{align}
&(1,1)(1,2)(1,3)(1,4)(1,5)(1,6) \tag{2.21}\\
&(2,1)(2,2)(2,3)(2,4)(2,5)(2,6) \tag{2.22}\\
&(3,1)(3,2)(3,3)(3,4)(3,5)(3,6) \tag{2.23}\\
&(4,1)(4,2)(4,3)(4,4)(4,5)(4,6) \tag{2.24}\\
&(5,1)(5,2)(5,3)(5,4)(5,5)(5,6) \tag{2.25}\\
&(6,1)(6,2)(6,3)(6,4)(6,5)(6,6) \tag{2.26}
\end{align}
$$

Thus, possible outcomes for S are

$$\left\{ 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12 \right\}.$$

Enumeration of outcomes yields

$$P(S) = \begin{cases} 1/36, & S = 2 \\ 2/36, & S = 3 \\ 3/36, & S = 4 \\ 4/36, & S = 5 \\ 5/36, & S = 6 \\ 6/36, & S = 7 \\ 5/36, & S = 8 \\ 4/36, & S = 9 \\ 3/36, & S = 10 \\ 2/36, & S = 11 \\ 1/36, & S = 12 \end{cases} \tag{2.27}$$

We can also compute $E(S)$ and $\text{Var}(S)$ as stated in Key Concept 2.1 and Key Concept 2.2.

```
# Vector of outcomes
S <- 2:12

# Vector of probabilities
PS <- c(1:6,5:1)/36

# Expectation of S
ES <- S %*% PS; ES
```

```
##      [,1]
## [1,]    7
```

```
# Variance of S
VarS <- (S - c(ES))^2 %*% PS; VarS
```

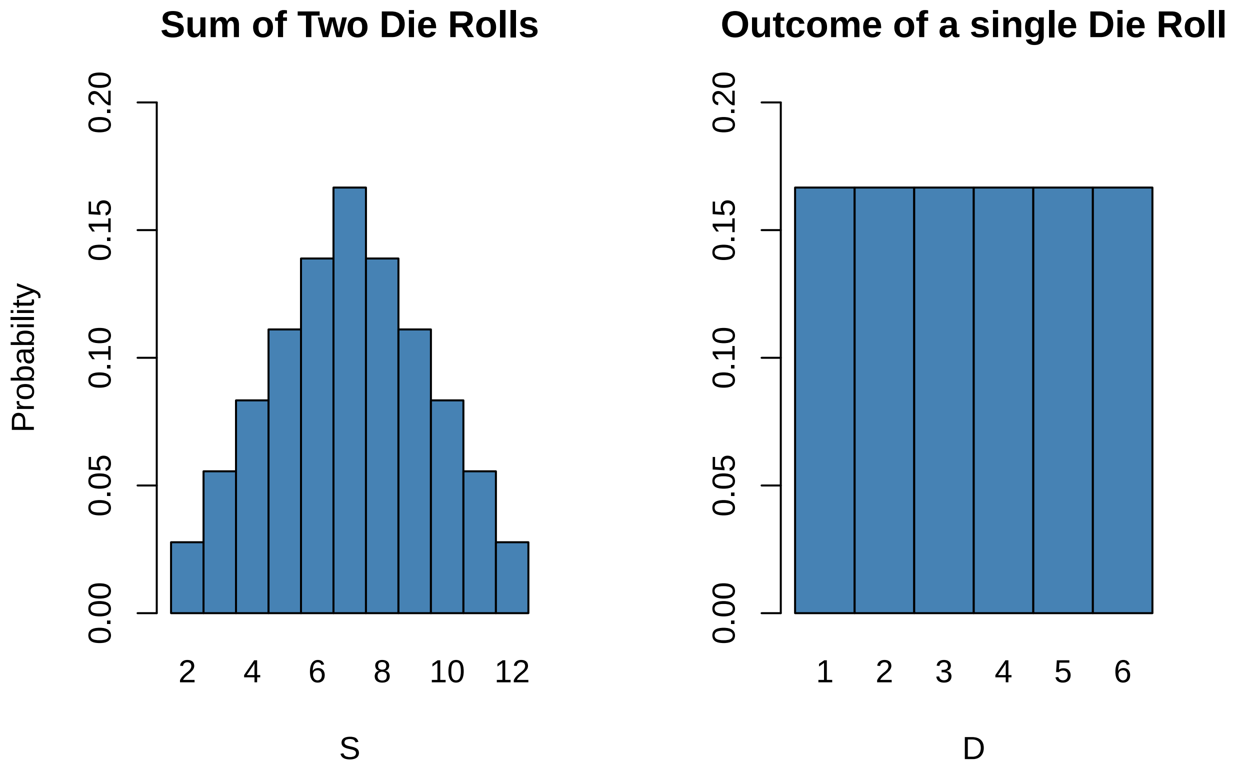
```
##          [,1]
## [1,] 5.833333
```

(The `%*%` operator is used to compute the scalar product of two vectors.)

So the distribution of S is known. It is also evident that its distribution differs considerably from the marginal distribution, i.e. the distribution of a single die roll's outcome, D . Let us visualize this using barplots.

```
# divide the plotting area in one row with two columns
par(mfrow = c(1, 2))

# plot the distribution of S
names(PS) <- 2:12

barplot(PS, ylim=c(0,0.2),
        xlab = "S",
        ylab ="Probability",
        col="steelblue",
        space=0,
        main="Sum of Two Die Rolls"
        )

# plot the distribution of D
probability <- rep(1/6,6)
```

```
names(probability) <- 1:6

barplot(probability,
        ylim=c(0,0.2),
        xlab = "D",
        col="steelblue",
        space = 0,
        main = "Outcome of a single Die Roll"
        )
```



Many econometric procedures deal with averages of sampled data. It is almost always assumed that observations are drawn randomly from a larger, unkown population. As demonstrated for the sample function S, computing an average of a random sample also has the effect to make the average a random variable itself. This random variable in turn has a probability distribution which is called the sampling distribution. Knowledge about the sampling distribution of an average is therefore crucial for understanding the performance of econometric procedures.

The *sample average* of a sample of n observations $Y_1, \dots, Y_n$ is

$$\overline{Y} = \frac{1}{n} \sum_{i=1}^{n} Y_i = \frac{1}{n}(Y_1 + Y_2 + \cdots + Y_n).$$

$\overline{Y}$ is also called the sample mean.

Mean and Variance of the Sample Mean

Denote μ_Y and σ_Y^2 the mean and the variance of the Y_i and suppose that all observations $Y_1, \dots, Y_n$ are i.i.d. such that in particular mean and variance are the same for all $i = 1, \dots, n$. Then we have that

$$E(\overline{Y}) = E\left(\frac{1}{n}\sum_{i=1}^{n} Y_i\right) = \frac{1}{n}E\left(\sum_{i=1}^{n} Y_i\right) = \frac{1}{n}\sum_{i=1}^{n} E\left(Y_i\right) = \frac{1}{n}\cdot n \cdot \mu_Y = \mu_Y$$

and

$$\begin{aligned}
\text{Var}(\overline{Y}) =& \text{Var}\left(\frac{1}{n}\sum_{i=1}^{n} Y_i\right) && (2.28)\\
=& \frac{1}{n^2}\sum_{i=1}^{n}\text{Var}(Y_i) + \frac{1}{n^2}\sum_{i=1}^{n}\sum_{j=1,j\neq i}^{n}\text{cov}(Y_i, Y_j) && (2.29)\\
=& \frac{\sigma_Y^2}{n} && (2.30)\\
=& \sigma_{\overline{Y}}^2. && (2.31)
\end{aligned}$$

Note that the second summand vanishes since $\text{cov}(Y_i, Y_j) = 0$ for $i \neq j$ due to independence of the observations.

Consequently, the standard deviation of the sample mean is given by

$$\sigma_{\overline{Y}} = \frac{\sigma_Y}{\sqrt{n}}.$$

It is worthwhile to mention that these results hold irrespective of the underlying distribution of the Y_i.

The Sampling Distribution of $\overline{Y}$ when Y Is Normally Distributed

If the $Y_1, \dots, Y_n$ are i.i.d. draws from a normal distribution with mean μ_Y and variance σ_Y^2, the following holds for their sample average $\overline{Y}$:

$$\overline{Y} \sim N(\mu_y, \sigma_Y^2/n) \qquad (2.4)$$

For example, if a sample Y_i with $i = 1, \dots, 10$ is drawn from a standard normal distribution with mean $\mu_Y = 0$ and variance $\sigma_Y^2 = 1$ we have

$$\overline{Y} \sim N(0, 0.1).$$

We can use R's random number generation facilities to verifiy this result. The basic idea is to simulate outcomes of the true distribution of $\overline{Y}$ by repeatedly drawing random samples of 10 observation from the $N(0, 1)$ distribution and computing their respective averages. If we do this for a large number of repititions, the simulated dataset of averages should quite accurately reflect the theoretical distribution of $\overline{Y}$ if the theoretical result holds.

The approach sketched above is an example of what is commonly known as *Monte Carlo Simulation* or *Monte Carlo Experiment*. To perform this simulation in R, we proceed as follows:

1. Choose a sample size `n` and the number of samples to be drawn `reps`.
2. Use the function `replicate()` in conjunction with `rnorm()` to draw `n` observations from the standard normal distribution `rep` times. **Note**: the outcome of `replicate()` is a matrix with dimensions `n` × `rep`. It contains the drawn samples as *columns*.
3. Compute sample means using `colMeans()`. This function computes the mean of each column i.e. of each sample and returns a vector.

```r
# Set sample size and number of samples
n <- 10
reps <- 10000

# Perform random sampling
samples <- replicate(reps, rnorm(n)) # 10 x 10000 sample matrix

# Compute sample means
sample.avgs <- colMeans(samples)
```

After performing these steps we end up with a vector of sample averages. You can check the vector property of `sample.avgs`:

```r
# Check that sample.avgs is a vector
is.vector(sample.avgs)
```

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

```r
# print the first few entries to the console
head(sample.avgs)
```

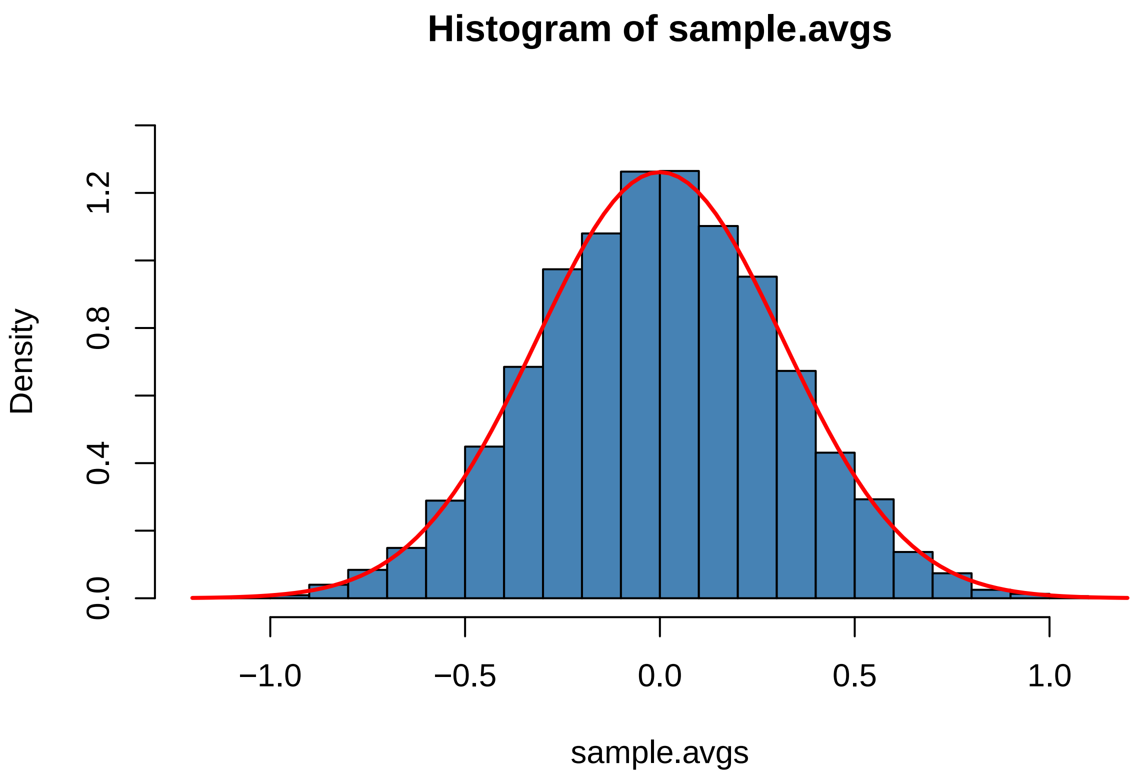
```
## [1] -0.12406767 -0.10649421 -0.01033423 -0.39905236 -0.41897968 -0.90883537
```

A straightforward approach to examine the distribution of univariate numerical data is to plot it as a histogram and compare it to some known or assumed distribution. This comparison can be done with help of a suitable statistical test or by simply eyeballing some graphical representations of these distributions. For our simulated sample averages, we will do the latter by means of the functions `hist()` and `curve()`.

By default, `hist()` will give us a frequency histogram i.e. a bar chart where observations are grouped into ranges, also called bins. The ordinate reports the number of observations falling into each of the bins. Instead, we want it to report density estimates for comparison purposes. This is achieved by setting the argument `freq = FALSE`. The number of bins is adjusted by the argument `breaks`.

Using `curve()`, we overlay the histogram with a red line which represents the theoretical density of a $N(0, 0.1)$ distributed random variable. Remember to use the argument `add = TRUE` to add the curve to the current plot. Otherwise R will open a new graphic device and discard the histogram plot!

```r
# Plot the density histogram
hist(sample.avgs,
     ylim=c(0,1.4),
     col="steelblue" ,
     freq = F,
     breaks = 20
     )

# overlay the theoretical distribution of sample averages on top of the histogram
curve(dnorm(x, sd = 1/sqrt(n)),
      col="red",
      lwd="2",
      add=T
      )
```



From inspection of the plot we can tell that the distribution of $\overline{Y}$ is indeed very close to that of a $N(0, 0.1)$ distributed random variable so that evidence obained from the Monte Carlo Simulation supports the theoretical claim.

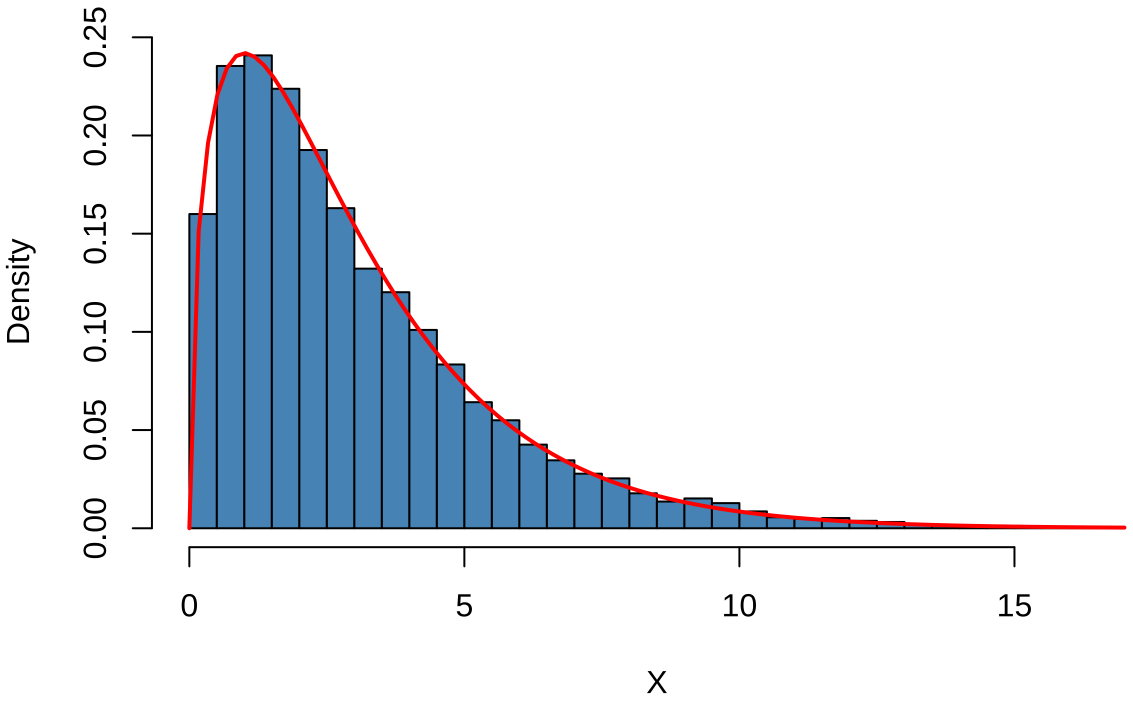
Let us discuss another example where using simple random sampling in a simulation setup helps to verify a well known result. As discussed before, the Chi-squared distribution with m degrees of freedom arises as the distribution of the sum of m independent squared standard normal distributed random variables.

To visualize the claim stated in equation (2.3), we proceed similarly as in the example before:

1. Choose the degrees of freedom `DF` and the number of samples to be drawn `reps`.
2. Draw `reps` random samples of size `DF` from the standard normal distribution using `replicate()`.
3. For each sample, by squaring the outcomes and summing them up columnwise. Store the results

Again, we produce a density estimate for the distribution underlying our simulated data using a density histogram and overlay it with a line graph of the theoretical density function of the χ^2_3 distribution.

```
# Number of repititions
reps <- 10000

# Set degrees of freedom of a chi-Square Distribution
DF <- 3

# Sample 10000 column vectors à 3 N(0,1) R.V.S
Z <- replicate(reps, rnorm(DF))

# Column sums of squares
X <- colSums(Z^2)

# Histogram of column sums of squares
hist(X,
     freq = F,
     col="steelblue",
     breaks = 40,
     ylab="Density",
     main=""
     )

# Add theoretical density
curve(dchisq(x, df = DF),
      type = 'l',
      lwd = 2,
      col="red",
      add = T
      )
```



Large Sample Approximations to Sampling Distributions

Sampling distributions as considered in the last section play an important role in the development of econometric methods. In general, there are two different approaches in characterizing sampling distributions: an "exact" approach and an "approximate" approach.

The exact approach aims to find a general formula for the sampling distribution that holds for any sample size n. We call this the *exact distribution* or *finite sample distribution*. In the previous examples of die rolling and normal variates, we have dealt with functionals of random variables whose sample distributions are *excactly known* in the sense that we can write them down as analytical expressions and do calculations. However, this is not always possible. For $\overline{Y}$, result (2.4) tells us that normality of the Y_i implies normality of $\overline{Y}$ (we demonstrated this for the special case of $Y_i \overset{i.i.d.}{\sim} N(0,1)$ with $n = 10$ using a simulation study that involves random sampling). Unfortunately, the *exact* distribution of $\overline{Y}$ is unknown, very hard to derive or even untractable if we drop the assumption of Y having a normal distribution.

Therefore, as can be guessed from its name, the "approximate" approach aims to find an approximation to the sampling distribution wherby it is required that the sample size n is large. A distribution that is used as a large-sample approximation to the sampling distribution is also called the *asymptotic distribution*. This is due to the fact that the asymptotic distribution *is* the sampling distribution for $n \to \infty$ i.e. the approximation becomes exact if the sample size goes to infinity. However, there are cases where the difference between the sampling distribution and the asymptotic distribution is negligible for moderate or even small samples sizes so that approximations work very good.

In this section we will discuss two well known results that are used to approximate sampling distributions and thus consitute key tools in econoemtric theory: the *law of large numbers* and the *central limit theorem*. The law of large numbers states that in large samples, $\overline{Y}$ is close to μ_Y with high probability. The central limit theorem says that the sampling distribution of the standardized sample average, that is $(\overline{Y} - \mu_Y)/\sigma_{\overline{Y}}$ is asymptotically normal distributed. It is particualarly interesting that both results do not depend on the distribution of Y. In other words, beeing unable to describe the complicated sampling distribution of $\overline{Y}$ if Y is not normal, approximations of the latter using the central limit theorem simplify the development and applicability of econometric procedures enormously. This is a key component underlying the theory of statistical inference for regression models. Both results are summarized in Key Concept 2.6 and Key Concept 2.7.

Key Concept 2.6

Convergence in Probability, Consistency and the Law of Large Numbers

The sample average $\overline{Y}$ converges in probability to μ_Y — we say that $\overline{Y}$ is *consistent* for μ_Y — if the probability that $\overline{Y}$ is in the range $(\mu_Y - \epsilon)$ to $(\mu_Y + \epsilon)$ becomes arbitrarily close to 1 as n increases for any constant $\epsilon > 0$. We write this short as

$$\overline{Y} \xrightarrow{p} \mu_Y.$$

Consider the independently and identically distributed random variables $Y_i, i = 1, \dots, n$ with expectation $E(Y_i) = \mu_Y$ and variance $\text{Var}(Y_i) = \sigma^2_Y$. Under the condition that $\sigma^2_Y < \infty$, that is large outliers are unlikely, the law of large numbers states

$$\overline{Y} \xrightarrow{p} \mu_Y.$$

The core statement of the law of large numbers is that under quite general conditions, the probability of obtaining a sample average $\overline{Y}$ that is close to μ_Y is high if we have a large sample size.

Consider the example of repeatedly tossing a coin where Y_i is the result of the i^{th} coin toss. Y_i is a Bernoulli distributed random variable with

$$P(Y_i) = \begin{cases} p, & Y_i = 1 \\ 1 - p, & Y_i = 0 \end{cases}$$

where $p = 0.5$ as we assume a fair coin. It is straightforward to show that

$$\mu_Y = p = 0.5.$$

Say p is the probabiliy of observing head and denote R_n the proportion of heads in the first n tosses,

$$R_n = \frac{1}{n} \sum_{i=1}^{n} Y_i. \tag{2.5}$$

According to the law of large numbers, the observed proportion of heads converges in probability to $\mu_Y = 0.5$, the probability of tossing head in a single coin toss,

$$R_n \xrightarrow{p} \mu_Y = 0.5 \ \text{ as } \ n \rightarrow \infty.$$

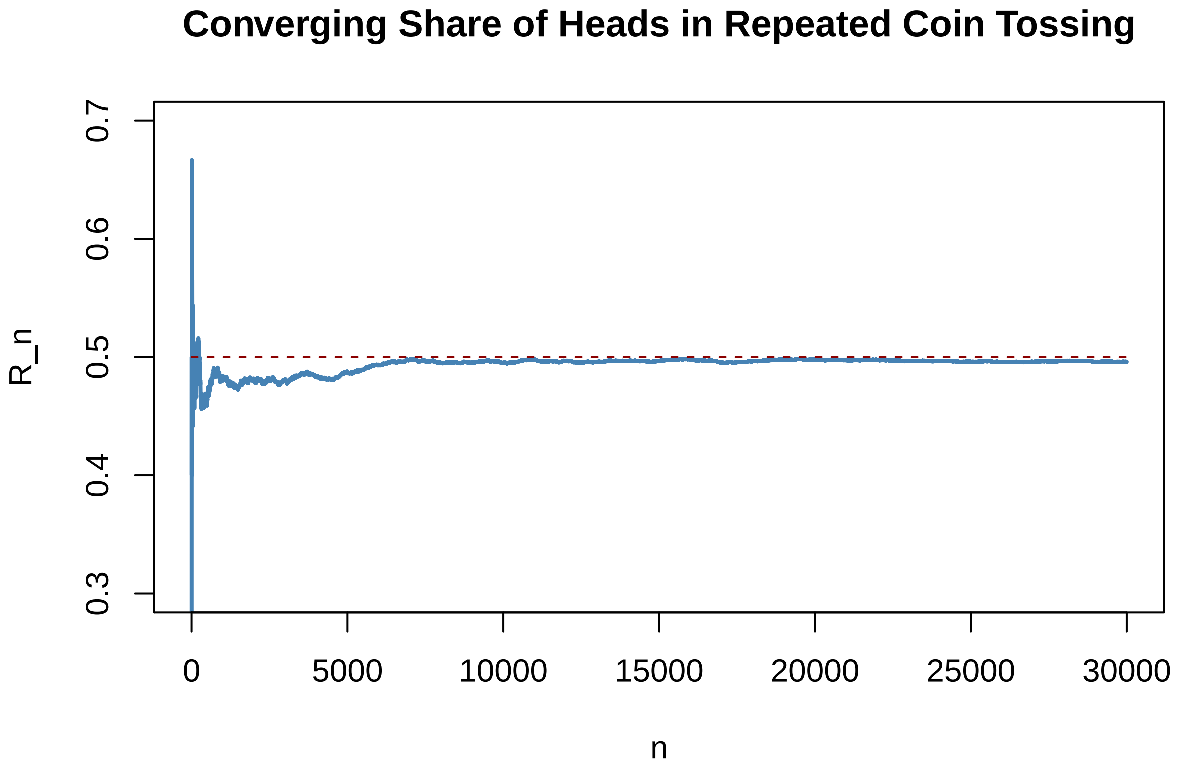
The following application simulates 1000 coin tosses with a fair coin and computes the fraction of heads observed for each additional toss interactively. The result is a random path that, as stated by the law of large numbers, shows a tendency to approach the vaule of 0.5 as n grows.

We can use R to compute and illustrate such paths by simulation. The procedure is as follows:

1. Sample `N` observations from the Bernoulli distribution e.g. using `sample()`.
2. Calculate the proportion of heads R_n as in (2.5). A way to achieve this is to call `cumsum()` on the vector of observations `Y` to obtain its cumulative sum and then divide by the respective number of observations.

We continue by plotting the path and also add a dashed line for the benchmark $R_n = p = 0.5$.

```r
# set random seed
set.seed(1)

# Set number of coin tosses and simulate
N <- 30000
Y <- sample(0:1, N, replace =T)

# Calculate R_n for 1:N
S <- cumsum(Y)
R <- S/(1:N)

# Plot the path.
plot(R,
     ylim=c(0.3, 0.7),
     type = "l",
     col = "steelblue",
     lwd = 2,
     xlab = "n",
     ylab = "R_n",
     main = "Converging Share of Heads in Repeated Coin Tossing"
     )

# Add a dashed line for R_n = 0.5
lines(c(0,N),
      c(0.5, 0.5),
      col = "darkred",
      lty = 2,
      lwd = 1
      )
```



There are several things to be said about this plot.

- The blue graph shows the observed proportion of heads when tossing a coin n times.
- Since the Y_i are radnom variables, R_n is a random variate, too. The path depicted is only one of many possible realisations of R_n as it is determined by the 30000 observations sampled from the Bernoulli distribution. Thus, the code chunk above produces a differnt path every time You execute it (try this!).
- If the number of coin tosses n is small, we observe the proportion of heads to be anything but close to its theoretical value, $\mu_Y = 0.5$. However, as more and more observation are included in the sample we find that the path stabilizes in neighbourhood of 0.5. This is the message to take away: the average of multiple trials shows a clear tendency to converge to its expected value as the sample size increases, just as claimed by the law of large numbers.

Key Concept 2.6

The Central Limit Theorem

Suppose that $Y_1, \dots, Y_n$ are independently and identically distributed random variables with expectation $E(Y_i) = \mu_Y$ and variance $\text{Var}(Y_i) = \sigma^2_Y$, $0 < \sigma^2_Y < \infty$. The central limit theorem states that, if the sample size n goes to infinity, the distribution of the scaled (by $\sqrt{n}$) standardized sample average

$$\frac{\overline{Y} - \mu_Y}{\sigma_{\overline{Y}}} = \frac{\overline{Y} - \mu_Y}{\sigma_Y/\sqrt{n}}$$

becomes arbitrarily well approximated by the standard normal distribution.

According to the central limit theorem, the distribution of the sample mean $\overline{Y}$ of the bernoulli distributed random variables Y_i, $i = 1, ..., n$ is well approximated by the normal distribution with parameters $\mu_Y = p = 0.5$ and $\sigma^2_{\overline{Y}} = p(1-p) = 0.25$ for large n. Consequently, for the standardized sample mean we conclude that the ratio

$$\frac{\overline{Y} - 0.5}{0.5/\sqrt{n}} \tag{2.6}$$

should be well approximated by the standard normal distribution $N(0, 1)$. We employ another simulation study to demonstrate this graphically. The idea is as follows.

Draw a large number of random samples, 10000 say, of size n from the Bernoulli distribution and compute the sample averages. Standardize the averages as shown in (2.6). Next, visualize the distribution of the generated standardized sample averages by means of a density histogram and compare to the standard normal distribution. Repeat this for different sample sizes n to see how increasing the sample size n impacts the simulated distribution of the averages.

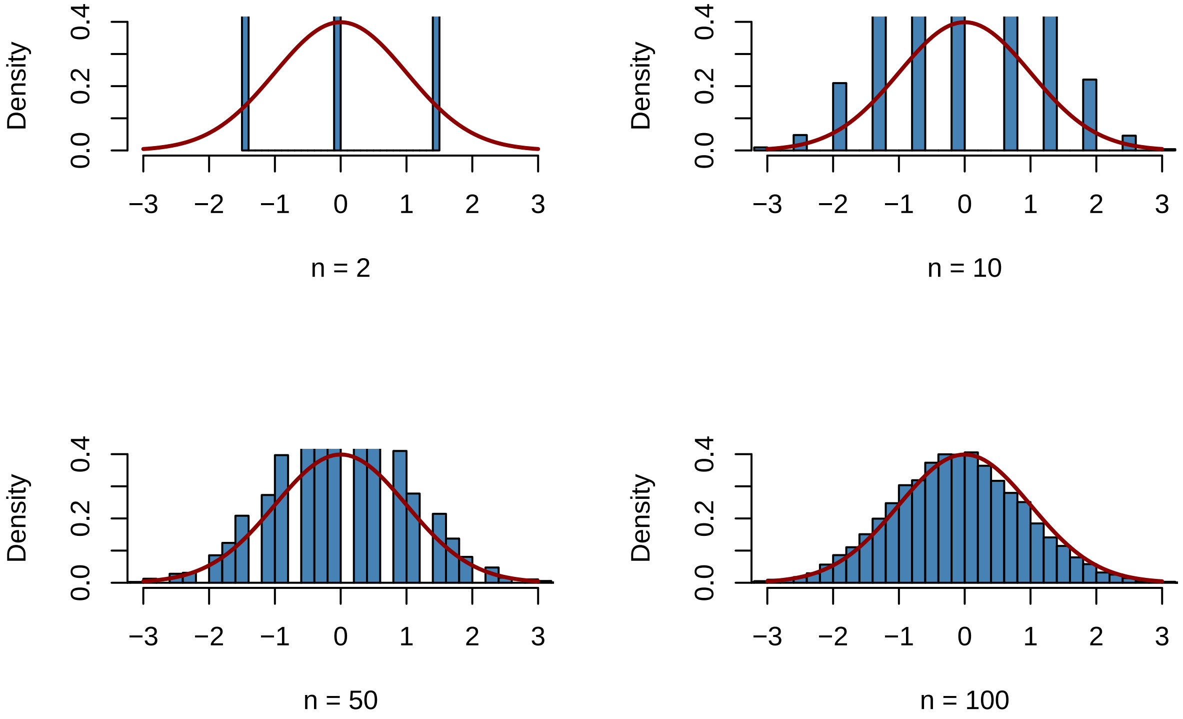
In R, we realized this as follows:

1. We start by defining that the next four subsequently generated figures shall be drawn in a 2×2 array such that they can be easily compared. This is done by calling `par(mfrow = c(2, 2))` before the figures are generated.

2. We define the number of repetitions `reps` as 10000 and create a vector of sample sizes named `sample.sizes`. We consider samples of sizes 2, 10, 50 and 100.

3. Next, we combine two `for()` loops to simulate the data and plot the distributions. The inner loop generates 10000 random samples, each consisting of `n` observations that are drawn from the bernoulli distribution, and computes the standardized averages. The outer loop executes the inner loop for the different sample sizes `n` and produces a plot for each iteration.

```r
# Subdivide the plot panel into a 2-by-2 array
par(mfrow = c(2, 2))

# Set number of repetitions and the sample sizes
reps <- 10000
sample.sizes <- c(2, 10, 50, 100)

# outer loop (loop over the sample sizes)
  for (n in sample.sizes) {

    samplemean <- rep(0,reps) #initialize the vector of sample menas
    stdsamplemean <- rep(0,reps) #initialize the vector of standardized sample menas

# inner loop (loop over repetitions)
    for (i in 1:reps) {
      x <- rbinom(n,1,0.5)
      samplemean[i] <- mean(x)
      stdsamplemean[i] <- sqrt(n)*(mean(x)-0.5)/0.5
    }

# plot the histogram and overlay it with the N(0,1) density for every iteration
    hist(stdsamplemean,
         col = "steelblue",
         breaks = 40,
         freq = FALSE,
         xlim=c(-3, 3),
         ylim = c(0, 0.4),
         xlab = paste("n =", n),
         main = ""
         )

    curve(dnorm(x),
          lwd = 2,
          col="darkred",
          add = TRUE
          )
  }
```



We see that the simulated sampling distribution of the standardized average tends to deviate strongly from the standard normal distribution if the sample size is small, e.g. for $n = 5$ and $n = 10$. However as n grows, the histograms are approaching the bell shape of a standard normal and we can be confident that the approximation works quite well as seen for $n = 100$.

Chapter 3

A Review of Statistics using R

This section reviews important statistical concepts:

- Estimation
- Hypothesis testing
- Confidence intervals

Since these types of statistical methods are heavily used in econometrics, we will discuss them in the context of inference about an unknown population mean and discuss several applications in R.

3.1 Estimation of the Population Mean

Key Concept 3.1

Estimators and Estimates

Estimators are functions of sample data that are drawn randomly from an unknown population. Estimates are numerical values computed by estimators based on the sample data. Estimators are random variables because they are functions of *random* data. Estimates are nonrandom numbers.

Think of some economic variable, for example hourly earnings of college graduates, denoted by Y. Suppose we are interested in μ_Y the mean of Y. In order to exactly calculate μ_Y we would have to interview every graduated member of the working population in the economy. We simply cannot do this for time and cost reasons. However, we could draw a random sample from n i.i.d. observations $Y_1, \dots, Y_n$ and estimate μ_Y using one of the simplest estimators in the sense of Key Concept 3.1 one can think of:

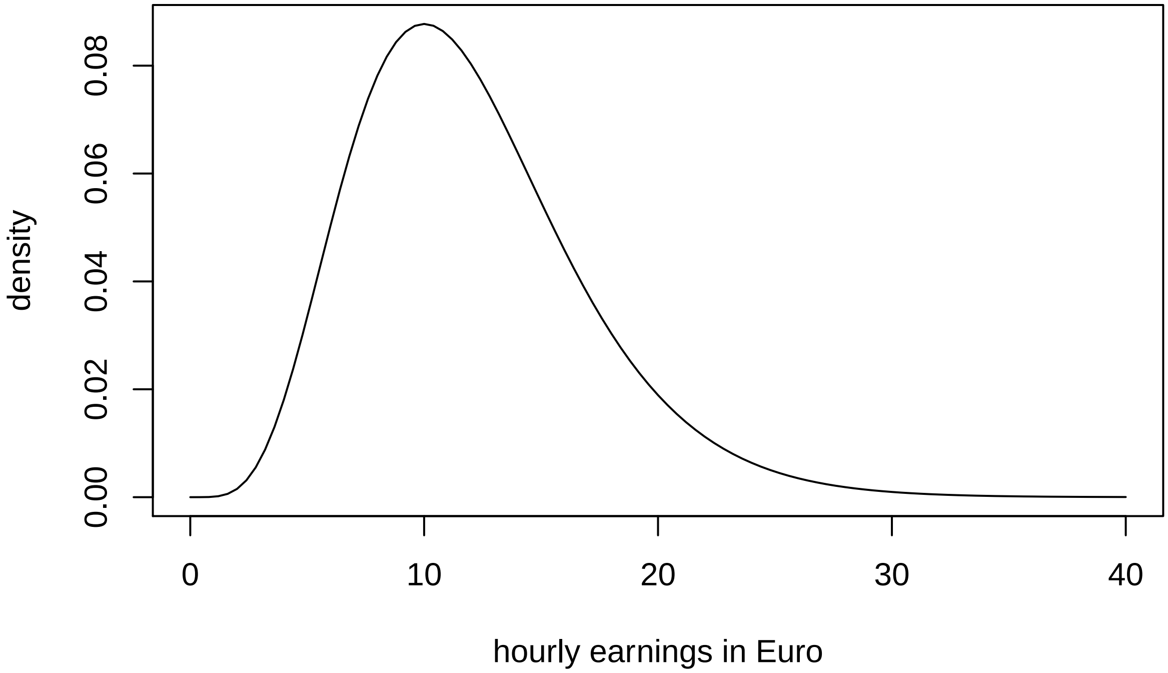
$$\overline{Y} = \frac{1}{n} \sum_{i=1}^{n} Y_i,$$

the sample mean of Y. Then again, we could use an even simpler estimator for μ_Y: the very first observation in the sample, Y_1. Is Y_1 a good estimator? For now, assume that

$$Y \sim \chi^2_{12}$$

which is not too unreasonable as the measure is nonnegative and we expect many hourly earnings to be in a range of 5 to 15. Moreover, it is common for income distributions to be skewed to the right.

```
# plot the chi_12^2 distribution
curve(dchisq(x, df=12),
      from = 0,
      to = 40,
      ylab = "density",
      xlab = "hourly earnings in Euro"
      )
```



We draw a sample of $n = 100$ observations and take the first observation Y_1 as an estimate for μ_Y

```
# set seed for reproducibility
set.seed(1)

# sample from the chi_12^2 distribution, keep only the first observation
rchisq(n = 100, df = 12)[1]
```

```
## [1] 8.257893
```

The estimate 8.26 is not too far away from $\mu_Y = 12$ but it is somewhat intuitive that we could do better: the estimator Y_1 discards a lot of information and its variance is the population variance:

$$\text{Var}(Y_1) = \text{Var}(Y) = 2 \cdot 12 = 24$$

This brings us to the following question: What is a 'good' estimator in the first place? This question is tackled in Key Concepts 3.2 and 3.3

Key Concept 3.2

Bias, Consistency and Efficiency

Disirable characteristics of an estimator are unbiasedness, consitency and Efficiency.

Unbiasedness:
If the mean of the sampling distribution of some estimator $\hat{\mu}_Y$ for the population mean μ_Y equals μ_Y

$$E(\hat{\mu}_Y) = \mu_Y$$

we say that the estimator is unbiased for μ_Y. The *bias* of $\hat{\mu}_Y$ is 0:

$$E(\hat{\mu}_Y) - \mu_Y = 0$$

Consistency:

We want the uncertainty of the estimator μ_Y to decrease as the number of observations in the sample grows. More precisely, we want the proabability that the estimate $\hat{\mu}_Y$ falls within a small interval of the true value μ_Y to get increasingly closer to 1 as n grows. We write this as

$$\hat{\mu}_Y \xrightarrow{p} \mu_Y.$$

Variance and efficiency:

We want the estimator to be efficient. Suppose we have two estimators, $\hat{\mu}_Y$ and $\overset{\sim}{\mu}_Y$ and for some given sample size n it holds that

$$E(\hat{\mu}_Y) = E(\overset{\sim}{\mu}_Y) = \mu_Y$$

but

$$\text{Var}(\hat{\mu}_Y) < \text{Var}(\overset{\sim}{\mu}_Y).$$

We then would prefer to use $\hat{\mu}_Y$ as it has a lower variance than $\overset{\sim}{\mu}_Y$, meaning that $\hat{\mu}_Y$ is more *efficient* in using the information provided by the observations in the sample.

Key Concept 3.3

Efficiency of $\overline{Y}$: The BLUE property

Let $\hat{\mu}_Y$ be a linear and unbiased estimator of μ_Y in the fashion of

$$\hat{\mu}_Y = \frac{1}{n} \sum_{i=1}^{n} a_i Y_i$$

with nonrandom constants a_i. We see that $\hat{\mu}_Y$ is a weighted average of the Y_i and the a_i are weights. For these type of estimators, $\overline{Y}$ with $a_i = 1$ for all $i = 1, \dots, n$ is the most efficient estimator. We say that $\overline{Y}$ is the BestLinear Unbiased Estimator (BLUE).

3.2 Properties of the Sample Mean

To examine properties of the sample mean as an estimator for the corresponding population mean, consider the following R example.

We generate a population `pop` which consists observations Y_i , $i = 1, \dots, 10000$ that stem from a normal distribution with mean $\mu = 10$ and variance $\sigma^2 = 1$. To investigate how the estimator $\hat{\mu} = \bar{Y}$ behaves we can draw random samples from this population and calculate $\bar{Y}$ for each of them. This is easily done by making use of the function `replicate()`. Its argument `expr` is evaluated `n` times. In this case we draw samples of sizes $n = 5$ and $n = 25$, compute the sample means and repeat this exactly $n = 25000$ times.

For comparison purposes we store results for the estimator Y_1, the first observation in a sample for a sample of size 5 separately.

```
# generate a fictive population
pop <- rnorm(10000, 10, 1)

# sample form pop and estimate the mean
est1 <- replicate(expr = mean(sample(x = pop, size = 5)), n = 25000)

est2 <- replicate(expr = mean(sample(x = pop, size = 25)), n = 25000)

fo <- replicate(expr = sample(x = pop, size = 5)[1], n = 25000)
```

Check that `est1` and `est2` are vectors of length 25000:

```
# check if object type is vector
is.vector(est1)
```

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

```
is.vector(est2)
```

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

```
# check lengths
length(est1)
```

```
## [1] 25000
```

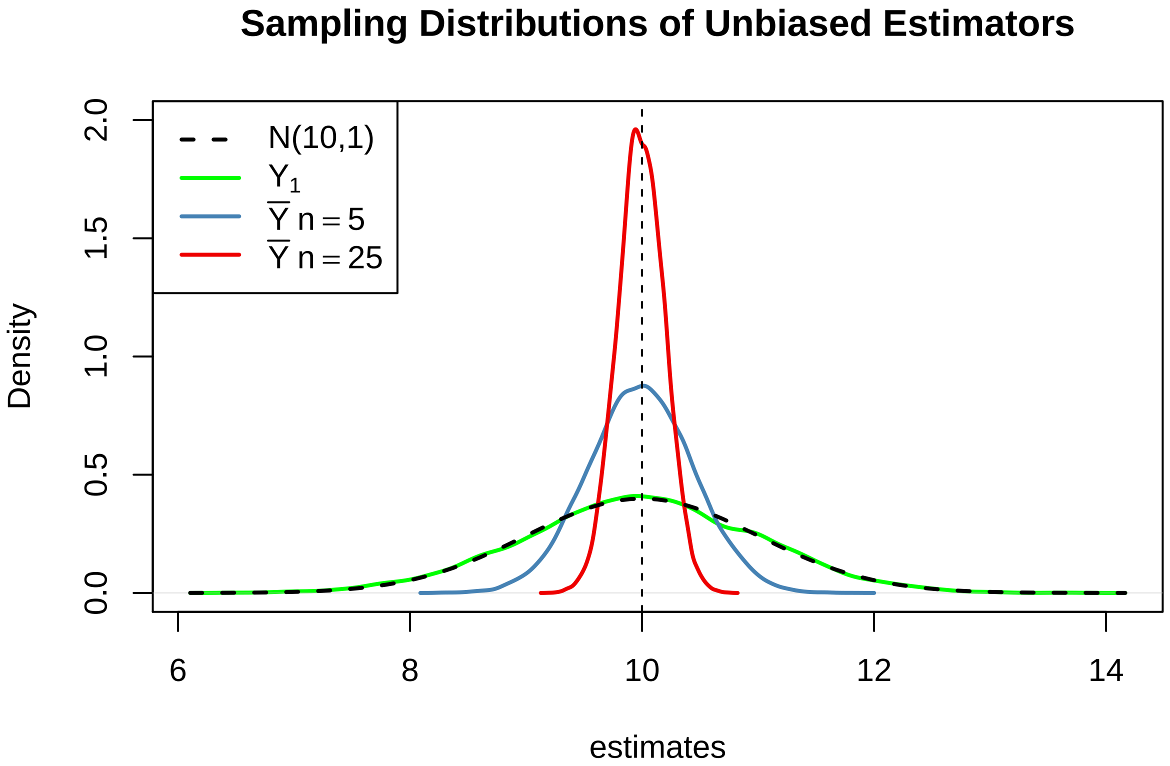
```
length(est2)
```

```
## [1] 25000
```

The code chunk below produces a plot of the sampling distributions of the estimators $\bar{Y}$ and Y_1 on the basis of the 25000 samples in each case. We also plot a curve depicting the density function of the $N(10, 1)$ distribution.

```
# plot density estimate Y_1
plot(density(fo),
      col = 'green',
      lwd = 2,
      ylim = c(0,2),
      xlab = 'estimates',
      main = 'Sampling Distributions of Unbiased Estimators'
      )

# add density estimate for the distribution of the sample mean with n=5 to the plot
lines(density(est1),
     col = 'steelblue',
     lwd = 2,
     bty = 'l'
     )

# add density estimate for the distribution of the sample mean with n=25 to the plot
lines(density(est2),
      col = 'red2',
      lwd = 2
      )

# add a vertical line marking the true parameter
abline(v = 10, lty = 2)
```

```
# add N(10,1) density to the plot
curve(dnorm(x, mean=10),
     lwd = 2,
     lty = 2,
     add = T
     )

# add a legend
legend("topleft",
       legend = c("N(10,1)",
                  expression(Y[1]),
                  expression(bar(Y) ~ n==5),
                  expression(bar(Y) ~ n==25)
                  ),
       lty = c(2, 1, 1, 1),
       col = c('black','green', 'steelblue', 'red2'),
       lwd = 2
       )
```



At first, notice how *all* sampling distributions (represented by the solid lines) are centered around $\mu = 10$. This is evidence for the *unbiasedness* of Y_1 and $\overline{Y}$. Of course, the theoretical density the $N(10,1)$ distribution is centered at 10, too.

Next, have a look add the spread of the sampling distributions. Several things are remarkable:

- First, the sampling distribution of Y_1 (green curve) tracks the density of the $N(10,1)$ distribution (black dashed line) pretty closely In fact, the sampling distribution of Y_1 *is* the $N(10,1)$ distribution. This is less surprising if You keep in mind that Y_1 estimator does nothing but reporting an observation that is randomly selected from a population with $N(10,1)$ distribution. Hence, $Y_1 \sim N(10,1)$. Note that this result is invariant to the sample size n: the sampling distribution of Y_1 is always the population distribution, no how large the sample is.

- Second, both sampling distributions of $\overline{Y}$ show less dispersion than the sampling distribution of Y_1. This means that $\overline{Y}$ has a lower variance than Y_1. In view of Key Concepts 3.2 and 3.3, we find that $\overline{Y}$ is a more efficient estimator than Y_1. In fact, one can show that this holds for all $n > 1$.
- Third, $\overline{Y}$ shows a behaviour that is termed consistency (see Key Concept 3.2). Notice that the blue and the red density curves are much more concentrated around $\mu = 10$ then the green one. As the number of observations is increased from 1 to 5, the sampling distribution tightens around the true parameter. This effect is more dominant as the sample size is increased to 25. This implies that the probability of obtaining estimates that are close to the true value increases with n.

A more precise way to express consitency of an estimator $\hat{\mu}$ for a parameter μ is

$$P(|\hat{\mu} - \mu| < \epsilon) \xrightarrow[n\rightarrow\infty]{p} 1 \quad \text{for any} \quad \epsilon > 0.$$

This expression says that the probability of observing a deviation from the true value μ that is smaller than some arbitrary $\epsilon > 0$ converges to 1 as n grows. Note that consistency does not require unbiasedness:

We encourage You to go ahead and modify the code. Try out different values for the sample size and see how the sampling distribution of $\overline{Y}$ changes!

$\overline{Y}$ is the least squares estimator of μ_Y

Assume You have some observations $Y_1, \dots, Y_n$ on $Y \sim N(10, 1)$ (which is unknown) and would like to find an estimator m that predicts the observations as good as possible where good means to choose m such that the total deviation between the predicted value and the observed values is small. Mathematically this means we want to find an m that minimizes

$$\sum_{i=1}^{n} (Y_i - m)^2. \tag{3.1}$$

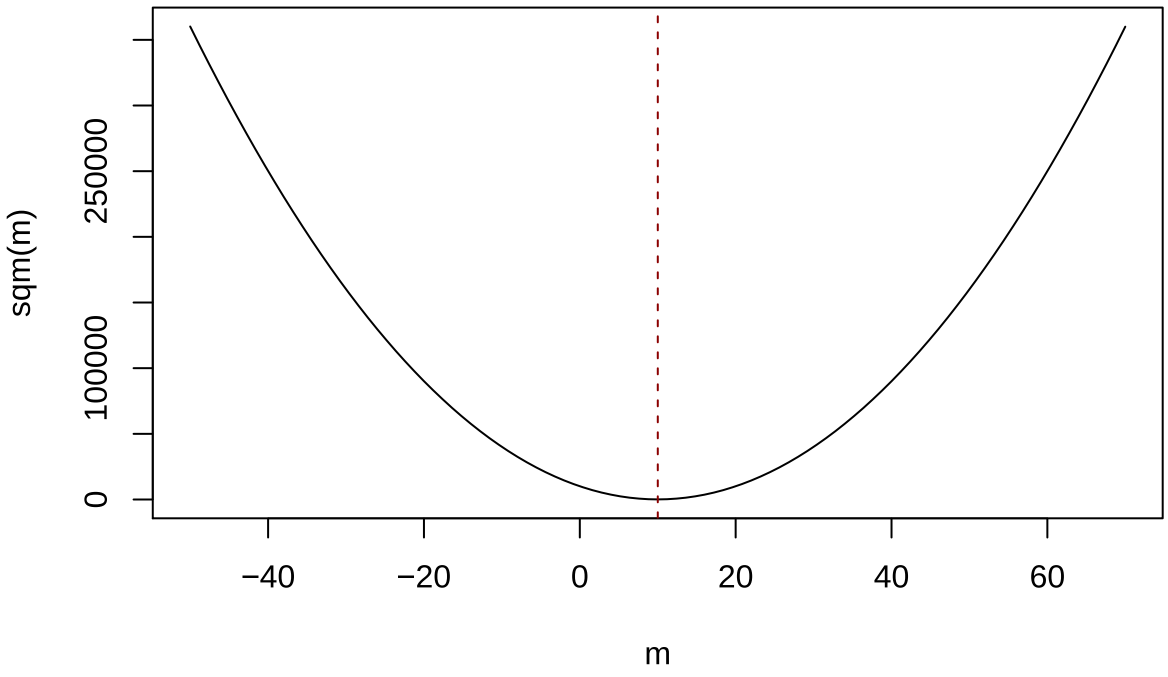
Think of $Y_i - m$ as the comitted mistake when predicting Y_i by m. We could just as well minimize the sum of absolute deviations from m but minimizing the sum of squared deviations is mathematically more convenient and leads, roughly speaking, to the same result. That is why the estimator we are looking for is called the *least squares estimator*. As It turns out $m = \overline{Y}$, the estimator of $\mu_Y = 10$ is this wanted estimator.

We can show this by generating a random sample of fair size and plotting (3.1) as a function of m.

```r
# define the function and vectorize it
sqm <- function(m) {
 sum((y-m)^2)
}
sqm <- Vectorize(sqm)

# draw random sample and compute the mean
y <- rnorm(100, 10, 1)
mean(y)
```

```
## [1] 10.00543
```

```r
# plot the objective function
curve(sqm(x),
      from = -50,
      to = 70,
      xlab = "m",
      ylab ="sqm(m)"
      )

# add vertical line at mean(y)
abline(v = mean(y),
       lty = 2,
       col = "darkred"
       )
```



Notice that (3.1) is a quadratic function so there is only one minimum. The plot shows that this minimum lies exactly at the sample mean of the sample data.

Some R functions can only interact with functions that take a vector as input evaluate the function body on every values of the vector, for example curve(). We call such functions vectorized functions and it is often a good idea to write vectorized functions although this is cumbersome in some cases. Having a vectorized function in R is never a drawback since these functions work on both single values and vectors.

Let us look at the function sqm() which is nonvectorized

```
sqm <- function(m) {
    sum((y-m)^2) #body of the function
}
```

Providing e.g. c(1,2,3) as the argument m would cause an error since then the operation y-m is invalid: the vecors y and m are of incompatible dimensions. This is why we cannot use sqm() in conjunction with curve().

Here comes Vectorize() into play. It generates a vectorized version of a non-vectorized function.

Why Random Sampling is important

So far, we assumed (somtimes implicitly) that observed data $Y_1, \dots, Y_n$ are the result of a sampling process that satisfies the assumption of i.i.d. random sampling. It is very important that this assumption is fulfilled when estimating a population mean using $\overline{Y}$. If this is not the case, estimates are biased.

Let us fall back to pop, the fictive population of 10000 observations and compute the population mean $\mu_{\texttt{pop}}$:

```
# compute the population mean of pop
mean(pop)
```

```
## [1] 9.992604
```

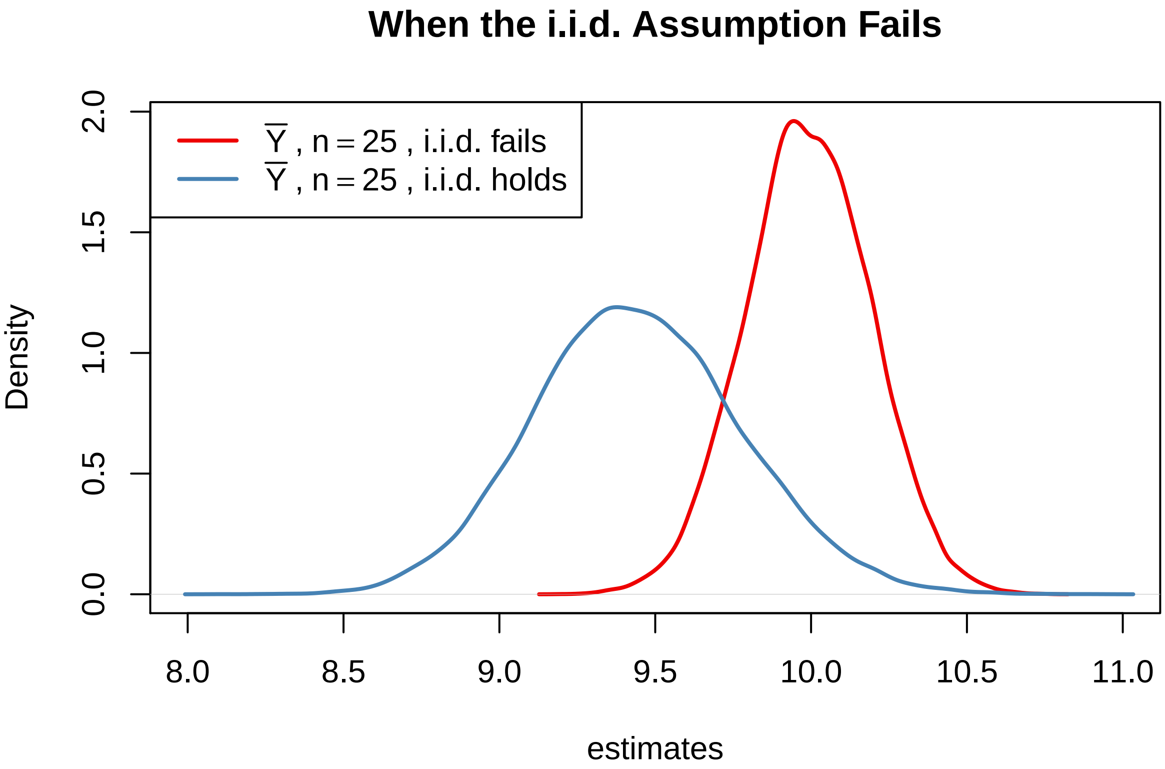
Next we sample 10 observations from pop with sample() and estimate $\mu_{\texttt{pop}}$ using $\overline{Y}$ repeatedly. However this time we use a sampling scheme that deviates from simple random sampling: instead of ensuring that each member of the population has the same chance to end up in a sample, we assign a higher probability of beeing sampled to the 2500 smallest observations of the population by setting the argument prop to a suitable vector of probability weights:

```
# simulate outcome for the sample mean when the i.i.d. assumption fails
est3 <-  replicate(n = 25000,
                   expr = mean(sample(x = sort(pop),
                                      size = 10,
                                      prob = c(rep(4,2500),rep(1,7500))
                                          )
                                    )
                  )

# compute the sample mean of the outcomes
mean(est3)
```

```
## [1] 9.443454
```

Next we plot the sampling distribution of $\overline{Y}$ for this non-i.i.d. case an compare it to the sampling distribution when the i.i.d. assumption holds.

```
# sampling distribution of sample mean, i.i.d. holds, n=25
plot(density(est2),
      col = 'red2',
      lwd = 2,
      xlim = c(8,11),
      xlab = 'estimates',
      main = 'When the i.i.d. Assumption Fails'
     )

# sampling distribution of sample mean, i.i.d. fails, n=25
lines(density(est3),
      col = 'steelblue',
      lwd = 2
      )

# add a legend
legend("topleft",
       legend = c(expression(bar(Y) ~ "," ~ n==25 ~ ", i.i.d. fails"),
                  expression(bar(Y) ~ "," ~ n==25 ~ ", i.i.d. holds")
                  ),
       lty = c(1, 1),
       col = c('red2', 'steelblue'),
       lwd = 2
       )
```



We find that in this case failure of the i.i.d. assumption implies that, on average, we underestimate μ_Y using $\overline{Y}$: the corresponding distribution of $\overline{Y}$ is shifted to the left. In other words, $\overline{Y}$ is a *biased* estimator for μ_Y if the i.i.d. assumption does not hold.

3.3 Hypothesis Tests Concerning the Population Mean

In this section we briefly review concepts in hypothesis testing and discuss how to conduct hypothesis tests in R. We focus on drawing inference about an unkown population mean.

About Hypotheses and Hypothesis Testing

In a significance test we want to exploit the information contained in a random sample as evidence in favour or against a hypothesis. Essentially, hypotheses are simple question that can be answered by 'yes' or 'no'. When conducting a hypothesis test we always deal with two different hypotheses:

- The null hypothesis, denoted H_0 is the hypothesis we are interested in testing
- The alternative hypothesis, denoted H_1, is the hypothesis that holds if the null hypothesis is false

The null hypothesis that the population mean of Y equals the value $\mu_{Y,0}$ is written down as

$$H_0 : E(Y) = \mu_{Y,0}.$$

The alternative hypothesis states what holds if the null hypothesis is false. Often the alternative hypothesis chosen is the most general one,

$$H_1 : E(Y) \neq \mu_{Y,0},$$

meaning that $E(Y)$ may be anything else but the value as the null hypothesis. This is called a two-sided alternative.

For brevity, we will only consider the case of a two-sided alternative in the subsequent sections of this chapter.

p-Value

Assume that the null hypothesis is *true*. The p-value is the probability of drawing data and observing a corresponding test statistics that is at least as adverse to what is stated under the null hypothesis as the test statistic actually computed using the sample data.

In context of population mean and sample mean, this definition can be stated mathematically in the following way:

$$p\text{-value} = P_{H_0}\left[|\overline{Y} - \mu_{Y,0}| > |\overline{Y}^{act} - \mu_{Y,0}|\right] \tag{3.2}$$

In (3.2), $\overline{Y}^{act}$ is the acutally computed mean of the random sample. Visualized, the p-value is the area in the part of tails of the distribution of $\overline{Y}$ that lies beyond

$$\mu_{Y,0} \pm |\overline{Y}^{act} - \mu_{Y,0}|.$$

Consequently, in order to compute the p-value as in (3.2), knowledge about the sampling distribution of $\overline{Y}$ when the null hypothesis is true is required. However in most cases the sampling distribution of $\overline{Y}$ is unkown. Furtunately, due to the large-sample normal approximation (see chapter 3) we know that under the null hypothesis

$$\overline{Y} \sim N(\mu_{Y,0}, \sigma^2_{\overline{Y}}) \quad , \quad \sigma^2_{\overline{Y}} = \frac{\sigma^2_Y}{n}$$

and thus

$$\frac{\overline{Y} - \mu_{Y,0}}{\sigma_Y/\sqrt{n}} \sim N(0,1).$$

So in large samples, the p-value can be computed *without* knowledge about the sampling distribution of $\overline{Y}$.

Calculating the p-Value When σ_Y Is Known

For now, let us assume that $\sigma_{\overline{Y}}$ is known. Then we can rewrite (3.2) as

$$p\text{-value} = P_{H_0}\left[\left|\frac{\overline{Y} - \mu_{Y,0}}{\sigma_{\overline{Y}}}\right| > \left|\frac{\overline{Y}^{act} - \mu_{Y,0}}{\sigma_{\overline{Y}}}\right|\right] \tag{3.3}$$

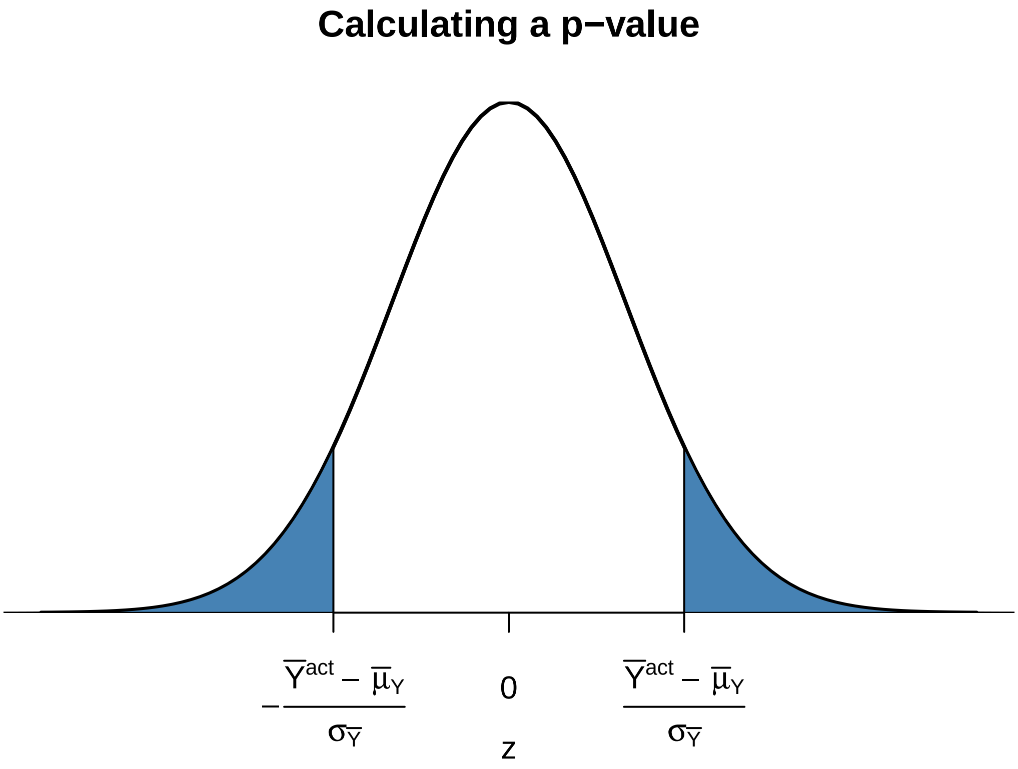
$$= 2 \cdot \Phi\left[-\left|\frac{\overline{Y}^{act} - \mu_{Y,0}}{\sigma_{\overline{Y}}}\right|\right]. \tag{3.4}$$

so the p-value can be seen as the area in the tails of the $N(0,1)$ distribution that lies beyond

$$\pm\left|\frac{\overline{Y}^{act}-\mu_{Y,0}}{\sigma_{\overline{Y}}}\right| \tag{3.5}$$

Whew, that was a lot of theory. Now we use R to visualize what is stated in (3.4) and (3.5). The next code chunck replicates figure 3.1 of the book.

```r
# plot the standard normal density on the domain [-4,4]
curve(dnorm(x),
      xlim = c(-4,4),
      main = 'Calculating a p-value',
      yaxs = 'i',
      xlab = 'z',
      ylab = '',
      lwd = 2,
      axes = 'F'
      )

# add x-axis
axis(1,
     at = c(-1.5,0,1.5),
     padj = 0.75,
     labels = c(expression(-frac(bar(Y)^"act"~-~bar(mu)[Y,0],sigma[bar(Y)])),
                0,
                expression(frac(bar(Y)^"act"~-~bar(mu)[Y,0],sigma[bar(Y)])))
     )

# shade p-value/2 region in left tail
polygon(x = c(-6, seq(-6,-1.5,0.01),-1.5),
        y = c(0, dnorm(seq(-6,-1.5,0.01)),0),
        col = 'steelblue'
        )

## shade p-value/2 region in right tail
polygon(x = c(1.5, seq(1.5, 6, 0.01), 6),
        y = c(0, dnorm(seq(1.5, 6, 0.01)), 0),
        col = 'steelblue'
        )
```



Sample Variance, Sample Standard Deviation and Standard Error

If σ^2_Y is unknown, it must be estimated. This can be done efficiently using the sample variance

$$s_y^2 = \frac{1}{n-1} \sum_{i=1}^n (Y_i - \overline{Y})^2. \tag{3.6}$$

Furthermore

$$s_y = \sqrt{\frac{1}{n-1} \sum_{i=1}^n (Y_i - \overline{Y})^2}. \tag{3.7}$$

is a suitable estimator for the standard deviation of Y. In R, s_y is implemented in the function `sd()`, see `?sd`.

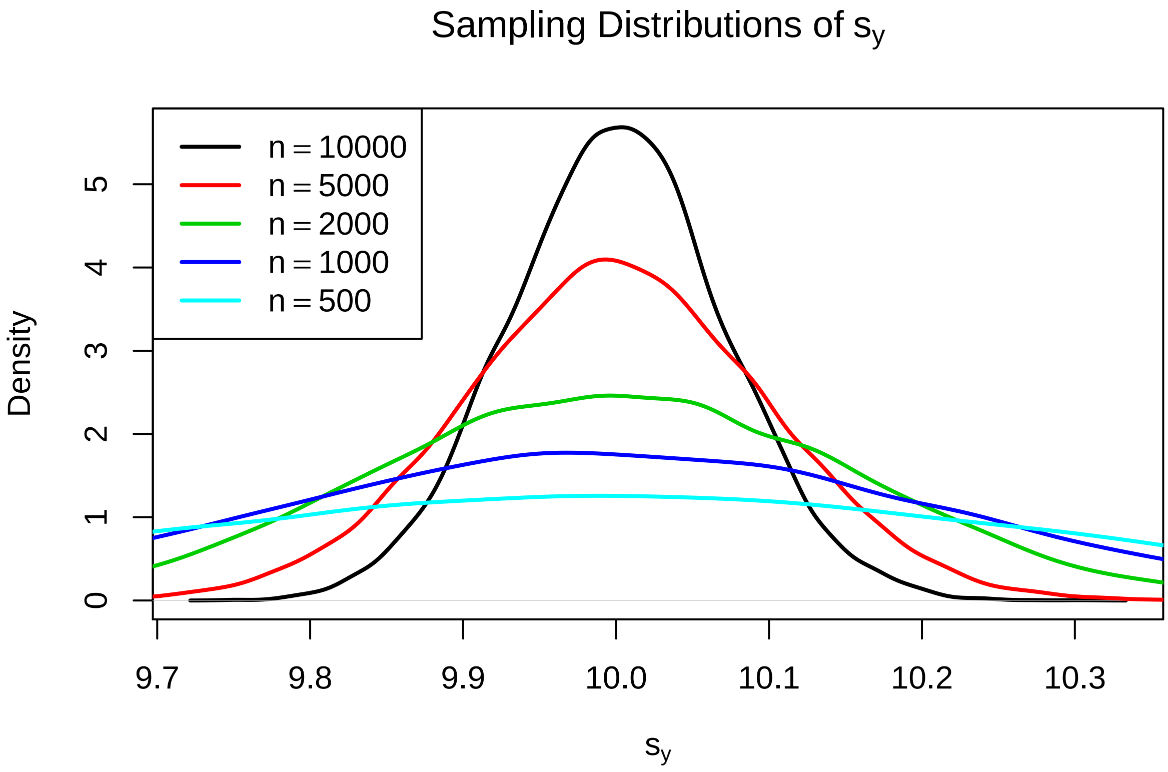
Using R we can get a notion that s_y is a consistent estimator for σ_Y, that is

$$s_Y \xrightarrow{p} \sigma_Y.$$

The idea here is to generate a large number of samples $Y_1, \dots, Y_n$ where $Y \sim N(10, 10)$, estimate σ_Y using s_y and investigate how the distribution of s_Y changes as n grows.

```r
# vector of sample sizes
n <- c(10000, 5000, 2000, 1000, 500)

# sample observations, estimate using sd() and plot estimated distributions
s2_y <- replicate(n = 10000, expr = sd(rnorm(n[1], 10, 10)))
```

```r
plot(density(s2_y),
     main = expression('Sampling Distributions of' ~ s[y]),
     xlab = expression(s[y]),
     lwd = 2
     )

for (i in 2:length(n)) {
  s2_y <- replicate(n = 10000, expr = sd(rnorm(n[i],10,10)))
  lines(density(s2_y),
        col=i,
        lwd=2)
}

# add a legend
legend("topleft",
       legend = c(expression(n==10000),
                  expression(n==5000),
                  expression(n==2000),
                  expression(n==1000),
                  expression(n==500)
       ),
       col = 1:5,
       lwd = 2
)
```



The plot shows that the distribution of s_Y tightens around the true value $\sigma_Y = 10$ as n increases.

The function that estimates the standard deviation of an estimator is called the *standard error of the estimator*. Key Concept 3.4 summarizes the terminology in the context of the sample mean.

Key Concept 3.4

The Standard Error of $\overline{Y}$

Take an i.i.d. sample $Y_1, \dots, Y_n$. The mean of Y can be consistently estimated using $\overline{Y}$, the sample mean of the Y_i. Since $\overline{Y}$ is a random variable, it has a sampling distribution with variance $\frac{\sigma_Y^2}{n}$.

The standard error of $\overline{Y}$, denoted $SE(\overline{Y})$ is an estimator of the standard deviation $\overline{Y}$:

$$SE(\overline{Y}) = \hat{\sigma}_{\overline{Y}} = \frac{s_Y}{\sqrt{n}}$$

The caret (^) over σ indicates that $\hat{\sigma}_{\overline{Y}}$ is an estimator for $\sigma_{\overline{Y}}$.

As an example to underpin Key Concept 3.4, consider a sample of $n = 100$ i.i.d. observations of the bernoulli distributed variable Y with success probability $p = 0.1$ and thus $E(Y) = p = 0.1$ and $\text{Var}(Y) = p(1-p)$. $E(Y)$ can be estimated by $\overline{Y}$ which then has variance

$$\sigma^2_{\overline{Y}} = p(1-p)/n = 0.0009$$

and standard deviation

$$\sigma_{\overline{Y}} = \sqrt{p(1-p)/n} = 0.03.$$

In this case the standard error of $\overline{Y}$ is given as

$$SE(\overline{Y}) = \sqrt{\overline{Y}(1-\overline{Y})/n}$$

Let verify whether $\overline{Y}$ and $SE(\overline{Y})$ estimate the respective true values on average.

```r
# draw 10000 samples of size 100 and estimate the mean of Y and
# estimate the standard error of the sample mean

mean_estimates <- numeric(10000)
se_estimates <- numeric(10000)

for (i in 1:10000) {
  s <- sample(0:1,
              size = 100,
              prob = c(0.9, 0.1),
              replace = T
              )
  mean_estimates[i] <- mean(s)
  se_estimates[i] <- sqrt(mean(s)*(1-mean(s))/100)
}

mean(mean_estimates)
```

```
## [1] 0.099693
```

```r
mean(se_estimates)
```

```
## [1] 0.02953467
```

Both estimators seem to be unbiased for the true parameters.

Calculating the p-value When σ_Y is Unknown

When σ_Y is unkown, the p-value for a hypothesis test about μ_Y using $\overline{Y}$ can be computed by replacing $\sigma_{\overline{Y}}$ in (3.4) by the standard error $SE(\overline{Y}) = \hat{\sigma}_Y$. Then,

$$p\text{-value} = 2 \cdot \Phi\left(- \left| \frac{\overline{Y}^{act} - \mu_{Y,0}}{SE(\overline{Y})} \right| \right).$$

This is easily done in R:

```
# sample and estimate, compute standard error and make a hypothesis
samplemean_act <- mean(
  sample(0:1,
         prob = c(0.9,0.1),
         replace = T,
         size = 100
         )
  )

SE_samplemean <- sqrt(samplemean_act * (1-samplemean_act)/100)

mean_h0 <- 0.1 #true null hypothesis

# compute the pvalue
pvalue <- 2 * pnorm(-abs(samplemean_act-mean_h0)/SE_samplemean)
pvalue
```

```
## [1] 0.5382527
```

The t-statistic

In hypothesis testing, the standardized sample average

$$t = \frac{\overline{Y} - \mu_{Y,0}}{SE(\overline{Y})} \tag{3.8}$$

is called t-statistic. This t-statistic has an important role when testing hypothesis about μ_Y. It is a prominent example of a test statistic.

Implicitly, we already have computed a t-statistic for $\overline{Y}$ in the previous code chunk.

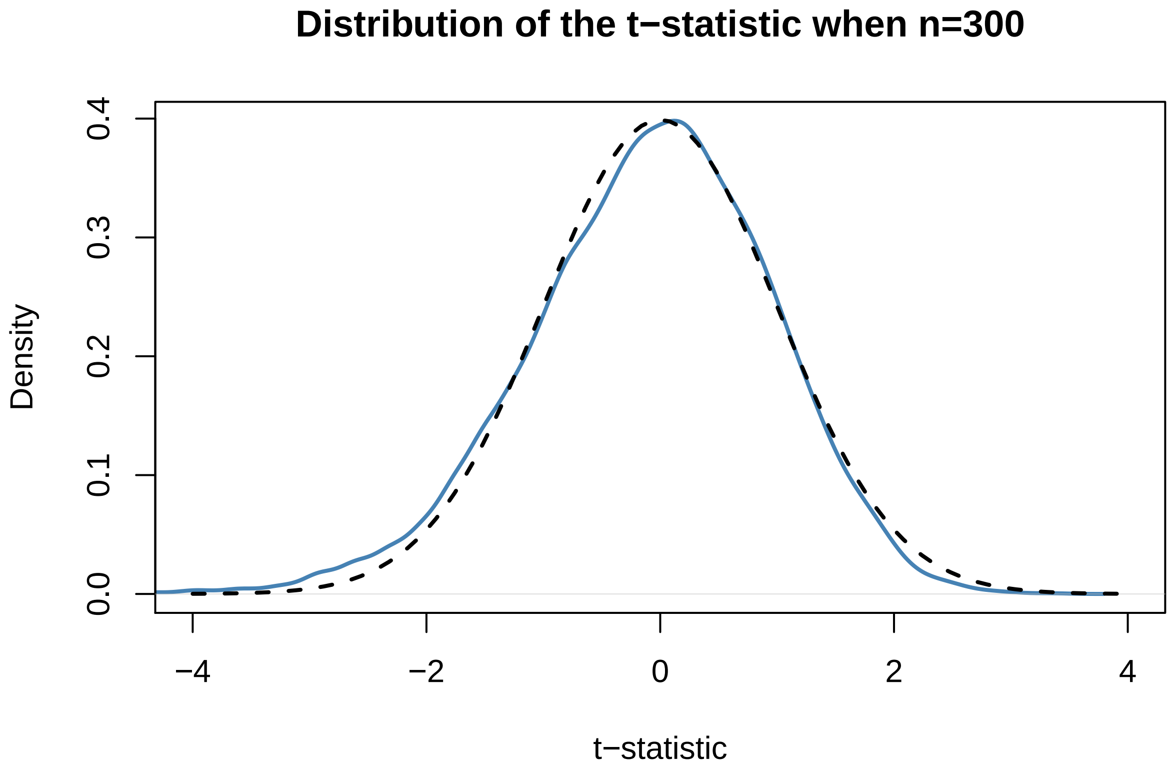
```
# compute a t-statistic for the sample mean
tstatistic <- (samplemean_act - mean_h0) / SE_samplemean
tstatistic
```

```
## [1] 0.6154575
```

Using R we can show that if $\mu_{Y,0}$ equals the true value, that is the null hypothesis is true, (3.8) is approximately distributed $N(0, 1)$ when n is large.

```
# initialize empty vector for t-statistics
tstatistics <- numeric(10000)

# set sample size
n <- 300
```

```
# simulate 10000 t-statistics
for (i in 1:10000) {
  s <- sample(0:1,
              size = n,
              prob = c(0.9, 0.1),
              replace = T
              )
  tstatistics[i] <- (mean(s)-0.1)/(sqrt(mean(s)*(1-mean(s))/n))
}

# plot density and compare to N(0,1) density
plot(density(tstatistics),
     xlab = 't-statistic',
     main = 'Distribution of the t-statistic when n=300',
     lwd = 2,
     xlim = c(-4,4),
     col = 'steelblue'
     )

# N(0,1) density (dashed)
curve(dnorm(x),
      add = T,
      lty = 2,
      lwd= 2
      )
```



Judging from the plot, the normal approximation works reasonably well for the chosen sample size. This normal approximation has already been used in the definition of the p-value, see (3.8).

Hypothesis Testing with a Prespecified Significance Level

Key Concept 3.5

The Terminology of Hypothesis Testing

In hypothesis testing, two types of mistakes are possible:

1. The null hypothesis *is* rejected although it is true (α-error / type-I-error)
2. The null hypothesis *is not* rejected although it is false (β-error / type-II-error)

The significance level of the test is the probability to commit a type-I-error we are willing to accept in advance. E.g. using a prespecified significance level of 0.05, we reject the null hypothesis if and only if the p-value is less than 0.05. The significance level is chosen before the test is conducted.

An equivalent procedure is to reject the null hypothesis if the test statistic observed is, in absolute value terms, larger than the critical value of the test statistic. The critical value is determined by the significance level chosen and defines two disjoint sets of values which are called acceptance region and rejection region. The acceptance region contains all values of the test statistic for which the test does not reject while the rejection region contains all the values for which the test does reject.

The p-value is the probability that, in repeated sampling under the same conditions, meaning i.i.d. sampling, the same null hypothesis and the same sample size, a test statistic is observed that provides just as much evidence against the null hypothesis as the test statistic actually observed.

The actual probability that the test rejects the true null hypothesis is called the size of the test. In an ideal setting, the size does not exceed the significance level.

The probability that the test correctly rejects a false null hypothesis is called power.

Reconsider `pvalue` computed further above:

```
# check whether p-value < 0.05
pvalue < 0.05
```

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

The condition is not fulfilled so we do not reject the null hypotheis (remember that the null hypothesis is true in this example).

When working with a t-statistic instead, it is equivalent to apply the following rule:

$$\text{Reject } H_0 \text{ if } |t^{act}| > 1.96$$

We reject the null hypothesis at the significance level of 5% if the computed t-statistic lies beyond the critical value of 1.96 in absolute value terms. 1.96 is the 0.05-quantile of the standard normal distribution.

```
# check the critical value
qnorm(p = 0.05)
```

```
## [1] -1.644854
```

```
# check whether the null is rejected using the t-statistic computed further above
abs(tstatistic) > 1.96
```

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

As when using the p-value, we cannot reject the null hypothesis using the corresponding t-statistic. Key Concept 3.6 summarizes the procedure of performing a two-sided hypothesis about the population mean $E(Y)$.

Key Concept 3.6

Testing the Hypothesis $E(Y) = \mu_{Y,0}$ Against the Alternative $E(Y) \neq \mu_{Y,0}$

1. Estimate μ_Y using $\overline{Y}$ and compute the standard error of $\overline{Y}$, $SE(\overline{Y})$.

2. Compute the t-statistic.

3. Compute the p-value and reject the null hypothesis at the 5% level of significance if the p-value is smaller than 0.05 or equivalently, if

$$\left|t^{act}\right| > 1.96.$$

One-sided Alternatives

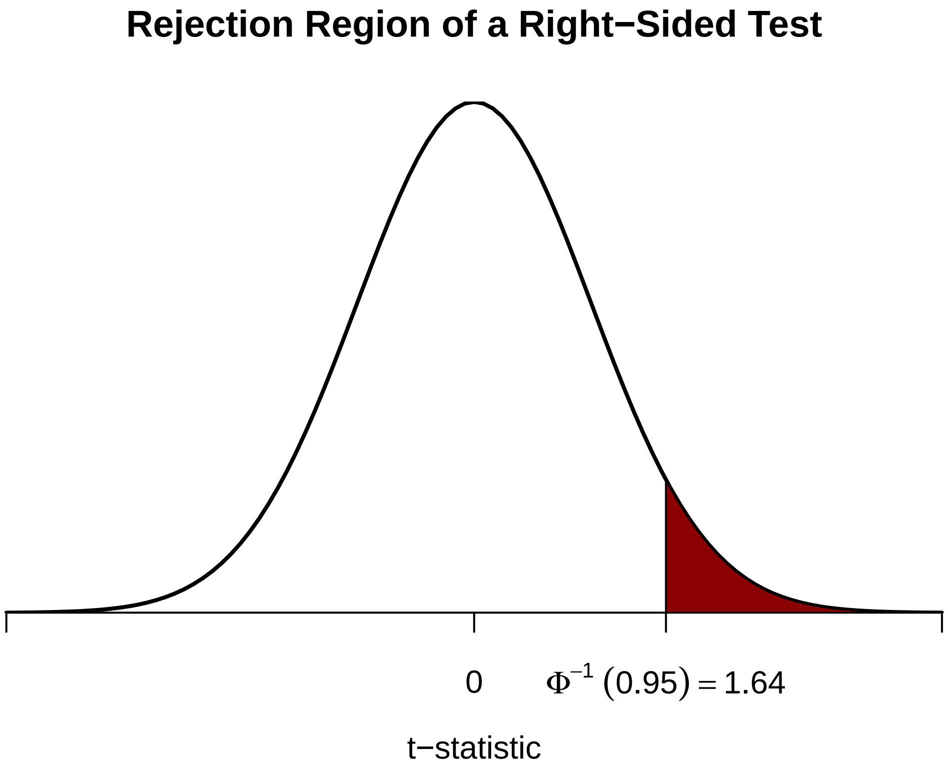
Sometimes we are interested in finding evidence that the mean is bigger or smaller than the some value hypothesized under the null. One can come up with many examples here but, to stick to the book, take the presumed wage differential between good and less educated working individuals. Since we hope that this differential exists, a relevant alternative (to the null hypothesis that there is no wage differential) is that good educated individuals earn more, i.e. that the average hourly wage for this group, μ_Y is *bigger* than $\mu_{Y,0}$ the know average wage of less educated workers.

This is an example of a *right-sided test* and the hypotheses pair is chosen as

$$H_0 : \mu_Y = \mu_{Y,0} \quad \text{vs} \quad H_1 : \mu_Y > \mu_{Y,0}.$$

We reject the null hypothesis if the computed test-statistic is larger than the critical value 1.64, the 0.95-quantile of the $N(0,1)$ distribution. This ensures that $1 - 0.95 = 5\%$ probability mass remains in the area to the right of the critical value. Similar as before we can visualize this in R using the function `polygon()`.

```r
# plot the standard normal density on the domain [-4,4]
curve(dnorm(x),
      xlim = c(-4,4),
      main = 'Rejection Region of a Right-Sided Test',
      yaxs = 'i',
      xlab = 't-statistic',
      ylab = '',
      lwd = 2,
      axes = 'F'
)

# add x-axis
axis(1,
     at = c(-4,0,1.64,4),
     padj = 0.5,
     labels = c('',0,expression(Phi^-1~(.95)==1.64),'')
)

# shade rejection region in right tail
polygon(x = c(1.64, seq(1.64, 4, 0.01), 4),
        y = c(0, dnorm(seq(1.64, 4, 0.01)), 0),
        col = 'darkred'
)
```



In an analogously manner for the *left-sided test* we have

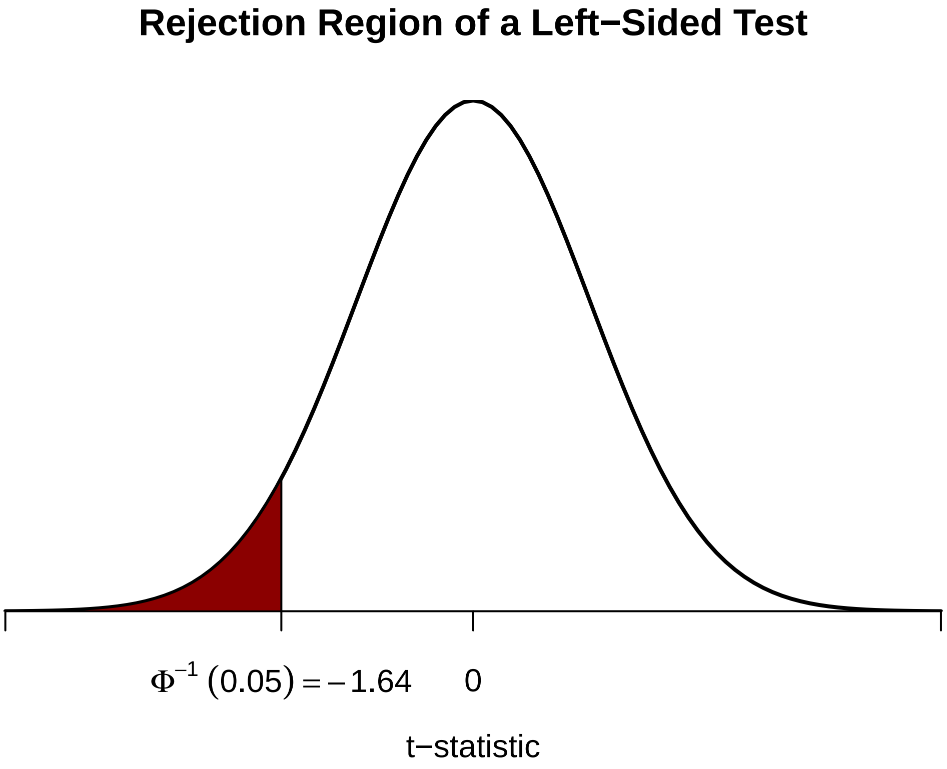
$$H_0 : \mu_Y = \mu_{Y,0} \text{ vs. } H_1 : \mu_Y < \mu_{Y,0}.$$

The null is rejected if the observed test statistic falls short of the critical value which, for a test at the 0.05 level of significance, is given by -1.64, the 0.05-quantile of the $N(0,1)$ distribution. 5% probability mass lies to the left of the critical value.

It is straight forward to adapt the code chunk above to the case of a left-sided test. We only have to fiddle with the color shading and the tick marks.

```
# plot the standard normal density on the domain [-4,4]
curve(dnorm(x),
      xlim = c(-4,4),
      main = 'Rejection Region of a Left-Sided Test',
      yaxs = 'i',
      xlab = 't-statistic',
      ylab = '',
      lwd = 2,
      axes = 'F'
)

# add x-axis
axis(1,
     at = c(-4,0,-1.64,4),
     padj = 0.5,
     labels = c('',0,expression(Phi^-1~(.05)==-1.64),'')
)

# shade rejection region in right tail
```

```
polygon(x = c(-4, seq(-4, -1.64, 0.01), -1.64),
        y = c(0, dnorm(seq(-4, -1.64, 0.01)), 0),
        col = 'darkred'
)
```



3.4 Confidence intervals for the Population Mean

As stressed before, we will never estimate the exact value of a the population mean of Y using a random sample. However, we can compute confidence intervals for the population mean. In general, a confidence interval for a unkown parameter is a set of values that contains the true parameter with a prespecified probability, the confidence level. Confidence intervals are computed using the information available in the sample. Since this information is the result of a random process, confidence intervals are random variables themselves.

Key Concept 3.7 shows how to compute confidence intervals for the unknown population mean $E(Y)$.

Key Concept 3.6

Confidence Intervals for the Population Mean

A 95% confidence interval for μ_Y is a random variable that contains the true μ_Y in 95% of all possible random samples. When n is large we can use the normal approximation. Then, 99%, 95%, 90% confidence intervals are

$$\text{99\% confidence interval for } \mu_Y = \left\{ \overline{Y} \pm 2.58 \times SE(\overline{Y}) \right\}. \tag{3.9}$$

$$\text{95\% confidence interval for } \mu_Y = \left\{ \overline{Y} \pm 1.96 \times SE(\overline{Y}) \right\}. \tag{3.10}$$

$$\text{90\% confidence interval for } \mu_Y = \left\{ \overline{Y} \pm 1.64 \times SE(\overline{Y}) \right\}. \tag{3.11}$$

These confidence intervals are sets of null hypotheses we cannot reject in a two-sided hypothesis test at the given level of confidence.

Now consider the following statements.

1. The interval
$$\left\{ \overline{Y} \pm 1.96 \times SE(\overline{Y}) \right\}$$
covers the true value of μ_Y with a probability of 95%.
2. We have computed $\overline{Y} = 5.1$ and $SE(\overline{Y} = 2.5$ so the interval
$$\left\{ 5.1 \pm 1.96 \times 2.5 \right\} = [0.2, 10]$$
covers the true value of μ_Y with a probability of 95%.

While 1. is right (this is exactly in line with the definition above), 2. is completely wrong and none of Your lecturers wants to read such a sentence in a term paper, written exam or similar, believe us. The difference is that, while 1. is the definition of a random variable, 2. is one possible *outcome* of this random variable so there is no meaning in making any probabilistic statement about it. Either the computed interval *does cover* μ_Y or it *does not*!

In R, testing hypothesis about the mean of a population on the basis of a random sample is very easy due to functions like `t.test()` from the stats package. It procudes an object of type list. Luckily, one of the most simple ways to use `t.test()` is when You want to obtain a 95% confidence interval for some population mean. We start by generating some random data and calling `t.test()` in conjunction with `ls()` to obtain a breakdown of the output components.

```r
# set random seed
set.seed(1)

# generate some sample data
sampledata <- rnorm(100,10,10)

# checke type
typeof(t.test(sampledata))
```

```
## [1] "list"
```

```r
# display list elements produced by t.test
ls(
  t.test(sampledata)
)
```

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

Though we find that many items are reported, at the moment we are interested in computing a 95% confidence set for the mean.

```r
t.test(sampledata)$"conf.int"
```

```
## [1]  9.306651 12.871096
## attr(,"conf.level")
## [1] 0.95
```

This tells us that the 95% confidence interval is

$$\left[9.31, 12.87 \right].$$

In this example, the computed interval does cover the true μ_Y which we know to be 10.

Let us have a look at the whole standard output produced by `t.test()`.

```
t.test(sampledata)
```

```
##
##  One Sample t-test
##
## data:  sampledata
## t = 12.346, df = 99, p-value < 2.2e-16
## alternative hypothesis: true mean is not equal to 0
## 95 percent confidence interval:
##   9.306651 12.871096
## sample estimates:
## mean of x
##  11.08887
```

We see that `t.test()` not only computes a 95% confidence interval but automatically conducts a two-sided significance test of the hypothesis $H_0 : \mu_Y = 0$ at the level of 5% and reports relevant parameters thereof: the alternative hypothesis, the estimated mean, the resulting t-statistic, the degrees of freedom of the underlying t distribution (`t.test()` does not perform the normal approximation) and the corresponding p-value. Very convenient!

In this example, we come to the conclusion that the population mean *is not* significantly different from 0 at the level of 5% (which is correct), since $\mu_Y = 0$ is element of the 95% confidence interval

$$0 \in [-0.27, 0.12] .$$

We come to an equivalent result when using the p-value rejection rule:

$$p = 0.456 > 0.05$$

3.5 Comparing Means from Different Populations

Suppose You are interested in the means of two different populations, denote them μ_1 and μ_2. More specifically You are interested whether these population means are different from each other and plan an using a hypothesis test to verifiy this on the basis of independent sample data from both populations. A suitable pair of hypotheses then is

$$H_0 : \mu_1 - \mu_2 = d_0 \quad \text{vs.} \quad H_1 : \mu_1 - \mu_2 \neq d_0 \tag{3.12}$$

where d_0 denotes the hypothesized difference in means. The book teaches us that H_0 can be tested with the t-statistic

$$t = \frac{(\overline{Y}_1 - \overline{Y}_2) - d_0}{SE(\overline{Y}_1 - \overline{Y}_2)} \tag{3.13}$$

where

$$SE(\overline{Y}_1 - \overline{Y}_2) = \sqrt{\frac{s_1^2}{n_1} + \frac{s_2^2}{n_2}}. \tag{3.14}$$

This is called a two sample t-test. For large n_1 and n_2, (3.13) is standard normal distributed under the null hypothesis. Anlog to the simple t-test we can compute confidence intervals for the true difference in population means:

$$(\overline{Y}_1 - \overline{Y}_2) \pm 1.96 \times SE(\overline{Y}_1 - \overline{Y}_2)$$

is a 95% confidence interval for d. In R, Hypotheses as in (3.12) can be tested with `t.test()`, too. Note that `t.test()` chooses $d_0 = 0$ by default. This can be changed by setting the argument `mu` accordingly.

```
# set random seed
set.seed(1)

# draw data from two different populations with equal mean
sample_pop1 <- rnorm(100, 10, 10)
sample_pop2 <- rnorm(100, 10, 20)

# perform a two sample t-test
t.test(sample_pop1, sample_pop2)
```

```
##
##  Welch Two Sample t-test
##
## data:  sample_pop1 and sample_pop2
## t = 0.872, df = 140.52, p-value = 0.3847
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
##  -2.338012  6.028083
## sample estimates:
## mean of x mean of y
## 11.088874  9.243838
```

We find that the two sample t-test does not reject the (true) null hypothesis that $d_0 = 0$.

3.6 An Application to the Gender Gap of Earnings

In this section discusses how to reproduce the results presented in the box '*The Gender Gap of Earnings of College Graduates in the United States*' in the book.

In order to reproduce table 3.1 You need to download the replication data which is hosted by Pearson and can be found and downloaded here. Download the data for chapter three as an excel spreadsheet (cps_ch3.xlsx). This data set contains data that ranges from 1992 to 2008 and earnings are reported in prices of 2008. There are several ways to import the .xlsx-files into R. Our suggestion is the function `read_excel()` from the readxl package. The package is not part of R's standard distribution and has to be installed manually.

```
# install and load the readxl package
## install.packages('readxl')
library(readxl)
```

You are now ready to import the data set. Make sure You use the correct path to the downloaded file! In our example, the file is saved in a subfolder (data) of the working directory. If You are not sure what Your current working directory is, use `getwd()`, see also `?getwd()`. This will give You the path that points to the place R is currently looking for files.

```
# import the data into R
cps <- read_excel(path = 'data/cps_ch3.xlsx')
```

Next, install and load the package dyplr. This package provides some handy functions that simplify data wrangling a lot. It makes use of the `%>%` operator.

> In general, the aim of pipe operators is to increase readability of written code. The pipe operator %>%, also known as magrittr, is relatively new to R. It was originally introduced with the package magrittr but is available for several R packages. The most prominent ones are plotly and dplyr. See the following link for more on the magrittr package.
> The basic idea is to simplify a sequece of function calls by chaining them. 1:10 %>% mean
> # [1] 5.5
> # is equivalent to mean(1:10)
> # [1] 5.5

```r
# install and load the dplyr package
## install.packages('dplyr')
library('dplyr')
```

First, get an overview over the data set. Next, use `%>%` and some functions from the `dplyr` package to group the observations by gender and year and compute descriptive statistics for both groups.

```r
# Get an overview of the data structure
head(cps)
```

```
## # A tibble: 6 x 3
##   a_sex  year    ahe08
##   <dbl> <dbl>    <dbl>
## 1     1  1992 17.16203
## 2     1  1992 15.33856
## 3     1  1992 22.94229
## 4     2  1992 13.28334
## 5     1  1992 22.12292
## 6     2  1992 12.16761
```

```r
# group data by gender and year and compute the mean, standard deviation
# and number of observations for each group
avgs <- cps %>%
        group_by(a_sex, year) %>%
        summarise(mean(ahe08),
                  sd(ahe08),
                  n()
                  )

# print results to the console
print(avgs)
```

```
## # A tibble: 10 x 5
## # Groups:   a_sex [?]
##    a_sex  year `mean(ahe08)` `sd(ahe08)` `n()`
##    <dbl> <dbl>         <dbl>       <dbl> <int>
##  1     1  1992      23.27382   10.172081  1594
##  2     1  1996      22.47544   10.103141  1379
##  3     1  2000      24.88314   11.599727  1303
##  4     1  2004      25.12169   12.008435  1894
##  5     1  2008      24.97840   11.778632  1838
##  6     2  1992      20.04629    7.868418  1368
##  7     2  1996      18.98048    7.951608  1230
##  8     2  2000      20.73938    9.359327  1181
##  9     2  2004      21.02373    9.363071  1735
## 10     2  2008      20.87478    9.657140  1871
```

With the pipe operator `%>%` we simply chain different R functions that produce compatible input and ouput. In the code above, we take the dataset `cps` and use it as an input for the function `group_by()`. The output of `group_by` is subsequently used as an input for `summarise()` and so forth.

Now that we have computed the statistics of interest for both genders, we can investigate how the gap in earnings between both groups evolves over time.

```
# split the data set by gender
male <- avgs %>% filter(a_sex == 1)
female <- avgs %>% filter(a_sex == 2)

# Rename columns of both splits
colnames(male)   <- c("Sex", "Year", "Y_bar_m", "s_m", "n_m")
colnames(female) <- c("Sex", "Year", "Y_bar_f", "s_f", "n_f")

# Estimate Gender gaps, compute standard errors and confidence intervals for all dates
gap <- male$Y_bar_m - female$Y_bar_f

gap_se <- sqrt(male$s_m^2 / male$n_m + female$s_f^2 / female$n_f)

gap_ci_l <- gap - 1.96 * gap_se

gap_ci_u <- gap + 1.96 * gap_se

result <- cbind(male[,-1], female[,-(1:2)], gap, gap_se, gap_ci_l, gap_ci_u)

# print results to the console
print(result, digits = 3)
```

```
##   Year Y_bar_m  s_m  n_m Y_bar_f  s_f  n_f  gap gap_se gap_ci_l gap_ci_u
## 1 1992    23.3 10.2 1594    20.0 7.87 1368 3.23  0.332     2.58     3.88
## 2 1996    22.5 10.1 1379    19.0 7.95 1230 3.49  0.354     2.80     4.19
## 3 2000    24.9 11.6 1303    20.7 9.36 1181 4.14  0.421     3.32     4.97
## 4 2004    25.1 12.0 1894    21.0 9.36 1735 4.10  0.356     3.40     4.80
## 5 2008    25.0 11.8 1838    20.9 9.66 1871 4.10  0.354     3.41     4.80
```

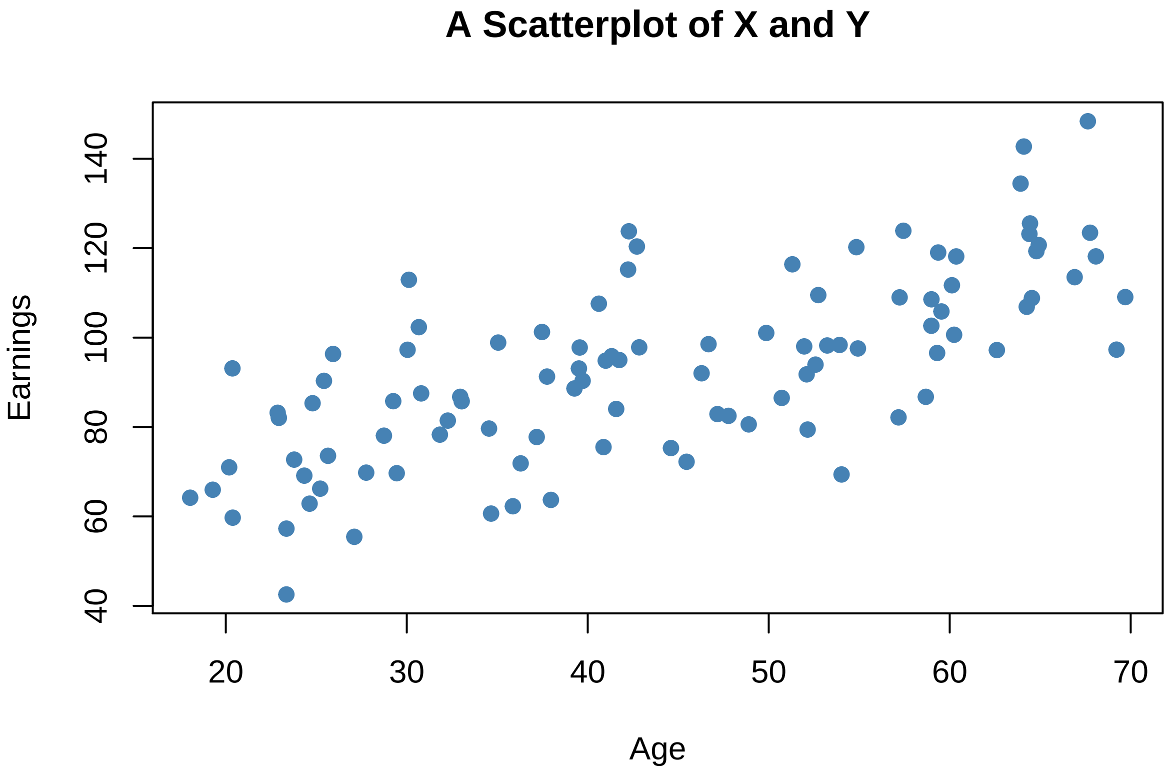
We observe virtually the same results as the ones presented in the book. the computed statistics suggest that there *is* a gender gap in earnings. Note that we can reject the null hypothesis that the gap is zero for all periodes. Further, estimates of the gap and bounds of the 95% confidence intervals indicate that the gap has been quite stable over the recent past.

3.7 Scatterplots, Sample Covariance and Sample Correlation

A scatterplot represents two dimensional data, for example n observation on X_i and Y_i, by points in a cartesian coordinate system. It is very easy to generate scatterplots using the `plot()` function in R. Let's generate some fictional data on age and earnings of workers and plot it.

```
# set random seed
set.seed(123)

# generate data set
```

```
X <- runif(n = 100,
           min = 18,
           max = 70
           )
Y <- X + rnorm(n=100, 50, 15)

# plot observations
plot(X,
     Y,
     type = "p",
     main = "A Scatterplot of X and Y",
     xlab = "Age",
     ylab = "Earnings",
     col = "steelblue",
     pch = 19
     )
```



The plot shows positive correlation between age and earnings. This in line with the assumption that older workers earn more than those that the joined the working population recently.

Sample Covariance and Correlation

By now You should be familiar with the concepts of variance and covariance. If not, we recommend You to work Your way through chapter 2 of the book (again).

As for the variance, covariance and correlation of two variables are properties that relate to the (unknown) joint probability distribution of these variable. Just as the individual population variances of both variables, we can estimate covariance and correlation by means of suitable estimators using a random sample (X_i, Y_i), $i = 1, \dots, n$.

The sample covariance

$$s_{XY} = \frac{1}{n-1} \sum_{i=1}^{n} (X_i - \overline{X})(Y_i - \overline{Y})$$

is an estimator for the population variance of X and Y whereas the sample correlation

$$r_{XY} = \frac{s_{XY}}{s_X s_Y}$$

can be used to estimate the population correlation, a standardized measure for the strength of the linear relationship between X and Y. See chapter 3.7 in the book for a more detailed treatment of these estimators.

As for variance and standard deviation, these estimators are implemented as R functions in the stats package. We can use them to estimate population covariance and population correlation the fictional data on age and earnings.

```
# compute sample covariance of X and Y
cov(X,Y)
```

```
## [1] 213.934
```

```
# compute sample correlation between X and Y
cor(X,Y)
```

```
## [1] 0.706372
```

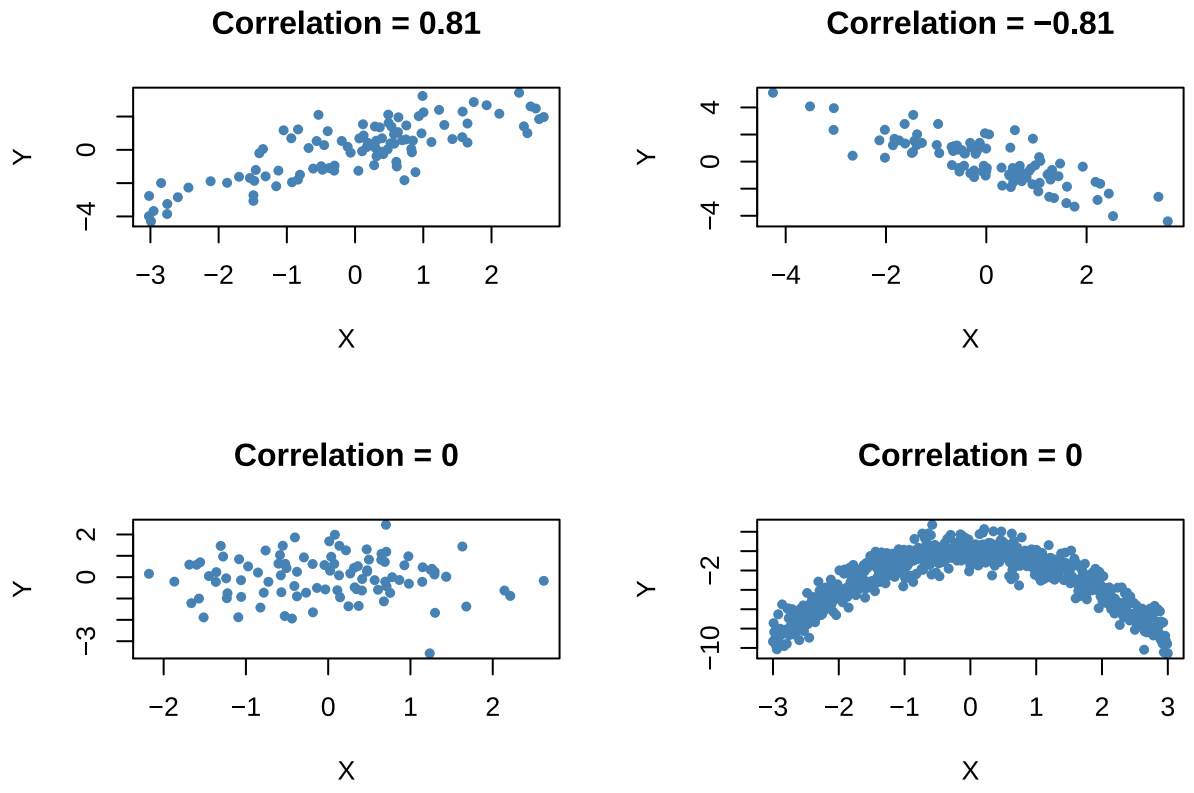
```
# equivalent way to compute the sample correlation
cov(X,Y)/(sd(X) * sd(Y))
```

```
## [1] 0.706372
```

The estimates indicate that X and Y are moderately correlated.

The next code chunk uses the function `mvnorm()` from package MASS to generate bivariate example data with different degree of correlation.

```
library(MASS)

# set random seed
set.seed(1)

# positive correlation (0.81)
example1 <- mvrnorm(100,
                    mu = c(0,0),
                    Sigma = matrix(c(2,2,2,3), ncol = 2),
                    empirical = TRUE
                    )

# negative correlation (-0.81)
example2 <- mvrnorm(100,
                    mu = c(0,0),
                    Sigma = matrix(c(2,-2,-2,3), ncol = 2),
                    empirical = TRUE
                    )

# no correlation
example3 <- mvrnorm(100,
                    mu = c(0,0),
                    Sigma = matrix(c(1,0,0,1), ncol = 2),
                    empirical = TRUE
                    )

# no correlation (quadratic relationship)
X <- seq(-3,3,0.01)
Y <- -X^2 + rnorm(length(X))

example4 <- cbind(X,Y)

# estimate

## Plots

# divide plot area as 2-by-2 array
par(mfrow=c(2,2))

plot(example1, col='steelblue', pch=20, xlab = 'X', ylab = 'Y', main="Correlation = 0.81")
plot(example2, col='steelblue', pch=20, xlab = 'X', ylab = 'Y', main="Correlation = -0.81")
plot(example3, col='steelblue', pch=20, xlab = 'X', ylab = 'Y', main="Correlation = 0")
plot(example4, col='steelblue', pch=20, xlab = 'X', ylab = 'Y', main="Correlation = 0")
```



Chapter 4

Linear Regression with One Regressor

This chapter introduces the basics in linear regression and shows how to perform regression analysis in R. In linear regression, the aim is to model the relationship between a dependent variable Y and one or more explanatory variables denoted as $X_1, X_2, \dots, X_k$. Following the book we will focus on the concept of simple linear regression throughout the whole chapter. In simple linear regression, there is just one explanatory variable X_1. If for example a school cuts the class sizes by hiring new teachers, that is the school lowers the student-teacher ratios of their classes, X_1, how would this affect the performance of the students involved in a standardized test,Y? With linear regression we can not only examine whether the student-teacher ratio *does have* an impact on the test results but we can also learn about the *direction* and the *strength* of this effect.

To start with an easy example, consider the following combinations of average test score and the average student-teacher ratio in some fictional school disctrics.

1

2

3

4

5

6

7

TestScore

680

640

670

660

630

660.0

635

STR

15

17

19

20

22

23.5

25

To work with these data in R we begin by creating two vectors: one for the student-teacher ratios (`STR`) and one for test scores (`TestScore`), both containing the data from the table above.

```
# Create sample data
STR <- c(15, 17, 19, 20, 22, 23.5, 25)
TestScore <- c(680, 640, 670, 660, 630, 660, 635)

# Print out sample data
STR
```

```
## [1] 15.0 17.0 19.0 20.0 22.0 23.5 25.0
```

```
TestScore
```

```
## [1] 680 640 670 660 630 660 635
```

If we use a simple linear regression model, we assume that the true relationship between both variables can be represented by a straight line, formally

$$Y = b \cdot X + a.$$

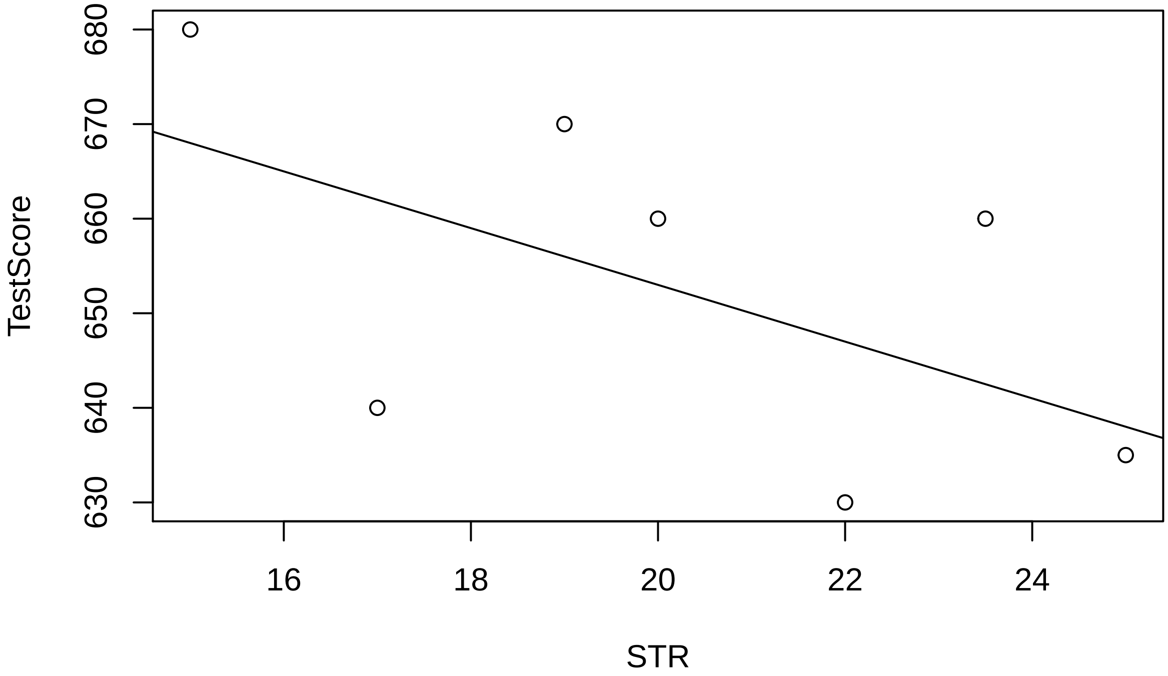
For now, let us suppose that the true function which relates test score and student-teacher ratio to each other is

$$TestScore = 713 - 3 \times STR.$$

If possible, it is always a good idea to visualize the data You work with in an appropriate way. For our purpose it is suitable to use the function `plot()` to produce a scatterplot with `STR` on the X-axis and `TestScore` on the Y axis. An easy way to do so is to call `plot(y_variable ~ x_variable)` whereby `y_variable` and `x_variable` are placeholders for the vectors of observations we want to plot. Furthermore, we might want to add the true relationship to the plot. To draw a straight line, R provides the function `abline()`. We just have to call this function with arguments `a` (representing the intercept) and `b` (representing the slope) after executing `plot()` in order to add the line to our scatterplot.

The following code reproduces figure 4.1 from the textbook.

```
# create a scatter plot of the data
plot(TestScore ~ STR)
# add the true relationship to the plot
abline(a = 713, b = -3)
```



We find that our line does not touch any of the points although we claimed that it represents the true relationship. The reason for this is the core problem of statistics, *randomness*. Most of the time there are influences which cannot be explained in a purely deterministic fashion and thus exacerbate finding the true relationship.

In order to account for these differences between observed data and the true relationship, we extend our model from above by an *error term u* which covers these random effects. Put differently, u accounts for all the differences between the true regression line and the actual observed data. Beside pure randomness, these deviations could also arise from measerment errors or, as will be discussed later, could be the consequence of leaving out other factors that are relevant in explaining the dependent variable. Which other factor are plausible in our example? For one thing, the test scores might be driven by the teachers quality and the background of the students. It is also imaginable that in some classes, the students were lucky on the test days and thus achieved higher scores. For now, we will summarize such influences by an additive component:

$$TestScore = \beta_0 + \beta_1 \times STR + \text{other factors}$$

Of course this idea is very general as it can be easily extented to other situations that can be described with a linear model. The basic linear regression function we will work with hence is

$$Y_i = \beta_0 + \beta_1 X_i + u_i.$$

Key Concept 4.1 summarizes the terminology of the simple linear regression model.

Key Concept 4.1

Terminology for the Linear Regression Model with a Single Regressor

The linear regression model is

$$Y_i = \beta_0 + \beta_1 X_1 + u_i$$

where

- the subscript i runs over the observations, $i = 1, \ldots, n$

- Y_i is the *dependent variable*, the *regressand*, or simply the *left-hand variable*
- X_i is the *independent variable*, the *regressor*, or simply the *right-hand variable*
- $Y = \beta_0 + \beta_1 X$ is the *population regression line* also called the *population regression function*
- β_0 is the *intercept* of the population regression line
- β_1 is the *slope* of the population regression line
- u_i is the *error term*

4.1 Estimating the Coefficients of the Linear Regression Model

In practice, the intercept β_0 and slope $\beta_1$of the population regression line are unknown. Therefore, we must employ data to estimate both unknown parameters. In the following a real world example will be used to demonstrate how this is achieved. We want to relate test scores to student-teacher ratios measured in californian schools. The test score is the district-wide average of reading and math scores for fifth graders. Again, the class size is measured as the number of students divided by the number of teachers (the student-teacher ratio). As for the data, the California School dataset (`CASchools`) comes with a R package called AER, an acronym for Applied Econometrics with R. After installing the package with `install.packages("AER")` and attaching it with `library("AER")` the dataset can be loaded using the `data` function.

```
# install the AER package (once)
install.packages("AER")

# load the AER package
library(AER)

# load the the data set in the workspace
data(CASchools)
```

Note that once a package has been installed it is available for use at further occasions when invoked with `library()` — there is no need to run `install.packages("...")` again!

For several reasons it is interesting to know what kind of object we are dealing with. `class(object_name)` returns the type (class) of an object. Depending on the class of an object some functions (such as `plot()` and `summary()`) behave differently.

Let us check the class of the object `CASchools`.

```
class(CASchools)
```

```
## [1] "data.frame"
```

It turns out that `CASchools` is of class `data.frame` which is a convienient format to work with.

With help of the function `head()` we get a first overview of our data. This function shows only the first 6 rows of the data set which prevents an overcrowded console output.

> Press ctrl + L to clear the console. This command deletes any code that has been typed in and executed by You or printed to the console by R functions. Good news is: anything else is left untouched. You neither loose defined variables and alike nor the code history. It is still possible to recall previously executed R commands using the up and down keys. If You are working in RStudio, press ctrl + Up on Your keyboard (CMD + Up on a mac) to review a list of previously entered commands.

```
head(CASchools)
```

```
##   district                          school  county grades students
## 1    75119              Sunol Glen Unified Alameda  KK-08      195
## 2    61499            Manzanita Elementary   Butte  KK-08      240
## 3    61549     Thermalito Union Elementary   Butte  KK-08     1550
## 4    61457 Golden Feather Union Elementary   Butte  KK-08      243
## 5    61523        Palermo Union Elementary   Butte  KK-08     1335
## 6    62042         Burrel Union Elementary  Fresno  KK-08      137
##   teachers calworks   lunch computer expenditure    income   english  read
## 1    10.90   0.5102  2.0408       67    6384.911 22.690001  0.000000 691.6
## 2    11.15  15.4167 47.9167      101    5099.381  9.824000  4.583333 660.5
## 3    82.90  55.0323 76.3226      169    5501.955  8.978000 30.000002 636.3
## 4    14.00  36.4754 77.0492       85    7101.831  8.978000  0.000000 651.9
## 5    71.50  33.1086 78.4270      171    5235.988  9.080333 13.857677 641.8
## 6     6.40  12.3188 86.9565       25    5580.147 10.415000 12.408759 605.7
##    math
## 1 690.0
## 2 661.9
## 3 650.9
## 4 643.5
## 5 639.9
## 6 605.4
```

We find that the dataset consists of plenty of variables and most of them are numeric.

By the way: an alternative to `class()` and `head()` is `str()` which is deduced from 'structure' and gives a comprehensive overview of the object. Try this!

Turning back to `CASchools`, the two variables we are intersted in (i.e. average test score and the student-teacher ratio) are *not* included. However, it is possible to calculate both from the provided data. To obtain the student-teacher ratios, we simply divide the number of students by the number of teachers. The avarage test score is the arithmetic mean of the test score for reading and the score of the math test. The next code chunk shows how the two variables can be constructed and how they are appended to `CASchools` which is a data.frame.

```
# compute STR and append it to CASchools
CASchools$STR <- CASchools$students/CASchools$teachers

# compute TestScore and append it to CASchools
CASchools$score <- (CASchools$read + CASchools$math)/2
```

If we ran `head(CASchools)` again we would find the two variables of interest as additional columns named `STR` and `score` (check this!).

Table 4.1 from the text book summarizes the distribution of test scores and student-teacher ratios. There are several functions which can be used to produce similar results within R:

- `mean()` (computes the arithmetic mean of the provided numbers)
- `sd()` (computes the sample standard deviation)
- `quantile()` (returns a vector of the specified quantiles for the data)

The next code chunk shows how to achieve this. First, we compute summary statistics on the coloumns `STR` and `score` of `CASchools`. In order to have a nice display format we gather the computed measures in a `data.frame` object named `DistributionSummary`.

```
# compute sample averages of STR and score
avg_STR <- mean(CASchools$STR)
avg_score <- mean(CASchools$score)
```

```
# compute sample standard deviations of STR and score
sd_STR <- sd(CASchools$STR)
sd_score <- sd(CASchools$score)

# set up a vector of percentiles and compute the quantiles
quantiles <- c(0.10, 0.25, 0.4, 0.5, 0.6, 0.75, 0.9)
quant_STR <- quantile(CASchools$STR, quantiles)
quant_score <- quantile(CASchools$score, quantiles)

# gather everything in a data.frame
DistributionSummary <- data.frame(
                                  Average = c(avg_STR, avg_score),
                                  StandardDeviation = c(sd_STR, sd_score),
                                  quantile = rbind(quant_STR, quant_score)
                                  )

# print the summary to the console
DistributionSummary
```

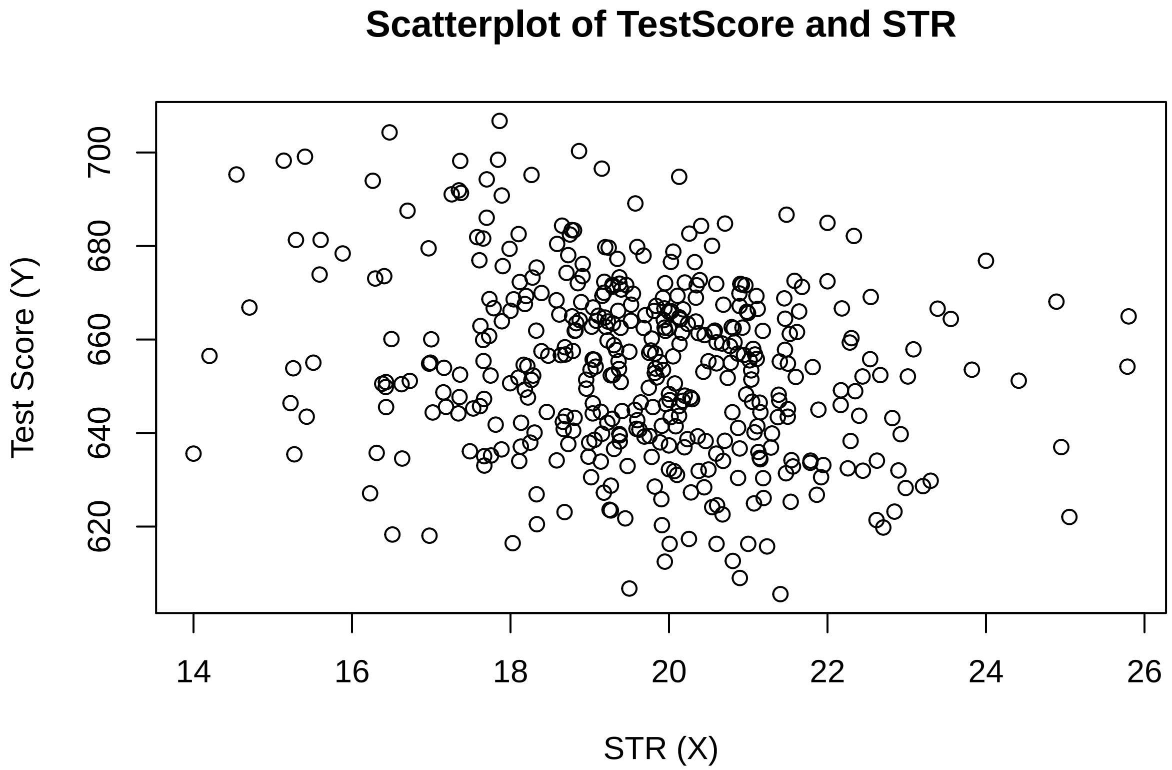
```
##               Average StandardDeviation quantile.10. quantile.25.
## quant_STR    19.64043          1.891812      17.3486     18.58236
## quant_score 654.15655         19.053347     630.3950    640.05000
##             quantile.40. quantile.50. quantile.60. quantile.75.
## quant_STR       19.26618     19.72321      20.0783     20.87181
## quant_score    649.06999    654.45000     659.4000    666.66249
##             quantile.90.
## quant_STR       21.86741
## quant_score    678.85999
```

The standard distribution (the Base R package) of R already contains a `summary` function which can be applied to objects of class `data.frame`. Type and execute `summary(STR)`!

As done for the sample data, we use `plot()` for a visual survey. This allows us to detect specific characteristics of our data, such as outliers which are hard to discover by looking at mere numbers. This time we add some additional arguments to the `plot()` function.

The first argument in our call of `plot()`, `score ~ STR`, is again a formula that states the dependent variable and the regressor. However, this time the two variables are not saved in seperate vectors but are columns of `CASchools`. Therefore, R would not find the variables without the argument `data` beeing correctly specified. `data` must be in accordance with the name of the `data.frame` to which the variables belong, in this case `CASchools`. Further arguments are used to change the appearance of the plot: while `main` adds a title, `xlab` and `ylab` are adding custom labels to both axes.

```
plot(score ~ STR,
     data = CASchools,
     main = "Scatterplot of TestScore and STR",
     xlab = "STR (X)",
     ylab = "Test Score (Y)"
)
```



The plot (figure 4.2 in the book) shows the scatterplot of all observations on student-teacher ratio and Test score. We see that the points are strongly scatterd and an apparent relationship cannot be detected by only looking at them. Yet it can be assumed that both variables are negatively correlated, that is we expect to observe lower test scores in bigger classes.

The function `cor()` (type and execute `?cor` for further info), can be used to compute the correlation between 2 *numerical* vectors.

```
cor(CASchools$STR, CASchools$score)
```

```
## [1] -0.2263627
```

As the scatterplot already suggests, the correlation is negative but rather weak.

The task we are facing now is to find a line which fits best to the data. Of course we could simply stick with graphical inspection and correlation analysis and then select the best fitting line by eyeballing. However, this is pretty unscientific and prone to subjective perception: different students would draw different regression lines. On this account, we are interested in techniques that are more sophisticated. Such a technique is ordinary least squares (OLS) estimation.

The Ordinary Least Squares Estimator

The OLS estimator chooses the regression coefficients such that the estimated regression line is as close as possible to the observed data points. Thereby closeness is measured by the sum of the squared mistakes made in predicting Y given X. Let b_0 and b_1 be some estimators of β_0 and β_1. Then the sum of squared estimation mistakes can be expressed as

$$\sum_{i=1}^{n}(Y_i - b_0 - b_1 X_i)^2.$$

The OLS estimator in the simple regression model is the pair of estimators for intercept and slope which minimizes the expression above. The derivation of the OLS estimators for both parameters are presented in Appendix 4.1 of the book. The results are summarized in Key Concept 4.2.

Key Concept 4.2

The OLS Estimator, Predicted Values, and Residuals

The OLS estimators of the slope β_1 and the intercept β_0 in the simple linear regression model are

$$\begin{align}
\hat\beta_1 &= \frac{\sum_{i=1}^{n}(X_i - \overline{X})(Y_i - \overline{Y})}{\sum_{i=1}^{n}(X_i - \overline{X})^2} \tag{4.1} \\
& \tag{4.2} \\
\hat\beta_0 &= \overline{Y} - \hat\beta_1 \overline{X} \tag{4.3}
\end{align}$$

The OLS predicted values $\widehat{Y}_i$ and residuals $\hat{u}_i$ are

$$\begin{align}
\widehat{Y}_i &= \hat\beta_0 + \hat\beta_1 X_i, \tag{4.4} \\
& \tag{4.5} \\
\hat{u}_i &= Y_i - \widehat{Y}_i. \tag{4.6}
\end{align}$$

The estimated intercept $\hat\beta_0$, the slope parameter $\hat\beta_1$, and the residuals $(\hat{u}_i)$ are computed from a sample of n observations of X_i and Y_i, i, ..., n. These are *estimates* of the unkown true population intercept (β_0), slope (β_1), and error term (u_i).

We are aware that the results presented in Key Concept 4.2 are not very intuitive at first glance. The following interactice application aims to help You understand the mechanics of OLS. You can add observations by clicking into the coordinate system where the data are represented by points. If two or more observations are available, the application computes a regression line using OLS and some statistics which are displayed in the right panel. The results are updated as You add further observations to the left panel. A double-click resets the application i.e. all data are removed.

There are many possible ways to compute $\hat\beta_0$ and $\hat\beta_1$ in R. For example, we could implement the formulas presented in Key Concept 4.2 with two of R's most basic functions: `mean()` and `sum()`.

```r
attach(CASchools) #allows to use the variables contained in CASchools directly
```

```
## The following objects are masked from CASchools (pos = 10):
##
##     calworks, computer, county, district, english, expenditure,
##     grades, income, lunch, math, read, school, score, STR,
##     students, teachers
```

```r
# compute beta_1
beta_1 <- sum((STR - mean(STR))*(score - mean(score))) / sum((STR - mean(STR))^2)

# compute beta_0
beta_0 <- mean(score) - beta_1 * mean(STR)

# print the results to the console
beta_1
```

```
## [1] -2.279808
```

```r
beta_0
```

```
## [1] 698.9329
```

Of course there are also other and even more manual ways to do the same tasks. Luckily, OLS is one of the most widely-used estimation techniques. Being a statistical programming language, R already contains a built-in function named `lm()` (**l**inear **m**odel) which can be used to carry out regression analysis.

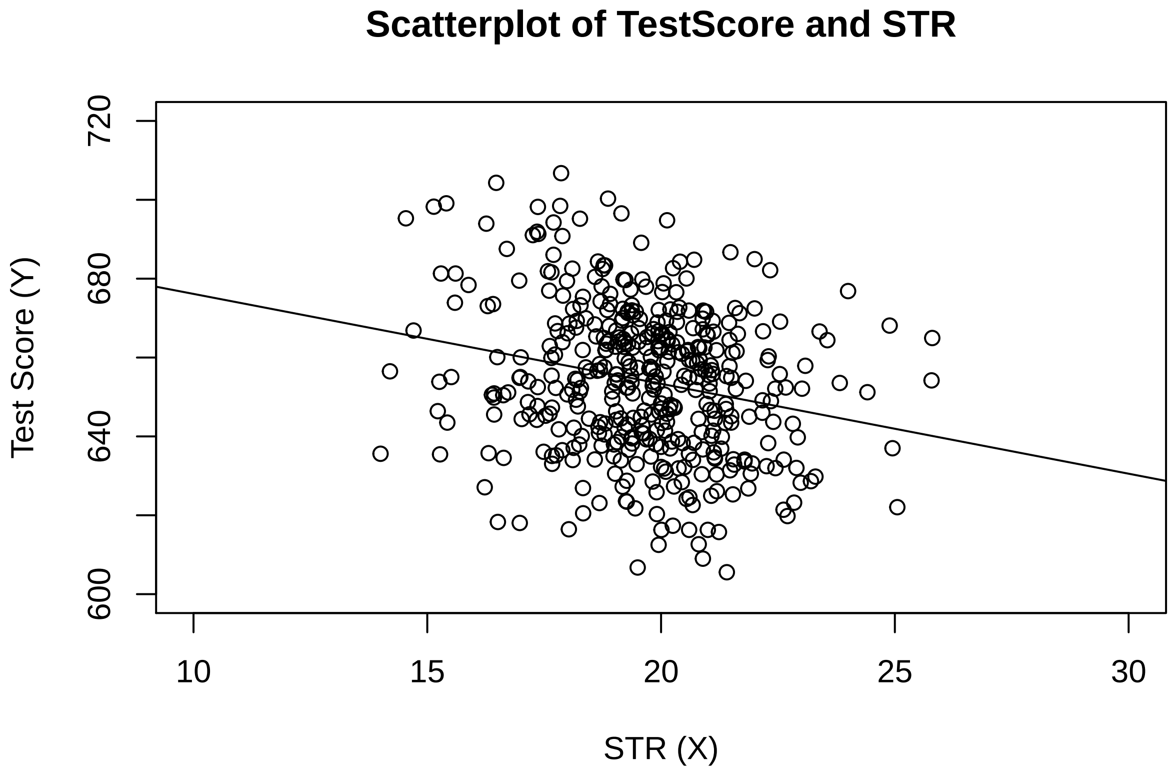
The first argument of the function to be specified is, similar as in `plot()`, the regression formula with the basic syntax `y ~ x` where `y` is the dependent variable and `x` the explanatory variable. The argument `data` sets the data set to be used in the regression. We now revisit the example from the book where the relationship between the test scores and the class sizes is analysed. The following code uses `lm()` to replicate the results presented in figure 4.3 in the book.

```r
# estimate the model and assign the result to linear_model
linear_model <- lm(score ~ STR, data = CASchools)

# Print the standard output of the estimated lm object to the console
linear_model
```

```
##
## Call:
## lm(formula = score ~ STR, data = CASchools)
##
## Coefficients:
## (Intercept)          STR
##      698.93        -2.28
```

Let us add the estimated regression line to the plot. This time we also enlarge ranges of both axes by setting the arguments `xlim` and `ylim`.

```r
# plot the data
plot(score ~ STR,
     data = CASchools,
     main = "Scatterplot of TestScore and STR",
     xlab = "STR (X)",
     ylab = "Test Score (Y)",
     xlim = c(10, 30),
     ylim = c(600, 720)
     )

# add the regression line
abline(linear_model)
```



Did you notice that this time, we did not pass the intercept and slope parameters to `abline`? If you call `abline` on an object of class `lm` that only contains a single regressor variable, R draws the regression line automatically!

4.2 Measures of Fit

After estimating a linear regression, the question occurs how well that regression line describes the data. Are the observations tightly clustered arround the regression line, or are they spread out? Both, the R^2 and the *standard error of the regression* (SER) measure how well the OLS Regression line fits the data.

The R^2

The R^2 is the fraction of sample variance of Y_i that is explained by X_i. Mathemethically, the R^2 can be written as the ratio of the explained sum of squares to the total sum of squares. The *explained sum of squares* (ESS) is the sum of squared deviations of the predicted values, $\hat{Y}_i$, from the average of the Y_i. The *total sum of squares* (TSS) is the sum of squared deviations of the Y_i from their average.

$$ESS = \sum_{i=1}^{n} \left(\hat{Y}_i - \overline{Y} \right)^2 \tag{4.7}$$

$$\tag{4.8}$$

$$TSS = \sum_{i=1}^{n} \left(Y_i - \overline{Y} \right)^2 \tag{4.9}$$

$$\tag{4.10}$$

$$R^2 = \frac{ESS}{TSS} \tag{4.11}$$

Since $TSS = ESS + SSR$ we can also write

$$R^2 = 1 - \frac{SSR}{TSS}$$

where SSR is the sum of squared residuals, a measure for the errors made when predicting the Y by X. The SSR is defined as

$$SSR = \sum_{i=1}^{n} \hat{u}_i^2.$$

R^2 lies between 0 and 1. It is easy to see that a perfect fit, i.e. no errors made when fitting the regression line, implies $R^2 = 1$ since then we have $SSR = 0$. On the contrary, if our estimated regression line does not explain any variation in the Y_i, we have $ESS = 0$ and consequently $R^2 = 0$.

Standard Error of the Regression

The *Standard Error of the Regression* (SER) is an estimator of the standard deviation of the regression error $\hat{u}_i$. As such it measure the magnitude of a typical deviation from the regression, i.e. the magnitude of a typical regression error.

$$SER = s_{\hat{u}} = \sqrt{s_{\hat{u}}^2} \quad \text{where} \quad s_{\hat{u}}^2 = \frac{1}{n-2} \sum_{i=1}^{n} \hat{u}_i^2 = \frac{SSR}{n-2}$$

Remember that the u_i are *unobserved.* That is why we use their estimated counterparts, the residuals $\hat{u}_i$ instead. See chapter 4.3 of the book for a more detailed comment on the SER.

Application to the Test Score Data

Both measures of fit can be obtained by using the function `summary()` with the `lm` object provided as the only argument. Whereas the function `lm()` only prints out the estimated coefficients to the console, `summary` provides additional predefined information such as the regression's R^2 and the SER.

```
mod_summary <- summary(linear_model)
mod_summary
```

```
##
## Call:
## lm(formula = score ~ STR, data = CASchools)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -47.727 -14.251   0.483  12.822  48.540
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept) 698.9329     9.4675  73.825  < 2e-16 ***
## STR          -2.2798     0.4798  -4.751 2.78e-06 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 18.58 on 418 degrees of freedom
## Multiple R-squared:  0.05124,    Adjusted R-squared:  0.04897
## F-statistic: 22.58 on 1 and 418 DF,  p-value: 2.783e-06
```

The R^2 in the output is called 'Multiple R-squared' and has the value 0.051. Hence, 5.1% of the variance of the dependent variable *score* is explained by the explanatory variable STR. That is the regression explains some of the variance but much of the variation in test scores remains unexplained (cf. figure 4.3 in the book).

The SER is called 'Residual standard error' and takes the value 18.58. The unit of the SER is the same as the unit of the dependent variable. In our context we can interpret the value as follows: on average the deviation of the actual achieved test score and the regression line is 18.58 points.

Now, let us check whether the `summary()` function uses the same definitions for R^2 and SER as we do by computing them manually.

```r
# compute R^2 manually
SSR <- sum(mod_summary$residuals^2)
TSS <- sum((score - mean(score))^2)
R2 <- 1 - SSR/TSS

# print the value to the console
R2
```

```
## [1] 0.05124009
```

```r
# compute SER manually
n <- nrow(CASchools)
SER <- sqrt(SSR / (n-2))

# print the value to the console
SER
```

```
## [1] 18.58097
```

We find that the results coincide. Note that the values provided by `summary()` are rounded to two decimal places. Can You Do this using R?

4.3 The Least Squares Assumptions

OLS performs well under a quite broad variety of different circumstances. However, there are some assumptions which are posed on the data which need to be satisfied in order to achieve reliable results.

Key Concept 4.3

The Least Squares Assumptions

$$Y_i = \beta_0 + \beta_1 X_i + u_i, \; i = 1, ..., n$$

where

1. The error term u_i has conditional mean zero given X_i: $E(u_i|X_i) = 0$
2. $(X_i, Y_i), i = 1, ..., n$ are independent and identically distributed (i.i.d.) draws from their joint distribution
3. Large outliers are unlikely: X_i and Y_i have nonzero finite fourth moments

Assumption #1: The Error Term has Conditional Mean of Zero

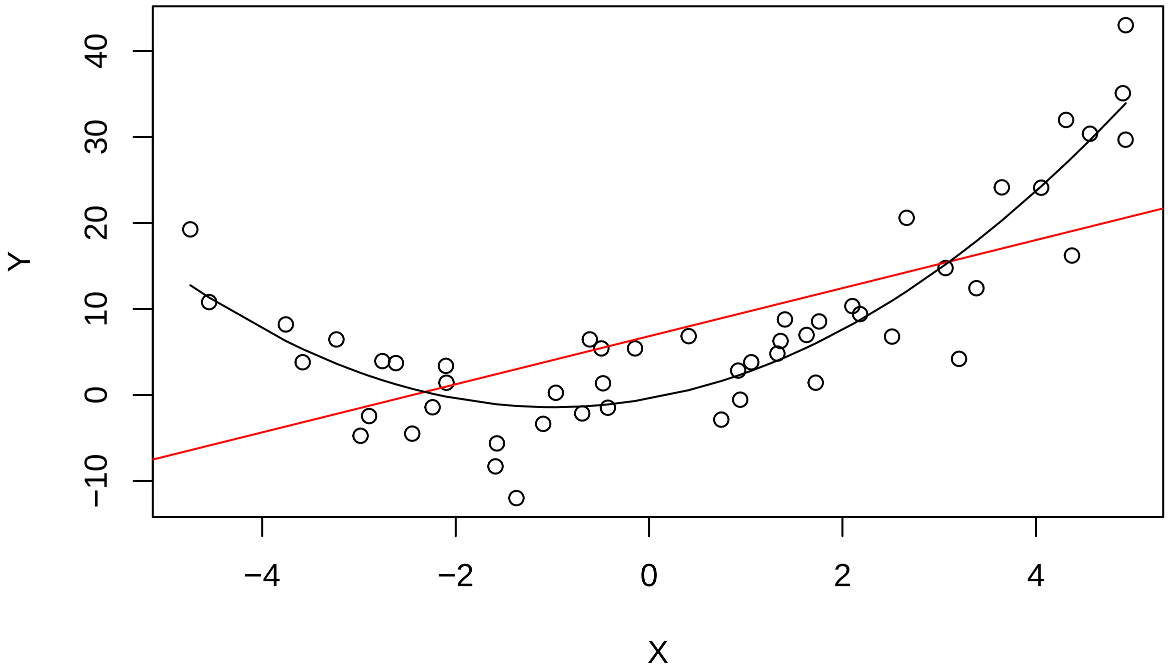
This means that no matter which value we choose for X, the error term u must not show any systematic pattern and must have a mean of 0. Consider the case that $E(u) = 0$ but for low and high values of X, the error term tends to be positive and for midrange values of X the error tends to be negative. We can use R to construct such an example. To do so we generate our own data using R's build in random number generators.

We will use the following functions You should be familiar with:

- `runif()` (generates uniformly distributed random numbers)
- `rnorm()` (generates nomally distributed random numbers)
- `predict()` (does predictions based on the results of model fitting functions like `lm()`)
- `lines()` (adds line segments to an existing plot)

We start by creating a vector containing values that are randomly scattered on the domain $[-5, 5]$. For our example we decide to generate uniformly distributed random numbers. This can be done with the function `runif()`. We also need to simulate the error term. For this we generate normally distributed random numbers with a mean equal to 0 and a variance of 1 using `rnorm()`. The Y values are obtained as a quadratic function of the X values and the error. After generating the data we estimate both a simple regression model and a quadratic model that also includes the regressor X^2. Finally, we plot the simulated data and add a the estimated regression line of a simple regression model as well as the predictions made with a quadratic model to compare the fit graphically.

```r
# set a random seed to make the results reproducible
set.seed(321)

# simulate the data
X <- runif(50, min = -5, max = 5)
u <- rnorm(50, sd = 5)
## the true relation
Y <- X^2 + 2*X + u

# estimate a simple regression model
mod_simple <- lm(Y ~ X)

# predict using a quadratic model
prediction <- predict(lm(Y ~ X +  I(X^2)), data.frame(X = sort(X)))

# plot the results
plot(Y ~ X)
abline(mod_simple, col = "red")
lines(sort(X), prediction)
```



This shows what is meant by $E(u_i|X_i) = 0$:

Using the quadratic model (represented by the black curve) we see that there are no systematic deviations of the observation from the predicted relation. It is credible that the assumption is not violated when such a model is employed. However, using a simple linear regression model we see that the assumption is probably violated as $E(u_i|X_i)$ varies with the X_i.

Assumption #2: All (X_i, Y_i) are Independently and Identically Distributed

Most common sampling schemes used when collecting data from populations produce i.i.d. samples. For example, we could use R's random number generator to randomly select student IDs from a university's enrollment list and record age X and earnings Y of the corresponding students. This is a typical example of simple random sampling and ensures that all the (X_i, Y_i) are drawn randomly from the same population.

A prominent example where the i.i.d. assumption is not fulfilled is time series data where we have observations on the same unit over time. For example, take X as the number of workers employed by a production company over the course of time. Due to technological change, the company makes job cuts periodically but there are also some non-deterministic influences that relate to economics, politics and alike. Using R we can simulate such a process and plot it.

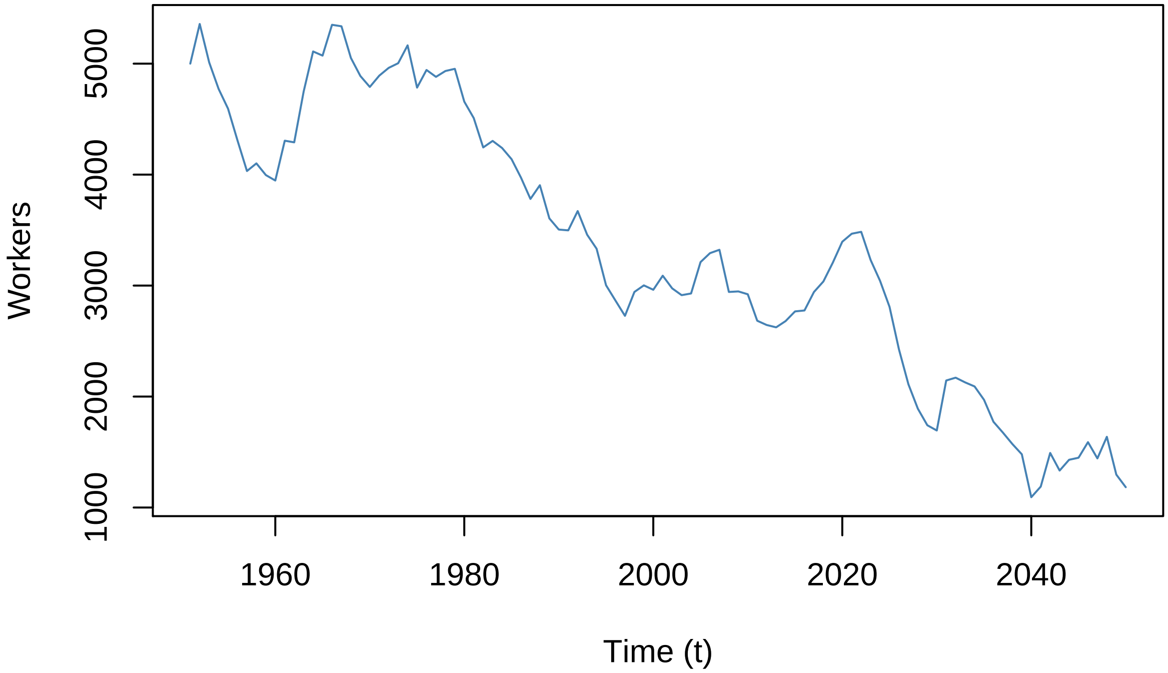
We start the series with a total of 5000 workers and simulate the reduction of employment with a simple autoregressive process that exhibits a downward trend and has normal distributed errors:[1]

$$employment_t = 0.98 \cdot employment_{t-1} + u_t$$

```
# set random seed
set.seed(7)

# initialize the employment vector
X <- c(5000,rep(NA,99))
```

[1] See chapter 14 in the book for more on autoregressive processes and time series analysis in general.

```r
# generate a date vector
Date <- seq(as.Date("1951/1/1"), as.Date("2050/1/1"), "years")

# generate time series observations with random influences
for (i in 2:100) X[i] <- 0.98*X[i-1] + rnorm(1, sd=200)

#plot the results
plot(Date, X, type = "l", col="steelblue", ylab = "Workers", xlab="Time (t)")
```



It is evident that the observations on X cannot be independnet in this example: the level of today's employment is correlated with tomorrows employment level. Thus, the i.i.d. assumption is violated for X.

Assumption #3: Large outliers are unlikely

It is easy to come up with situations where extreme observations, i.e. observations that deviate considerably from the usual range of the data, may occur. Such observations are called outliers. Technically speaking, assumption #3 requires that X and Y have a finite kurtosis.[2]

Common cases where we want to exclude or (if possible) correct such outliers is when they are apperently typos, conversion errors or measurement errors. Even if it seems that extreme observations have been recorded correctly, it is advisable to exclude them before estimating a model since OLS suffers from *sensitivity to outliers*.

What does this mean? One can show that extreme observation receive heavy weighting in the computation done with OLS. Therefore, outliers can lead to strongly distorted estimates of regression coefficient. To get a better impression of this, consider the following application where we have placed some sample data on X and Y which are highly correlated. The relation between X and Y seems to be explained pretty good by the plotted regression line: all of the blue dots lie close to the red line and we have $R^2 = 0.92$.

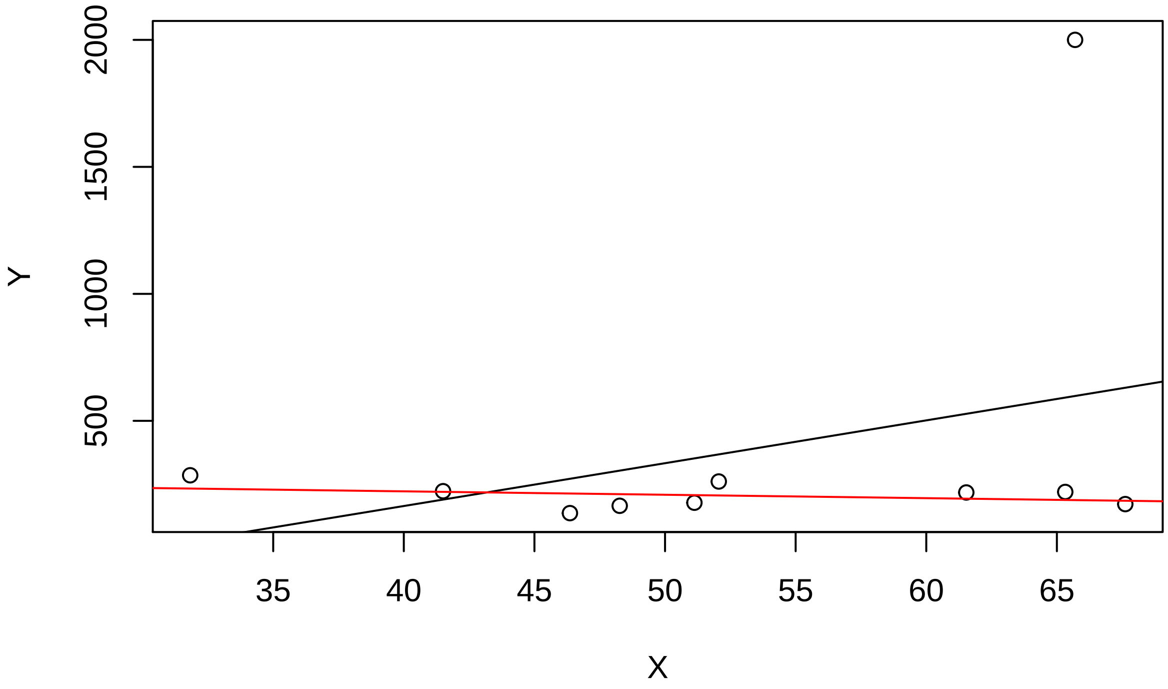
Now go ahead and add a further observation at, say, $(18, 2)$. This clearly is an outlier. The result is quite striking: the estimated regression line differs greatly from the one we adjudged to fit the data well. The slope

[2] See chapter 4.4 in the book.

is heavily downward biased and R^2 decreased to a mere 29%! Double-click inside the coordinate system to reset the app. Feel free to experiment. Choose different coordinates for the outlier or add additional ones.

The following code roughly reproduces what is shown in figure 4.5 in the book. As done above we use sample data generated using R's random number functions `rnorm()` and `runif()`. We estimate simple regression models based on the original data set and a modified set where one observation is change to be an outlier and plot the results. In order to understand the complete code You should be familiar with the function `sort()` which sorts the entries of a numeric vector in ascending order.

```
# set random seed
set.seed(123)

# generate the data
X <- sort(runif(10, min = 30, max = 70 ))
Y <- rnorm(10 , mean = 200, sd = 50)
Y[9] <- 2000

# fit model with outlier
fit <- lm(Y ~ X)

# fit model without outlier
fitWithoutOutlier <- lm(Y[-9] ~ X[-9])

# plot the results
plot(Y ~ X)
abline(fit)
abline(fitWithoutOutlier, col = "red")
```



4.4 The Sampling Distribution of the OLS Estimator

Because the OLS estimators $\hat{\beta}_0$ and $\hat{\beta}_1$ are computed from a randomly drawn sample, the estimators themselves are random variables with a probability distribution — the so-called sampling distribution of the estimators — which describes the values they could take over different random samples. Although the sampling distribution of $\hat{\beta}_0$ and $\hat{\beta}_1$ can be complicated when the sample size is small and generally differs with the number of observation, n, it is possible to make certain statements about it that hold for all n. In particular

$$E(\hat{\beta}_0) = \beta_0 \quad \text{and} \quad E(\hat{\beta}_1) = \beta_1,$$

that is, $\hat{\beta}_0$ and $\hat{\beta}_1$ are unbiased estimators of β_0 and β_1, the true parameters. If the sample is sufficiently large, by the central limit theorem the *joint* sampling distribution of the estimators is well approximated by the bivariate normal distribution (2.1). This implies that the marginal distributions are also normal in large samples. Core facts on the large-sample distribution of β_0 and β_1 are presented in Key Concept 4.4.

Key Concept 4.4

Large Sample Distribution of $\hat{\beta}_0$ and $\hat{\beta}_1$

If the least squares assumptions in Key Concept 4.3 hold, then in large samples $\hat{\beta}_0$ and $\hat{\beta}_1$ have a jointly normal sampling distribution. The large sample normal distribution of $\hat{\beta}_1$ is $N(\beta_1, \sigma^2_{\hat{\beta}_1})$, where the variance of the distribution, $\sigma^2_{\hat{\beta}_1}$, is

$$\sigma^2_{\hat{\beta}_1} = \frac{1}{n} \frac{Var\left[(X_i - \mu_X)\, u_i\right]}{\left[Var\left(X_i\right)\right]^2}. \tag{4.1}$$

The large sample normal distribution of $\hat{\beta}_0$ is $N(\beta_0, \sigma^2_{\hat{\beta}_0})$, where

$$\sigma^2_{\hat{\beta}_0} = \frac{1}{n} \frac{Var\left(H_i u_i\right)}{\left[E\left(H_i^2\right)\right]^2}, \quad \text{where} \quad H_i = 1 - \left[\frac{\mu_X}{E\left(X_i^2\right)}\right] X_i. \tag{4.2}$$

R Simulation Study 1

Whether Key Koncept 4.4 really holds can be verified using R. First we build our own population of 100000 observations in total. To do this we need values for our independent variable X, for the error term u, and the regression parameters β_0 and β_1. With all this combined in a simple regression model, we can compute our dependent variable Y. In our example we generate the numbers X_i, $i = 1$, ... ,100000 by drawing a random sample from a uniform distribution on the interval $[0, 20]$. The realisations of the error terms u_i are drawn from a standard normal distribution with parameters $\mu = 0$ and $\sigma^2 = 100$ (note that `rnorm()` requires σ as input for the argument `sd`, see `?rnorm`). Furthermore we chose $\beta_0 = -2$ and $\beta_1 = 3.5$ so the true model is

$$Y_i = -2 + 3.5 \cdot X_i.$$

Finally, we store the results in a data.frame.

```r
# simulate data
N <- 100000
X <- runif(N, min = 0, max = 20)
u <- rnorm(N, sd = 10)

# population regression
Y <- -2 + 3.5 * X + u
population <- data.frame(X, Y)
```

From now on we will consider the previously generated data as the true population (which of course would be *unknown* in a real world application, otherwise there would not be a reason to do draw a random sample in the first place). The knowledge about the true population and the true relationship between Y and X can be used to verify the statements made in Key Concept 4.4.

First, let us calculate the true variances $\sigma^2_{\hat{\beta}_0}$ and $\sigma^2_{\hat{\beta}_1}$ for a randomly drawn sample of size $n = 100$.

```
# set sample size
n <- 100

# compute the variance of hat_beta_0
H_i <- 1 - mean(X) / mean(X^2) * X
var_b0 <- var(H_i * u) / (n * mean(H_i^2)^2 )

# compute the variance of hat_beta_1
var_b1 <- var( ( X - mean(X) ) * u ) / (100 * var(X)^2)
```

```
# print variances to the console
var_b0
```

```
## [1] 4.045066
```

```
var_b1
```

```
## [1] 0.03018694
```

Now let us assume that we do not know the true values of β_0 and β_1 and that it is not possible to observe the whole population. However, we can observe a random sample of n observations. Then, it would not be possible to compute the true parameters but we could obtain estimates of β_0 and β_1 from the sample data using OLS. However, we know that these estimates are outcomes of random variables themselves since the observations are randomly sampled from the population. Key Concept 4.4. describes their distributions for large n. When drawing a single sample of size n it is not possible to make any statement about these distributions. Things change if we repeat the sampling scheme many times and compute the estimates for each sample: using such a procedure we simulate outcomes of the respective distributions.

To achieve this in R, we employ the following approach:

- We assign the number of repetitions, say 10000, to `reps`. Then we initialize a matrix `fit` were the estimates obtained in each sampling iteration shall be stored row-wise. Thus `fit` has to be an array of dimensions `reps`×2.
- In the next step we draw `reps` random sample of size `n` from the population and obtain the OLS estimates for each sample. The results are stored as row entries in the outcome matrix `fit`. This is done using a `for()` loop.
- At last, we estimate variances of both coefficient estimators using the sampled outcomes and plot histograms of the latter. We also add plot of the density functions belonging to the distributions that follow from Key Concept 4.4. The function `bquote()` is used to obtain math expressions in the titels and labels of both plots. See `?bquote`.

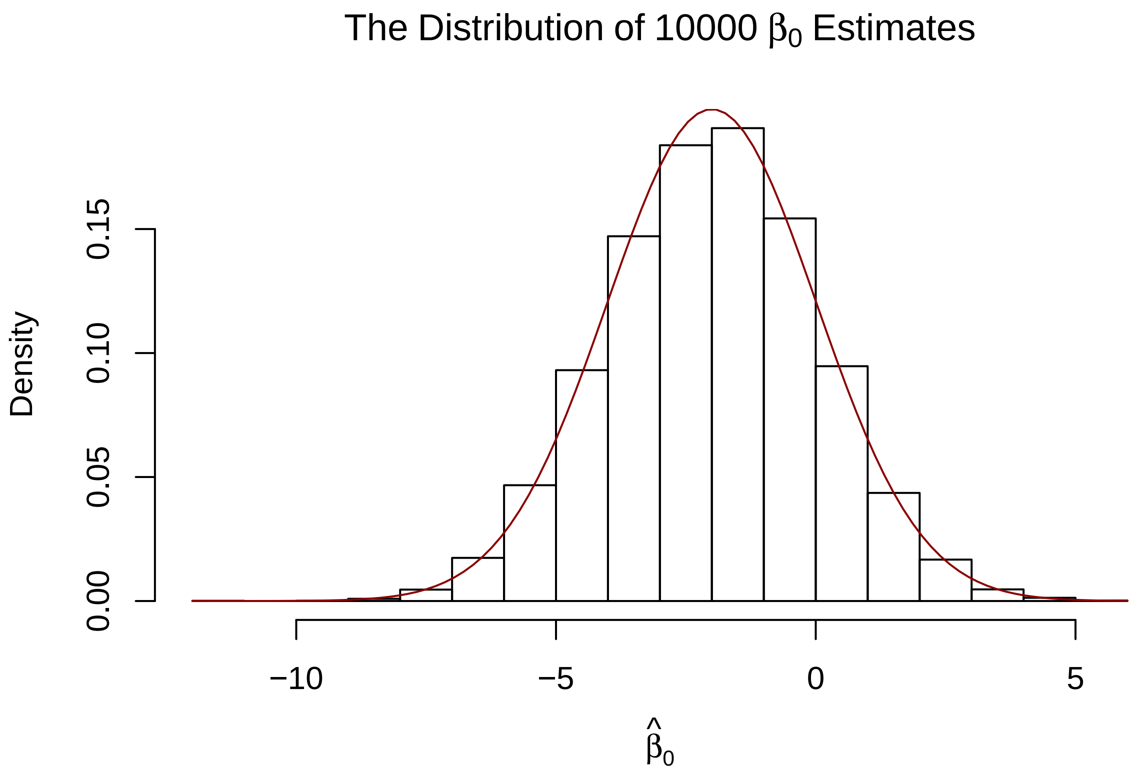
```
# set repetitions and sample size
n <- 100
reps <- 10000

# initialize the matrix of outcomes
fit <- matrix(ncol = 2, nrow = reps)

# loop sampling and estimating of the coefficients
for (i in 1:reps){
 sample <- population[sample(1:N, n),]
 fit[i, ] <- lm(Y ~ X, data = sample)$coefficients
}

# compute variance estimates using outcomes
var(fit[ ,1])
```

```
## [1] 4.057089
```

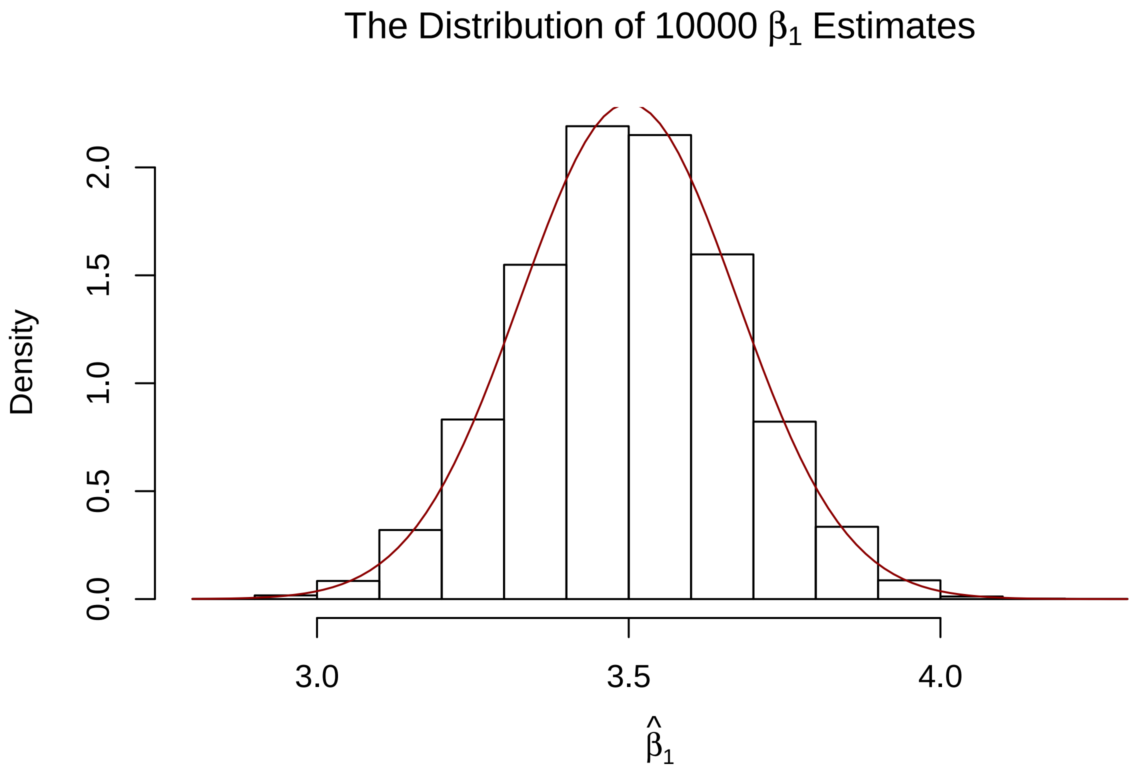
```
var(fit[ ,2])
```

```
## [1] 0.03021784
```

```
# plot histograms of beta_0 estimates
hist(fit[ ,1],
     main = bquote(The ~ Distribution  ~ of ~ 10000 ~ beta[0] ~ Estimates),
     xlab = bquote(hat(beta)[0]),
     freq = F)
# add true distribution to plot
curve(dnorm(x,-2,sqrt(var_b0)), add = T, col="darkred")
```



```
# plot histograms of beta_1 estimates
hist(fit[ ,2],
     main = bquote(The ~ Distribution  ~ of ~ 10000 ~ beta[1] ~ Estimates),
     xlab = bquote(hat(beta)[1]),
     freq = F)

# add true distribution to plot
curve(dnorm(x,3.5,sqrt(var_b1)), add = T, col="darkred")
```



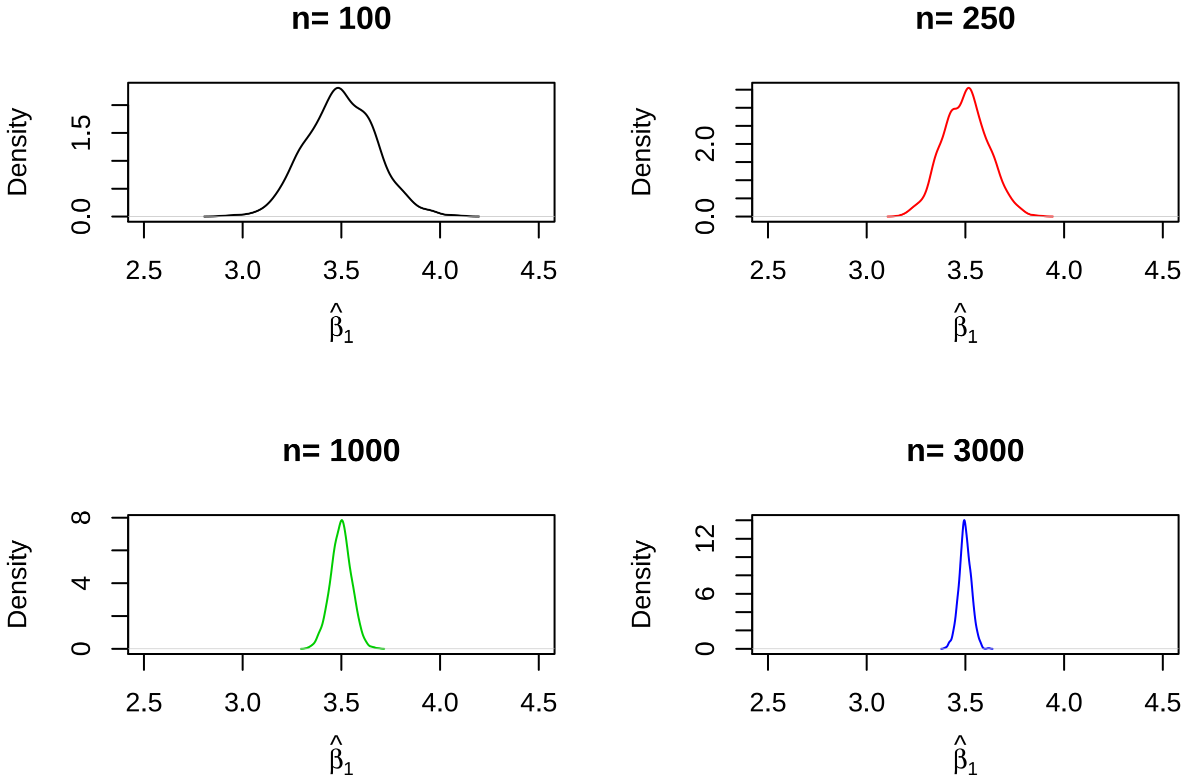
We are now able to say the following: first, our variance estimates are in favour of the claims made in Key Concept 4.4 since they come close to the computed theoretical values. Second, the histograms suggest that the estimators distributions indeed follow normal distributions which can be fairly approximated by the respective normal distributions stated in Key Concept 4.4.

R Simulation Study 2

A further result implied by Key Concept 4.4 is that both estimators are consistent i.e. they converge in probability to their true value. This is since their variances converge to 0 as n increases. We can check this by repeating the simulation above for an increasing sequence of sample sizes. This means we no langer assign the sample size but a *vector* of sample sizes: `n <- c(...)`. Let us look at the distributions of β_1. The idea here is to add an additional call of `for()` to the code. This is done in order to loop over the vector of sample sizes `n`. For each of the sample sizes we carry out the same simulation as before but plot a density estimate for the outcomes of each iteration over `n`. Notice that we have to change `n` to `n[j]` in the inner loop to ensure that the `j`th element of `n` is used. In the simulation, we use sample sizes $100, 250, 1000$ and 3000. Consequently we have a total of four distinct simulations using different sample sizes.

```
# set random seed for reproducibility
set.seed(1)

# set repetitions and the vector of sample sizes
reps <- 1000
n <- c(100, 250, 1000, 3000)

# initialize the matrix of outcomes
fit <- matrix(ncol = 2, nrow = reps)

# devide the plot panel in a 2-by-2 array
par(mfrow = c(2,2))
```

```
#### Loop sampling and plotting ####

# outer loop over n
for (j in 1:length(n)) {

  # inner loop: sampling and estimating of the coefficients
  for (i in 1:reps){
    sample <- population[sample(1:N, n[j]), ]
    fit[i, ] <- lm(Y ~ X, data = sample)$coefficients
  }

  # draw density estimates
  plot(density(fit[,2]), xlim=c(2.5,4.5), col=j,
       main = paste("n=", n[j]), xlab = bquote(hat(beta)[1]))

}
```



We find that, as n increases, the distribution of $\hat{\beta}_1$ concentrates around its mean, i.e. its variance decreases. Put differently, the likelihood of observering estimates close to the true value of $\beta_1 = 3.5$ grows as we increase the sample size. The same behaviour could be observed if we would analyze the distribution of $\hat{\beta}_0$ instead.

R Simulation Study 3

Furthermore, (4.1) reveals that the variance of the OLS estimator for β_1 decreases as the variance of the X_i increases. In other words, as we increase the amount of information provided by the regressor, that is increasing $Var(X)$, which is used to estimate β_1, we are more confident that the estimate is close to the true value (i.e. $Var(\hat{\beta}_1)$ decreases). We can visualize this by reproducing figure 4.6 from the book. To do this, we sample 100 observations (X, Y) from a bivariate normal distribution with

$$E(X) = E(Y) = 5,$$

$$Var(X) = Var(Y) = 5$$

and

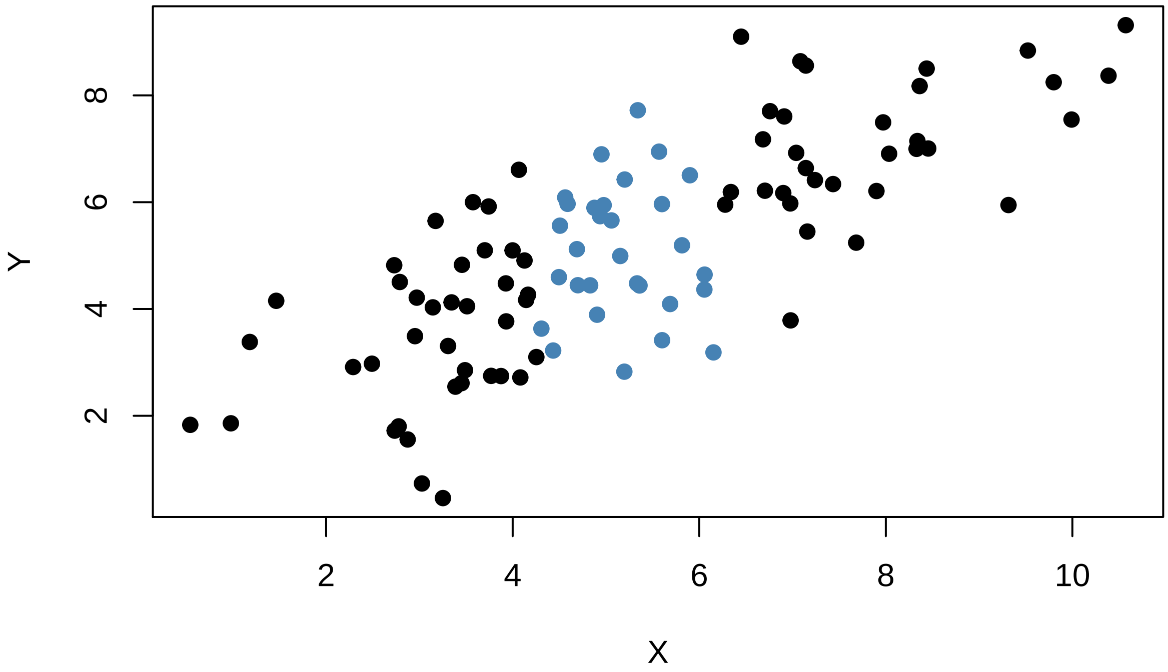
$$Cov(X, Y) = 4.$$

Formally, this is written down as

$$\begin{pmatrix} X \\ Y \end{pmatrix} \overset{i.i.d.}{\sim} \mathcal{N}\left[\begin{pmatrix} 5 \\ 5 \end{pmatrix}, \begin{pmatrix} 5 & 4 \\ 4 & 5 \end{pmatrix}\right]. \tag{4.3}$$

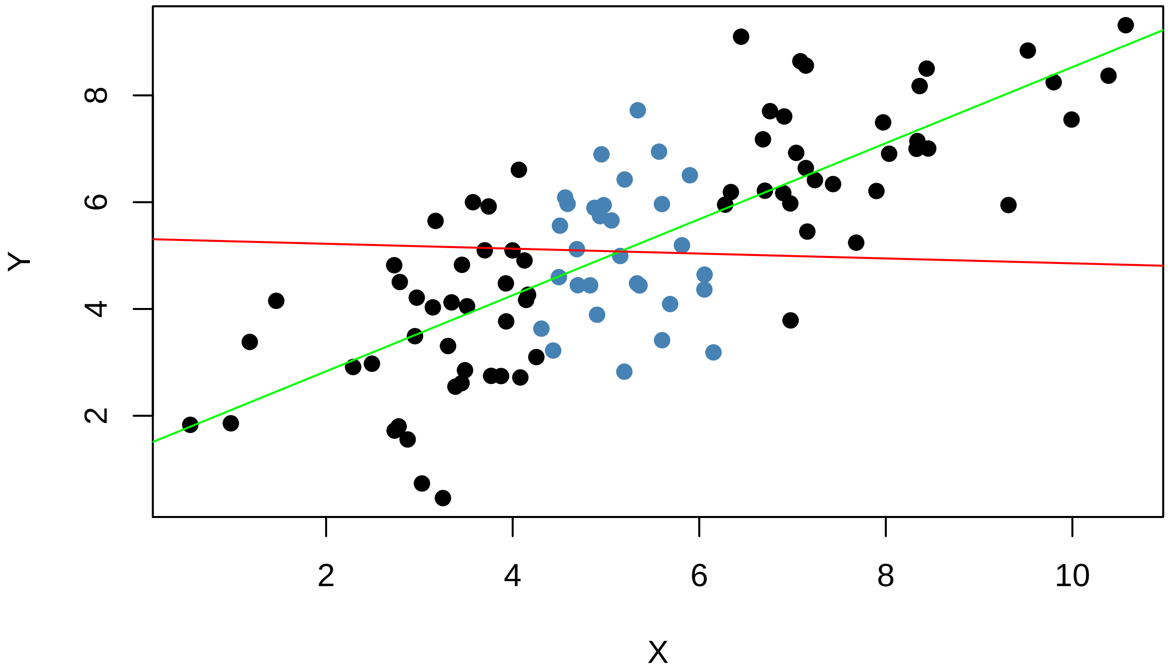
To carry out the random sampling, we make use of the function `mvtnorm()` from the package `MASS` which allows to draw random samples from multivariate normal distributions, see `?mvtnorm`. Next, we use the `subset()` function to split the sample into two subsets such that the first set, `set1`, consists of observations that fulfill the condition $|X - \overline{X}| > 1$ and the second set, `set2`, includes the remainder of the sample. We then plot both sets and use different colors to make them distinguishable.

```r
# load the MASS package
library(MASS)

# set random seed for reproducibility
set.seed(4)

# simulate bivarite normal data
bvndata <- mvrnorm(100,
                mu = c(5,5),
                Sigma = cbind(c(5,4),c(4,5))
                )

# assign column names / convert to data.frame
colnames(bvndata) <- c("X","Y")
bvndata <- as.data.frame(bvndata)

# subset the data
set1 <- subset(bvndata, abs(mean(X) - X) > 1)
set2 <- subset(bvndata, abs(mean(X) - X) <= 1)

# plot both data sets
plot(set1, xlab = "X", ylab = "Y", pch = 19)
points(set2, col = "steelblue", pch = 19)
```



It is clear that observations that are close to the sample average of the X_i have less variance than those that are farther away. Now, if we were to draw a line as accurately as possible through either of the two sets it is obvious that choosing the observations indicated by the black dots, i.e. using the set of observations which has larger variance than the blue ones, would result in a more precise line. Now, let us use OLS to estimate and draw the regression lines for both sets of observations.

```r
# estimate both regression lines
lm.set1 <- lm(Y ~ X, data = set1)
lm.set2 <- lm(Y ~ X, data = set2)

# add both lines to the plot
abline(lm.set1, col="green")
abline(lm.set2, col="red")
```



Evidently, the green regression line does far better in describing data sampled from the bivariate normal distribution stated in (4.3) than the red line. This is a nice example why we are interested in a high variance of the regressor X: more variance in the X_i means more information from which the precision of the estimation benefits.

Chapter 5

Hypothesis Tests and Confidence Intervals in the Simple Linear Regression Model

In this chapter, we continue with the treatment of the simple linear regression model. The following subsction discuss how we may use our knowledge about the sampling distribution of the OLS estimator in order to make statements regarding its uncertainty. These subsections cover the following topics:

- Testing Hypotheses about regression coefficients
- Confidence intervals for regression coefficients
- Regression when X is a dummy variable
- Heteroskedasticity and Homoskedasticity

5.1 Testing Two-Sided Hypotheses Concerning β_1

Using the fact that $\hat{\beta}_1$ is approximately normal distributed in large samples (see Key Concept 4.4), testing hypothesis about the true value β_1 can be done with the same approach as discussed in chapter 3.2.

Key Concept 5.1

General Form of the t-Statistic

Remember from chapter 3 that a general t-statistic has the form

$$t = \frac{\text{estimated value} - \text{hypothesized value}}{\text{standard error of the estimator}}.$$

Key Concept 5.2

Testing Hyothesis about β_1

For testing the hypothesis $H_0 : \beta_1 = \beta_{1,0}$, we need to perform the following steps:

1. Compute the standard error of $\hat{\beta}_1$, $SE(\hat{\beta}_1)$

$$SE(\hat{\beta}_1) = \sqrt{\hat{\sigma}^2_{\hat{\beta}_1}} \quad , \quad \hat{\sigma}^2_{\hat{\beta}_1} = \frac{1}{n} \times \frac{\frac{1}{n-2}\sum_{i=1}^n (X_i - \overline{X})^2 \hat{u_i}^2}{\left[\frac{1}{n}\sum_{i=1}^n (X_i - \overline{X})^2\right]^2}.$$

2. Compute the t-statistic

$$t = \frac{\hat{\beta}_1 - \beta_{1,0}}{SE(\hat{\beta}_1)}.$$

3. Now, given a two sided alternative ($H_1 : \beta_1 \neq \beta_{1,0}$) we reject at the 5% level if $|t^{act}| > 1.96$ or, equivalently, if the p-value is less than 0.05.
   Recall the definition of the p-value:

$$\begin{aligned} p\text{-value} =& \Pr_{H_0}\left[\left|\frac{\hat{\beta}_1 - \beta_{1,0}}{SE(\hat{\beta}_1)}\right| > \left|\frac{\hat{\beta}_1^{act} - \beta_{1,0}}{SE(\hat{\beta}_1)}\right|\right] & (5.1) \\ =& \Pr_{H_0}(|t| > |t^{act}|) & (5.2) \\ =& 2 \cdot \Phi(-|t^{act}|) & (5.3) \end{aligned}$$

   The last equality holds due to the normal approximation for large samples.

Consider again the OLS regression stored in `linear_model` from Chapter 4 that gave us the regression line

$$\widehat{TestScore} \ = \underset{(9.47)}{698.9} - \underset{(0.49)}{2.28} \times STR \ , \ R^2 = 0.051 \ , \ SER = 18.6.$$

For testing a hypothesis about the slope parameter (the coefficient on STR), we need $SE(\hat{\beta}_1)$, the standard error of the respective point estimator. As common in the literature, standard errors are presented in parantheses below the point estimates.

As can be witnessed in Key Concept 5.1 it is rather cumbersome to compute the standard error and thus the t-statistic by hand. The question You should be asking Yourself right now is obvious: can we obtain these values with minimum effort using R? Yes, we can. Let us first use `summary()` to get a summary on the estimated coefficients in `linear_model`.

```r
# print the summary of coefficients to the console
summary(linear_model)$coefficients
```

```
##               Estimate Std. Error   t value      Pr(>|t|)
## (Intercept) 698.932949  9.4674911 73.824516 6.569846e-242
## STR          -2.279808  0.4798255 -4.751327  2.783308e-06
```

When looking at the second column of the coefficients' summary, we discover values for $SE(\hat{\beta}_0)$ and $SE(\hat{\beta}_1)$. Also, in the third column, named `t value`, we find t-statistics t^{act} suitable for tests of the individual hypotheses $H_0 : \beta_0 = 0$ and $H_0 : \beta_1 = 0$. Furthermore, the output provides us with p-values corresponding to both tests against the two-sided alternatives $H_1 : \beta_0 \neq 0$ respectively $H_1 : \beta_1 \neq 0$ in the fourth column of the table.

Let us have a closer look at the test of

$$H_0 : \beta_1 = 0 \quad vs. \quad H_1 : \beta_1 \neq 0.$$

Using our revisited knowledge about t-statistics we find that

$$t^{act} = \frac{-2.279808 - 0}{0.4798255} \approx -4.75.$$

What does this tell us about the significance of the estimated coefficient? We reject the null hypothesis at the 5% level of significance since $|t^{act}| > 1.96$ that is the observed test statistic falls into the region of rejection. Or, alternatively and leading to the same result, we have p-value $= 2.78 * 10^{-6} < 0.05$. We conclude that the coefficient is significantly different from zero. With other words, our analysis provides evidence that the clase size *has an influence* on the students test scores. We say that β_1 is significantly different from 0 at the level of 5%.

Note that, although the difference is negligible in the present case as we will see later, `summary()` does not perform the normal approximation but calculates p-values using the appropriate t-distribution instead. Generally, the degrees of freedom are determined in the following manner:

$$\text{DF} = n - k - 1$$

where n is the number of observations used to estimate the model and k is the number of regressors, excluding the intercept. In our case, we have $n = 420$ observations and the only regressor is STR so $k = 1$. A sleek way to determine the model degress of freedom using R is

```
# determine degrees of freedom
linear_model$df.residual
```

```
## [1] 418
```

Hence, for the sampling distribution of $\hat{\beta}_1$ we have

$$\hat{\beta}_1 \sim t_{418}$$

such that the p-value for a two-sided significance test can be obtained by executing the following code:

```
2 * pt(-4.751327, df = 418)
```

```
## [1] 2.78331e-06
```

The result is very close to the value provided by `summary`. However since n is sufficiently large one could just as well use the standard normal density to compute the p-value:

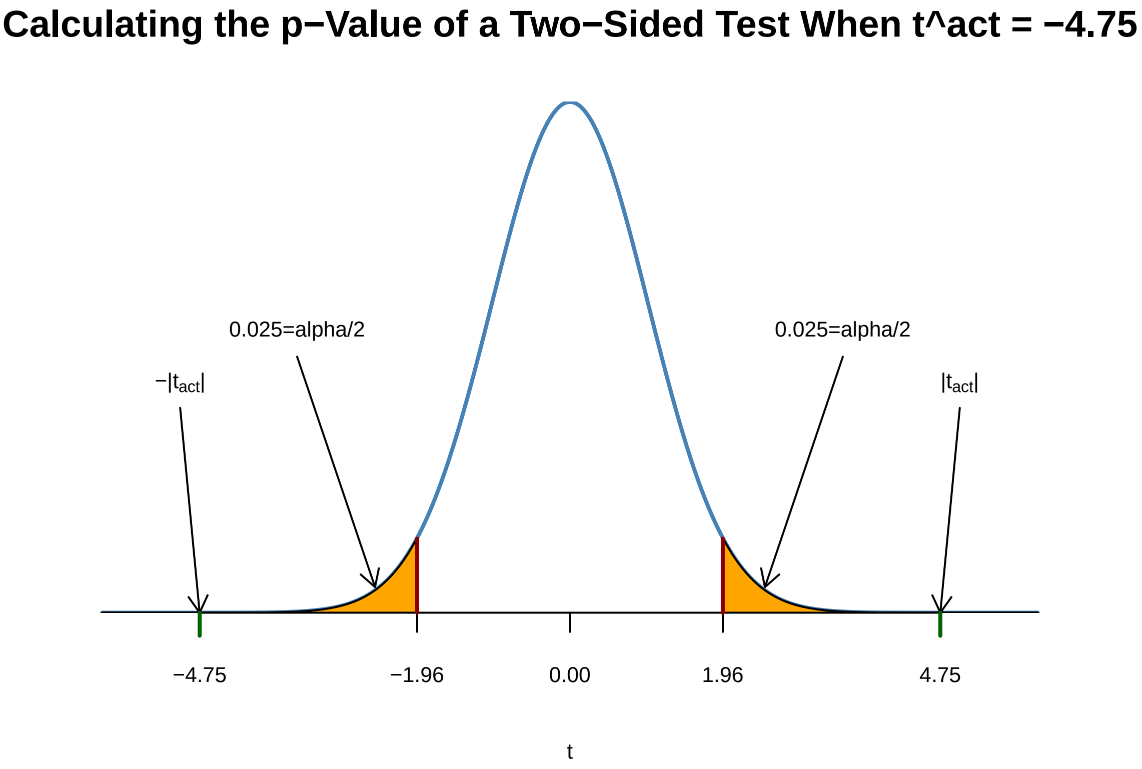
```
2 * pnorm(-4.751327)
```

```
## [1] 2.02086e-06
```

The difference is indeed negligible. These findings tell us that, if $H_0 : \beta_1 = 0$ is true and we were to repeat the whole process of gathering observations and estimating the model, chances of observing a $\hat{\beta}_1 \geq |-4.75|$ are roughly 1 : 359285 — so higher chances than winning the lottery next saturday but still very unlikely!

Using R we may visualise how such a statement is made when using the normal approximation. This reflects the principles depicted in figure 5.1 in the book. Do not let the following code chunk deter You: the code is somewhat longer than the usual examples and looks unappealing but there is **a lot** of repetition since color shadings and annotations are added on both tails of the normal distribution. We recommend You to execute the code step by step in order to see how the graph is augmented with the annotations.

```
# Plot the standard normal on the domain [-6,6]
t <- seq(-6,6,0.01)

plot(x = t,
     y = dnorm(t, 0, 1),
     type = "l",
     col = "steelblue",
     lwd = 2,
     yaxs = "i",
     axes = F,
     ylab = "",
     main = "Calculating the p-Value of a Two-Sided Test When t^act = -4.75",
     cex.lab = 0.7
     )

tact <- -4.75

axis(1, at = c(0,-1.96,1.96,-tact,tact), cex.axis=0.7)

# Shade the critical regions using polygon()

## critical region in left tail
polygon(x = c(-6, seq(-6,-1.96,0.01),-1.96),
        y = c(0, dnorm(seq(-6,-1.96,0.01)),0),
        col = 'orange'
        )

## critical region in right tail

polygon(x = c(1.96, seq(1.96, 6, 0.01), 6),
        y = c(0, dnorm(seq(1.96, 6, 0.01)), 0),
        col = 'orange'
        )

# Add arrows and texts indicating critical regions and the p-value
arrows(-3.5, 0.2, -2.5, 0.02, length = 0.1)
arrows(3.5, 0.2, 2.5, 0.02, length = 0.1)

arrows(-5, 0.16, -4.75, 0, length = 0.1)
arrows(5, 0.16, 4.75, 0, length = 0.1)

text(-3.5,0.22, labels = paste("0.025=",expression(alpha),"/2",sep = ""), cex = 0.7)
text(3.5,0.22, labels = paste("0.025=",expression(alpha),"/2",sep = ""), cex = 0.7)

text(-5,0.18, labels = expression(paste("-|",t[act],"|")), cex = 0.7)
text(5,0.18, labels = expression(paste("|",t[act],"|")), cex = 0.7)

# Add ticks indicating critical values at the 0.05-level, t^act and -t^act
rug(c(-1.96,1.96), ticksize  = 0.145, lwd = 2, col = "darkred")
rug(c(-tact,tact), ticksize  = -0.0451, lwd = 2, col = "darkgreen")
```



The p-Value is the area under the curve to left of -4.75 plus the area under the curve to the right of 4.75. As we already know from the calculations above, this value is very small.

5.2 Confidence Intervals for Regression Coefficients

As we already know, estimates of the regression coefficients β_0 and β_1 are afflicted with sampling uncertainty, see chapter 4. Therefore, we will *never* estimate the exact true value of these parameters from sample data in an empirical application. However, we may construct confidence intervals for the intercept and the slope parameter.

A 95% confidence interval for β_i has two equivalent definitions:

- The interval is the set of values for which a hypothesis test to the level of 5% cannot be rejected.
- The interval has a probability of 95% to contain the true value of β_i. So in 95% of all samples that could be drawn, the confidence interval will cover the true value of β_i.

We also say that the interval has a confidence level of 95%. The idea is summarized in Key Concept 5.3.

Key Concept 5.3

A Confidence Interval for β_i

Imagine You could draw all possible random samples of given size. The interval that contains the true value β_i in 95% of all samples is given by the expression

$$\text{KI}_{0.95}^{\beta_i} = \left[\hat{\beta}_i - 1.96 \times SE(\hat{\beta}_i) \, , \, \hat{\beta}_i + 1.96 \times SE(\hat{\beta}_i)\right] .$$

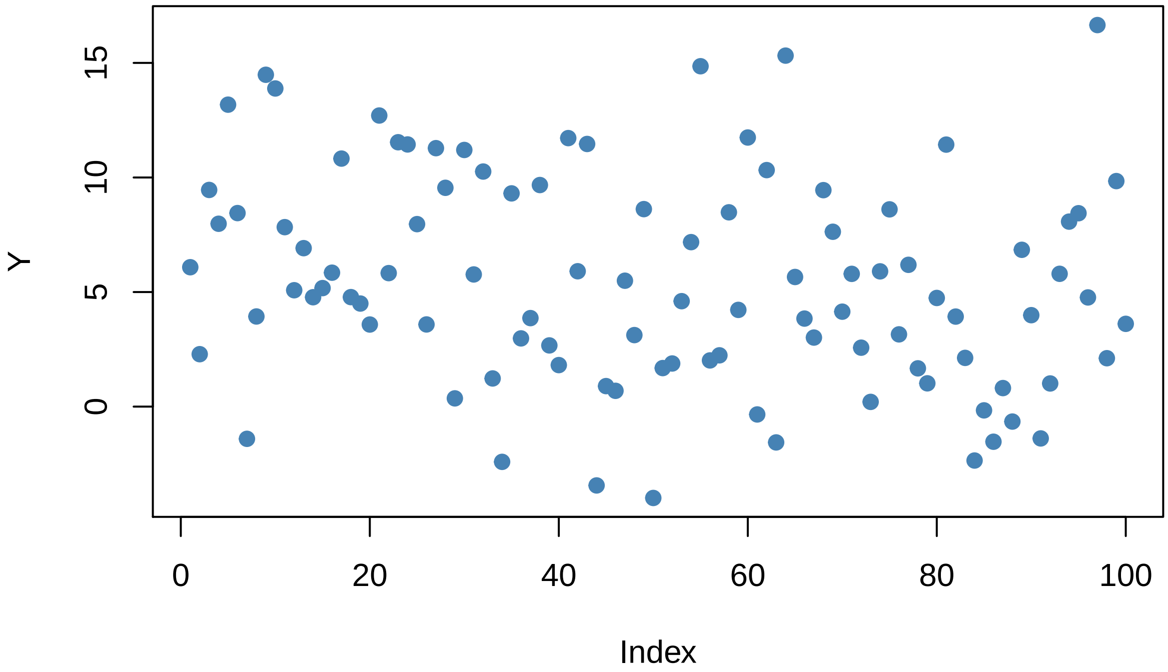
Equivalently, this interval can be seen as the set of null hypotheses for which a 5% two-sided hypothesis test does not reject.

R Simulation Study 5.1

To get a better understanding of confidence intervalls we will conduct another simulation study. For now, assume that we are confronted with the following sample of $n = 100$ observations on a single variable Y where

$$Y_i \overset{i.i.d}{\sim} N(5,25) \ \ \forall \ i = 1, \dots, 100.$$

```
# set random seed for reproducibility
set.seed(4)

# generate and plot the sample data
Y <- rnorm(n = 100,
           mean = 5,
           sd =5
           )

plot(Y,
     pch=19,
     col = "steelblue"
     )
```



We assume that the data is generated by the model

$$Y_i = \mu + \epsilon_i$$

where μ is the unknown constant and we know that $\epsilon_i \overset{i.i.d.}{\sim} N(0,25)$. In this model, the OLS estimator for μ is given by

$$\hat{\mu} = \overline{Y} = \frac{1}{n} \sum_{i=1}^{n} Y_i$$

(try to verify this!) i.e. the sample average of the Y_i. It further holds that

$$SE(\hat{\mu}) = \frac{\sigma_\epsilon}{\sqrt{n}} = \frac{5}{\sqrt{100}}.$$

A large sample 95% confidence intervall for μ is then given by

$$KI^{\mu}_{0.95} = \left[\hat{\mu} - 1.96 \times \frac{5}{\sqrt{100}} \ , \ \hat{\mu} + 1.96 \times \frac{5}{\sqrt{100}}\right]. \tag{5.4}$$

It is fairly easy to compute this interval in R by hand. The following code chunck generates a named vector containing the interval bounds:

```
cbind(
  CIlower = mean(Y) - 1.96 * 5/10,
  CIupper = mean(Y) + 1.96 * 5/10
)
```

```
##       CIlower  CIupper
## [1,] 4.502625 6.462625
```

Nowing that $\mu = 5$ we see that our example covers the true value for the present sample. As opposed to real world examples, we can use R to get a better understanding of confidence intervals by repeatedly sampling data, estimating μ and computing the confidence interval for μ as in (5.4).

The procedure is as follows:

- We initialize the vectors `lower` and `upper` in which the simulated interval boundaries are to be saved. We want to simulate 10000 intervals so both vectors are set to have this length.
- We use a `for()` loop to sample 100 observations from the $N(5, 25)$ distribution and compute $\hat{\mu}$ as well as the boundaries of the confidence interval in every iteration of the loop.
- At last we join `lower` and `upper` in an array.

```
# set random seed
set.seed(1)

# initialize vectors of lower and upper interval boundaries
lower <- numeric(10000)
upper <- numeric(10000)

# loop sampling / estimation / CI
for(i in 1:10000) {
  Y <- rnorm(100, mean = 5, sd =5)
  lower[i] <- mean(Y) - 1.96 * 5/10
  upper[i] <- mean(Y) + 1.96 * 5/10
}

# join vectors of interval boundaries
CIs <- cbind(lower, upper)
```

According to Key Concept 5.3 we expect that the fraction of the 10000 simulated intervals saved in the array `CIs` that contain the true value $\mu = 5$ should be roughly 95%. We can check this using logical operators.

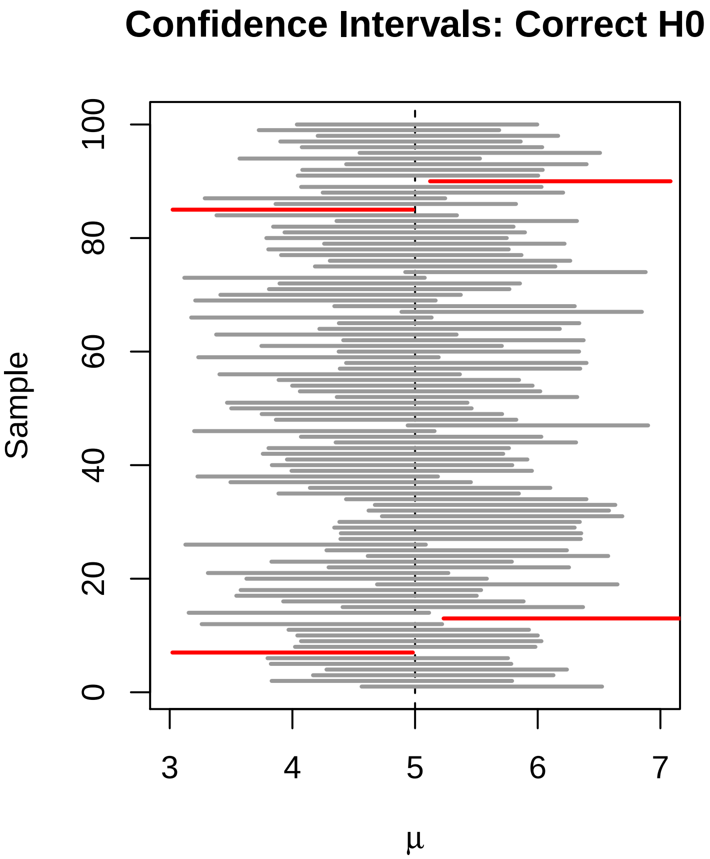
```
sum(CIs[,1] <= 5 & 5 <= CIs[,2])/10000
```

```
## [1] 0.9487
```

The simulation shows that the fraction of intervals covering $\mu = 5$, i.e. those intervals for which $H_0 : \mu = 5$ cannot be rejected is close to the theoretical value of 95%.

Let us draw a plot of the first 100 simulated confidence intervals and indicate those which *do not* cover the true value of μ. We do this by adding horizonal lines representing the confidence intervals on top of each other.

```
# identify intervals not covering mu
# (4 intervals out of 100)
ID <- which(!(CIs[1:100,1] <= 5 & 5 <= CIs[1:100,2]))

# initialize the plot
plot(0,
     xlim = c(3,7),
     ylim = c(1,100),
     ylab = "Sample",
     xlab = expression(mu),
     main = "Confidence Intervals: Correct H0")

# setup color vector
colors <- rep(gray(0.6), 100)
colors[ID] <- "red"

# draw reference line at mu=5
abline(v=5, lty=2)

# add horizontal bars representing the CIs
for(j in 1:100) {
  lines(c(CIs[j,1], CIs[j,2]),
        c(j,j),
        col = colors[j],
        lwd=2)
}
```



We find that for the first 100 samples, the true null hypthesis is rejected in four cases so these intervals do not cover $\mu = 5$. We have indicated the intervals which lead to a rejection of the true null hypothesis by red color.

Let us now turn back to the example of test scores and class sizes.The regression model from chapter 4 is stored in `linear_model`. An easy way to get 95% confidence intervals for β_0 and β_1, the coefficients on `(intercept)` and `STR`, is to use the function `confint()`. We only have to provide a fitted model object as the argument `object` to this function. The confidence level is set to 95% by default but can be modified by setting the argument `level`, see `?confint`.

```
confint(object = linear_model)
```

```
##                  2.5 %     97.5 %
## (Intercept) 680.32312 717.542775
## STR          -3.22298  -1.336636
```

Let us check if the calculation is done as we expect it to be. For β_1, that is the coefficient on `STR`, according to the formula presented above the interval borders are computed as

$$-2.279808 \pm 1.96 \times 0.4798255 \;\Rightarrow\; \text{KI}_{0.95}^{\beta_1} = [-3.22, -1.34]$$

so this actually leads to the same interval. Obviously, this interval *does not* contain the value zero what, as we have already seen in the previous section, leads to rejection of the null hypothesis $\beta_{1,0} = 0$.

5.3 Regression when X is a Binary Variable

Instead of using a continuous regressor X, we might be interested in running the regression

$$Y_i = \beta_0 + \beta_1 D_i + u_i \tag{5.2}$$

where D_i is binary variable, a so-called *dummy variable*. For example, we may define D_i in the following way:

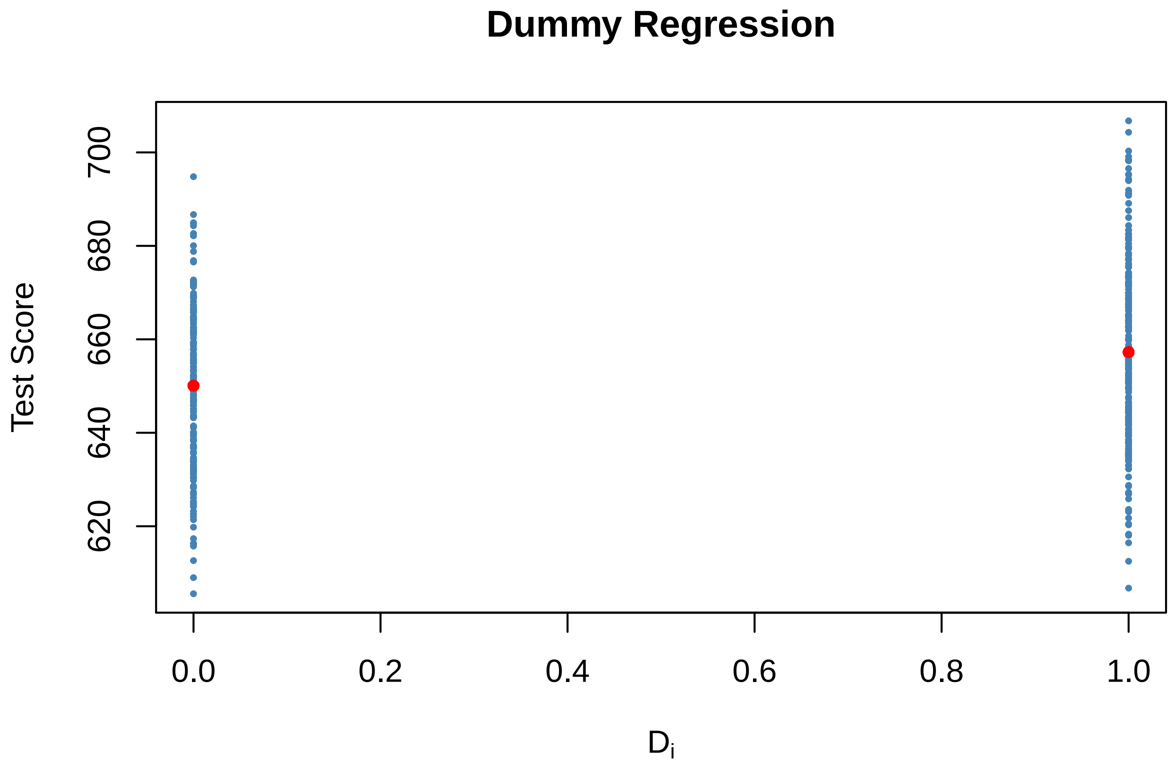
$$D_i = \begin{cases} 1 & \text{if } STR \text{ in } i^{th} \text{ school district} < 20 \\ 0 & \text{if } STR \text{ in } i^{th} \text{ school district} \geq 20 \end{cases} \tag{5.3}$$

The regression model now is

$$TestScore_i = \beta_0 + \beta_1 D_i + u_i. \tag{5.4}$$

Let us see how these data look like in a scatter plot:

```r
# Create the dummy variable as defined above using a for loop
for (i in 1:nrow(CASchools)) {
  if (CASchools$STR[i] < 20) {
    CASchools$D[i] <- 1
    } else {
      CASchools$D[i] <- 0
    }
  }

# Plot the data
plot(CASchools$D, CASchools$score,          # provide the data to be ploted
     pch=20,                                # use filled circles as plot symbols
     cex=0.5,                               # set size of plot symbols to 0.5
     col="Steelblue",                       # set the symbols' color to "Steelblue"
     xlab=expression(D[i]),                 # Set title and axis names
     ylab="Test Score",
     main = "Dummy Regression"
     )
```



We see that with D as the regressor, it is not useful to think of β_1 as a slope parameter since $D_i \in \{0, 1\}$, i.e. we only observe two discrete values instead of a continuoum of regressor values lying (in some range) on the real line. Simply put, there is no continuous line depicting the conditional expectation function $E(TestScore_i|D_i)$ since this function is solely defined for X-positions 0 and 1.

Therefore, the interpretation of the coefficients in our regression model is as follows:

- $E(Y_i|D_i = 0) = \beta_0$ so β_0 is the expected test score in districts where $D_i = 0$ i.e. where STR is below 20.
- $E(Y_i|D_i = 1) = \beta_0 + \beta_1$ or, using the result above, $\beta_1 = E(Y_i|D_i = 1) - E(Y_i|D_i = 0)$. Thus, β_1 is the difference in group specific expectations, i.e. the difference in expected test score between districts with $STR < 20$ and those with $STR \geq 20$.

We will now use R to estimate the dummy regression model as defined by equations (5.2) - (5.3) .

```
# estimate the dummy regression model
dummy_model <- lm(score ~ D, data = CASchools)
summary(dummy_model)
```

```
##
## Call:
## lm(formula = score ~ D, data = CASchools)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -50.496 -14.029  -0.346  12.884  49.504
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)  650.077      1.393 466.666  < 2e-16 ***
## D              7.169      1.847   3.882  0.00012 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 18.74 on 418 degrees of freedom
## Multiple R-squared:  0.0348, Adjusted R-squared:  0.0325
## F-statistic: 15.07 on 1 and 418 DF,  p-value: 0.0001202
```

One can see that the expected test score in districts with $STR < 20$ ($D_i = 1$) is predicted to be $650.1 + 7.17 = 657.27$ while districs with $STR \geq 20$ ($D_i = 0$) are expected to have an average test score of only 650.1.

Group specific predictions can be added to the plot by execution of the following code chunk:

```r
# add group specific predictions to the plot
points(x = CASchools$D,
       y = predict(dummy_model),
       col = "red",
       pch = 20
       )
```

Here we use the function `predict()` to obtain estimates of the group specific means. The red dots represent these sample group averages. Accordingly, $\hat{\beta}_1 = 7.17$ can be seen as the difference in group averages.

By inspection of the output generated with `summary(dummy_model)` we may also find an answer to the question whether there is a statistically significant difference in group means. This in turn would support the hypothesis that students perform differently when they are taught in small classes rather than in large groups. We can assess this by a two-tailed test of the hypothesis $H_0 : \beta_1 = 0$. Conviniently the t-statistic and the corresponding p-value for this test are computed defaultly by `summary()`!

Since `t value` $= 3.88 > 1.96$ we reject the null hypothesis at the 5% level of significance. The same conclusion can be made when using the p-value which reports significance to the 0.00012% level.

As done with `linear_model`, we may alternatively use the `confint()` function to compute a 95% confidence interval for the true difference in means and see if the hypothesised value is an element of this confidence set.

```r
# confidence intervals for coefficients in the dummy regression
confint(dummy_model)
```

```
##                  2.5 %    97.5 %
## (Intercept) 647.338594 652.81500
## D             3.539562  10.79931
```

We reject the hypothesis that there is no difference between group means at the 5% significance level since $\beta_{1,0} = 0$ lies outside of $[3.54, 10.8]$, the 95% confidence interval for the coefficient on D.

5.4 Heteroskedasticity and Homoskedasticity

All inference made in the previous chapters relies on the assumption that the error variance does not vary as regressor values change. But this will not necessarily be the case in most empirical applications.

Key Concept 5.4

Heteroskedasticity and Homoskedasticity

- We say that the error term of our regression model is homoskedastic if the variance of the conditional distribution of u_i given X_i, $Var(u_i|X_i = x)$, is constant *for all* observations in our sample

$$\text{Var}(u_i|X_i = x) = \sigma^2 \ \forall \ i = 1, \dots, n.$$

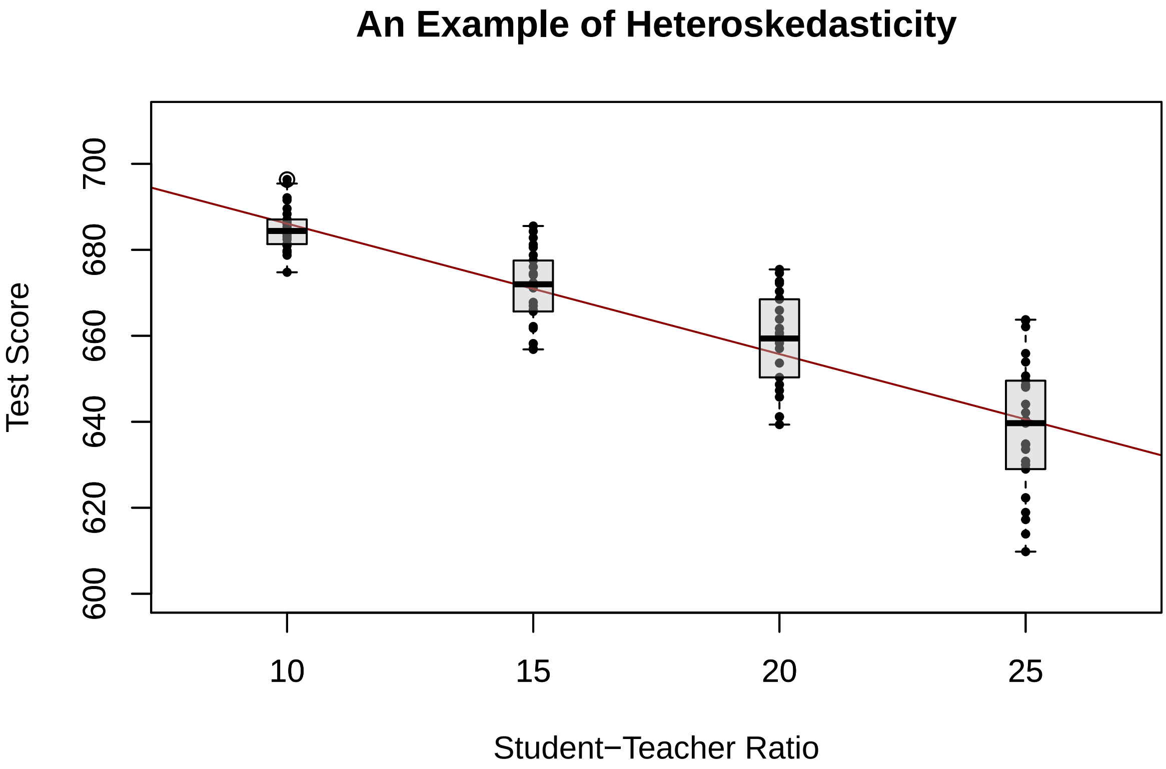
- If instead there is dependence of the conditional variance of u_i on X_i, the error term is said to be heteroskedastic. We then write

$$\text{Var}(u_i|X_i = x) = \sigma_i^2 \ \forall \ i = 1, \dots, n.$$

- Homoskedasticity is a *special case* of heteroskedasticity.

For a better understanding of heteroskedasticity, we generate some bivariate heteroskedastic data, estimate a linear regression model and then use boxplots to depict the conditional distributions of the residuals.

```r
# load scales package for custom color opacities
library(scales)

# Genrate some heteroskedastic data
set.seed(123)
x <- rep(c(10,15,20,25),each=25)
e <- rnorm(100, sd=12)
i <- order(runif(100, max=dnorm(e, sd=12)))
y <- 720 - 3.3 * x + e[rev(i)]

# Estimate the model
mod <- lm(y ~ x)

# Plot the data
plot(x=x,
     y=y,
     main="An Example of Heteroskedasticity",
     xlab = "Student-Teacher Ratio",
     ylab = "Test Score",
     cex = 0.5,
     pch = 19,
     xlim = c(8,27),
     ylim = c(600,710)
     )

# Add the regression line to the plot
abline(mod, col="darkred")

# Add boxplots to the plot
boxplot(y ~ x,
        add = TRUE,
        at = c(10,15,20,25),
        col = alpha("gray", 0.4),
        border = "black"
        )
```



For this artificial data it is straightforward to see that we face unequal conditional error variances. Specifically, we observe that the variance in test scores (and therefore the variance of the errors committed) *increases* with the student teacher ratio.

A Real-World Example for Heteroskedasticity

Think about the economic value of education: if there would not be an expected economic value-added to receiving education at university, You probably would not be reading this script right now. A starting point to empirical verification of such a relation exists is to have data on individuals that are in an employment relationship. More precisely, we need data on wages and education in order to work with a model like

$$wage_i = \beta_0 + \beta_1 \cdot education_i + u_i.$$

What can be presumed about this relation? It is likely that, on average, higher educated workers earn more money than workers with less education so we expect to estimate an upward sloping regression line. Also it seems plausible that workers with better education are more likely to meet the requirements for the well-paid jobs. However, workers with low education will have no shot at those well-paid jobs. Therefore it seems plausible that the distribution of earnings spreads out as education increases. In other words: we expect that there is heteroskedasticity!

To verify this empirically we may use real data on hourly earnings and the number of years of education of employees. Such data can be found in `CPSSWEducation`. This data set is part of the package `AER` and stems from the Current Population Survey (CPS) which is conducted periodically by the Bureau of Labor Statistics in the US.

The subsequent code chunks demonstrate how to load the data into R and how to produce a plot in the fashion of figure 5.3 in the book.

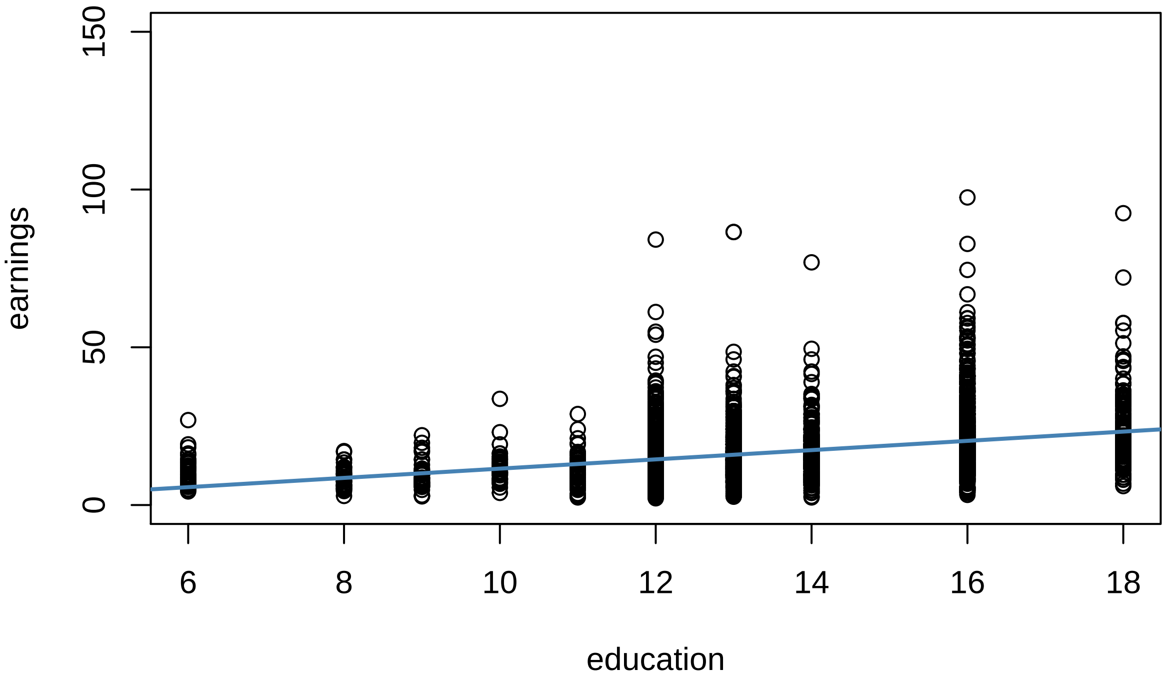
```
# load package and attach data
library(AER)
data("CPSSWEducation")
attach(CPSSWEducation)
```

```
## The following objects are masked from CPSSWEducation (pos = 9):
##
##     age, earnings, education, gender
```

```
# get an overview
summary(CPSSWEducation)
```

```
##       age          gender        earnings        education
##  Min.   :29.0   female:1202   Min.   : 2.137   Min.   : 6.00
##  1st Qu.:29.0   male  :1748   1st Qu.:10.577   1st Qu.:12.00
##  Median :29.0                 Median :14.615   Median :13.00
##  Mean   :29.5                 Mean   :16.743   Mean   :13.55
##  3rd Qu.:30.0                 3rd Qu.:20.192   3rd Qu.:16.00
##  Max.   :30.0                 Max.   :97.500   Max.   :18.00
```

```
# estimate a simple regression model
labor_model <- lm(earnings ~ education)

# plot observations and add the regression line
plot(education,
     earnings,
     ylim = c(0,150)
     )

abline(labor_model, col="steelblue", lwd=2)
```



From inspecting the plot we can tell that the mean of the distribution of earnings increases with the level of education. This is also suggested by formal analysis: the estimated regression model stored in `labor_mod` asserts that there is a positive relation between years of education and earnings.

```
labor_model
```

```
##
## Call:
## lm(formula = earnings ~ education)
##
## Coefficients:
## (Intercept)    education
##      -3.134        1.467
```

The estimated regression equation states that, on average, an additional year of education increases a workers hourly earnings by about \$1.47. Once more we use `confint()` to obtain a 95% confidence interval for both regression coefficients.

```
confint(labor_model)
```

```
##                  2.5 %    97.5 %
## (Intercept) -5.015248 -1.253495
## education    1.330098  1.603753
```

Since the intervall is $[1.33, 1.60]$ we can reject the hypothesis that the coefficient on `education` is zero at the 5% level.

What is more, the plot indicates that there is heteroskedasticity: if we assume the regression line to be a reasonably good representation of the conditional mean function $E(earnings_i|education_i)$, the dispersion of hourly earnings around that function cleary increases with the level of education, i.e. the variance of the distribution of earnings increases. In other words: the variance of the residuals increases with the years of education so that the regression errors are heteroskedastic. This example makes a case that it is doubtful to assume homoskedasticity in many economic applications.

Should We Care About Heteroskedasticity?

To answer this question, let us see how the variance of $\hat{\beta}_1$ is computed under the assumption of homoskedasticity. In this case we have

$$\sigma^2_{\hat{\beta}_1} = \frac{\sigma^2_u}{n \cdot \sigma^2_X} \tag{5.5}$$

which is a simplified version of the general equation (4.1) presented in Key Concept 4.4. See Appendix 5.1 of the book for details on the derivation. The `summary()` function in R estimates (5.5) by

$$\overset{\sim}{\sigma}^2_{\hat{\beta}_1} = \frac{SER^2}{\sum_{i=1}^n (X_i - \overline{X})^2} \ \text{ where } \ SER = \frac{1}{n-2} \sum_{i=1}^n \hat{u}_i^2.$$

Thus `summary()` estimates the *homoskedasticity-only* standard error

$$\sqrt{\overset{\sim}{\sigma}^2_{\hat{\beta}_1}} = \sqrt{\frac{SER^2}{\sum (X_i - \overline{X})^2}}.$$

This in fact is an estimator for the standard deviation of the estimator $\hat{\beta}_1$ that is *inconsistent* for the true value $\sigma^2_{\hat{\beta}_1}$ when there is heteroskedasticity. The implication is that t-statistics computed in the manner of Key Concept 5.1 do not have a standard normal distribution, even in large samples. This issue may invalidate inference drawn when using the previously treated tools for hypothesis testing: we should be cautious when making statements about the significance of regression coefficients on the basis of t-statistics as computed by `summary()` or confidence intervals produced by `confint()` if it is doubtful for the assumption of homoskedasticity to hold!

We will now use R to compute the homoskedasticity-only standard error estimate for $\hat{\beta}_1$ in the test score regression model `linear_model` by hand and see if it matches the value produced by `summary()`.

```
# Store model summary in 'mod'
model <- summary(linear_model)

# Extract the standard error of the regression from model summary
SER <- model$sigma

# Compute the variation in 'size'
V <- (nrow(CASchools)-1) * var(CASchools$STR)

# Compute the standard error of the slope parameter's estimator and print it
SE.beta_1.hat <- sqrt(SER^2/V)
SE.beta_1.hat
```

```
## [1] 0.4798255
```

```
# Use logical operators to see if the value computed by hand matches the one provided # in mod$coeffici

round(model$coefficients[2,2], 4) == round(SE.beta_1.hat, 4)
```

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

Indeed, the estimated values are equal.

Computation of Heteroskedasticity-Robust Standard Errors

Cosistent estimation of $\sigma_{\hat{\beta}_1}$ under heteroskedasticity is granted when the following *robust* estimator is used.

$$SE(\hat{\beta}_1) = \sqrt{\frac{\frac{1}{n-2}\sum_{i=1}^{n}(X_i-\overline{X})^2\hat{u}_i^2}{\left[\frac{1}{n}\sum_{i=1}^{n}(X_i-\overline{X})^2\right]^2}} \tag{5.6}$$

Standard error estimates computed this way are also referred to as Eicker-Huber-White standard errors. It can be quite cumbersome to do this calculation by hand. Luckily, there are R function for that purpose. A convenient one, named `vcovHC()` is part of the `sandwich` package. This function can compute a variety of standard error estimators. The one brought forward in (5.6) is computed when the argument `type` is set to `"HC0"`.

Let us now compute robust standard error estimates for the coefficients in `linear_model`.

```
# load the sandwich package
library(sandwich)

# compute robust standard error estimates
vcov <- vcovHC(linear_model, type = "HC0")
vcov
```

```
##              (Intercept)        STR
## (Intercept)   106.908469 -5.3383689
## STR            -5.338369  0.2685841
```

The output of `vcovHC()` is the variance-covariance matrix of coefficient estimates. We are interested in the square root of the diagonal elements of this matrix since these values are the standard error estimates we seek.

> When we have k > 1 regressors, writing down the equations for a regression model becomes very messy. A more convinient way to denote and estimate so-called multiple regression models is matrix algebra. This is why functions like vcovHC() produce matrices. In the simple linear regression model, the variances and covariances of the coefficient estimators can be gathered in the variance-covariance matrix
>
> $$\text{Var}\begin{pmatrix}\hat\beta_0\\ \hat\beta_1\end{pmatrix} = \begin{pmatrix}\text{Var}(\hat\beta_0) & \text{Cov}(\hat\beta_0,\hat\beta_1)\\ \text{Cov}(\hat\beta_0,\hat\beta_1) & \text{Var}(\hat\beta_1)\end{pmatrix} \tag{5.5}$$
>
> which is a symmetric matrix. So vcovHC() gives us $\widehat{\text{Var}}(\hat\beta_0)$, $\widehat{\text{Var}}(\hat\beta_1)$ and $\widehat{\text{Cov}}(\hat\beta_0,\hat\beta_1)$ but most of the time we are interested in the diagonal elements of the estimated matrix.

```
# compute the square root of the diagonal elements in vcov
robust_se <- sqrt(diag(vcov))
robust_se
```

```
## (Intercept)         STR
##   10.339655    0.518251
```

Now assume we want to generate a coefficient summary as provided by `summary()` but with *robust* standard error estimates for the coefficient estimators, robust t-statistics and corresponding p-values for the regression model `linear_model`. This can be done using `coeftest()` from the package `lmtest`, see `?coeftest`. Further we specify in the argument `vcov.` that `vcov`, the Eicker-Huber-White estimate of the variance matrix we have computed before should be used.

```
# We invoke the function `coeftest()` on our model
coeftest(linear_model, vcov. = vcov)
```

```
##
## t test of coefficients:
##
##              Estimate Std. Error t value  Pr(>|t|)
## (Intercept) 698.93295   10.33966  67.597 < 2.2e-16 ***
## STR          -2.27981    0.51825  -4.399 1.382e-05 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

We see that values reported in the column `Std. Error` equal the ones received using `sqrt(diag(vcov))`.

How severe are the implications of using homoskedasticity-only standard errors in the presence of heteroskedasticity? The answer is: it depends. As mentioned above we may face the risk of drawing wrong conclusions when conducting significance tests. Let us illustrate this by generating another example of a heteroskedastic data set and use it to estimate a simple regression model. We take

$$Y_i = \beta_1 \cdot X_i + u_i \quad , \quad u_i \overset{i.i.d.}{\sim} N(0, 0.36 \cdot X_i^2)$$

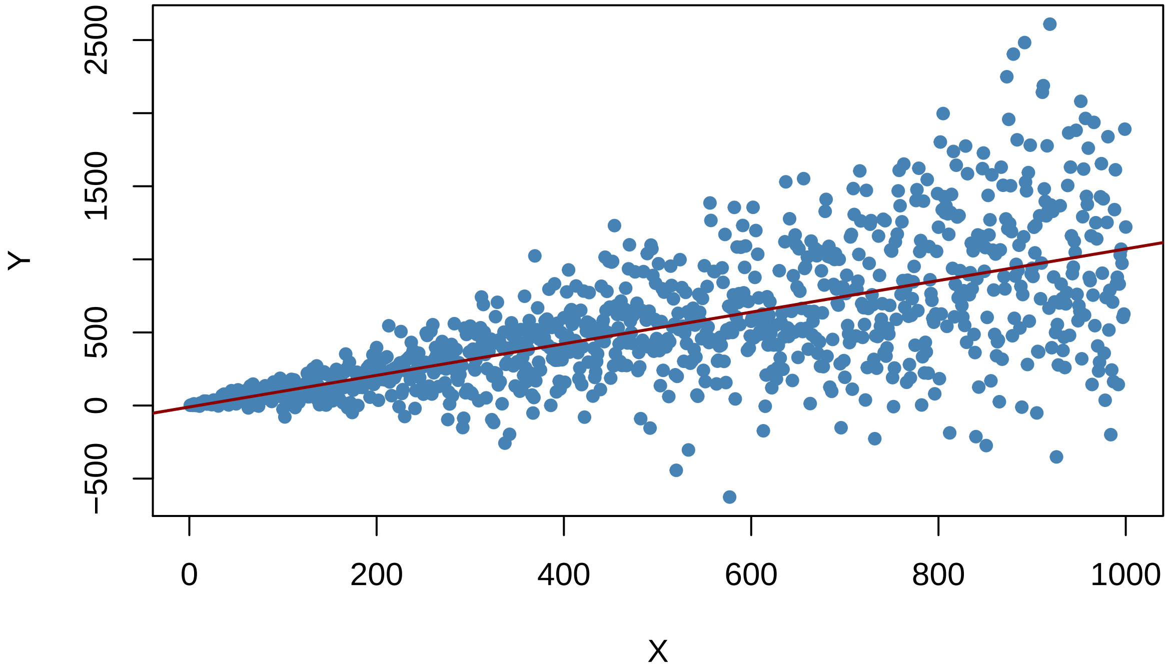
with $\beta_1 = 1$ as the data generating process. The assumption of homoskedasticity is violated since the variance of the errors is a non-linear increasing function of X_i but the errors have zero mean and are i.i.d. such that the assumptions made in Key Concept 4.3 are not violated. As before, the true conditional mean function we are interested in estimating is

$$E(Y_i|X_i) = X_i.$$

```r
# set random seed
set.seed(21)

# generate heteroskedastic data
X <- 1:1000
Y <- rnorm(n = 1000, mean = X, sd = 0.6*X)

# estimate a simple regression model
reg <- lm(Y ~ X)
```

We plot the data and add the regression line.

```r
# plot the data
plot(X, Y, pch = 19, col="steelblue", cex = 0.8)

# add the regression line to the plot
abline(reg, col = "darkred", lwd = 1.5)
```



The plot clearly shows that the data are heteroskedastic as the variance of Y grows with X. We continue by conducting a significance test of the (true) null hypothesis $H_0 : \beta_1 = 1$ twice, once using the homoskedasticity-only standard error formula and once with the robust version (5.6). An idiomatic way to do this in R is the function `linearHypothesis()` from the package `car`, see `?linearHypothesis`. It allows to test linear hypotheses about parameters in linear models in a similar way as done with a t-statistic and offers various robust covariance matrix estimators. We test by comparing the tests' p-values to the significance level of 5%.

linearHypothesis() computes a test statistic that follows an F distribution under the null hypothesis. We will not loose too much words on the theory behind it at this time. In general, the core idea of the F test is to compare the fit of different models. When testing a hypothesis about a *single* coefficient using a F test, one can show that the test statistic is simply the square of the corresponding t-statistic:

$$F = t^2 = \frac{\hat{\beta}_i - \beta_{i,0}}{SE(\hat{\beta}_i)} \sim F_{1,n-k-1}$$

In linearHypothesis(), the hypothesis must be provided as a *string*. The function returns an object of class anova which contains further information on the test that can be accessed using the $ operator. For example, we can obtain the test's p-value by adding $'Pr(>F)' right behind the function call.

```
# test using default standard error
linearHypothesis(reg, hypothesis.matrix = "X = 1")$'Pr(>F)'[2] < 0.05
```

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

```
# test using robust standard error
linearHypothesis(reg, hypothesis.matrix = "X = 1", white.adjust = "hc0")$'Pr(>F)'[2] < 0.05
```

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

This is a good example of what can go wrong if we do not care for heteroskedasticity: for the data set at hand the default method rejects the null hypothesis $\beta_1 = 1$ although it is true. Using the robust standard error though the test does not reject the null. Of course we could argue that this is just a coincidence and both tests are equally well in maintaining the type I error rate of 5%. This can be further investigated by computing Monte Carlo estimates of the rejection frequencies of both tests on the basis of a large number of random samples. We proceed as follows:

- initialize vectors `t` and `t.rob` as type `numeric` with length 10000.
- Using a `for()` loop, we generate 10000 heteroskedastic random samples of size 1000, estimate the regression model and check whether the tests wrongly reject the null at the level of 5% using comparison operators. The results are stored in the respective vectors `t` and `t.rob`.
- After the simulation, we compute the fraction of rejections for both tests.

```
# initialize vectors t and t.rob
t <- numeric(10000)
t.rob <- numeric(10000)

# loop sampling and estimation
for (i in 1:10000) {

  # sample data
  X <- 1:1000
  Y <- rnorm(n = 1000, mean = X, sd = 0.6*X)

  # estimate regression model
  reg <- lm(Y ~ X)

  # homoskedasdicity-only significance test
  t[i] <- linearHypothesis(reg, "X = 1")$'Pr(>F)'[2] < 0.05

  # robust significance test
  t.rob[i] <- linearHypothesis(reg, "X = 1", white.adjust = "hc0")$'Pr(>F)'[2] < 0.05
}

# compute fraction of rejections
cbind(t = sum(t), t.rob = sum(t.rob)) / 10000
```

```
##           t  t.rob
## [1,] 0.0762 0.0524
```

The results show that we face an increased risk of falsely rejecting the null using the homoskedasticity-only standard error for the testing problem at hand: with the common standard error estimator, 7.62% of all tests reject the null hypothesis falsely. In contrast, with the robust test statistic we are close to the nominal level of 5%.

5.5 The Gauss-Markov Theorem

When estimating regression models, we know that the results of the estimation procedure are outcomes of a random process. However, when using unbiased estimators, at least on average, we estimate the true parameter. When comparing different unbiased estimators, it is therefore interesting to know which one has the highest precision: being aware that the likelihood of estimating the *exact* value of the parameter of interest is 0 in an empirical application, we want to make sure that the likelihood of obtaining an estimate very close to the true value is as high as possible. We want to use the estimator with the lowest variance of all unbiased estimators. The Gauss-Markov theorem states that the OLS estimator has this property under certain conditions.

Key Concept 5.5

The Gauss-Markov Theorem for $\hat{\beta}_1$

Suppose that the assumptions made in Key Concept 4.3 hold *and* that the errors are *homoskedastic*. The OLS estimator is the best (in the sense of smallest variance) linear conditionally unbiased estimator (BLUE) in this setting.

Let us have a closer look at what this means:

- Estimators of β_1 that are linear functions of the $Y_1, \dots, Y_n$ and that are unbiased conditionally on the regressor $X_1, \dots, X_n$ can be written as
$$\overset{\sim}{\beta}_1 = \sum_{i=1}^{n} a_i Y_i$$
where the a_i are weights that are allowed to depend on the X_i but *not* on the Y_i.

- We already know that $\overset{\sim}{\beta}_1$ has a sampling distribution: $\overset{\sim}{\beta}_1$ is a linear function of the Y_i which are random variables. If now
$$E(\overset{\sim}{\beta}_1 | X_1, \dots, X_n) = \beta_1$$
we say that $\overset{\sim}{\beta}_1$ is a linear unbiased estimator of β_1, conditionally on the $X_1, \dots, X_n$.

- We may ask if $\overset{\sim}{\beta}_1$ is also the *best* estimator in this class, i.e. the most efficient one of all linear unbiased estimators where "most efficient" means smallest variance. The weights a_i play an important role here and it turns out that OLS uses just the right weights to have the BLUE property.

R Simulation Study: BLUE Estimator

Consider the case of a regression of $Y_i, \dots, Y_n$ only on a constant. Here, the Y_i are assumed to be a random sample from a population with mean μ and variance σ^2. We know that the OLS estimator in this model is simply the sample mean:

$$\hat{\beta}_1 = \overline{\beta}_1 = \sum_{i=1}^{n} \underbrace{\frac{1}{n}}_{=a_i} Y_i \tag{5.6}$$

Clearly, each observation is weighted by

$$a_i = \frac{1}{n}.$$

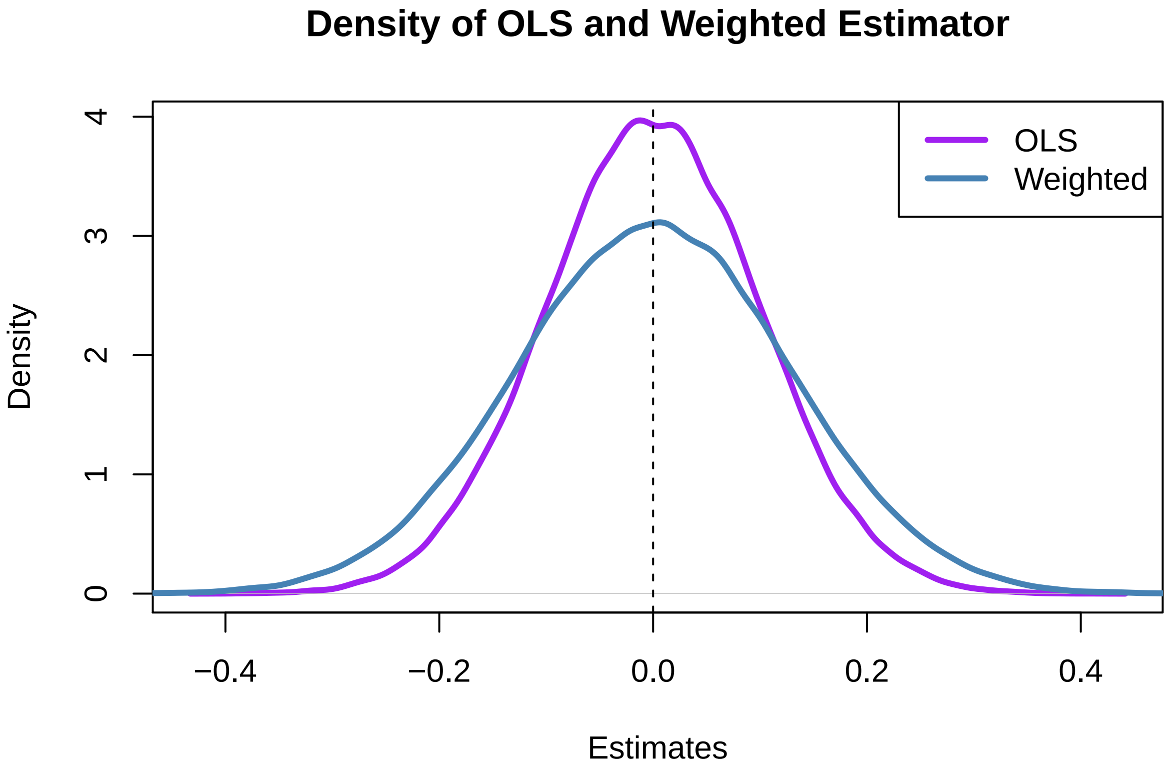
and We also know that $\text{Var}(\hat{\beta}_1) = \text{Var}(\hat{\beta}_1) = \frac{\sigma^2}{n}$.

We will now use R for a simulation study that illustrates what happens to the variance of (5.6) if different weights

$$w_i = \frac{1 \pm \epsilon}{n}$$

are assigned to either half of the sample $Y_1, \dots, Y_n$ instead of using $\frac{1}{n}$, the weights implied by OLS.

```r
# Set sample size and number of repititions
n <- 100
reps <- 1e5

# Choose epsilon and create a vector of weights as defined above
epsilon <- 0.8
w <- c(rep((1+epsilon)/n,n/2),
       rep((1-epsilon)/n,n/2)
      )

# Draw a random sample y_1,...,y_n from the standard normal distribution,
# use both estimators 1e5 times and store the result in thr vectors ols and
# weightedestimator

ols <- rep(NA, reps)
weightedestimator <- rep(NA, reps)

for (i in 1:reps) {
  y <- rnorm(n)
  ols[i] <- mean(y)
  weightedestimator[i] <- crossprod(w,y)
}

# Plot kernel density estimates of the estimators' distributions

## OLS
plot(density(ols),
     col = "purple",
     lwd = 3,
     main = "Density of OLS and Weighted Estimator",
     xlab = "Estimates"
     )

## Weighted
lines(density(weightedestimator),
      col = "steelblue",
      lwd = 3
      )

## Add a dashed line at 0 and a legend to the plot
abline(v = 0, lty = 2)
legend('topright',
       c("OLS","Weighted"),
       col = c("purple","steelblue"),
       lwd = 3
       )
```



What conclusion can we draw from the result?

- Both estimators seem to be unbiased: the means of their estimated distributions are zero.
- The `weightedestimator` is less efficient than the `ols` estimator: there is higher dispersion when weights are $w_i = \frac{1\pm0.8}{100}$ instead of $w_i = \frac{1}{100}$ as required by the OLS solution.

Hence, our simulation results confirm what is stated by the Gauss-Markov Theorem.

5.6 Using the t-Statistic in Regression When the Sample Size Is Small

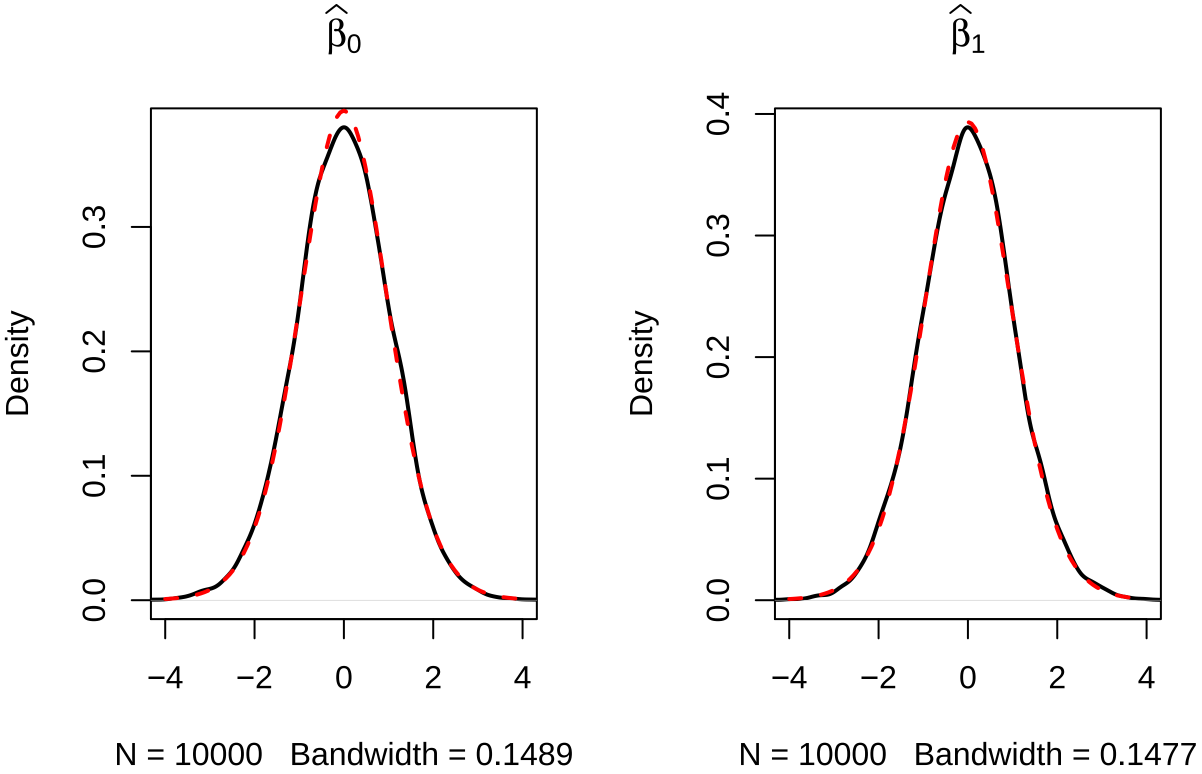
The three OLS assumptions discussed in chapter 4 (see Key Concept 4.3) are the foundation results on the large sample distribution of the OLS estimators in the simple regression model. What can be said about the distribution of the estimators and their t-statistics when the sample size is small and the population distribution of the data is unkown? Provided that the three least squares assumptions hold and the errors are normally distributed and homoskedastic (we refer to these conditions as the homoskedastic normal regression assumptions), we have normally distributed estimators and t-distributed test tatistics. Recall the definition of a t-distributed variable

$$\frac{Z}{\sqrt{W/m}} \sim t_m$$

where Z is a standard normal random variable, W is χ^2 distributed with m degrees of freedom and Z and W are independent. See section 5.6 in the book for a more detailed discussion of the small sample distribution of t-statistics in regression.

Let us simulate the distribution of regression t-statistics based on a large number of small random samples ($n = 20$) and compare their simulated distributions to their theoretical distribution which sould be t_{18}, the t-distribution with 18 degrees of freedom (recall that $\text{DF} = n - k - 1$).

```r
# initialize vectors
beta_0 <- numeric(10000)
beta_1 <- numeric(10000)

# loop sampling / estimation / t statistics
for (i in 1:10000) {

  X <- runif(20,0,20)
  Y <- rnorm(n = 20, mean = X)
  reg <- summary(lm(Y ~ X))
  beta_0[i] <- (reg$coefficients[1,1] - 0)/(reg$coefficients[1,2])
  beta_1[i] <- (reg$coefficients[2,1] - 1)/(reg$coefficients[2,2])

}

# plot distributions and compare with t_18 density function
par(mfrow = c(1,2))

# plot simulated density of beta_0
plot(density(beta_0),
     lwd= 2 ,
     main = expression(widehat(beta)[0]),
     xlim = c(-4, 4)
    )

# add t_18 density to the plot
curve(dt(x, df = 18),
      add = T,
      col = "red",
      lwd = 2,
      lty = 2
      )

# plot simulated density of beta_1
plot(density(beta_1),
     lwd = 2,
     main = expression(widehat(beta)[1]), xlim=c(-4,4)
     )

# add t_18 density to the plot
curve(dt(x, df = 18),
      add = T,
      col = "red",
      lwd = 2,
      lty = 2
      )
```



The outcomes are consistent with our expectations: the empirical distributions of both estimators seem to track the t_{18} distribution quite closely.

Chapter 6

Regression Models with Multiple Regressors

In what follows we introduce linear regression models that use more than just one explanatory variable and discuss important key concepts in multiple regression. As we broaden our scope beyond the relationship of only two variables (dependent and independent variable), some potential issues arise, such as multicollinearity and omitted variable bias. In particular, this chapter deals with omitted variables and their hazard to causal interpretation of OLS-estimated coefficients. Naturally, we will introduce estimation of multiple regression models using R. We will also advocate thoughtful usage of multiple regression models by simulation sudies in R that demonstrate consequences of using highly correlated regressors or a misspecified model.

6.1 Omitted Variable Bias

Previous analysis of the relationship between test score and class size discussed in Chapters 4 and 5 has a major flaw: we ignored other potentially important determinants of test scores that vary with our regressor. The influences of those variables were collected in the error term. This might induce an estimation bias, i.e. the mean of the OLS estimator's sampling distribution is no longer equal to the true mean and we measure a wrong effect on test scores of a unit change in the student-teacher ratio. This is called omitted variable bias, see Key Concept 6.1.

Key Concept 6.1

Omitted Variable Bias in Regression with a Single Regressor

Omitted variable bias is the bias in the OLS estimator that arises when the regressor, X, is *correlated* with an omitted variable. For omitted variable bias to occur, two conditions must be fulfilled:

1. X is correlated with the omitted variable.
2. The omitted variable is a determinant of the dependent variable Y.

Together, 1. and 2. result in a violation of the first OLS assumption $E(u_i|X_i) = 0$. Formally, the resulting bias can be expressed as

$$\hat{\beta}_1 \xrightarrow{p} \beta_1 + \rho_{Xu}\frac{\sigma_u}{\sigma_X}. \tag{6.1}$$

See Appendix 6.1 in the book for a detailed derivation. (6.1) states that OVB is a problem that cannot be aleviated by increasing the numner of observations used to estimate β_1 since then $\hat{\beta}_1$ is inconsistent: OVB prevents the estimator to converge in probability to the true parameter value. Strength and direction of the bias are driven by ρ_{Xu}, the correlation between the error term and the regressor.

In our example of test score and class size, it is fairly easy to come up with variables that may cause such a bias if omitted. As mentioned in the book, a highly relevant variable could be the percentage of english learners in the school district: it is plausible that the ability to speak, read and write english is an important factor for successful learning. Therefore, students that are still learning english are likely to perform worse in the tests than native speakers are. Also, it is conceivable that the share of english learning students is larger in school districts where class sizes are large. Think of less well-off urban districs were a lot of immigrants live.

Let us think about a possible bias induced by omitting the share of english learning students ($PctEL$) in view of (6.1) when the estimated regression model excludes $PctEL$ although the true DGP is

$$TestScore = \beta_0 + \beta_1 \times STR + \beta_2 \times PctEL \tag{6.2}$$

where STR and $PctEL$ are correlated,

$$corr(STR, PctEL) \neq 0.$$

After defining our variables in R, we compute the correlation between STR and $PctEL$ as well as the correlation between STR and $TestScore$.

```r
# load the AER package
library(AER)

# load the data set
data(CASchools)

# define variables
CASchools$STR <- CASchools$students/CASchools$teachers
CASchools$score <- (CASchools$read + CASchools$math)/2

# compute correlations
cor(CASchools$STR, CASchools$score)
```

```
## [1] -0.2263627
```

```r
cor(CASchools$STR, CASchools$english)
```

```
## [1] 0.1876424
```

The fact that $\widehat{corr}(STR, Testscore) = -0.2264$ is cause for concern that omitting $PctEL$ leads to a negatively biased estimate $\hat{\beta}_1$ since then $\rho_{Xu} < 0$ and we have $\sigma_X > 0$, $\sigma_u > 0$ by definition. As consequence we expect $\hat{\beta}_1$, the coefficient on STR, to be too large in absolute value. Put differently, the OLS estimate of $\hat{\beta}_1$ suggests that small classes improve test scores but the estimated effect of small classes is too strong as it captures the effect of having fewer English learners, too.

What happens to the magnitude of $\hat{\beta}_1$ if we add the variable $PctEL$ to the regression, that is if we estimate the model

$$TestScore = \beta_0 + \beta_1 \times STR + \beta_2 \times PctEL + u$$

instead? And what do we expect about the sign of, $\hat{\beta}_2$, the estimated coefficient on $PctEL$? Following the reasoning above we should end up with a (still) negative but larger coefficient estimate $\hat{\beta}_1$ and a negative estimate $\hat{\beta}_2$.

Let us estimate both regression models and compare. Performing a multiple regression in R is straightforward. One can simply add additional variables to the right hand side of the `formula` argument of the function `lm()` by using their names and the `+` operator. Notice that `english` is the name of the column in the data set `CASchools` which contains observations on the share of English learning students.

```
# estimate both regression models
mod <- lm(score ~ STR, data = CASchools)
mult.mod <- lm(score ~ STR + english, data = CASchools)

mod
```

```
##
## Call:
## lm(formula = score ~ STR, data = CASchools)
##
## Coefficients:
## (Intercept)          STR
##      698.93        -2.28
```

```
mult.mod
```

```
##
## Call:
## lm(formula = score ~ STR + english, data = CASchools)
##
## Coefficients:
## (Intercept)          STR      english
##    686.0322      -1.1013      -0.6498
```

We find the outcomes to be consistent with our expectations. The following section discusses some thoery on multiple regression models.

6.2 The Multiple Regression Model

In a multiple regression model we extend the basic concept of the simple regression model discussed in Chapter 4 and 5. A multiple regression model enables us to estimate the effect on Y_i of changing a regressor X_{1i} if the remaining regressors $X_{2i}, X_{3i} \dots, X_{ki}$ *do not vary*. In fact we already have performed estimation of the multiple regression model (6.2) using R in the previous section. Recall that the interpretation of the coefficient on student-teacher ratio is the effect on test scores of a one unit change student-teacher ratio if the percentage of English learners is kept constant.

As in the simple regression model, we assume the true relationship between Y and $X_{2i}, X_{3i} \dots$ to be linear. On average, this relation is given by the population regression function

$$E(Y_i|X_{1i} = x_1, X_{2i} = x_2, X_{3i} = x_3, \dots, X_{ki} = x_k) = \beta_0 + \beta_1 x_1 + \beta_2 x_2 + \beta_3 x_3 + \dots + \beta_k x_k. \tag{6.3}$$

As in the simple regression model, this relation does not hold exactly since there are disturbing influences to the dependent variable Y we cannot observe as explanatory variables. Therefore we add an error term u which represents deviations of the observations from the population regression line to (6.3). This yields the population multiple regression model

$$Y_i = \beta_0 + \beta_1 X_{1i} + \beta_2 X_{2i} + \beta_3 X_{3i} + \dots + \beta_k X_{ki} + u_i \ \ , \ \ i = 1, \dots, n. \tag{6.4}$$

Key Concept 6.2

The Multiple Regression Model

The multiple regression model is

$$Y_i = \beta_0 + \beta_1 X_{1i} + \beta_2 X_{2i} + \beta_3 X_{3i} + \cdots + \beta_k X_{ki} + u_i \ \ , \ \ i = 1, \dots, n.$$

Designations are similar to those in the simple regression model:

- Y_i is the i^{th} observation in the dependent variable. Observations on the k regressors are denoted by $X_{1i}, X_{2i}, \dots, X_{ki}$ and u_i is the error term.
- The average relationship between Y and the regressors is given by the population regression line

$$E(Y_i | X_{1i} = x_1, X_{2i} = x_2, X_{3i} = x_3, \dots, X_{ki} = x_k) = \beta_0 + \beta_1 x_1 + \beta_2 x_2 + \beta_3 x_3 + \cdots + \beta_k x_k.$$

- β_0 is the intercept; it is the expected value of Y when all Xs equal 0. $\beta_j \ , \ j = 1, \dots, k$ are the coefficients on $X_j \ , \ j = 1, \dots, k$. β_1 measures the expected change in Y_i that results from a one unit change in X_{1i} while holding all other regressors $X_{ji} \ , \ j \neq 1$ constant.

Key Concept 6.2 summarizes the core concepts of the multiple regression model. How can we estimate the coefficients of the multiple regression model (6.4)? We will not go to much into detail on this issue as our focus lies on usage of R instead of the technical refinements. However it should be pointed out that, similarly to the simple regression model, the coefficients of the multiple regression model can be estimated using OLS. As in the simple model, we seek to minimize the sum of squared prediction mistakes by choosing estimates $b_0, b_1, \dots, b_k$ for the coefficients $\beta_0, \beta_1, \dots, \beta_k$ such that

$$\sum_{i=1}^{n} (Y_i - b_0 - b_1 X_{1i} - b_2 X_{2i} - \cdots - b_k X_{ki})^2 \tag{6.5}$$

is minimized. Note that (6.5) is simply an extension of SSR in the case with just one regressor and an intercept. The estimators that minimize (6.5) are hence denoted $\hat\beta_0, \hat\beta_1, \dots, \hat\beta_k$ and, as in the simple regression model, we call them the ordinary least squares estimators of $\beta_0, \beta_1, \dots, \beta_k$. For the predicted value of Y_i given the regressors and the estimates $\hat\beta_0, \hat\beta_1, \dots, \hat\beta_k$ we have

$$\hat{Y}_i = \hat\beta_0 + \hat\beta_1 X_{1i} + \cdots + \hat\beta_k X_{ki}.$$

and, as before, the difference of Y_i and its predicted value $\hat{Y}_i$ is called the OLS residual of observation i: $\hat{u} = Y_i - \hat{Y}_i$.

For further information regarding the theory behind multiple regression, see Chapter 18.1 in the book which inter alia presents a derivation of the OLS estimator in the multiple regression model using matrix notation.

Now let us jump back to the example of test scores and class sizes. The estimated model object is `mult.mod`. As for simple regression models we can use the `summary()` function to obtain information on estimated coefficients and model statistics.

```r
summary(mult.mod)$coef
```

```
##                Estimate Std. Error    t value      Pr(>|t|)
## (Intercept) 686.0322445 7.41131160  92.565565 3.871327e-280
## STR          -1.1012956 0.38027827  -2.896026  3.978059e-03
## english      -0.6497768 0.03934254 -16.515882  1.657448e-47
```

So the estimated multiple regression model is

$$\widehat{TestScore} = \underset{(7.41)}{686.03} - \underset{(0.38)}{1.10} \times STR - \underset{(0.04)}{0.65} \times PctEL. \tag{6.6}$$

Unlike in the simple regression model where the data can be represented by points in the two-dimensional cartesian coordinate system, we are now dealing with three dimensions. Hence observations can be represented by points in the three-dimensional real space, denoted $\mathbb{R}^3$. Therefore (6.6) is now longer a regression line but a *regression plane*. This idea extends to higher dimensions when we further expand the number of regressors k. We then say that the regression model can be represented a hyperplane in the $k+1$ dimensional space. It is already hard to imagine such a space if $k = 3$ and we best stick with the general idea that, in the multiple regression model, the dependent variable is explained by a *linear combination of the regressors*. However, in the present case we are able to visualize the situation. The following figure is an interactive 3D visualization of the data and the estimated regression plane (6.6).

We observe that the estimated regression plane fits the data reasonably well — at least with regard to the shape and spatial poistion of the point cloud. The color of the markers is an indicator for the absolute deviation from the predicted regression plane. Observations that are coloured more reddish lie close to the regression plane while the color shifts to blue with growing distance. An anomaly that can be seen from the plot is that there might be heteroskedasticity: we see that the dispersion of regression errors made, i.e. the distance of observations to the regression plane shows a tendency to decrease as the share of English learning students increases.

6.3 Measures of Fit in Multiple Regression

In multiple regression, common summary statistics are SER, $R\hat{}2$ and the adjusted R^2.

Taking the code from Section 6.3 You could simply use `summary(mult.mod)` to print the SER, R^2 and adjusted-R^2. For multiple regression models the SER is computed as

$$SER = s_{\hat{u}} = \sqrt{s_{\hat{u}}^2}$$

where, in contrast to the simple regression model we apply a modification to the denominator of the premultiplied factor in $s_{\hat{u}}^2$ in order to accommodate for additional regressors. Thus,

$$s_{\hat{u}}^2 = \frac{1}{n-k-1} \, SSR$$

with k the number of regressors *excluding* the intercept. While `summary()` computes the R^2 just as in the case of a single regressor, it is not a reliable measure for multiple regression models. This is due to R^2 becoming larger every time an additional regressor is added to the model since adding a regressor decreases the SSR — at least unless the respective estimated coefficient is exactly zero what practically never happens to be the case (see chapter 6.4 in the book). The adjusted R^2 takes this into consideration by "punishing" the addition of regressors using a correction factor. So the adjusted R^2 or simply $\overline{R^2}$ is a modified version of R^2.

$$\overline{R^2} = 1 - \frac{n-1}{n-k-1} \frac{SSR}{TSS}$$

As You may have already suspected, `summary()` adjusts the formula for SER by itself and it computes $\overline{R^2}$ and of course R^2 by default, therby leaving the decision which measure to rely on up to the user.

You can find the measures at the bottom of the output produced by calling `summary(mult.mod)`.

```r
summary(mult.mod)
```

```
##
## Call:
## lm(formula = score ~ STR + english, data = CASchools)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -48.845 -10.240  -0.308   9.815  43.461
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept) 686.03224    7.41131  92.566  < 2e-16 ***
## STR          -1.10130    0.38028  -2.896  0.00398 **
## english      -0.64978    0.03934 -16.516  < 2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 14.46 on 417 degrees of freedom
## Multiple R-squared:  0.4264, Adjusted R-squared:  0.4237
## F-statistic:   155 on 2 and 417 DF,  p-value: < 2.2e-16
```

We can also compute the measures by hand using the formulas above. Let us check if the results coincide with the values provided by `summary()`.

```
# define the components
n <- nrow(CASchools)                            # number of observations (rows)
k <- 2                                          # number of regressors

y_mean <- mean(CASchools$score)                 # mean of avg. test-scores

SSR <- sum(residuals(mult.mod)^2)               # sum of squared residuals
TSS <- sum((CASchools$score - y_mean )^2)       # total sum of squares
ESS <- sum((fitted(mult.mod) - y_mean)^2)       # explained sum of squares

# compute the measures

SER <- sqrt(1/(n-k-1) * SSR)                    # standard error of the regression
Rsq <- 1 - (SSR / TSS)                          # R^2
adj_Rsq <- 1 - (n-1)/(n-k-1) * SSR/TSS          # adj. R^2

# Print the measures to the console
c("SER" = SER, "R2" = Rsq, "Adj.R2" = adj_Rsq)
```

```
##        SER         R2     Adj.R2
## 14.4644831  0.4264315  0.4236805
```

We find that the results do match. Now, what can be said about the fit of our multiple regression model for test scores with the percentage of english learners as an additional regressor? Does it improve on the simple model including only an intercept and a measure of the class size? The answer is yes: this is easily seen by comparing these measures of fit with those for the simple regression model `mod`.

```
# SER
summary(mod)$sigma
```

```
## [1] 18.58097
```

```
# R^2
summary(mod)$r.squared
```

```
## [1] 0.05124009
```

```
# Adj. R^2
summary(mod)$adj.r.squared
```

```
## [1] 0.04897033
```

Including $PctEL$ as a regressor boots the R^2 from about 5% to 42.6%. Qualitatively the same is observed for $\overline{R^2}$ which we deem to be more reliable in view of the discussion above. Notice that the difference between R^2 and $\overline{R^2}$ is small since $k = 2$ and n is large. Condensed, the fit of (6.6) improves vastly on the fit of the simple regression model with STR as the only regressor. Comparing prediction errors we find that the prediction precision of the multiple regression model (6.6) improves upon the simple model as adding $PctEL$ lowers the SER from 18.6 to 14.5 units of test score.

As already mentioned R^2 and $\overline{R^2}$ may be used to quantify how good a model fits the data. However it is rarely a good idea to maximize these measures by stuffing the model with regressors in general. You will (hopefully) not find any serious study that does so. Instead it is more fruitful to include regressors that improve estimation of the causal effect of interest which is *not* assessed by means of a low SSR. The issue of variable selection is covered in Chapter 7 of this script and Chapter 7 in the book.

6.4 OLS Assumptions in Multiple Regression

In the multiple regression model we extend the known three least squares assumptions imposed for the simple regression model (see Chapter 4, Key Concept 4.3) and add a fourth assumption. These assumptions are presented in Key Concept 6.4. While we will not go into the details of assumptions 1, 2 and 3 since their ideas have been discussed before and are easily generalized to the case of multiple regressors, we will devote our attention to the fourth assumption. This forth assumption forbids the occurence of perfect correlation between any pair of regressors.

Key Concept 6.4

The Least Squares Assumptions in the Multiple Regression Model

The multiple regression model is given by

$$Y_i = \beta_0 + \beta_1 X_{1i} + \beta_1 X_{2i} + \dots + \beta_k X_{ki} + u_i \ , \ i = 1, \dots, n.$$

The OLS assumptions in the multiple regression model are an extension of the ones made for the simple regression model:

1. Regressors $(X_{1i}, X_{2i}, \dots, X_{ki}, Y_i)$, $i = 1, \dots, n$ are drawn such that the i.i.d. assumption holds.
2. u_i is an error term with conditional zero given the regressors, i.e.

$$E(u_i | X_{1i}, X_{2i}, \dots, X_{ki}) = 0.$$

3. Large outliers are unlikely, formally $X_{1i}, \dots, X_{ki}$ and Y_i have finite fourth moments.
4. No perfect multicollinearity.

Multicollinearity

If two or more regressors in a multiple regression model are *strongly* correlated we say that there is *multicollinearity*. If the correlation between two or more regressors is perfect (correlation coeficient equals 1), we refer to the situation as *perfect multicollinearity*. Perfectly multicollinear regressors can be written as linear combinations of each other. While strong multicollinearity in general is unpleasent as it causes the variance of the OLS estimator to be large (we will discuss is in more detail later), the presence of perfect multicollinearity makes it even impossible to solve for the OLS estimator, that is the model cannot be estimated at all.

The next section presents some examples of perfect multicollinearity and demonstrates how R, specifically the `lm` function deals with them.

Examples of Perfect Multicollinearity

How does R react if we want it to estimate a model with perfectly correlated regressors?

If we use the `lm` function to estimate a model with a set of regressors that suffer from perfect multicollinearity the system will produce a warning in the first line of the coefficient section of the output (1 not defined because of singularities) and ignore the regressor(s) which is (are) assumed to be a linear combination of the others. See the following example where we add another variable `FracEL`, the fraction of Englisch learners to `CASchools` where observations are scaled values of the observations for `english` and use it as a regressor together with `STR` and `english` in a multiple regression model. In this example `english` and `FracEL` are perfectly collinear. The R code is as follows.

```
# define the fraction of english learners
CASchools$FracEL <- CASchools$english/100

# estimate the model
mult.mod <- lm(score ~ STR + english + FracEL, data = CASchools)

# obtain a summary of the model
summary(mult.mod)
```

```
##
## Call:
## lm(formula = score ~ STR + english + FracEL, data = CASchools)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -48.845 -10.240  -0.308   9.815  43.461
##
## Coefficients: (1 not defined because of singularities)
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept) 686.03224    7.41131  92.566  < 2e-16 ***
## STR          -1.10130    0.38028  -2.896  0.00398 **
## english      -0.64978    0.03934 -16.516  < 2e-16 ***
## FracEL             NA         NA      NA       NA
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 14.46 on 417 degrees of freedom
## Multiple R-squared:  0.4264, Adjusted R-squared:  0.4237
## F-statistic:   155 on 2 and 417 DF,  p-value: < 2.2e-16
```

Notice that the row `FracEL` in the coefficients section of the output consists of `NA` entries since `FracEL` was excluded from the model.

If we were to compute OLS by hand we would run into the problem as well but no one would be helping us out! The computation simply fails. Why is this the case? Take the following example:

Assume You want to estimate a simple linear regression model with an intercept and one regressor:

$$Y_i = \beta_0 + \beta_1 X_i + u_i$$

As mentioned above, for perfect multicollinearity to be present X has to be a linear combination of the other regressors. Since the only other regressor is a constant (think of the right hand side of the model equation as $\beta_0 \times 1 + \beta_1 X_i + u_i$ so that β_1 is always multiplied by 1 for every observation), X has to be constant as well. When we recap the formula for $\hat{\beta}_1$ and rewrite it somewhat, we have

$$\hat{\beta}_1 = \frac{\sum_{i=1}^n (X_i - \bar{X})(Y_i - \bar{Y})}{\sum_{i=1}^n (X_i - \bar{X})^2} = \frac{\frac{1}{n-1}\sum_{i=1}^n (X_i - \bar{X})(Y_i - \bar{Y})}{\frac{1}{n-1}\sum_{i=1}^n (X_i - \bar{X})^2} = \frac{\widehat{cov}(X,Y)}{\widehat{Var}(X)}. \tag{6.7}$$

So the variance of the regressor X stands in the denominator. Since the variance of a constant is zero, we are not able to compute this fraction and $\hat{\beta}_1$ remains undefined.

Note: In this special case the nominator in (6.7) equal zero, too. Can You show that?

Let us behold two further examples where our selection of regressors induces perfect multicollinearity. First, assume that we intend to analyse the effect of class size on test score by using a dummy variable that identifies "Not very small" classes (NVS). We define that a school has the NVS attribute when the school's average student-teacher ratio is at least 12.

$$NVS = \begin{cases} 0 & \text{if STR} < 12 \\ 1 & \text{otherwise} \end{cases}$$

We add the corresponding column to `CASchools` and estimate a multiple regression model with covariates `computer` and `english`.

```
# if STR smaller 12, NVS = 0, else NVS = 1
CASchools$NVS <- ifelse(CASchools$STR < 12, 0, 1)

# estimate the model
mult.mod <- lm(score ~ computer + english + NVS, data = CASchools)

# obtain a model summary
summary(mult.mod)
```

```
##
## Call:
## lm(formula = score ~ computer + english + NVS, data = CASchools)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -49.492  -9.976  -0.778   8.761  43.798
##
## Coefficients: (1 not defined because of singularities)
##               Estimate Std. Error t value Pr(>|t|)
## (Intercept) 663.704837   0.984259 674.319  < 2e-16 ***
## computer      0.005374   0.001670   3.218  0.00139 **
## english      -0.708947   0.040303 -17.591  < 2e-16 ***
## NVS                 NA         NA      NA       NA
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 14.43 on 417 degrees of freedom
## Multiple R-squared:  0.4291, Adjusted R-squared:  0.4263
## F-statistic: 156.7 on 2 and 417 DF,  p-value: < 2.2e-16
```

Again, the output of `summary(mult.mod)` tells us that inclusion of `NVS` in the regression would render the estimation infeasible. What happened here? This is an example where we made a logical mistake when defining the regressor `NVS`: if we had taken a closer look at `NVS`, the redefined measure for class size, we would have noticed that there is not a single school with $STR < 12$ hence NVS equals one for all observations. We can check this by printing the contents of `CASchools$NVS` to the console or by using the function `table`, see `?table`.

```
table(CASchools$NVS)
```

```
##
##   1
## 420
```

`CASchools$NVS` is a vector of 420 ones and our data set includes 420 observations. This obviously violates assumption 4 of Key Concept 6.4: remember that observations for the intercept are always 1 so we have

$$\begin{align} intercept &= \lambda \cdot NVS \tag{6.1}\\ & \tag{6.2}\\ \begin{pmatrix}1\\ \vdots \\ 1\end{pmatrix} &= \lambda \cdot \begin{pmatrix}1\\ \vdots \\ 1\end{pmatrix} \tag{6.3}\\ &\Leftrightarrow \lambda = 1. \tag{6.4}\end{align}$$

Since both regressors can be written as a linear combination of each other, we face perfect multicollinearity and R excludes NVS from the model. Thus the message to take away is: think carefully about how regressors You created Yourself could possibly interact with unrecognized features of the data set!

Another example of perfect multicollinearity is known as the "dummy variable trap". This may occur when multiple dummy variables are used as regressors. A common case for this is when the dummies are used to sort the data set into mutually exclusive categories. For example, suppose we have spatial information that indicates whether a school is located in the North, West, South or East of the US which allows us to create the dummy variables

$$\begin{align} North_i &= \begin{cases} 1 & \text{if located in the north} \\ 0 & \text{otherwise} \end{cases} \tag{6.5}\\ & \tag{6.6}\\ West_i &= \begin{cases} 1 & \text{if located in the west} \\ 0 & \text{otherwise} \end{cases} \tag{6.7}\\ & \tag{6.8}\\ South_i &= \begin{cases} 1 & \text{if located in the south} \\ 0 & \text{otherwise} \end{cases} \tag{6.9}\\ & \tag{6.10}\\ East_i &= \begin{cases} 1 & \text{if located in the east} \\ 0 & \text{otherwise.} \end{cases} \tag{6.11}\end{align}$$

Since the directions are mutually exclusive, for every school $i = 1, \dots, n$ we have

$$North_i + West_i + South_i + East_i = 1.$$

We run into problems when trying to estimate a model that includes a constant and *all four* direction dummies, e.g. in the model

$$TestScore = \beta_0 + \beta_1 \times STR + \beta_2 \times english + \beta_3 \times North_i + \beta_4 \times West_i + \beta_5 \times South_i + \beta_6 \times East_i + u_i \tag{6.8}$$

since then for all observations $i = 1, \dots, n$ the constant term can be written as a linear combination of the dummies:

$$
\begin{align}
intercept &= \lambda_1 \cdot (North + West + South + East) \tag{6.12}\\
\tag{6.13}\\
\begin{pmatrix} 1 \\ \vdots \\ 1 \end{pmatrix} &= \lambda \cdot \begin{pmatrix} 1 \\ \vdots \\ 1 \end{pmatrix} \tag{6.14}\\
&\Leftrightarrow \lambda = 1 \tag{6.15}
\end{align}
$$

and we have perfect multicollinearity. This is what is meant by the "dummy variable trap": not paying attention and erroneously including all dummies and an intercept term in a regression model.

How does the `lm` function in R handle a regression like (6.8)? To answer this we first generate some artifical categorical data and append a new column named `directions` to `CASchools` and see what `lm` does when asked to estimate the model above.

```r
# set random seed for reproducibility
set.seed(1)

# Generate artificial data on location
CASchools$direction <- sample(c("West","North","South","East"), 420, replace = T)

# estimate the model
mult.mod <- lm(score ~ STR + english + direction, data = CASchools)

# obtain a model summary
summary(mult.mod)
```

```
##
## Call:
## lm(formula = score ~ STR + english + direction, data = CASchools)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -48.018 -10.098  -0.556   9.304  42.596
##
## Coefficients:
##                 Estimate Std. Error t value Pr(>|t|)
## (Intercept)    685.67356    7.43308  92.246  < 2e-16 ***
## STR             -1.12246    0.38231  -2.936  0.00351 **
## english         -0.65096    0.03934 -16.549  < 2e-16 ***
## directionNorth   1.60680    1.92476   0.835  0.40431
## directionSouth  -1.17013    2.07665  -0.563  0.57342
## directionWest    2.44340    2.05191   1.191  0.23442
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 14.45 on 414 degrees of freedom
## Multiple R-squared:  0.4315, Adjusted R-squared:  0.4246
## F-statistic: 62.85 on 5 and 414 DF,  p-value: < 2.2e-16
```

Notice that R solves the problem sketched above on its own by generating and including the dummies `directionNorth`, `directionSouth` and `directionWest` but ommitting `directionEast`. Of course, omission of every other dummy instead would be achieve the same. This is done by convention. Another solution would be to exclude the intercept and include all dummies instead. Does this mean that the information on schools located in the East is discarded? Furtunately, this is not the case: exclusion of `directEast` just alters the interpretation of coefficient estimates on the remaining dummies from absolute to relative. For example, the coefficient estimate on `directionNorth` states that, on average, test scores in the North are about 1.61 points higher than in the East.

A last example considers the case where a perfect linear relationship arises from redundant regressors. Suppose we have a regressor $PctES$, the percentage of English speakers in the school where

$$PctES = 100 - PctEL$$

and both $PctES$ and $PctEL$ are included in a regression model. One regressor is redundant since the other one conveys the same information. Since this obviously is a case where the regressors can be written as linear combination, we end up with perfect multicollinearity, again.

Let us do this in R.

```r
# Percentage of english speakers
CASchools$PctES <- 100 - CASchools$english

# estimate the model
mult.mod <- lm(score ~ STR + english + PctES, data = CASchools)

# obtain a model summary
summary(mult.mod)
```

```
##
## Call:
## lm(formula = score ~ STR + english + PctES, data = CASchools)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -48.845 -10.240  -0.308   9.815  43.461
##
## Coefficients: (1 not defined because of singularities)
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept) 686.03224    7.41131  92.566  < 2e-16 ***
## STR          -1.10130    0.38028  -2.896  0.00398 **
## english      -0.64978    0.03934 -16.516  < 2e-16 ***
## PctES              NA         NA      NA       NA
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 14.46 on 417 degrees of freedom
## Multiple R-squared:  0.4264, Adjusted R-squared:  0.4237
## F-statistic:   155 on 2 and 417 DF,  p-value: < 2.2e-16
```

Once more, the `lm` function refuses to estimate the full model using OLS and excludes `PctES`.

See chapter 18.1 of the book for an explanation of perfect multicollinearity and its consequences to the OLS estimator in general multiple regression models using matrix notation.

Imperfect Multicollinearity

As opposed to perfect multicollinearity, imperfect multicollinearity is — to a certain extend — not a problem at all. In fact, imperfect multicollinearity is the reason why we are interested in estimating multiple regression models in the first place: the OLS estimator allows us to *isolate* influences of *correlated* regressors on the dependent variable. So if it was not for these dependencies, there would not be a reason to resort to a multiple regression approach and we could simply work with a single-regressor model. However, reality is complicated and this is rarely the case. Moreover, we already know that ignoring dependencies among regressors which influence the outcome variable has an adverse effect on estimation results (keyword: omitted variable bias!).

So when and why is imperfect multicollinearity a problem? Suppose You got the regression model

$$Y_i = \beta_0 + \beta_1 X_{1i} + \beta_2 X_{2i} + u_i \tag{6.9}$$

and You are interested in estimating β_1, the effect on Y_i of a one unit change in X_{1i} while holding X_{2i} constant. You do not know that the true model indeed includes X_2 but You follow some reasoning and add X_2 as a covariate to the model in order to address a potential omitted variable bias. You are confident that $E(u_i|X_{1i}, X_{2i}) = 0$ for all observations and there is no reason to suspect violation of the assumptions 2 and 3 made in Key Concept 6.4. If now X_1 and X_2 are highly correlated, OLS has its difficulties to estimate β_1 precisely. That means although $\hat{\beta}_1$ is a consistent and unbiased estimator for β_1, it has a large variance due to X_2 being included in the model. If the errors are homoskedastic, this issue can be better understood from inspecting the formula for the variance of $\hat{\beta}_1$ in the model (6.9) (cf. Appendix 6.2 of the book):

$$\sigma^2_{\hat{\beta}_1} = \frac{1}{n} \left(\frac{1}{1 - \rho^2_{X_1,X_2}} \right) \frac{\sigma^2_u}{\sigma^2_{X_1}} \tag{6.10}$$

Firstly, notice that if $\rho_{X_1,X_2} = 0$ i.e. if there is no correlation between both regressors, including X_2 in the model has no influence on the variance of $\hat{\beta}_1$. Secondly, if X_1 and X_2 are correlated, $\sigma^2_{\hat{\beta}_1}$ is inversely proportional to $1 - \rho^2_{X_1,X_2}$ so the stronger the correlation between X_1 and X_2, the smaller is $1 - \rho^2_{X_1,X_2}$ and thus the bigger is the variance of $\hat{\beta}_1$. Thirdly, (6.10) reveals that, in any case, increasing the sample size helps to reduce the variance of $\hat{\beta}_1$. Of course, this is not limited to the case with two regressors: in general multiple regression, imperfect multicollinearity inflates the variance of one or more coefficient estimators and it is an empirical question which estimators are severly affected by this and which are not. So is the decision whether one wants to hazard the consequences of adding a large number of covariates when the sample size is small.

In sum, undesirable consequences of imperfect multicollinearity are not the result of a logical error made by the researcher (as is often the case for perfect multicollinearity) but are rather a problem that is linked to the data used, the model to be estimated and the research question at hand.

Let us conduct a simulation study to illustrate the issues sketched above.

1. We use (6.9) as the data generating process and choose $\beta_0 = 5$, $\beta_1 = 2.5$ and $\beta_2 = 3$ and u_i is an error term distributed as $\mathcal{N}(0, 5)$. In a first step, we sample the regressor data from a bivariate normal distribution:
$$X_i = (X_{1i}, X_{2i}) \overset{i.i.d.}{\sim} \mathcal{N} \left[\begin{pmatrix} 0 \\ 0 \end{pmatrix}, \begin{pmatrix} 10 & 2.5 \\ 2.5 & 10 \end{pmatrix} \right]$$
It is straightforward to see that the correlation between X_1 and X_2 in the population is rather low:
$$\rho_{X_1,X_2} = \frac{cov(X_1, X_2)}{\sqrt{Var(X_1)}\sqrt{Var(X_2)}} = \frac{2.5}{10} = 0.25$$
2. Next, we estimate the model (6.9) and save the estimates for β_1 and β_2. This is repeated 10000 times with a `for` loop so we end up with a large number of estimates that allow us to describe the distributions of $\hat{\beta}_1$ and $\hat{\beta}_2$.

3. We repeat steps 1 and 2 but increase the covariance between X_1 and X_2 from 2.5 to 8.5 such that the correlation between the regressors is high:

$$\rho_{X_1,X_2} = \frac{cov(X_1,X_2)}{\sqrt{Var(X_1)}\sqrt{Var(X_2)}} = \frac{8.5}{10} = 0.85$$

4. In order to assess the effect on the precision of the estimators of increasing the collinearity between X_1 and X_2 we compute estimates of the variances of $\hat{\beta}_1$ and $\hat{\beta}_2$ and compare.

```
# load packages
library(MASS)
library(mvtnorm)

# set number of observations
n <- 50

# initialize vectors of coefficients
coefs1 <- cbind("hat_beta_1" = numeric(10000), "hat_beta_2" = numeric(10000))
coefs2 <- coefs1

# set random seed
set.seed(1)

# loop sampling and estimation
for (i in 1:10000) {

  # for cov(X_1,X_2) = 0.25
  X <- rmvnorm(n, c(50,100), sigma = cbind(c(10,2.5), c(2.5,10)))
  u <- rnorm(n, sd=5)
  Y <- 5 + 2.5*X[,1] + 3*X[,2] + u
  coefs1[i,] <- lm(Y ~ X[,1] + X[,2])$coefficients[-1]

  # for cov(X_1,X_2) = 0.85
  X <- rmvnorm(n, c(50,100), sigma = cbind(c(10,8.5), c(8.5,10)))
  Y <- 5 + 2.5*X[,1] + 3*X[,2] + u
  coefs2[i,] <- lm(Y ~ X[,1] + X[,2])$coefficients[-1]
}

# estimate the variances
var(coefs1)
```

```
##             hat_beta_1  hat_beta_2
## hat_beta_1  0.05674375 -0.01387725
## hat_beta_2 -0.01387725  0.05712459
```

```
var(coefs2)
```

```
##            hat_beta_1 hat_beta_2
## hat_beta_1  0.1904949 -0.1610405
## hat_beta_2 -0.1610405  0.1909056
```

Since we call `var` on matrices rather than vectors, the oucomes are variance-covariance matrices. We are interested in the variances which are the diagonal elements. We see that due to the high collinearity, the variances of $\hat{\beta}_1$ and $\hat{\beta}_2$ have more than tripled: in Econometrics lingo we say that it has become more difficult to estimate the true coefficients precisely.

6.5 The Distribution of the OLS Estimators in Multiple Regression

As in simple linear regression, different samples will produce different values of the OLS estimators in the multiple regression model. Here again this variation leads to uncertainty of those estimators and we seek to describe it using their sampling distribution(s). In short, if the assumption made in Key Concept 6.4 hold, the large sample distribution of $\hat\beta_0, \hat\beta_1, \dots, \hat\beta_k$ is multivariate normal and the individual estimators themselves are also normally distributed. Key Concept 6.5 summarizes the corresponding statements made in Chapter 6.6 of the book. A more technical derivation of these results can be found in Chapter 18 of the book.

Key Concept 6.5

Large-sample distribution of $\hat\beta_0, \hat\beta_1, \dots, \hat\beta_k$

If the least squares assumptions in the multiple regression model (see Key Concept 6.4) hold, then in large samples, the OLS estimators $\hat\beta_0, \hat\beta_1, \dots, \hat\beta_k$ are jointly normally distributed. We also say that their joint distribution is *multivariate* normal. Further, each $\hat\beta_j$ is distributed as $N(\beta_j, \sigma^2_{\beta_j})$.

Essentially, Key Concept 6.5 states that, if the sample size is large, we can approximate the individual sampling distributions of the coefficient estimators by specific normal distributions and their joint sampling distribution by a multivariate normal distribution.

How can we use R two get a notion of what the joint PDF of the coefficient estimators in multiple regression model looks like? When estimating some model on arbitrary data once, we would end up with a set of point estimates that do not reveal any information on the joint density of the estimators. However, with a large number of estimations using repeatedly randomly sampled data from the same population we could generate a large set of point estimates that allows us to plot an *estimate* of the joint density function.

The approach we will use is a follows:

- Generate 10000 random samples of size 75 using the DGP

$$Y_i = 5 + 2.5 \cdot X_{1i} + 3 \cdot X_{2i} + u_i$$

where the regressors X_{1i} and X_{2i} are sampled for each observations as

$$X_i = (X_{1i}, X_{2i}) \sim \mathcal{N}\left[\begin{pmatrix}0\\0\end{pmatrix}, \begin{pmatrix}10 & 2.5\\2.5 & 10\end{pmatrix}\right]$$

and

$$u_i \sim \mathcal{N}(0, 5)$$

is an error term.

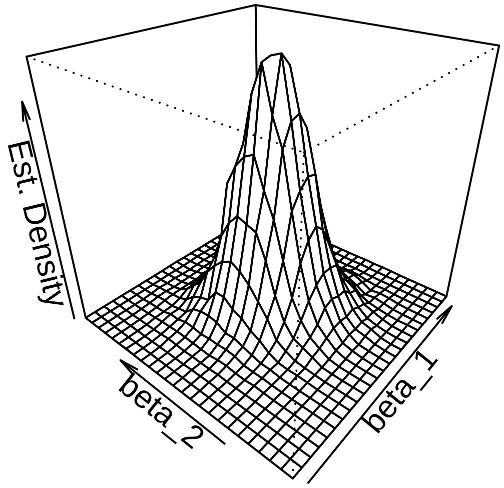
- For each of the 10000 simulated sets of sample data, we estimate the model

$$Y_i = \beta_0 + \beta_1 X_{1i} + \beta_2 X_{2i} + u_i$$

and save the coefficient estimates $\hat\beta_1$ and $\hat\beta_2$.

- We compute a density estimate of the joint distribution of $\hat\beta_1$ and $\hat\beta_2$ in the model above using the function `kde2d` from the package `MASS`, see `?MASS`. This estimate is then plotted using the function `persp`.

```
# load packages
library(MASS)
library(mvtnorm)

# set sample size
n <- 50

# initialize vector of coefficients
coefs <- cbind("hat_beta_1" = numeric(10000), "hat_beta_2" = numeric(10000))

# set random seed for reproducibility
set.seed(1)

# loop sampling and estimation
for (i in 1:10000) {
  X <- rmvnorm(n, c(50,100), sigma = cbind(c(10,2.5), c(2.5,10)))
  u <- rnorm(n, sd=5)
  Y <- 5 + 2.5*X[,1] + 3*X[,2] + u
  coefs[i,] <- lm(Y ~ X[,1] + X[,2])$coefficients[-1]
}

# Compute density estimate
kde <- kde2d(coefs[,1], coefs[,2])

# plot density estimate
persp(kde,  theta = 310, phi = 30, xlab = "beta_1", ylab = "beta_2", zlab = "Est. Density")
```



From the plot above we can see that the density estimate has some similarity to a bivariate normal distribution (see chapter 2) though it is not very pretty and probably a little rough. Furthermore, there is correlation between the estimators such that $\rho \neq 0$ in (2.1). Also, the distribution's shape deviates from the symmetric bell shape of the bivariate standard normal distribution and has an eliptical surface area instead.

```
# estimate correlation between estimators
cor(coefs[,1], coefs[,2])
```

```
## [1] -0.2503028
```

Where does this correlation come from? Notice that, due to the way we generated the data, there is correlation between the regressors X_1 and X_2. Correlation between the regressors in a multiple regression model always translates to correlation between the estimators (see Appendix 6.2 of the book). In our case, the positive correlation between X_1 and X_2 translates to negative correlation between $\hat{\beta}_1$ and $\hat{\beta}_2$. To get a better feeling You can vary the point of view in the subsequent smooth interactive 3D plot of the same density estimate used for plotting with `persp`. Here You can see that the shape of the distribution is somewhat stretched due to $\hat{\rho} = -0.20$ and it is also apparent that both estimators are unbiased since their joint density seems to be centered close to the true parameter vector $(\beta_1, \beta_2) = (2.5, 3)$.

Chapter 7

Hypothesis Tests and Confidence intervals in Multiple Regression

This chapter discusses methods that allow to quantify the sampling uncertainty inherent to the OLS estimator of coefficients in multiple regression models. The basis for this are standard errors, hypothesis tests and confidence intervals which, just as for the simple linear regression model, can be computed using basic R functions. We will also tackle the issue of testing joint hypothesis on coefficients of multiple regression models.

7.1 Hypothesis Tests and Confidence Intervals for a Single Coefficient

First, we will discuss how to compute standard errors, how to test hypotheses and how to construct confidence intervals for a single regression coefficient β_j in a multiple regression model. The basic idea is summarized in Key Concept 7.1.

Key Concept 7.1

Testing the Hypothesis $\beta_j = \beta_{j,0}$ Against the Alternative $\beta_j \neq \beta_{j,0}$

1. Compute the standard error of $\hat{\beta}_j$
2. Compute the t-statistic,
$$t = \frac{\hat{\beta}_j - \beta_{j,0}}{SE(\hat{\beta}_j)}$$
3. Compute the p-value,
$$p\text{-value} = 2\Phi(-|t^{act}|)$$

where t^{act} is the value of the t-statistic actually computed. Reject the hypothesis at the 5% significance level if the p-value is less than 0.05 or, equivalently, if $|t^{act}| > 1.96$. The standard error and (typically) the t-statistic and the corresponding p-value for testing $\beta_j = 0$ are computed automatically by statistical software, e.g. by `summary()`.

It is straightforward to verify that principles of testing single hypothesis about the significance of coefficients in the multiple regression model are just as in in the simple regression model.

You can easily see this by inspecting the coefficient summary of the regression model

$$TestScore = \beta_0 - \beta_1 \times size - \beta_2 \times english + u$$

already discussed in chapter 6. Let us review this:

```
model <- lm(score ~ size + english, data = CASchools)
summary(model)
```

```
##
## Call:
## lm(formula = score ~ size + english, data = CASchools)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -48.845 -10.240  -0.308   9.815  43.461
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept) 686.03224    7.41131  92.566  < 2e-16 ***
## size         -1.10130    0.38028  -2.896  0.00398 **
## english      -0.64978    0.03934 -16.516  < 2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 14.46 on 417 degrees of freedom
## Multiple R-squared:  0.4264, Adjusted R-squared:  0.4237
## F-statistic:   155 on 2 and 417 DF,  p-value: < 2.2e-16
```

You may check that these quantities are computed as in the simple regression model by computing the t-statistics or p-values by hand using the output above and R as a calculator.

For example, using the definition of the p-value for a two-sided test as given in Key Concept 7.1, we can confirm the p-value for a test of the hypothesis that the coeffiecient β_0, that is the coefficient on `(intercept)`, is zero to be approximatley zero.

```
2*(1-pnorm(abs(92.566)))
```

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

Remember that, given a vector of quantiles, `pnorm()` calculates associated probabilities for the standard normal distribution by default which is suitable here since we approximate with the standard normal distribution.

Key Concept 7.2

Confidence Intervals for a Single Coefficient in Multiple Regression

A 95% two-sided confidence interval for the coefficient β_j is an interval that contains the true value of β_j with a 95% probability; that is, it contains the true value of β_j in 95% of all randomly drawn samples. Equivalently, it is the set of values of β_j that cannot be rejected by a 5% two-sided hypothesis test. When the sample size is large, the 95% confidence interval for β_j is

$$\left[\hat\beta_j - 1.96 \times SE(\hat\beta_j), \hat\beta_j + 1.96 \times SE(\hat\beta_j)\right].$$

7.2 An Application to Test Scores and the Student-Teacher Ratio

Let us take a look at the regression from section 6.3 again.

Computing individual confidence intervals for the coefficients in the multiple regression model can be done analogously as in the simple regression model using the function `confint()`.

```
model <- lm(score ~ size + english, data = CASchools)
confint(model)
```

```
##                   2.5 %      97.5 %
## (Intercept) 671.4640580 700.6004311
## size         -1.8487969  -0.3537944
## english      -0.7271113  -0.5724424
```

We note that 95% confidence intervals for all three coefficients are computed.

If we want to compute confidence intervals at another level of $\alpha = 0.1$ say, we just have to set the argument `level` in our call of `confint()` accordingly.

```
confint(model, level = 0.9)
```

```
##                     5 %        95 %
## (Intercept) 673.8145793 698.2499098
## size         -1.7281904  -0.4744009
## english      -0.7146336  -0.5849200
```

The output now reports the desired 90% confidence intervals for all model coefficients.

Knowing how to use to make inference about the coefficients in multiple regression models, You can now answer the following question:

Can the null hypothesis that a change in the student-teacher ratio, `size`, has no significant influence on test scores, `scores`, — if we control for the percentage of students learning English in the district, `english`, — be rejected at the 10% and the 5% level of significance?

The outputs above tell us that zero is not an element of the computed confidence intervals for the coefficient of `size` such that we can reject the null hypothesis at significance levels of 5% and 10%.

Note that rejection at the 5%-level implies rejection at the 10% level (why?).

The same conclusion can be made when beholding the p-value for `size`: $0.00398 < 0.05 = \alpha$.

The 95% confidence interval tells us that we can be 95% confident that a one-unit decrease in the student-teacher ratio has an effect on test scores that lies in the interval with a lower bound of -1.8488 and an upper bound of -0.3538.

Another Augmentation of the Model

What is the average effect on test scores of reducing the student-teacher ratio when the expenditures per pupil and the percentage of english learning pupils are held constant?

We can pursue this question by augmenting our model equation by an additional regressor that is a measure for spendings per pupil. Using `?CASchools` we find that `CASchools` contains the variable expenditure which provides expenditures per student.

The model we want the estimate now is

$$TestScore = \beta_0 + \beta_1 \times size + \beta_2 \times english + \beta_3 \times expenditure + u$$

with *expenditure* the total amount of expenditures per pupil in the district (thousands of dollars).

Let us now estimate the model:

```
# Scale expenditure to thousands of dollars
CASchools$expenditure <- CASchools$expenditure/1000
```

```r
# estimate the model
model <- lm(score ~ size + english + expenditure, data = CASchools)
summary(model)
```

```
##
## Call:
## lm(formula = score ~ size + english + expenditure, data = CASchools)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -51.340 -10.111   0.293  10.318  43.181
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept) 649.57795   15.20572  42.719  < 2e-16 ***
## size         -0.28640    0.48052  -0.596  0.55149
## english      -0.65602    0.03911 -16.776  < 2e-16 ***
## expenditure   3.86790    1.41212   2.739  0.00643 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 14.35 on 416 degrees of freedom
## Multiple R-squared:  0.4366, Adjusted R-squared:  0.4325
## F-statistic: 107.5 on 3 and 416 DF,  p-value: < 2.2e-16
```

We see that the estimated effect of a one unit change in the student-teacher ratio on test scores with expenditures per pupil and the share of english learning pupils held constant is rather small (-0.29). What is more, the coefficient on *size* is not significantly different from zero anymore even at the level of 10% since p-value $= 0.55$. Can You come up with an interpretation for these findings (see chapter 7.1 of the book)? Mathematically, the insignificance of β_1 could be due to a larger standard error of $\hat{\beta}_1$ resulting from adding $expenditure$ to the model so that we are estimating the true coefficent on *size* less precisely. This illustrates the issue of strongly correlated regressors (imperfect multicollinearity). The correlation between *size* and $expenditures$ can be computed using `cor()`.

```r
cor(CASchools$size, CASchools$expenditure)
```

```
## [1] -0.6199822
```

Altogether we conclude that the new model provides no evidence that changing the student-teacher ratio, e.g. by hiring new teachers, has any effect on the test scores while keeping expenditures per student and the share of english learners constant at the same time.

7.3 Joint Hypothesis Testing Using the F-Statistic

The estimated model is

$$\widehat{TestScore} = 649.58 - 0.29 \times size - 0.66 \times english + 3.87 \times expenditure.$$

Now, can we reject the hypothesis that the coefficient on *size* and and the coefficient on $expenditure$ are zero? To answer this question, we have to resort to methods that allow joint hypothesis testing. A joint hypothesis imposes restrictions on multiple regression coefficients. This is different from conducting individual t-tests where a single resitriction is imposed on a single coefficient. Chapter 7.2 of the book explains why testing the individual coefficients one at a time is different from testing them jointly.

The homoskedasticity-only F-Statistic is given by

$$F = \frac{(SSR_{restricted} - SSR_{unrestricted})/q}{SSR_{unrestricted}/(n - k_{unrestricted} - 1)}$$

with $SSR_{restricted}$ the sum of squared residuals from the restricted regression, i.e. the regression where we impose the restriction. $SSR_{unrestricted}$ is the sum of squared residuals from the full model, q is the number of restriction under the null and k is the number of regressors in the unrestricted regression.

Luckily, it is fairly easy to conduct F-tests in R. We can use the function `linearHypothesis()` which is contained in the `car` package.

```r
# estimate the multiple regression model
model <- lm(score ~ size + english + expenditure, data = CASchools)

# execute the function on the model object and provide both linear restrictions
# to be tested as strings
linearHypothesis(model, c("size=0", "expenditure=0"))
```

```
## Linear hypothesis test
##
## Hypothesis:
## size = 0
## expenditure = 0
##
## Model 1: restricted model
## Model 2: score ~ size + english + expenditure
##
##   Res.Df   RSS Df Sum of Sq      F   Pr(>F)
## 1    418 89000
## 2    416 85700  2    3300.3 8.0101 0.000386 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

From the output we can infer that the F-statistic for this joint hypothesis test is about 8.01 and the corresponding p-value is 0.0004. Thus we can reject the null hypothesis that both coefficients are zero at any level of significance commonly used in practice.

Note:

The standard output of a model summary also reports an F-statistic and the corresponding p-value. The null hypothesis belonging to this F-test is that all of the population coefficients in the model except for the intercept are zero, so the hypotheses pair is

$$H_0 : \beta_1 = 0, \ \beta_2 = 0, \ \beta_3 = 0 \quad \text{vs.} \quad H_1 : \beta_j \neq 0 \text{ for at least one } j = 1, 2, 3.$$

This is also called the "overall" regression F-statistic and the null hypothesis is obviously different from testing if only β_1 and β_3 are zero.

We will now check that the F-statistic belonging to the p-value listed in the model's summary coincides with the result reported by `linearHypothesis()`.

```r
# execute the function on the model object and provide the linear restriction
# to be tested as strings
linearHypothesis(model, c("size=0","english=0","expenditure=0"))
```

```
## Linear hypothesis test
```

```
##
## Hypothesis:
## size = 0
## english = 0
## expenditure = 0
##
## Model 1: restricted model
## Model 2: score ~ size + english + expenditure
##
##   Res.Df    RSS Df Sum of Sq      F    Pr(>F)
## 1    419 152110
## 2    416  85700  3     66410 107.45 < 2.2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```r
# Access the F-statistic from the model's summary
summary(model)$fstatistic
```

```
##    value    numdf    dendf
## 107.4547   3.0000 416.0000
```

The test rejects the null hypothesis that the model has no power in explaining test scores rather clearly.

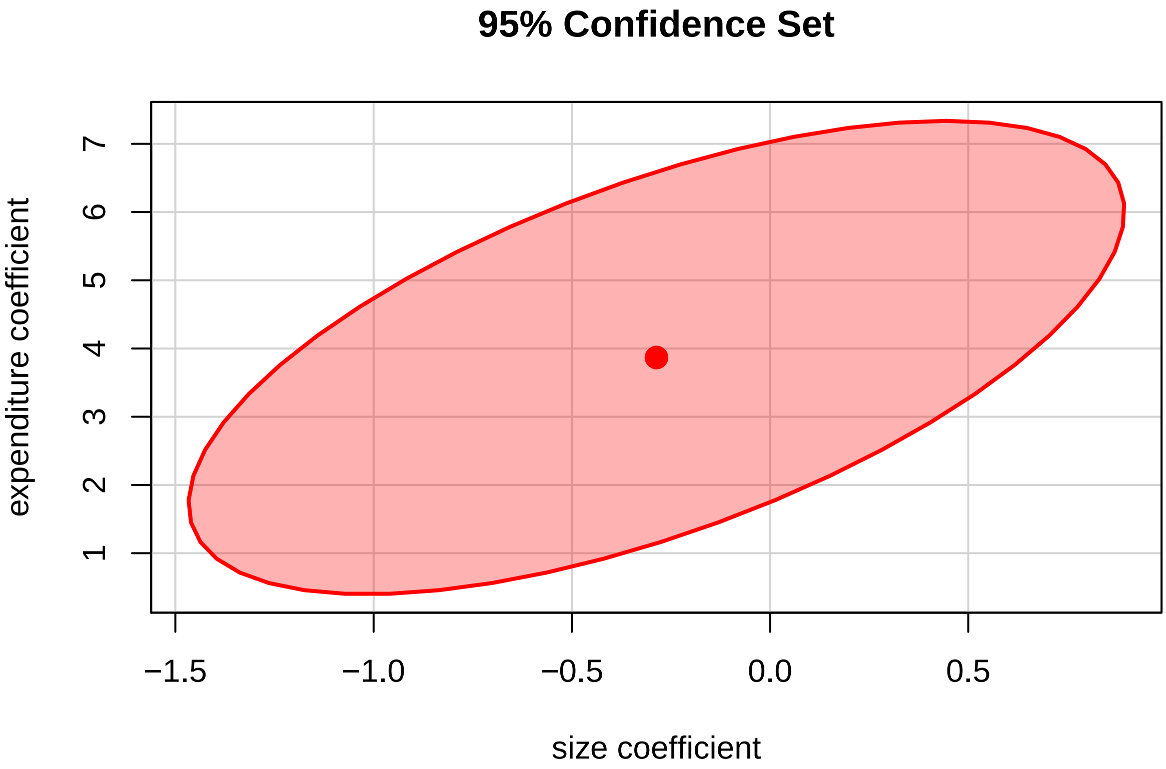
7.4 Confidence Sets for Multiple Coefficients

Based on the F-statistic that we have previously encountered, we can specify confidence sets. Confidence sets are analogous to confidence intervals for single coefficients. As such, confidence sets consist of combinations of coefficients that contain the true combination of coefficients in, 95% say, of all cases if we could infinitely draw random samples, just as in the univariate case. Put differently, a confidence set is the set of coefficient combinations for which we cannot reject a joint null hypothesis tested using a F-test.

If we consider two coefficients, their confidence set is an ellipse which is centered around the point defined by both coefficient estimates. Again, there is a very convenient way to plot the confidence set for two coefficients of model objects, namely the function `confidenceEllipse()` which is also coming with the `car` package.

In the following, we plot the 95% confidence ellipse for the coefficients on `size` and `expenditure` from the regression conducted above. By specifying the additional argument `fill`, the confidence set is colored which gives us a better impression which set of coefficients is meant.

```r
# Draw the 95% confidence set for coefficients on size and expenditure
confidenceEllipse(model,
                  fill = T,
                  which.coef = c("size","expenditure"),
                  main = "95% Confidence Set"
                  )
```



We see that the ellipse is centered around $(-0.29, 3.87)$ i.e. the pair of coefficients estimates on *size* and *expenditure*. What is more, $(0,0)$ is not element of the 95% confidence set so that we can reject $H_0 : \beta_1 = 0,\ \beta_3 = 0$.

7.5 Model Specification for Multiple Regression

Choosing a regression specifaction i.e. selecting the variables to be included in a regression model can be quite cumbersome. However, there are some guidelines how to do this. The goal is clear: obtaining an unbiased estimation of the causal effect of interest. As a starting point, one should think about omitted variables, that is to avoid a possible estimation bias by using suitable control variables (omitted variables bias in the context of multiple regression is explained in Key Concept 7.3). A second step could be to compare different regression model specifications by measures of fit. However, as we shall see one should not rely solely on $\overline{R^2}$.

Key Concept 7.3

Omitted Variable Bias in Multiple Regression

Omitted variable bias is the bias in the OLS estimator that arises when one or more included regressors are correlated with an omitted variable. For omitted variable bias to arise, two things must be true:

1. At least one of the included regressors must be correlated with the omitted variable.
2. The omitted variable must be a determinant of the dependent variable, Y.

We will now discuss an example were we face a potential omitted variable bias in a multiple regression model:

Consider again the estimated regression equation

$$\widehat{TestScore} = \underset{(8.7)}{686.0} - \underset{(0.43)}{1.10} \times size - \underset{(0.031)}{0.650} \times english.$$

We are interested in estimated the causal effect of class size on test score. In this estimation, there might be a bias due to omitting "outside learning opportunities" from our regression sice a measure like this could be a determinant of the students test scores and could also be correlated with both regressors already included in the model (so that both conditions of Key Concept 7.3 are fulfilled). "outside learning opportunities" is a complicated concept that is difficult to quantify. A surrogate we can consider instead is the students' economic backgroud which should be strongly related to the outside learning opportunities: think of wealthy parents that are able to provide time and/or money for private tuition of there children. We thus augment the model with the variable `lunch`, the percentage of students that qualify for a free or subsidized lunch in school due to family incomes below a certain threshold, and estimate the model again.

```r
# estimate the model and print summary to console
model <- lm(score ~ size + english + lunch, data = CASchools)
summary(model)
```

```
##
## Call:
## lm(formula = score ~ size + english + lunch, data = CASchools)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -32.849  -5.151  -0.308   5.243  31.501
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept) 700.14996    4.68569 149.423  < 2e-16 ***
## size         -0.99831    0.23875  -4.181 3.54e-05 ***
## english      -0.12157    0.03232  -3.762 0.000193 ***
## lunch        -0.54735    0.02160 -25.341  < 2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 9.08 on 416 degrees of freedom
## Multiple R-squared:  0.7745, Adjusted R-squared:  0.7729
## F-statistic: 476.3 on 3 and 416 DF,  p-value: < 2.2e-16
```

Thus, the estimated regression line is

$$\widehat{TestScore} = \underset{(4.7)}{700.15} - \underset{(0.24)}{1.00} \times size - \underset{(0.032)}{0.12} \times english + \underset{(0.022)}{0.55} \times lunch.$$

We observe no substantial changes in the conclusion about the effect of `size`: the coefficient changes by only 0.1 and keeps its significance.

Although the difference in estimated coefficients is not big in this case, it might be a good idea to keep `lunch` in the model to make the assumption of conditional mean independence more credible (see chapter 7.5 of the book).

Model Specification in Theory and in Practice

Key Concept 7.4

R^2 and $\overline{R^2}$: What They Tell You — and What They Don't

The R^2 and $\overline{R^2}$ tell you whether the regressors are good at predicting, or "explaining" the values of the independent variable in the sample of data at hand. if the R^2 (or $\overline{R^2}$) is nearly 1, then the regressors produce good prediction of the dependent variable in that sample, in the sense that the variance of OLS residuals is small compared to the variance of the dependent variable. If the R^2 (or $\overline{R^2}$) is nearly 0, the opposite is true.

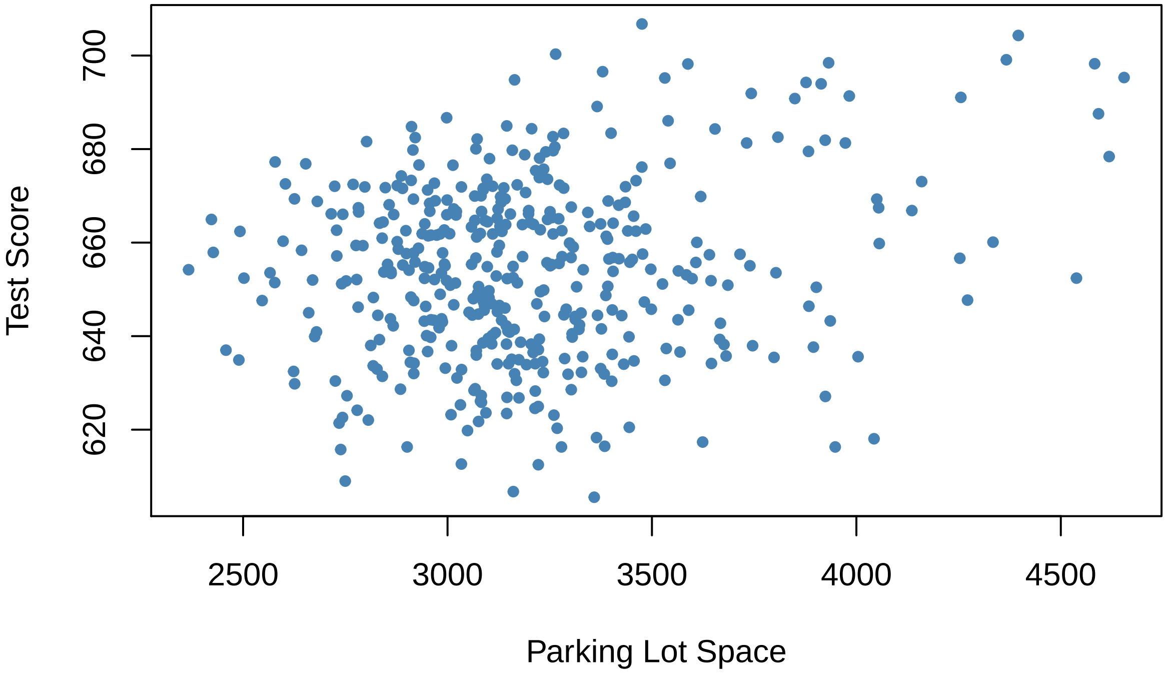
The R^2 and $\overline{R^2}$ do not tell you whether:

1. An included variable is statistically significant.
2. The regressors are true cause of the movements in the dependent variable
3. There is omitted variable bias, or
4. You have chosen the most appropriate set of regressors.

Key Concept 7.4 names some common pitfalls when using R^2 and $\overline{R^2}$ to evaluate the predictive ability of regression models.

For example, think of regressing $TestScore$ on PLS which measures the available parking lot space in thousand square feet. You are likely to observe a significant coefficient of reasonable magnitude and moderate to high values for R^2 and $\overline{R^2}$. The reason for this is that parking lot space is correlated with many determinants of the test score like location, class size, financial endowment and so on. Although we do not have observations on PLS, we can use R to generate some relatively realistic data.

```
# Generate observations for parking lot space
CASchools$PLS <- 5 + 0.6*CASchools$expenditure + 0.6*CASchools$income + CASchools$size/100 + rnorm(nrow

# plot parking lot space against test score
plot(CASchools$PLS,
     CASchools$score,
     xlab = "Parking Lot Space",
     ylab = "Test Score",
     pch = 20,
     col = "steelblue"
     )
```



```
# regress test score on PLS
summary(lm(score ~ PLS, data = CASchools))
```

```
##
## Call:
```

```
## lm(formula = score ~ PLS, data = CASchools)
##
## Residuals:
##    Min     1Q Median     3Q    Max
## -50.16 -14.25   0.65  13.56  49.88
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept) 6.224e+02  7.715e+00  80.679  < 2e-16 ***
## PLS         9.915e-03  2.393e-03   4.144 4.13e-05 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 18.7 on 418 degrees of freedom
## Multiple R-squared:  0.03946,    Adjusted R-squared:  0.03717
## F-statistic: 17.17 on 1 and 418 DF,  p-value: 4.131e-05
```

PLS is generated as a linear function of *expenditure*, *income*, *size* and random disturbances. Therefore the data suggest that there is some postive relationship between parking lot space and test score. In fact, when estimating the model

$$\widehat{TestScore} = \beta_0 + \beta_1 \times PLS + u \tag{7.1}$$

using `lm()` we find that the coefficient on PLS is positive and significantly different from zero. Also R^2 and $\overline{R^2}$ are about 0.47 which is a lot more than the roughly 0.05 observed when regressing test score on class size only.

This suggests that increasing the parking lot space boosts a school's test scores and that model (7.1) does even better in explaining heterogeneity in the dependent variable than a model with *size* as the only regressor. Keeping in mind how PLS is constructed this comes of no surprise. It is evident that the high R^2 cannot be used to the conclude that the estimated relation between parking lot space and test scores is causal: the (relatively) high R^2 is due to correlation between PLS and other determinantes and/or control variables. Increasing parking lot space is not an appropriate measure to generate more learning success!

7.6 Analysis of the Test Score Data Set

Chapter 6 and some of the previous sections have stressed that it is important to include control variables in regression models if it is plausible that there are omitted factors that cannot be measured directly. Recall that in our example of test scores, we are interested in estimating the causal effect of a change in the student-teacher ratio on test scores. In what follows, we will provide an example how to use multiple regression models in order to alleviate omitted variable bias and we will demonstrate how to report results using R.

So far we have considered two variables that control for unobservable student characteristics which correlate with the student-teacher ratio and are assumed to have an impact on test scores:

- *english*, the percentage of english learning students
- *lunch*, the share of students that qualify for a subsidized or even a free lunch at school

Another new variable provided with `CASchools` is *calworks*, the percentage of students that qualify for the CalWorks income assistance programm. Students eligible for CalWorks live in families with a total income below the threshold for the subsidized lunch programm so both variables are indicators for the share of economically disadvantaged children. Using R we can confirm that both indicators are highly correlated:

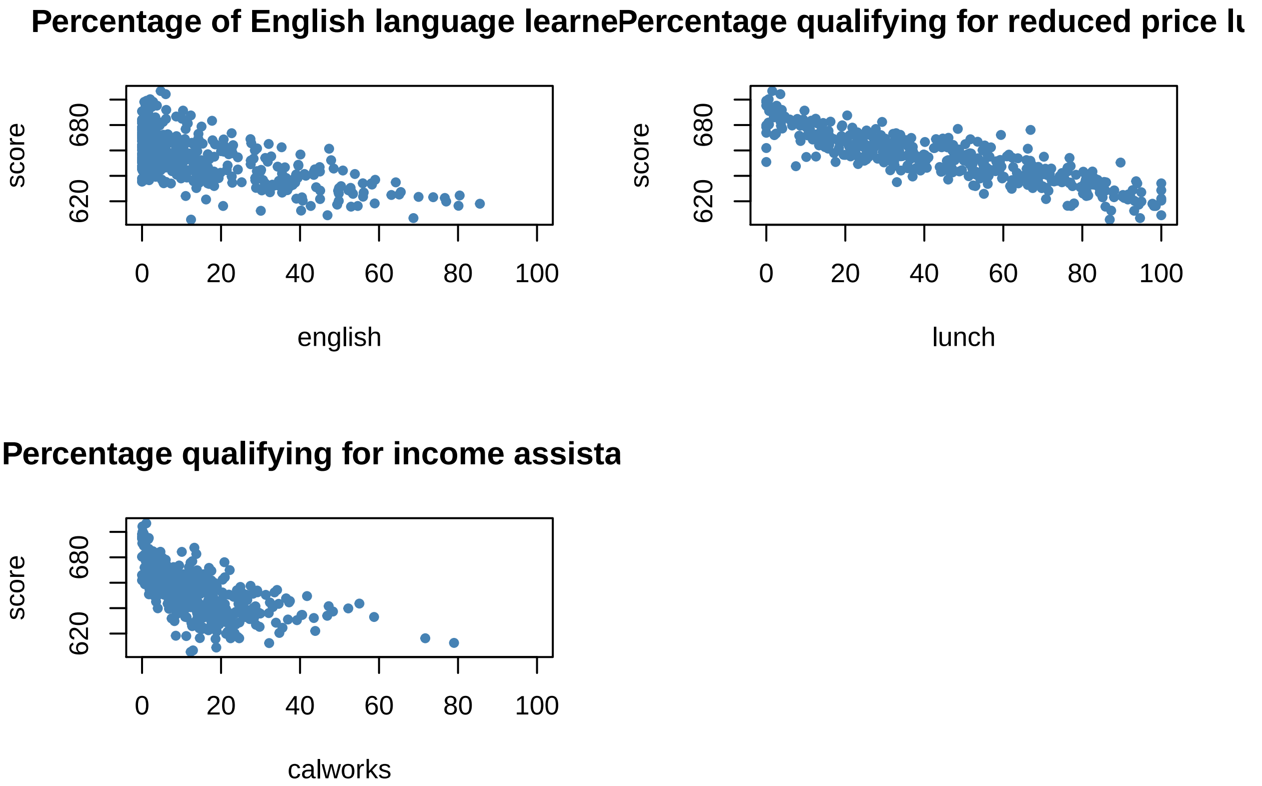
```
# estimate correlation between calworks and lunch
cor(CASchools$calworks, CASchools$lunch)
```

```
## [1] 0.7394218
```

There is no unabigious way to proceed when deciding which variable to use. In any case it is not a good idea to use both variables as regressors having in mind consequences of colinearity. Therefore, we will also consider alternative model specifications.

For a start, we plot student characteristics against test scores.

```
par(mfrow = c(1,3))

m <- rbind(c(1, 2), c(3, 0))
layout(m)

plot(score ~ english,
     data = CASchools,
     col = "steelblue",
     pch = 20,
     xlim = c(0,100),
     main = "Percentage of English language learners")

plot(score ~ lunch,
     data = CASchools,
     col = "steelblue",
     pch = 20,
     main = "Percentage qualifying for reduced price lunch")

plot(score ~ calworks,
     data = CASchools,
     col = "steelblue",
     pch = 20,
     xlim = c(0,100),
     main = "Percentage qualifying for income assistance")
```



Percentage of English language learne

Percentage qualifying for reduced price lu

Percentage qualifying for income assista

We see that all relationships are negative. We can use R to estimate the correlation coefficients.

```r
# estimate correlation between student characteristics and test scores
cor(CASchools$score, CASchools$english)
```

```
## [1] -0.6441238
```

```r
cor(CASchools$score, CASchools$lunch)
```

```
## [1] -0.868772
```

```r
cor(CASchools$score, CASchools$calworks)
```

```
## [1] -0.6268533
```

We will consider 5 different model equations:

$$\begin{aligned}
(I) \quad & \widehat{TestScore} = \beta_0 + \beta_1 \times size + u \\
(II) \quad & \widehat{TestScore} = \beta_0 + \beta_1 \times size + \beta_2 \times english + u \\
(III) \quad & \widehat{TestScore} = \beta_0 + \beta_1 \times size + \beta_2 \times english + \beta_3 \times lunch + u \\
(IV) \quad & \widehat{TestScore} = \beta_0 + \beta_1 \times size + \beta_2 \times english + \beta_4 \times calworks + u \\
(V) \quad & \widehat{TestScore} = \beta_0 + \beta_1 \times size + \beta_2 \times english + \beta_3 \times lunch + \beta_4 \times calworks + u
\end{aligned}$$

The best way to communicate regression results is in a table. The `stargazer` package is very convenient for this purpose. It provides a function that generates professionally looking HTML and LATEX tables that satisfy scienctific standards. One simply has to provide one or multiple object(s) of class `lm` and the rest is done by the function `stargazer()`.

```r
# load the stargazer library
library(stargazer)

# estimate different model specifications
spec1 <- lm(score ~ size , data = CASchools)
spec2 <- lm(score ~ size + english, data = CASchools)
spec3 <- lm(score ~ size + english + lunch, data = CASchools)
spec4 <- lm(score ~ size + english + calworks, data = CASchools)
spec5 <- lm(score ~ size + english + lunch + calworks, data = CASchools)

# generate a Latex table using stargazer
stargazer(spec1, spec2, spec3, spec4, spec5,
          column.labels = c("(I)", "(II)", "(III)", "(IV)", "(V)")
          )
```

Dependent variable:

score

(I)

(II)

(III)

(IV)

(V)

spec1

spec2

spec3

spec4

spec5

size

-2.280***

-1.101***

-0.998***

-1.308***

-1.014***

(0.480)

(0.380)

(0.239)

(0.307)

(0.240)

english

-0.650***

-0.122***

-0.488***

-0.130***

(0.039)

(0.032)

(0.033)

(0.034)

lunch

-0.547***

-0.529***

(0.022)

(0.032)

calworks

-0.790***

-0.048

(0.053)

(0.061)

Constant

698.933***

686.032***

700.150***

697.999***

700.392***

(9.467)

(7.411)

(4.686)

(6.024)

(4.698)

Observations

420

420

420

420

420

R2

0.051

0.426

0.775

0.629

0.775

Adjusted R2

0.049

0.424

0.773

0.626

0.773

Residual Std. Error

18.581 (df = 418)

14.464 (df = 417)

9.080 (df = 416)

11.654 (df = 416)

9.084 (df = 415)

F Statistic

22.575*** (df = 1; 418)

155.014*** (df = 2; 417)

476.306*** (df = 3; 416)

234.638*** (df = 3; 416)

357.054*** (df = 4; 415)

Note:

p<0.1; ***p<0.05;*** p<0.01

The table states that *scores* is the dependent variable and that we consider 5 models. We see that the coloumns of Table 7.1 contain all the information provided by `summary()` for the regression models `spec1` to `spec5`: the coefficient section of the table presents coefficients estimates equipped with signifiance codes (asterisks) and standard errors in parantheses below. Although there a no t-statistics, it is straightforward for the reader to compute them simply by dividing a coefficient estimate by the correspondung standard error. In the botton of the table we find summary statistics for each model and a legend. For an in-depth discussion of the tabular presentation of regression results, see chapter 7.6 of the book.

What can we conclude from the model comparison?

1. We see that adding control variables roughly halves the coefficient on `size`. Also the coefficient is not very sensitive to the set of control variables used. The conclusion is that decreasing the student-teacher ratio ceteris paribus by one unit leads to an estimated average increase in test scores of about 1 point.

2. Adding student characteristics as controls boosts R^2 and $\overline{R^2}$ from 0.049 (`spec1`) up to 0.773 (`spec3` and `spec5`), so we can consider these variables as suitable predictors for test scores. Morever, the estimated coefficients on all control variables are consistent with the impressions gained from figure 7.2.

3. We see that the control variables are not always individually statistically significant: for example in `spec5` we see that the coefficient on *calworks* is not significantly different from zero at the level of 5% since $|-0.048/0.061| = 0.79 < 1.64$. We also observe that the effect on the estimate (and its standard error) of the coefficient on *size* of adding *calworks* to the base specification `spec3` is negligible. We can therefore consider `calworks` as a redundant control variable in this setting.

Chapter 8

Nonlinear Regression Functions

Until now we assumed the regression function to be linear, i.e. we have treated the slope of the regression function as a constant. This implies that the effect on Y of a one unit change in X does not depend on the level of X. If however the effect of a change in X on Y does depend on the value of X, we have to use a nonlinear regression function.

8.1 A General Strategy for Modeling Nonlinear Regression Functions

Let us have a look at an example where in fact using a nonlinear regression function is better suited for estimation of the population relationship between the regressor, X, and the regressand, Y: the relationship between the income of schooling districts and their test scores.

```
#Prepare the data
library(AER)
data(CASchools)
CASchools$size <- CASchools$students/CASchools$teachers
CASchools$score <- (CASchools$read + CASchools$math)/2
```

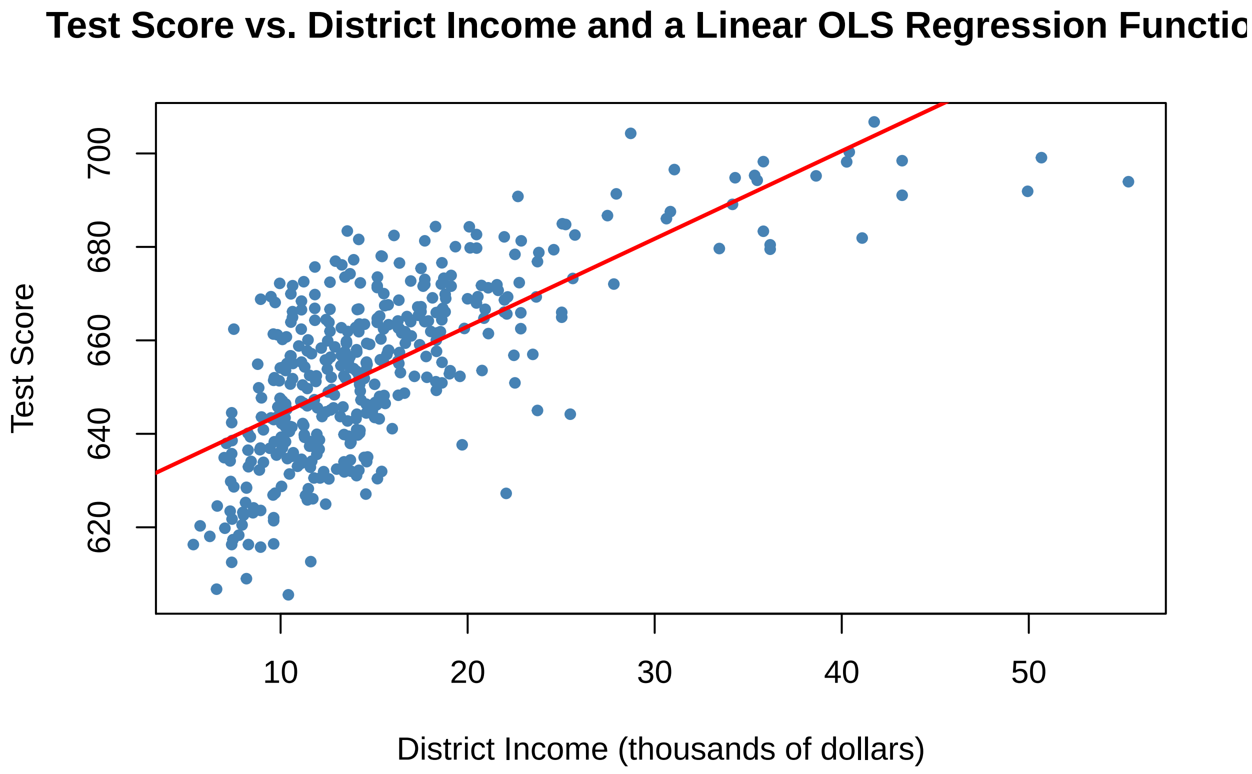
We start our analysis by computing the correlation between the two variables.

```
cor(CASchools$income, CASchools$score)
```

```
## [1] 0.7124308
```

The correlation coefficient is about 0.71. This means that income and test scores are positively correlated. In other words, children whose parents have an above average income tend to achieve above average test scores. Can we use the correlation coefficient to assess whether a linear regression model does fit the data adequately? To answer this question we visualize the data and add a linear regression line to the plot.

```
#Fit linear model
linear_model<- lm(score ~ income, data = CASchools)

# Plot observations
plot(CASchools$income, CASchools$score,
     col = "steelblue",
     pch = 20,
     xlab = "District Income (thousands of dollars)",
     ylab = "Test Score",
     main = "Test Score vs. District Income and a Linear OLS Regression Function")

# Add the regression line to the plot
abline(linear_model, col="red", lwd=2)
```



As Stock and Watson point out, the linear regression line seems to overestimate the true relationship when income is very high or very low and underestimates it in the midrange.

Fortunately, usage of the OLS is not restricted to linear functions of the regressors. Thus we can for example model test scores as a function of income and the square of income. The corresponding regression model is

$$TestScore_i = \beta_0 + \beta_1 Income_i + \beta_2 Income_i^2 + u_i.$$

This equation is called the *quadratic regression model*. Note, that $Income^2$ is treated as an additional explanatory variable. Hence, the quadratic model is a special case of a multivariate regression model. When fitting the model with `lm()` we have to use the `^` operator in conjunction with the function `I()` to add the quadratic term as an additional regressor to the `formula` argument.

```
# Fit the quadratic Model
quadratic_model <- lm(score ~ income + I(income^2), data = CASchools)

# Generate model summary
summary(quadratic_model)
```

```
##
## Call:
## lm(formula = score ~ income + I(income^2), data = CASchools)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -44.416  -9.048   0.440   8.347  31.639 
## 
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)    
## (Intercept) 607.30174    3.04622 199.362  < 2e-16 ***
## income        3.85099    0.30426  12.657  < 2e-16 ***
## I(income^2)  -0.04231    0.00626  -6.758 4.71e-11 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 
## Residual standard error: 12.72 on 417 degrees of freedom
## Multiple R-squared:  0.5562, Adjusted R-squared:  0.554 
## F-statistic: 261.3 on 2 and 417 DF,  p-value: < 2.2e-16
```

The output tells us that the estimated model equation is

$$\widehat{TestScore}_i = \underset{(3.05)}{607.3} + \underset{(0.30)}{3.85} \times Income_i - \underset{(0.01)}{0.0423} \times Income_i^2.$$

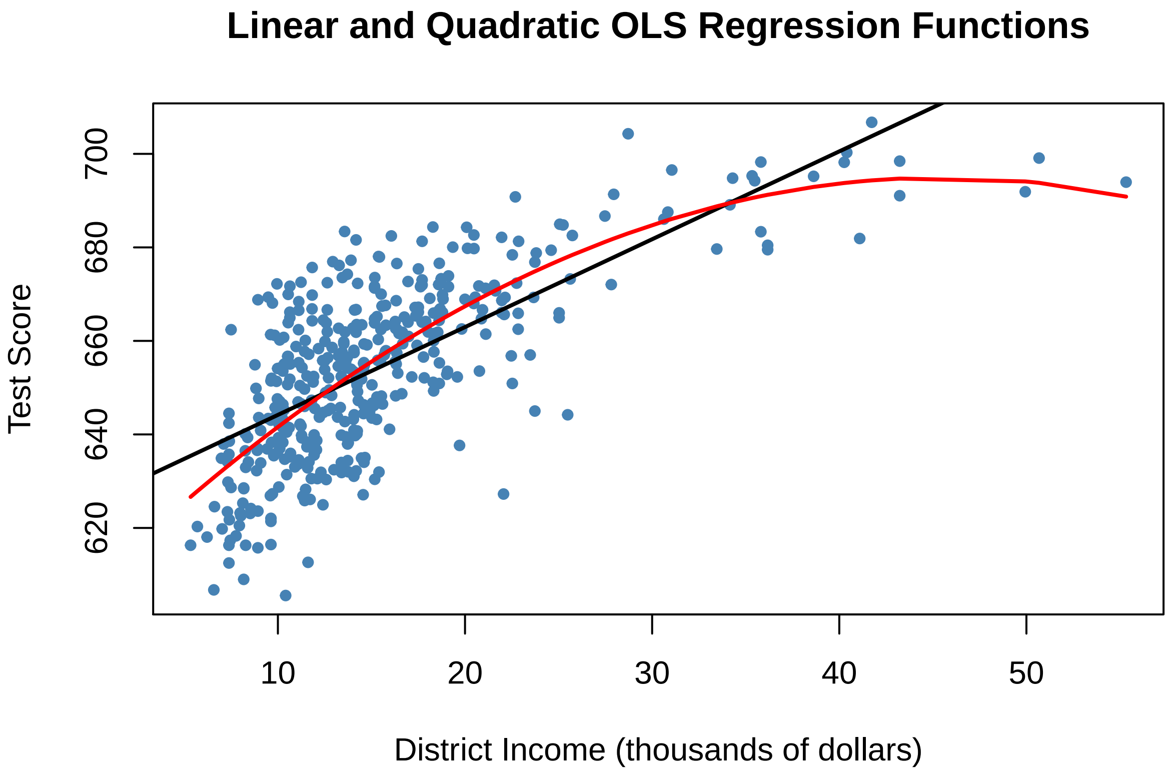
Notice that this estimated model equation allows us to test the hypothesis that the relationship between test scores and district income is linear against the alternative hypothesis that it is nonlinear. This corresponds to testing

$$H_0 : \beta_2 = 0 \ \text{ vs. } \ H_1 : \beta_2 \neq 0,$$

since $\beta_2 = 0$ corresponds to a simple linear equation and and $\beta_2 \neq 0$ implies a quadratic relationship. We find that $t = (\hat\beta_2 - 0)/SE(\hat\beta_2) = -0.0423/0.01 = -4.23$ so the null is rejected at any common level of significance and we conclude that the relationship is nonlinear. This is consistent with our informal inspection of the plotted data.

We can now draw the same scatterplot as for the linear model and add the regression line for the quadratic model. Because `abline()` can only draw straight lines, it cannot be used for this task. A function which can be used to draw lines without being restricted to straight lines is `lines()`, see `?lines`. The most basic call of `lines()` is `lines(x_values, y_values)` where `x_values` and `y_values` are vectors of the same length that provide coordinates of the points to be sequentially connected by a line. This makes it necessary to sort the coordinate pairs according to the X-values. Otherwise You will not get the desired result! In this example we use the function `order()` to sort the fitted values of $TestScore$ according to the observations for $income$.

```r
# Scatterplot of observatuib for income and TestScore
plot(CASchools$income, CASchools$score,
     col  = "steelblue",
     pch = 20,
     xlab = "District Income (thousands of dollars)",
     ylab = "Test Score",
     main = "Linear and Quadratic OLS Regression Functions")

#Add linear function to the plot
abline(linear_model , col="black", lwd=2)

#Add quatratic function to the plot
order_id <- order(CASchools$income)

lines(x = CASchools$income[order_id],
      y = fitted(quadratic_model)[order_id],
      col="red",
      lwd=2)
```



We see that the quadratic model does much better in fitting the data than the linear model.

8.2 Nonlinear Functions of a Single Independent Variable

Polynomials

The approach used to obtain a quadratic model can be generalized to polynomial models of arbitrary order r.

$$Y_i = \beta_0 + \beta_1 X_i + \beta_2 X_i^2 + \ldots + \beta_r X_i^r + u_i$$

A cubic model ($r = 3$) for instance can be estimated in the same way as the quadratic model — we just have to add `I(income^3)` to the `formula` argument in our call of `lm()`.

```
cubic_model <- lm(score ~ income + I(income^2) + I(income^3), data = CASchools)
```

In practice the question will arise which polynomial order should be chosen. First note that, similarly as for $r = 2$, we can test the null hypothesis that the true relation is linear against the alternative hypothesis that the relationship is a polynomial of degree r:

$$H_0 : \beta_2 = 0, \ \beta_3 = 0, \ldots, \beta_r = 0 \quad \text{vs.} \quad H_1 : \text{at least one } \beta_j \neq 0, \ j = 2, \ldots, r$$

This is a joint null hypothesis with $r - 1$ restrictions so it can be tested using the F-test presented in chapter 7. Remember that the function `linearHypothesis()` can compute such test statistics. If, for example, we would like to test the null hypothesis of a linear model against the alternative of a polynomial of a maximal degree $r = 3$ we could simply do the following:

```
library(car)

# test the hypothesis
linearHypothesis(cubic_model,
                 c("I(income^2)=0", "I(income^3)=0")
)
```

```
## Linear hypothesis test
## 
## Hypothesis:
## I(income^2) = 0
## I(income^3) = 0
## 
## Model 1: restricted model
## Model 2: score ~ income + I(income^2) + I(income^3)
## 
##   Res.Df   RSS Df Sum of Sq      F    Pr(>F)    
## 1    418 74905                                  
## 2    416 67170  2    7735.5 23.954 1.424e-10 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

The p-value for this test is very small so that we reject the null hypothesis. However, this does not tell us which r to choose. In practice, one approach to determine degree of the polynomial is to use sequential testing:

1. Estimate a polynomial model for some maximum value r.
2. Use a t-test to test whether $\beta_r = 0$. Rejection of the null means that X^r belongs in the regression equation.
3. Acceptance of the null in step 2 means that X^r can be eliminated from the model. Continue by repeating step 1 with order $r-1$ and test whether $\beta_{r-1} = 0$. If the test rejects, use a polynomial model of order $r-1$.
4. If the tests from step 3 rejects, continue with the procedure until the coefficient on the highest power is statistically significant.

There is no unambigous guideline how to choose r in step one. However as Stock and Watson point out, economic data is often smooth such that it is appropriate to choose small orders like 2, 3, or 4.

We will now demonstrate how to apply sequential testing in the example of a cubic model.

```
summary(cubic_model)
```

```
## 
## Call:
## lm(formula = score ~ income + I(income^2) + I(income^3), data = CASchools)
## 
## Residuals:
##    Min     1Q Median     3Q    Max 
## -44.28  -9.21   0.20   8.32  31.16 
## 
## Coefficients:
##               Estimate Std. Error t value Pr(>|t|)    
## (Intercept)  6.001e+02  5.830e+00 102.937  < 2e-16 ***
## income       5.019e+00  8.595e-01   5.839 1.06e-08 ***
## I(income^2) -9.581e-02  3.736e-02  -2.564   0.0107 *  
## I(income^3)  6.855e-04  4.720e-04   1.452   0.1471    
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 12.71 on 416 degrees of freedom
## Multiple R-squared:  0.5584, Adjusted R-squared:  0.5552
## F-statistic: 175.4 on 3 and 416 DF,  p-value: < 2.2e-16
```

The estimated cubic model stored in `cubic_model` is

$$\widehat{TestScore}_i = \underset{(5.83)}{600.1} + \underset{(0.86)}{5.02} \times Income + \underset{(0.03)}{-0.96} \times Income^2 + \underset{(-0.00047)}{0.00069} \times Income^3.$$

Summary tells us that the t-statistic on $Income^3$ is 1.42 so the null that the relationship is quadratic cannot be rejected, even at the 10% level. This is contrary to the result of the book which reports robust standard errors throughout so we will also use robust variance-covariance estimation to reproduce these results.

```
# load the lmtest package for coeftest()
library(lmtest)

# test the hypothesis using robust standard errors
coeftest(cubic_model, vcov. = vcovHC(cubic_model, type = "HC1"))
```

```
##
## t test of coefficients:
##
##                 Estimate  Std. Error  t value  Pr(>|t|)
## (Intercept)   6.0008e+02  5.1021e+00 117.6150 < 2.2e-16 ***
## income        5.0187e+00  7.0735e-01   7.0950 5.606e-12 ***
## I(income^2) -9.5805e-02  2.8954e-02  -3.3089  0.001018 **
## I(income^3)   6.8549e-04  3.4706e-04   1.9751  0.048918 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Notice that the reported standard errors have changed. Furthermore, the coefficient for `income^3` is now significant at the 5% level. This means we reject the hypothesis that the regression function is quadratic against the alternative that it is cubic. Furthermore, we can also test if the coefficients for `income^2` and `income^3` are jointly significant using a robust version of the F-test.

```
# robust F-test for
linearHypothesis(cubic_model,
                 vcov. = vcovHC(cubic_model, type = "HC1"),
                 c("I(income^2)=0", "I(income^3)=0")
                 )
```

```
## Linear hypothesis test
##
## Hypothesis:
## I(income^2) = 0
## I(income^3) = 0
##
## Model 1: restricted model
## Model 2: score ~ income + I(income^2) + I(income^3)
##
## Note: Coefficient covariance matrix supplied.
##
##   Res.Df Df      F    Pr(>F)
## 1    418
## 2    416  2 37.691 9.043e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

With a *p*-value of `9.043e-16`, i.e. much less than 0.05, the null hypothesis of linearity is rejected in favour of the alternative that the relationship is quadratic or cubic.

Interpretation of Coefficients in Nonlinear Regression Models

The coefficients in polynomial regression do not have a simple interpretation. Think of a quadratic model. It is not helpful to think of the coefficient on X as the expected change in Y associated with a change in X holding the other regressors constant because one other is X^2 which changes as X is varied. This is also the case for other deviations from linearity, for example in models where regressors and/or the dependent variable are log-transformed. The best way to approach this is to calculate the estimated effect on Y associated with a change in X for one or more values of X. This idea is summarized in Key Concept 8.1.

Key Concept 8.1

The Expected Effect on Y of a Change in X_1 in a Nonlinear Regression Model

Consider the nonlinear population regression model

$$Y_i = f(X_{1i}, X_{2i}, \dots, X_{ki}) + u_i \ , \ i = 1, \dots, n,$$

where $f(X_{1i}, X_{2i}, \dots, X_{ki})$ is the population regression function and u_i is the error term.

The expected change in Y, ΔY, associated with the change in X_1, ΔX_1, holding $X_2, \cdots, X_k$ constant. That is, the expected change in Y is the difference:

$$\Delta Y = f(X_1 + \Delta X_1, X_2, \cdots, X_k) - f(X_1, X_2, \cdots, X_k).$$

The estimator of this unknown population difference is the difference between the predicted values for these two cases. Let $\hat{f}(X_1, X_2, \cdots, X_k)$ be the predicted value of of Y based on the estimator $\hat{f}$ of the population regression function. Then the predicted change in Y is

$$\Delta \hat{Y} = \hat{f}(X_1 + \Delta X_1, X_2, \cdots, X_k) - \hat{f}(X_1, X_2, \cdots, X_k).$$

For example, we may ask the following: what is the predicted change in test scores associated with a one unit change (i.e. \$1000), based on the estimated quadratic regression function

$$\widehat{TestScore} = 607.3 + 3.85 \times Income - 0.0423 \times Income^2 \ ?$$

Because the regression function is quadratic, this effect depends on the initial district income. We therefore consider two cases: an increase in district income form 10 to 11 (i.e. from \$10000 per capita to \$11000) and an increase in district income from 40 to 41 (that is from \$40000 to \$41000).

In order to obtain the $\Delta \hat{Y}$ associated with a change in income form 10 to 11, we use the following formula:

$$\Delta \hat{Y} = \left(\hat{\beta}_0 + \hat{\beta}_1 \times 11 + \hat{\beta}_2 \times 11^2\right) - \left(\hat{\beta}_0 + \hat{\beta}_1 \times 10 + \hat{\beta}_2 \times 10^2\right)$$

To compute $\hat{Y}$ using R we may use `predict()`.

```
# compute and assign the quadratic model
quadriatic_model <- lm(score ~ income + I(income^2), data = CASchools)

# set up data to predict
new_data <- data.frame(income = c(10, 11))

# do the prediction
Y_hat <- predict(quadriatic_model, newdata = new_data)

# compute the difference
diff(Y_hat)
```

```
##        2
## 2.962517
```

Analogously we can compute the effect of a change in *income* from 40 to 11:

```
# set up data to predict
new_data <- data.frame(income = c(40, 41))

# do the prediction
Y_hat <- predict(quadriatic_model, newdata = new_data)

# compute the difference
diff(Y_hat)
```

```
##         2
## 0.4240097
```

So for the quadratic model, the expected change in $TestScore$ induced by an increase in *income* from 10 to 11 is about 2.96 points but an increase in *income* from 40 to 41 increases the predicted score by only 0.42. Hence the slope of the estimated quadratic regression function is steeper at low levels of income than at the higher levels.

Logarithms

Another way to specify a nonlinear regression function is to use the natural logarithm of Y and/or X. Logarithms convert changes in variables into percentage changes which is convenient as many relationships are naturally expressed in terms of percentages.

There are three different cases in which logarithms might be used.

1. X could be transformed by taking its logarithm but Y is not.
2. We could transform Y to its logarithm but leave X at level.
3. A third case is that both Y and X are transformed to their logarithms. The interpretation of the regression coefficients is different in each case.

Case I: X is in logarithm, Y is not.

The regression model then is

$$Y_i = \beta_0 + \beta_1 \times \ln(X_i) + u_i,\ i = 1, ..., n.$$

Similar as for polynomial regression we do not have to create a new variable by computing $\ln(X)$. We can simply adjust the `formula` argument of `lm()` to tell R that the log-transformation of a variable should be used.

```
# estimate a level-log model
LinearLog_model <- lm(score ~ log(income), data = CASchools)

# compute robust summary
coeftest(LinearLog_model,
         vcov = vcovHC(LinearLog_model, type = "HC1")
         )
```

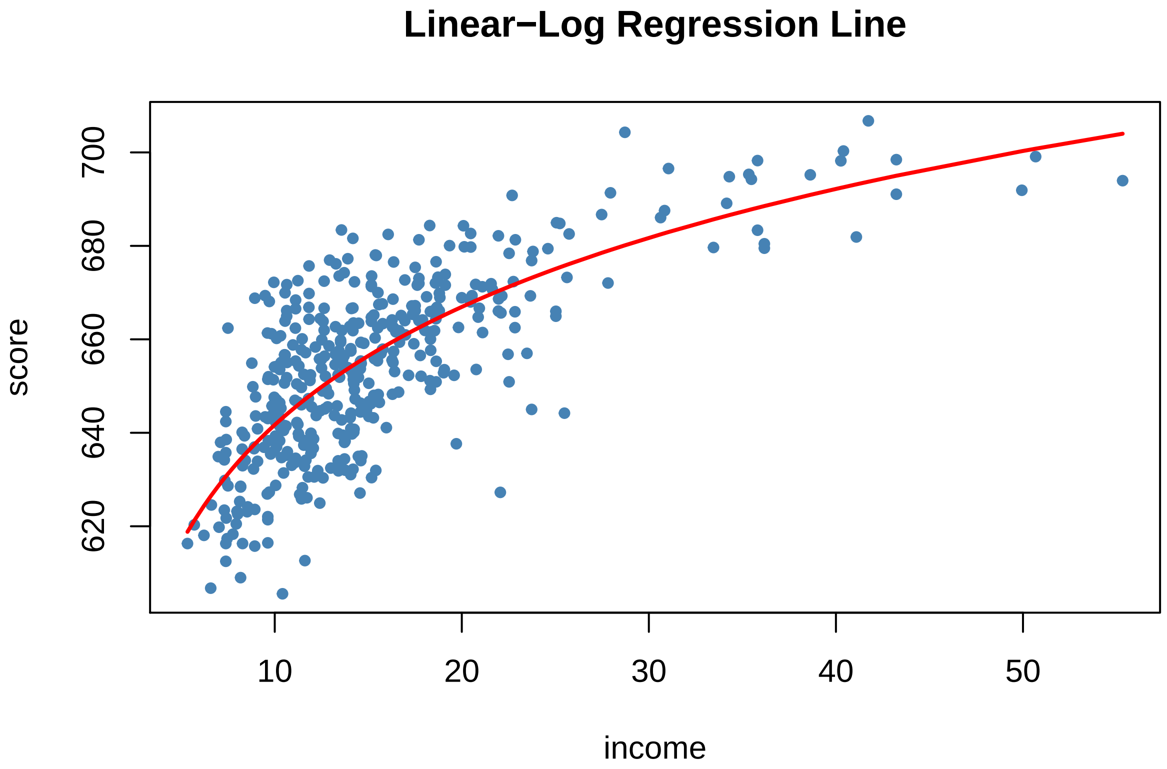
```
##
## t test of coefficients:
##
##             Estimate Std. Error t value  Pr(>|t|)
## (Intercept) 557.8323     3.8399 145.271 < 2.2e-16 ***
## log(income)  36.4197     1.3969  26.071 < 2.2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

According to the output the estimated regression function is:

$$\widehat{TestScore} = 557.8 + 36.42 \times \ln(Income).$$

Let us draw a plot of this function.

```
# draw scatterplot
plot(score ~ income,
     col = "steelblue",
     pch = 20,
     data = CASchools,
     main = "Linear-Log Regression Line")

# add Linear-Log regression line
order_id  <- order(CASchools$income)

lines(CASchools$income[order_id],
      fitted(LinearLog_model)[order_id],
      col = "red",
      lwd = 2)
```



We can interpret $\hat{\beta}_1$ as follows: a 1% increase in income is associated with an increase in test scores of $0.01 \times 36.42 = 0.36$ points. In order to get the estimated effect of a one unit change in income (that is a change in the original units,thousands of dollars, not in logarithms) on test scores, the method presented in Key Concept 8.1 can be used.

```
# set up new data
new_data <- data.frame(income = c(10, 11, 40, 41))

# predict outcomes
Y_hat <- predict(LinearLog_model, newdata = new_data)

# compute expected difference
changes <- matrix(Y_hat, nrow = 2, byrow = TRUE)
changes[ ,2] - changes[ ,1]
```

```
## [1] 3.471166 0.899297
```

The estimated model states that for an income increase from $\$10,000$ to $\$11,000$, test scores increase by an expected amount of 3.47 points. When income increases from $\$40,000$ to $\$41,000$, the expected increase in test scores is only about 0.90 points.

Case II: Y is in logarithm, X is not

If You want to learn about the absolute impact of an explanatory variable on Your dependent variable, it is not recommended to log-transform the latter. There are, however, cases where we want to learn about $\ln(Y)$ instead of Y.

The corresponding regression then model is

$$\ln(Y_i) = \beta_0 + \beta_1 \times X_i + u_i \quad , \quad i = 1, ..., n.$$

```
# estimate a log-linear model
LogLinear_model <- lm(log(score) ~ income, data = CASchools)

# compute a robust summary
coeftest(LogLinear_model,
         vcov = vcovHC(LogLinear_model, type = "HC1")
         )
```

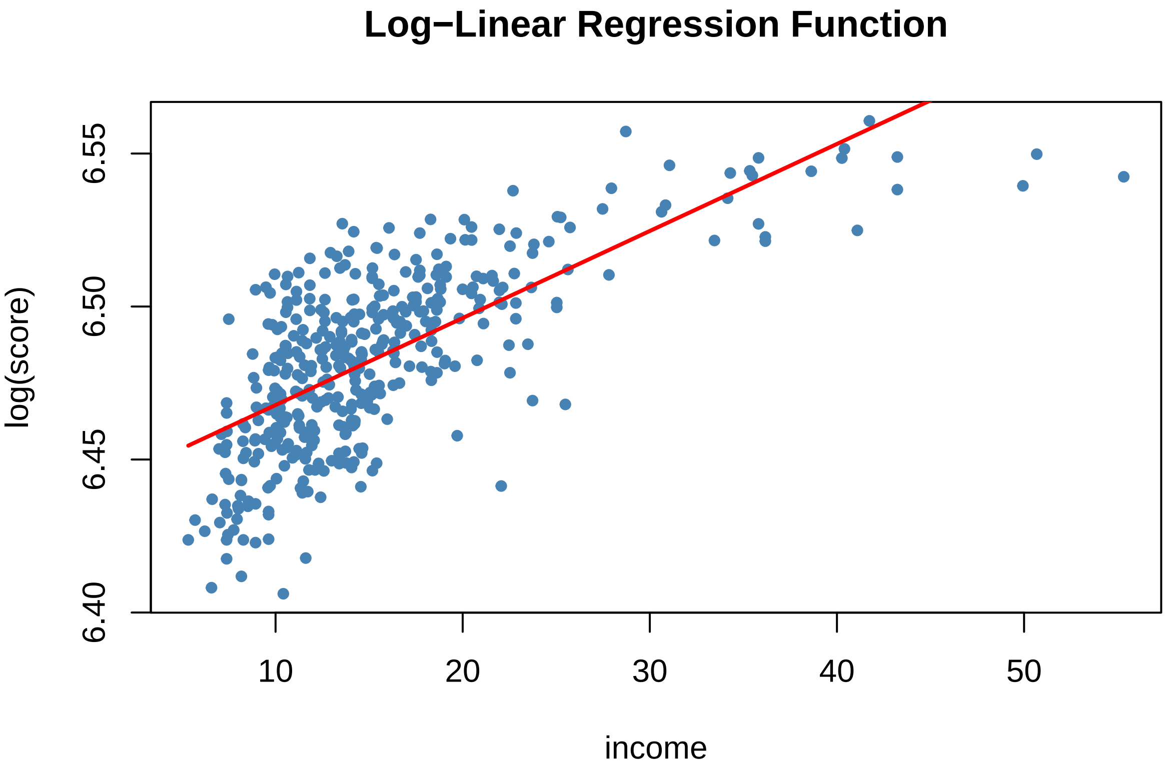
```
##
## t test of coefficients:
##
##               Estimate Std. Error  t value  Pr(>|t|)
## (Intercept) 6.43936234 0.00289382 2225.210 < 2.2e-16 ***
## income      0.00284407 0.00017509   16.244 < 2.2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

The estimated regression function is

$$\ln(\widehat{TestScore}) = 6.439 + 0.00284 \times income.$$

Since we are interested in $\ln(Y)$ rather than Y, we do not retransform the dependent variable.

```
# scatterplot
plot(log(score) ~ income,
     col="steelblue",
     pch=20,
     data = CASchools,
     main = "Log-Linear Regression Function"
     )

# add the Log-Linear regression line
order_id  <- order(CASchools$income)

lines(CASchools$income[order_id],
      fitted(LogLinear_model)[order_id],
      col = "red",
      lwd = 2)
```



Note that the Y-Axis is now log-transformed.

In a log-linear model, a one-unit change in X is associated with an estimated $100 \times \hat{\beta}_1\%$ change in Y. This time we left the X values unchanged.

```
# do predictions
Y_hat <- predict(LogLinear_model, newdata = new_data)

# calculate changes
changes <- matrix(Y_hat, nrow = 2, byrow = TRUE)
changes[ ,2] - changes[ ,1]
```

```
## [1] 0.00284407 0.00284407
```

Case III: X and Y are in logarithms

The log-log regression model is

$$\ln(Y_i) = \beta_0 + \beta_1 \times \ln(X_i) + u_i \quad , \quad i = 1, ..., n.$$

```
# Estimate the log-log model
LogLog_model <- lm(log(score) ~ log(income), data = CASchools)

# print robust summary to the console
coeftest(LogLog_model,
         vcov = vcovHC(LogLog_model, type = "HC1")
         )
```

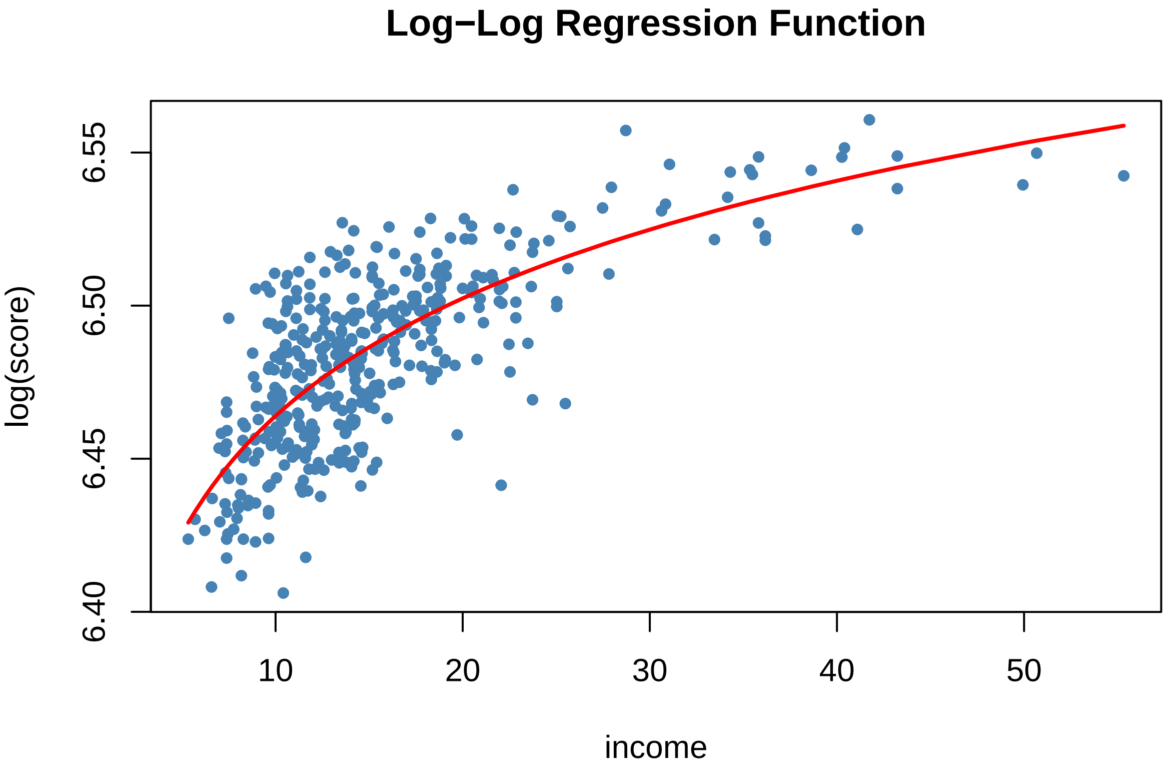
```
##
## t test of coefficients:
```

```
##
##              Estimate Std. Error  t value  Pr(>|t|)
## (Intercept) 6.3363494  0.0059246 1069.501 < 2.2e-16 ***
## log(income) 0.0554190  0.0021446   25.841 < 2.2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

The estimated regression function hence is

$$\ln(\widehat{TestScore}) = 6.336 + 0.0554 \times income.$$

```
# scatterplot
plot(log(score) ~ income,
     data = CASchools,
     col = "steelblue",
     pch = 20,
     main = "Log-Log Regression Function")

# plot the estimate log-log regression line
lines(sort(CASchools$income),
      fitted(LogLog_model)[order(CASchools$income)],
      col = "red",
      lwd = 2)
```



In a log-log model, a 1% change in X is associated with an estimated $\hat{\beta}_1$% change in Y.

```
# predict Y
Y_hat <- predict(LogLog_model, newdata = new_data)

# compute changes
changes <- matrix(Y_hat, nrow = 2, byrow = TRUE)
```

```r
changes[ ,2] - changes[ ,1]
```

```
## [1] 0.005281992 0.001368439
```

Key Concept 8.2 summarizes the three logarithmic regression models.

Key Concept 8.2

Logarithms in Regression: Three Cases

Logarithms can be used to transform the dependent variable Y or the independent variable X, or both (the variable being transformed must be positive). The following table summarizes these three cases and the interpretation of the regression coefficient β_1. In each case, β_1, can be estimated by applying OLS after taking the logarithm(s) of the dependent and/or the independent variable.

Case

Model Specification

Interpretation of β_1

(I)

$Y_i = \beta_0 + \beta_1 \ln X_i + u_i$

A 1% change in X is associated with a change in Y of $0.01 \times \beta_1$.

(II)

$\ln(Y_i) = \beta_0 + \beta_1 X_i + u_i$

A change in X by one unit ($\Delta X = 1$) is associated with a $100 \times \beta_1 \%$ change in Y.

(III)

$\ln(Y_i) = \beta_0 + \beta_1 \ln(X_i) + u_i$

A 1% change in X is associated with a $100 \times \beta_1 \%$ change in Y, so β_1 is the elasticity of Y with respect to X.

Of course we can also estimate a polylog model like

$$TestScore_i = \beta_0 + \beta_1 \times \ln(income_i) + \beta_2 \times \ln(income_i)^2 + \beta_3 \times \ln(income_i)^3 + u_i$$

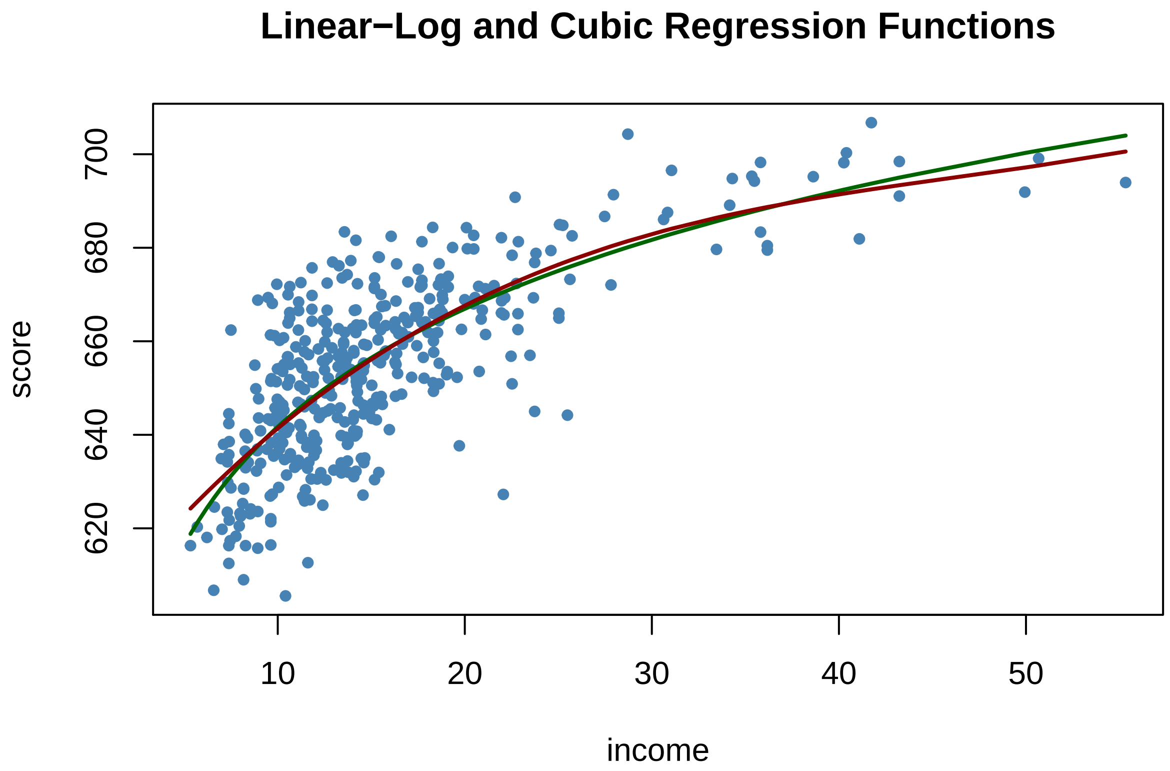
which models the dependent variable $TestScore$ by a third-degree polynomial of the log-transformed regressor $income$

```r
# estimate the polylog model
polyLog_model <- lm(score ~ log(income) + I(log(income)^2) + I(log(income)^3),
                    data = CASchools)

# print robust summary to the console
coeftest(polyLog_model,
         vcov = vcovHC(polyLog_model, type = "HC1"))
```

```
##
## t test of coefficients:
##
##                   Estimate Std. Error t value  Pr(>|t|)
## (Intercept)       486.1341    79.3825  6.1239 2.115e-09 ***
## log(income)       113.3820    87.8837  1.2901    0.1977
## I(log(income)^2) -26.9111    31.7457 -0.8477    0.3971
## I(log(income)^3)   3.0632     3.7369  0.8197    0.4128
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Which of the models presented here is the most suitable? Comparing by $\overline{R^2}$ we find that, leaving out the log-linear model, all models have a similar fit. In the class of polynomial models, the cubic specification has the highest $\overline{R^2}$ whereas the linear-log specification is the best of the log-models (check this!). Let us first compare both models graphically by plotting the corresponding estimated regression functions

```
# scatter plot
plot(score ~ income,
     data = CASchools,
     col = "steelblue",
     pch = 20,
     main = "Linear-Log and Cubic Regression Functions")

# add Linear-Log regression line
order_id  <- order(CASchools$income)

lines(CASchools$income[order_id],
      fitted(LinearLog_model)[order_id],
      col = "darkgreen",
      lwd = 2)

# add cubic regression line
lines(x = CASchools$income[order_id],
      y = fitted(cubic_model)[order_id],
      col="darkred",
      lwd=2)
```



We see that both regression lines are nearly identical. Here the linear-log model is preferable since it has a slightly higher $\overline{R^2}$ and is more parsimonious in terms of regressors: it does not need higher-degree polynomials.

8.3 Interactions Between Independent Variables

There are research questions where it is interesting to know how the effect on Y of a change in one independent variables dependends on the value of another independent variable. For example, we could ask if districts with many english learners benefit differentially from a decrease in class sizes than those with few english learning students. To answer this, we need to include an interaction term into a multiple regression model. We will consider three cases:

1. Interactions between two binary variables
2. Interactions between a binary and a continuous variable
3. Interactions between two continuous variables

The following subsections discuss those cases briefly and demonstrate how to perform such regressions using R.

Interactions Between Two Binary Variables

Take two binary variables D_1 and D_2 and the population regression

$$Y_i = \beta_0 + \beta_1 \times D_{1i} + \beta_2 \times D_{2i} + u_i.$$

Now assume

$$
\begin{align}
Y_i &= \ln(Earnings_i), \tag{8.1}\\
&\tag{8.2}\\
D_{1i} &= \begin{cases} 1 & \text{if } i^{th} \text{ person has a college degree} \\ 0 & \text{else,} \end{cases} \tag{8.3}\\
&\tag{8.4}\\
D_{2i} &= \begin{cases} 1 & \text{if } i^{th} \text{ person is female} \\ 0 & \text{if } i^{th} \text{ person is male.} \end{cases} \tag{8.5}\\
&\tag{8.6}
\end{align}
$$

By now You should know that β_1 measures the average difference in $\ln(Earnings)$ between individuals with and without a college degree and β_2 is the gender differential in $\ln(Earnings)$, ceteris paribus. This model does not allow us to determine if there is a geneder specific effect of heaving a college degree and, if so, how strong this is. Luckily it is easy to come up with a model specification that allows to investigate this:

$$Y_i = \beta_0 + \beta_1 \times D_{1i} + \beta_2 \times D_{2i} + \beta_3 \times (D_{1i} \times D_{2i}) + u_i$$

$(D_{1i} \times D_{2i})$ is called an interaction term and β_3 measures the difference in the effect of having a college degree for women versus men.

Key Concept 8.3

A Method for Interpreting Coefficients in Regression with Binary Variables

Compute expected values of Y for each possible set described by the set of binary variables. Compare the expected values. The coefficients can be expressed either as expected values or as the difference between at least two expected values.

Following Key Concepts 8.1 we have

$$\begin{aligned}
E(Y_i|D_{1i}=0,D_{2i}=d_2) &= \beta_0+\beta_1\times 0+\beta_2\times d_2+\beta_3\times(0\times d_2)\\
&= \beta_0+\beta_2\times d_2.
\end{aligned}$$

Changing D_{1i} from 0 to 1 we obtain

$$\begin{aligned}
E(Y_i|D_{1i}=1,D_{2i}=d_2) &= \beta_0+\beta_1\times 1+\beta_2\times d_2+\beta_3\times(1\times d_2)\\
&= \beta_0+\beta_1+\beta_2\times d_2+\beta_3 d_2
\end{aligned}$$

and hence the overall effect is

$$E(Y_i|D_{1i}=1,D_{2i}=d_2)-E(Y_i|D_{1i}=0,D_{2i}=d_2)=\beta_1+\beta_3 d_2$$

so the effect is a difference of expected values.

8.3.0.0.1 Application to the student-teacher ratio and the percentage of English learners

Now let

$$HiSTR=\begin{cases}1, & \text{if } STR\geq 20\\ 0, & \text{else,}\end{cases}$$

$$HiEL=\begin{cases}1, & \text{if } PctEL\geq 10\%\\ 0, & \text{else.}\end{cases}$$

We may use R construct the variables above.

```r
# Add HiSTR to CASchools
CASchools$HiSTR <- as.numeric(CASchools$size >= 20)

# Add HiEL to CASchools
CASchools$HiEL <- as.numeric(CASchools$english >= 10)
```

We proceed by estimating the model

$$TestScore_i=\beta_0+\beta_1\times HiSTR+\beta_2\times HiEL+\beta_3\times(HiSTR\times HiEL)+u_i$$

using `lm()`. There are several ways to add an interaction term to the model `formula` argument of `lm()` but the most intuitive is to use the product of both variables `HiEL * HiSTR`.

```r
# estimate the model with binary interaction term
bi_model <- lm(score ~ HiSTR + HiEL + HiSTR * HiEL, data = CASchools)

# print summary
summary(bi_model)
```

```
## 
## Call:
## lm(formula = score ~ HiSTR + HiEL + HiSTR * HiEL, data = CASchools)
## 
## Residuals:
##     Min      1Q  Median      3Q     Max 
## -39.078 -10.679  -1.282   9.665  45.522 
## 
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)    
## (Intercept)  664.143      1.316 504.852  < 2e-16 ***
## HiSTR         -1.908      2.235  -0.854    0.394    
## HiEL         -18.316      2.144  -8.544 2.49e-16 ***
## HiSTR:HiEL    -3.260      3.223  -1.012    0.312    
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 
## Residual standard error: 16.06 on 416 degrees of freedom
## Multiple R-squared:  0.2948, Adjusted R-squared:  0.2897 
## F-statistic: 57.97 on 3 and 416 DF,  p-value: < 2.2e-16
```

The estimated regression model is

$$\widehat{TestScore} = 664.1 - 1.9 \times HiSTR - 18.3 \times HiEL - 3.3 \times (HiSTR \times HiEL)$$

and it predicts that the effect of moving from a school district with a low student-teacher ratio to a district with a high student-teacher ratio, depending on high or low percentage of english learners is $-1.9 - 3.3 \times HiEL$. So for districts with a low share of english learners ($HiEL = 0$), the estimated effect is a decrease of 1.9 points in test scores while for districts with a big fraction of english learner ($HiEL = 1$), the predicted decrease in test scores amounts to $1.9 + 3.3 = 5.2$ points.

We can also use the model to estimate the mean test score for each combination of binary variables.

```
# estimate means for all combinations of HiSTR and HiEL
predict(bi_model, newdata = data.frame("HiSTR"=0, "HiEL"=0))
```

```
##        1 
## 664.1433
```

```
predict(bi_model, newdata = data.frame("HiSTR"=0, "HiEL"=1))
```

```
##        1 
## 645.8278
```

```
predict(bi_model, newdata = data.frame("HiSTR"=1, "HiEL"=0))
```

```
##        1 
## 662.2354
```

```
predict(bi_model, newdata = data.frame("HiSTR"=1, "HiEL"=1))
```

```
##        1 
## 640.6598
```

Interactions Between a Continuous and a Binary Variable

Now consider a continuous variable X_i, the years of working experience of person i instead of the gender. We than have

$$Y_i = \ln(Earnings_i)$$

$$X_i = \text{working experience of person } i$$

$$D_i = \begin{cases} 1, & \text{if } i^{th} \text{ person has a college degree} \\ 0, & \text{else.} \end{cases}$$

The base model thus is

$$Y_i = \beta_0 + \beta_1 \times X_i + \beta_2 \times D_i + u_i,$$

a simple multiple regression model that allows us to estimate the average benefit of having a college degree holding working experience constant and the average effect on earnings of a change in working experience holding college degree constant.

By adding the interaction term $X_i \times D_i$ we allow the effect of an additional year of work experience to differ for person with and without college degree.

$$Y_i = \beta_0 + \beta_1 \times X_i + \beta_2 \times D_i + \beta_3 \times (X_i \times D_i) + u_i$$

Here, β_3 measures the difference in the effect of an additional year of work experience for college graduates versus nongraduates. A further possible specifications is

$$Y_i = \beta_0 + \beta_1 X_i + \beta_2 (X_i \times D_i) + u_i.$$

This model states that the expected impact of an additional year of work experience on earnings is the same for individuals without college degree but differs for college graduates. All three population regression functions can be visualized by straight lines. Key Concept 8.4 summarizes the differences.

Key Concept 8.4

Interactions Between Binary and Continuous Variables

An interaction term like $X_i \times D_i$ (where X is continuous and D is binary) allows for the slope to depend on the binary variable D. There are three possibilities:

1. Different intercept and same slope:

$$Y_i = \beta_0 + \beta_1 X_i + \beta_2 D_i + u_i$$

2. Different intercept and different slope:

$$Y_i = \beta_0 + \beta_1 X_i + \beta_2 D_i + \beta_3 \times (X_i \times D_i) + u_i$$

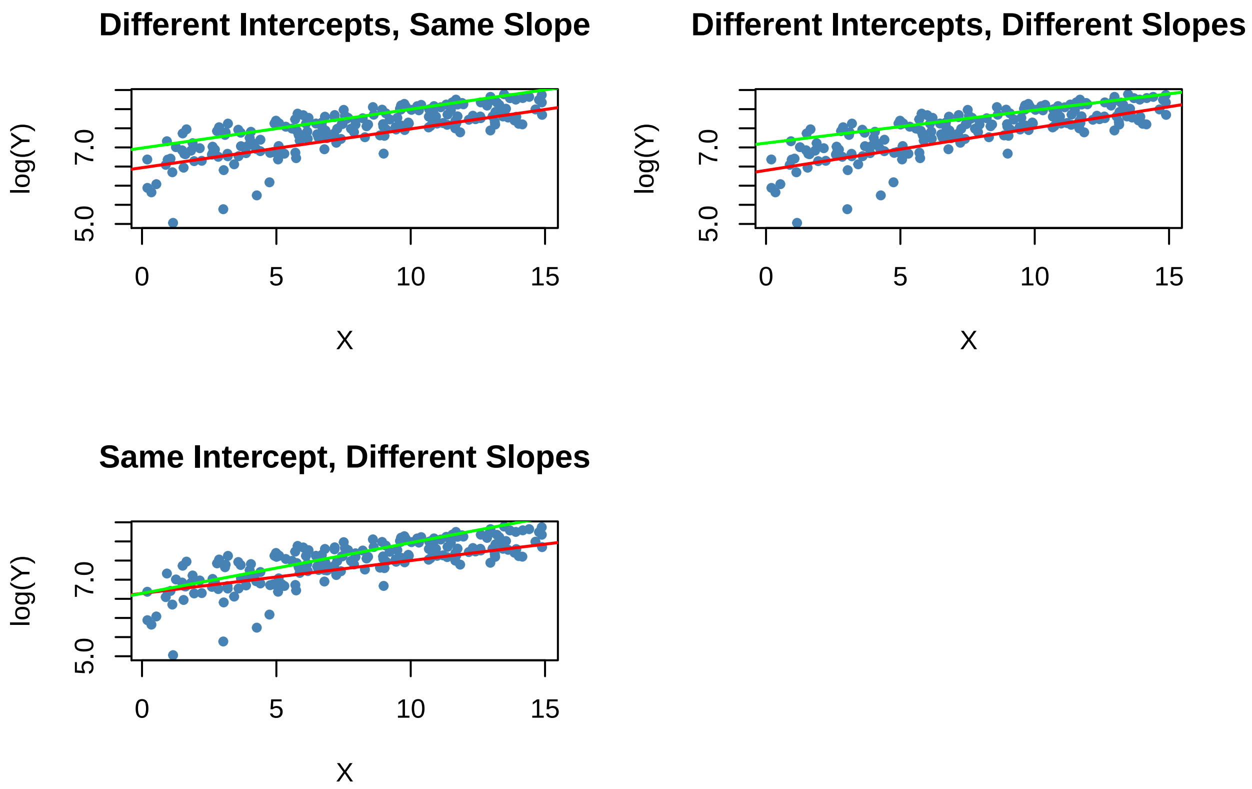
3. Same intercept and different slope:

$$Y_i = \beta_0 + \beta_1 X_i + \beta_2 (X_i \times D_i) + u_i$$

The following code chunk shows how replicate the results shown in Figure 8.8 using fictional data.

```
# generate fictional data
set.seed(1)

X <- runif(200,0, 15)
D <- sample(0:1, 200, replace = T)
Y <- 450 +  150 * X + 500 * D + 50 * (X * D) + rnorm(200, sd=300)

# divide plotting area
m <- rbind(c(1, 2), c(3, 0))
layout(m)

# Estimate models and plot regression lines

# 1.(base model)
plot(X,log(Y),
     pch = 20,
     col = "steelblue",
     main = "Different Intercepts, Same Slope"
)
mod1_coef <- lm(log(Y) ~ X + D)$coefficients

abline(coef = c(mod1_coef[1], mod1_coef[2]),
       col = "red",
       lwd = 1.5
       )

abline(coef = c(mod1_coef[1] + mod1_coef[3], mod1_coef[2]),
       col = "green",
       lwd = 1.5
       )


# 2. (base model + interaction term)
plot(X,log(Y),
     pch = 20,
     col = "steelblue",
     main = "Different Intercepts, Different Slopes"
)

mod2_coef <- lm(log(Y) ~ X + D + X:D)$coefficients

abline(coef = c(mod2_coef[1], mod2_coef[2]),
       col = "red",
       lwd = 1.5
)

abline(coef = c(mod2_coef[1] + mod2_coef[3], mod2_coef[2] + mod2_coef[4]),
       col = "green",
       lwd = 1.5
)

# 3. (omission of D as regressor + interaction term)
```

```
plot(X,log(Y),
     pch = 20,
     col = "steelblue",
     main = "Same Intercept, Different Slopes"
)

mod3_coef <- lm(log(Y) ~ X + X:D)$coefficients

abline(coef = c(mod3_coef[1], mod3_coef[2]),
       col = "red",
       lwd = 1.5
)

abline(coef = c(mod3_coef[1], mod3_coef[2] + mod3_coef[3]),
       col = "green",
       lwd = 1.5
)
```



8.3.0.0.2 Application to the student-teacher ratio and the percentage of English learners

Using a model specification like 2. in Key Concept 8.3 we may answer the question whether the effect on test scores of decreasing the student-teacher ratio depends on the whether there are many or few English learners. We estimate the regression model

$$\widehat{TestScore}_i = \beta_0 + \beta_1 \times size_i + \beta_2 \times HiEL_i + \beta_2(size_i \times HiEL_i) + u_i.$$

```
# estimate the model
bci_model <- lm(score ~ size + HiEL + size * HiEL, data = CASchools)
```

```
# print summary to console
summary(bci_model)
```

```
##
## Call:
## lm(formula = score ~ size + HiEL + size * HiEL, data = CASchools)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -37.356 -10.790  -0.841   9.911  46.457
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept) 682.2458    10.5109  64.908   <2e-16 ***
## size         -0.9685     0.5398  -1.794   0.0735 .
## HiEL          5.6391    16.7177   0.337   0.7360
## size:HiEL    -1.2766     0.8441  -1.512   0.1312
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 15.88 on 416 degrees of freedom
## Multiple R-squared:  0.3103, Adjusted R-squared:  0.3054
## F-statistic:  62.4 on 3 and 416 DF,  p-value: < 2.2e-16
```

The estimated regression model is

$$\widehat{TestScore} = 682.2 - 0.97 \times size + 5.6 \times HiEL - 1.28 \times (size \times HiEL).$$

We find that the estimated regression line for districts with a low fraction of English learners ($HiEL_i = 0$) is

$$\widehat{TestScore} = 682.2 - 0.97 \times size_i.$$

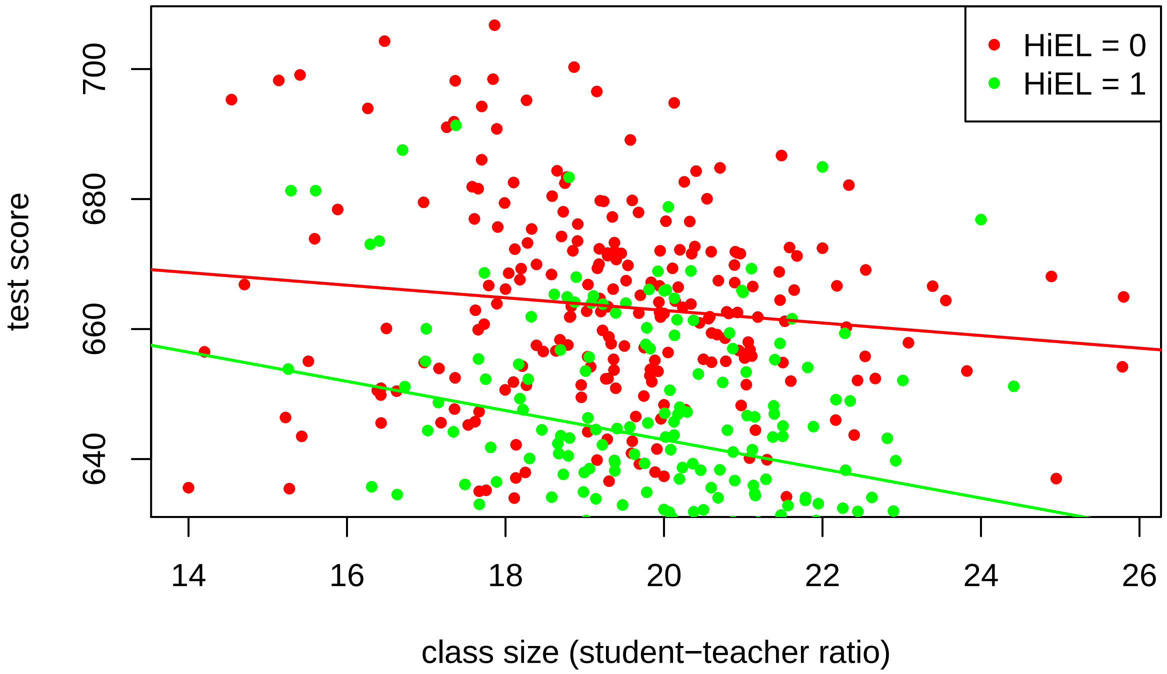
For districts with a high fraction of English learners we have

$$\begin{aligned}\widehat{TestScore} &= 682.2 + 5.6 - 0.97 \times size_i - 1.28 \times size_i && (8.7)\\ &= 687.8 - 2.25 \times size_i && (8.8)\end{aligned}$$

so the predicted increase in test scores following a reduction of the student-teacher ratio by 1 is about 0.97 points in districts where the fraction of English learners is low but 2.25 in districts with a high share of English learners. The difference between these effects is 1.28, the magnitude of the coefficient on the interaction term $size \times HiEL$.

The next code chunk draws both lines belonging to the model. In order to make observations with $HiEL = 0$ distinguishable from those with $HiEL = 0$, we assign different colors.

```
# identify observations PctEL >= 10
id <- CASchools$english >= 10

# plot observations with HiEL = 0 as red dots
plot(CASchools$size[!id], CASchools$score[!id],
     pch = 20,
     col = "red",
     main = "",
     xlab = "class size (student-teacher ratio)",
     ylab = "test score"
     )

# plot observations with HiEL = 1 as green dots
points(CASchools$size[id], CASchools$score[id],
     pch = 20,
     col = "green"
     )

# read out estimated coefficients of bci_model
coefs <- bci_model$coefficients

# Draw the estimated regression line for HiEL = 0
abline(coef = c(coefs[1], coefs[2]),
       col = "red",
       lwd = 1.5
       )

# Draw the estimated regression line for HiEL = 1
abline(coef = c(coefs[1]+coefs[3], coefs[2]+coefs[4]),
       col = "green",
       lwd = 1.5
       )

# Add a legend to the plot
legend("topright",
       pch=c(20,20),
       col = c("red","green"),
       legend = c("HiEL = 0", "HiEL = 1")
       )
```



Interactions Between Two Continuous Variables

If we have a regression model with Y the log earnings and two continuous regressors X_1, the years of work experience, and X_2, the years of schooling, a simple multiple regression model cannot be used to estimate the effect on wages of an additional year of work experience depending on a given level of schooling. This effect can be assessed by including the interaction term $(X_{1i} \times X_{2i})$ in the model:

$$Y_i = \beta_0 + \beta_1 X_{1i} + \beta_2 X_{2i} + \beta_3 \times (X_{1i} \times X_{2i}) + u_i$$

Following Key Concept 8.1 we find that the effect on Y of a change on X_1 given X_2 is

$$\frac{\Delta Y}{\Delta X_1} = \beta_1 + \beta_3 X_2.$$

In the earnings example, a positive β_3 implies that the effect on log earnings of an additional year of work experience grows linearly with years of schooling.

Vice versa we have

$$\frac{\Delta Y}{\Delta X_2} = \beta_2 + \beta_3 X_1.$$

as the effect on log earnings of an additional year of schooling holding work experience constant.

Altogether we find that β_3 measures the effect of a unit increase in X_1 and X_2 beyond the effects of increasing X_1 alone and X_2 alone by one unit. The overall change in Y is thus

$$Y_i = (\beta_1 + \beta_3 X_2)\Delta X_1 + (\beta_2 + \beta_3 X_1)\Delta X_2 + \beta_3 \Delta X_1 \Delta X_2. \tag{8.9}$$

Key Concept 8.5 summarizes interactions between two regressors in multiple regression.

Key Concept 8.5

Interactions in Multiple Regression

The interaction term between the two regressors X_1 and X_2 is given by their product $X_1 \times X_2$. Adding this interaction term as a regressor to the model

$$Y_i = \beta_0 + \beta_1 X_1 + \beta_2 X_2 + u_i$$

allows the effect of change on X_2 to depend on the value of X_1 and vice versa. Thus the coefficient β_3 in the model

$$Y_i = \beta_0 + \beta_1 X_1 + \beta_2 X_2 + \beta_3 (X_1 \times X_2) + u_i$$

measures the effect of a one-unit increase in both X_1 and X_2 above and beyond the sum of both individual effects. This holds for continuous and binary regressors.

8.3.0.0.3 Application to the student-teacher ratio and the percentage of English learners

We will now examine the interaction between student-teacher ratio and the percentage of english learners which both are continuous variables.

```r
# estimate regression model including the interaction between 'PctEL' and 'size'
cci_model <- lm(score ~ size + english + english:size, data = CASchools)

# print a summary to the console
summary(cci_model)
```

```
##
## Call:
## lm(formula = score ~ size + english + english:size, data = CASchools)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -48.836 -10.226  -0.343   9.796  43.447
##
## Coefficients:
##                Estimate Std. Error t value Pr(>|t|)
## (Intercept)  686.338527   9.402603  72.995   <2e-16 ***
## size          -1.117018   0.482537  -2.315   0.0211 *
## english       -0.672912   0.437985  -1.536   0.1252
## size:english   0.001162   0.021905   0.053   0.9577
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 14.48 on 416 degrees of freedom
## Multiple R-squared:  0.4264, Adjusted R-squared:  0.4223
## F-statistic: 103.1 on 3 and 416 DF,  p-value: < 2.2e-16
```

The estimated model equation is

$$\widehat{TestScore} = 686.3 - 1.12 \times STR - 0.67 \times PctEL + 0.0012(STR \times PctEL).$$

For the interpretation, let us consider some quartiles of $PctEL$.

```r
summary(CASchools$english)
```

```
##    Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
##   0.000   1.941   8.778  15.768  22.970  85.540
```

According to (8.9), if $PctEL$ is at its median 8.78 the slope of the regression function relating test scores and the student teacher ratio is predicted to be $-1.12 + 0.0012 \times 8.78 = -1.11$. This means that increasing STR by one unit deteriorates test scores by estimated 1.11 points. For the 75% quantile the estimated change on $TestScore$ of a one-unit increase in STR is estimated by $-1.12 + 0.0012 \times 23.0 = -1.09$ so the slope is somewhat lower. The interpretation is that for a school district with 23% english learners, a reduction of the studtent-teacher ratio by one unit is expected to increase the test scores by only 1.09 points.

Note, however, that the output produced by summary indicates that the difference of the effect for the median and the 75% quantile is not statistically significant. The p-value for the test $H_0 : \beta_3 = 0$ cannot be rejected at the 5% level of significance. Using robust standard errors, one can show that β_3 is not significantly different from zero even at the level of 10% (verify this using R!).

Example: The Demand for Economic Journals

In this section we replicate the empirical example *The Demand for Economic Journals* presented at pages 336 - 337 of the book. The central question is: how elastic is the demand by libraries for economic journals? The idea here is to analyze the relationship between the number of subscription to a journal at U.S. libraries and the journal's subscription price. The study uses the dataset `Journals` wich is provided with the `AER` package and contains observations for 180 economic journals for the year 2000. You can use the help function (`?Journals`) to get more information on the data after loading the package.

```r
# load package and the dataset
library(AER)
data("Journals")
```

We measure the price as "price per citation" and have to compute journal age and the number of character manually. For consistency with the book we also rename the variables.

```r
# define and rename variables
Journals$PricePerCitation <- Journals$price/Journals$citations
Journals$Age <- 2000 - Journals$foundingyear
Journals$Characters <- Journals$charpp * Journals$pages/10^6
Journals$Subscriptions <- Journals$subs
```

Note that the range of "price per citation" is quite large:

```r
# compute summary statistics for price per citation
summary(Journals$PricePerCitation)
```

```
##      Min.   1st Qu.    Median      Mean   3rd Qu.      Max.
##  0.005223  0.464495  1.320513  2.548455  3.440171 24.459459
```

The lowest price observed is a mere 0.5¢ per citation while the highest price is more than 20¢ per citation.

After loading and preparing the data, we estimate the four different model specifications. All models are log-log models. This is useful because it allows us to directly interpret the ceofficients as elasticities, see Key Concept 8.2. (I) is a simple linear model. To aleviate a possible omitted variable bias, (II) augments (I) by the covariates $\ln(Age)$ and $\ln(Characters)$. The largest model (III) attempts to capture nonlinearities in the relationship of $\ln(Subscriptions)$ and $\ln(PricePerCitation)$ using a cubic regression function of $\ln(PricePerCitation)$ and also adds the interaction term $(PricePerCitation \times Age)$ while specfication (IV) does not include the cubic term.

$$(I) \quad \ln(Subscriptions_i) = \beta_0 + \beta_1 \ln(PricePerCitation_i) + u_i$$

$$(II) \quad \ln(Subscriptions_i) = \beta_0 + \beta_1 \ln(PricePerCitation_i) + \beta_4 \ln(Age_i) + \beta_6 \ln(Characters_i) + u_i$$

$$\begin{aligned}(III) \quad \ln(Subscriptions_i) = {} & \beta_0 + \beta_1 \ln(PricePerCitation_i) + \beta_2 \ln(PricePerCitation_i)^2 \\ & + \beta_3 \ln(PricePerCitation_i)^3 + \beta_4 \ln(Age_i) + \beta_5 \left[\ln(Age_i) \times \ln(PricePerCitation_i)\right] \\ & + \beta_6 \ln(Characters_i) + u_i\end{aligned}$$

$$(IV) \quad \ln(Subscriptions_i) = \beta_0 + \beta_1 \ln(PricePerCitation_i) + \beta_4 \ln(Age_i) + \beta_5 + \beta_6 \ln(Characters_i) + u_i$$

```r
# Estimate models (I) - (IV)
Journals_mod1 <- lm(log(Subscriptions) ~ log(PricePerCitation), data = Journals)

Journals_mod2 <- lm(log(Subscriptions) ~ log(PricePerCitation) + log(Age) +
    log(Characters), data = Journals)

Journals_mod3 <- lm(log(Subscriptions) ~ log(PricePerCitation) + I(log(PricePerCitation)^2) +
    I(log(PricePerCitation)^3) + log(Age) + log(Age):log(PricePerCitation) +
    log(Characters), data = Journals)

Journals_mod4 <- lm(log(Subscriptions) ~ log(PricePerCitation) + log(Age) +
    log(Age):log(PricePerCitation) + log(Characters), data = Journals)
```

Using `summary()`, we obtain the following estimated model equations:

$$(I) \quad \ln(\widehat{Subscriptions}_i) = 4.77 - 0.53 \ln(PricePerCitation_i)$$

$$(II) \quad \ln(\widehat{Subscriptions}_i) = 3.21 - 0.41 \ln(PricePerCitation_i) + 0.42 \ln(Age_i) + 0.21 \ln(Characters_i)$$

$$\begin{aligned}(III) \quad \ln(\widehat{Subscriptions}_i) = {} & 3.41 - 0.96 \ln(PricePerCitation_i) + 0.02 \ln(PricePerCitation_i)^2 \\ & + 0.004 \ln(PricePerCitation_i)^3 + 0.37 \ln(Age_i) \\ & + 0.16 \left[\ln(Age_i) \times \ln(PricePerCitation_i)\right] \\ & + 0.23 \ln(Characters_i)\end{aligned}$$

$$\begin{aligned}(IV) \quad \ln(\widehat{Subscriptions}_i) = {} & 3.43 - 0.90 \ln(PricePerCitation_i) + 0.37 \ln(Age_i) \\ & + 0.14 \left[\ln(Age_i) \times \ln(PricePerCitation_i)\right] + 0.23 \ln(Characters_i)\end{aligned}$$

It is of interest whether the coefficients the nonlinear transformations of $\ln(PricePerCitation)$ in Model (III) are statistically significant. To answer this, we use a F-Test:

```r
# F-Test for significance of cubic terms
linearHypothesis(Journals_mod3,
                 c("I(log(PricePerCitation)^2)=0","I(log(PricePerCitation)^3)=0")
                 )
```

```
## Linear hypothesis test
```

```
##
## Hypothesis:
## I(log(PricePerCitation)^2) = 0
## I(log(PricePerCitation)^3) = 0
##
## Model 1: restricted model
## Model 2: log(Subscriptions) ~ log(PricePerCitation) + I(log(PricePerCitation)^2) +
##     I(log(PricePerCitation)^3) + log(Age) + log(Age):log(PricePerCitation) +
##     log(Characters)
##
##   Res.Df    RSS Df Sum of Sq      F Pr(>F)
## 1    175 82.738
## 2    173 82.500  2    0.2379 0.2494 0.7795
```

We cannot reject the null hypothesis $H_0 : \beta_3 = \beta_4 = 0$ in model (III).

We will now use the `stargazer()` function to generate a verbose tabular representation of all four estimated models.

```
# load the stargazer package
library(stargazer)

# generate a Latex table using stargazer
stargazer(Journals_mod1, Journals_mod2, Journals_mod3, Journals_mod4,
          column.labels = c("(I)", "(II)", "(III)", "(IV)")
          )
```

Dependent variable:

log(Subscriptions)

(I)

(II)

(III)

(IV)

log(PricePerCitation)

-0.533***

-0.408***

-0.961***

-0.899***

(0.036)

(0.042)

(0.189)

(0.162)

I(log(PricePerCitation)2)

0.017

(0.024)

I(log(PricePerCitation)3)

0.004

(0.007)

log(Age)

0.424***

0.373***

0.374***

(0.090)

(0.089)

(0.089)

log(Characters)

0.206*

0.235**

0.229**

(0.107)

(0.106)

(0.105)

log(PricePerCitation):log(Age)

0.156***

0.141***

(0.055)

(0.045)

Constant

4.766***

3.207***

3.408***

3.434***

(0.056)

(0.314)

(0.318)

(0.315)

Observations

180

180

180

180

R2

0.557

0.613

0.635

0.634

Adjusted R2

0.555

0.607

0.622

0.626

Residual Std. Error

0.750 (df = 178)

0.705 (df = 176)

0.691 (df = 173)

0.688 (df = 175)

F Statistic

224.037*** (df = 1; 178)

93.009*** (df = 3; 176)

50.149*** (df = 6; 173)

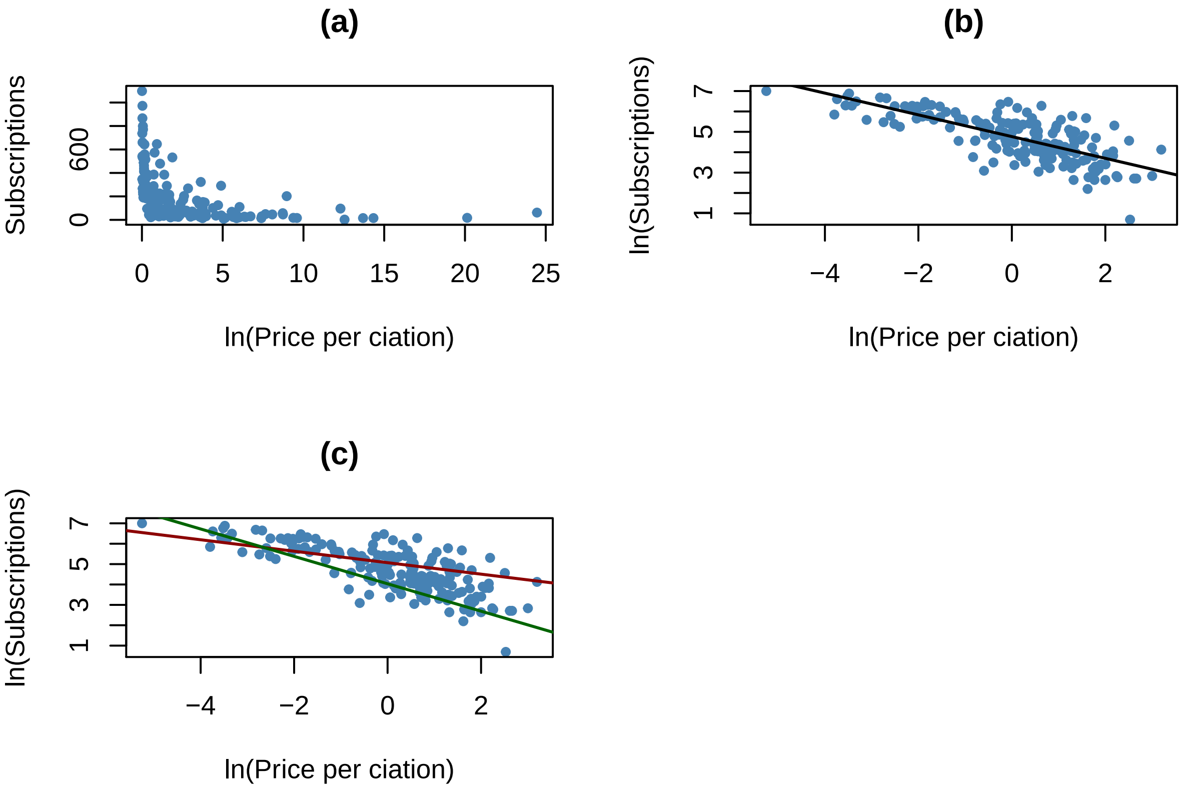
75.749*** (df = 4; 175)

Note:

p<0.1; ***p<0.05;*** p<0.01

The subsequent code chunk reproduces figure 8.9 of the book:

```r
# divide plotting area
m <- rbind(c(1, 2), c(3, 0))
layout(m)

# scatterplot
plot(Journals$PricePerCitation,
     Journals$Subscriptions,
     pch = 20,
     col = "steelblue",
     ylab = "Subscriptions",
     xlab = "ln(Price per ciation)",
     main = "(a)"
     )

# log-log scatterplot and estimated regression line (I)
plot(log(Journals$PricePerCitation),
     log(Journals$Subscriptions),
     pch = 20,
     col = "steelblue",
     ylab = "ln(Subscriptions)",
     xlab = "ln(Price per ciation)",
     main = "(b)"
     )

abline(Journals_mod1,
       lwd = 1.5
       )

# log-log scatterplot and regression lines (IV) for Age = 5 and Age = 80
plot(log(Journals$PricePerCitation),
     log(Journals$Subscriptions),
     pch = 20,
     col = "steelblue",
     ylab = "ln(Subscriptions)",
     xlab = "ln(Price per ciation)",
     main = "(c)"
     )

JM4C <-Journals_mod4$coefficients

# Age = 80
abline(coef = c(JM4C[1] + JM4C[3] * log(80),
                JM4C[2] + JM4C[5] * log(80)
                ),
       col = "darkred",
       lwd = 1.5
)

# Age = 5
abline(coef = c(JM4C[1] + JM4C[3] * log(5),
                JM4C[2] + JM4C[5] * log(5)
                ),
       col = "darkgreen",
       lwd = 1.5
)
```



As can be seen from plots (a) and (b), the relation between subscriptions and the citation price is inverse and nonlinear and log-transforming both variables makes it approximately linear. Plot (c) shows that the price elasticity of journal subscriptions depends on the journal's age: the red line shows the estimated relationship for $Age = 80$ while the green line represents the prediction from model (IV) for $Age = 5$.

Which conclusion can be made?

1. We conclude that the demand for journals is more elastic for young journals than for old journals.
2. For model (III) we cannot reject the null hypothesis that the coefficients on $\ln(PricePerCitation)^2$ and $\ln(PricePerCitation)^3$ are both zero using an F-test. This is evidence supporting a linear relation between log-subscriptions and log-price.
3. Demand is greater for Journals with more characters, holding price and age constant.

Hence we have found evidence, that the price elasticity of demand for economic journals depends on the age of the journal. Altogether our estimates suggest that the demand is very inelastic, i.e. the librararies' demand for economic journals is quite insensitve to the price: using model (IV), even for a young journal $(Age = 5)$ we estimate the price elasticity to be $-0,899 + 0,374 \times \ln(5) + 0,141 \times [\ln(1) \times \ln(5)] \approx -0.3$ so that a one percent increase in price is predicted to reduce the demand by only 0.3 percent.

This finding comes at no surprise since providing the most recent research is a necessity for libraries.

8.4 Nonlinear Effects on Test Scores of the Student-Teacher Ratio

In this section we will discuss three specific questions about the relatin between test scores and the student-teacher ratio:

1. Does the effect on test scores of decreasing the student-teacher ratio depend on the fraction of english learners when we control for economic idiosyncracies of different districts?

2. Does this effect depend on the the student-teacher ratio?
3. How strong is the effect of decreasing the student-teacher ratio (by two students per teacher) if we take into account economic characteristics and nonlinearities?

Two answer these questions we will consider a total of seven models, some of which are nonlinear regression specifications of the types that have been discussed before. As measures for the students' economic backgrounds, we will additionally consider the regressors *lunch* and $\ln(income)$. We use the logarithm of *income* because the analysis discussed in chapter 8.2 showed that the nonlinear relationship between *income* and *TestScores* is approximately logarithmic. We do not include expenditures per pupil (*expenditure*) because doing so allows the expenditures to vary with the student-teacher ratio, see chapter 7.2.

8.4.0.0.1 Nonlinear Regression Models of Test Scores

The considered model specifications are:

$$
\begin{align}
\widehat{TestScore}_i &= \beta_0 + \beta_1 size_i + \beta_4 english_i + \beta_9 lunch_i + u_i \tag{8.10}\\
& \tag{8.11}\\
\widehat{TestScore}_i &= \beta_0 + \beta_1 size_i + \beta_4 english_i + \beta_9 lunch_i + \beta_{10}\ln(income_i) + u_i \tag{8.12}\\
& \tag{8.13}\\
\widehat{TestScore}_i &= \beta_0 + \beta_1 size_i + \beta_5 HiEL_i + \beta_6 (HiEL_i \times size_i) + u_i \tag{8.14}\\
& \tag{8.15}\\
\widehat{TestScore}_i &= \beta_0 + \beta_1 size_i + \beta_5 HiEL_i + \beta_6 (HiEL_i \times size_i) + \beta_9 lunch_i + \beta_{10}\ln(income_i) + u_i \tag{8.16}\\
& \tag{8.17}\\
\widehat{TestScore}_i &= \beta_0 + \beta_1 size_i + \beta_2 size_i^2 + \beta_5 HiEL_i + \beta_9 lunch_i + \beta_{10}\ln(income_i) + u_i \tag{8.18}\\
& \tag{8.19}\\
\widehat{TestScore}_i &= \beta_0 + \beta_1 size_i + \beta_2 size_i^2 + \beta_3 size_i^3 + \beta_5 HiEL_i + \beta_6 (HiEL \times size) \tag{8.20}\\
&\quad + \beta_7 (HiEL_i \times size_i^2) + \beta_8 (HiEL_i \times size_i^3) + \beta_9 lunch_i + \beta_{10}\ln(income_i) + u_i \tag{8.21}\\
& \tag{8.22}\\
\widehat{TestScore}_i &= \beta_0 + \beta_1 size_i + \beta_2 size_i^2 + \beta_3 size_i^3 + \beta_4 english + \beta_9 lunch_i + \beta_{10}\ln(income_i) + u_i \tag{8.23}
\end{align}
$$

```r
# Estimate all models
TestScore_mod1 <- lm(score ~ size + english + lunch, data = CASchools)

TestScore_mod2 <- lm(score ~ size + english + lunch + log(income), data = CASchools)

TestScore_mod3 <- lm(score ~ size + HiEL + HiEL:size, data = CASchools)

TestScore_mod4 <- lm(score ~ size + HiEL + HiEL:size + lunch + log(income),
    data = CASchools)

TestScore_mod5 <- lm(score ~ size + I(size^2) + I(size^3) + HiEL + lunch + log(income),
    data = CASchools)

TestScore_mod6 <- lm(score ~ size + I(size^2) + I(size^3) + HiEL + HiEL:size +
    HiEL:I(size^2) + HiEL:I(size^3) + lunch + log(income), data = CASchools)

TestScore_mod7 <- lm(score ~ size + I(size^2) + I(size^3) + english + lunch +
    log(income), data = CASchools)
```

Next, we may use `summary()` to assess the models. Using `stargazer()` we may also obtain a LATEX-based tabular representation of all regression outputs and which is more convenient for comparison of the models.

```r
# generate a latex table of regression outputes
stargazer(TestScore_mod1, TestScore_mod2, TestScore_mod3, TestScore_mod4, TestScore_mod5,
    TestScore_mod6, TestScore_mod7, column.labels = c("(1)", "(2)", "(3)", "(4)",
        "(5)", "(6)", "(7)"))
```

Dependent variable:

score

(1)

(2)

(3)

(4)

(5)

(6)

(7)

size

-1.00***

-0.73***

-0.97*

-0.53*

64.34**

83.70***

65.29**

(0.24)

(0.23)

(0.54)

(0.30)

(25.46)

(29.69)

(25.48)

english

-0.12***

-0.18***

-0.17***

(0.03)

(0.03)

(0.03)

I(size2)

-3.42***

-4.38***

-3.47***

(1.29)

(1.51)

(1.29)

I(size3)

0.06***

0.07***

0.06***

(0.02)

(0.03)

(0.02)

lunch

-0.55***

-0.40***

-0.41***

-0.42***

-0.42***

-0.40***

(0.02)

(0.03)

(0.03)

(0.03)

(0.03)

(0.03)

log(income)

11.57***

12.12***

11.75***

11.80***

11.51***

(1.74)

(1.77)

(1.73)

(1.75)

(1.73)

HiEL

5.64

5.50

-5.47***

816.08*

(16.72)

(9.14)

(1.03)

(434.61)

size:HiEL

-1.28

-0.58

-123.28*

(0.84)

(0.46)

(66.35)

I(size2):HiEL

6.12*

(3.35)

I(size3):HiEL

-0.10*

(0.06)

Constant

700.15***

658.55***

682.25***

653.67***

252.05

122.35

244.81

(4.69)

(7.68)

(10.51)

(8.89)

(165.82)

(192.18)

(165.93)

Observations

420

420

420

420

420

420

420

R2

0.77

0.80

0.31

0.80

0.80

0.80

0.80

Adjusted R2

0.77

0.79

0.31

0.79

0.80

0.80

0.80

Residual Std. Error

9.08 (df = 416)

8.64 (df = 415)

15.88 (df = 416)

8.63 (df = 414)

8.56 (df = 413)

8.55 (df = 410)

8.57 (df = 413)

F Statistic

476.31*** (df = 3; 416)

405.36*** (df = 4; 415)

62.40*** (df = 3; 416)

325.80*** (df = 5; 414)

277.21*** (df = 6; 413)

185.78*** (df = 9; 410)

276.52*** (df = 6; 413)

Note:

p<0.1; ***p<0.05;*** p<0.01

Let us summarize what can be concluded from the table above:

First of all, it is apparent that the student-teacher ratio is statistically significant in all seven models. Adding $\ln(income)$ to model (1) we find that the corresponding coefficient is statistically significant at the level of 1% while all other coefficients remain at their significance level. Furthermore, the estimate for the coefficient on $size$ is roughly 0.27 points larger which could be a sign of attenuated omitted variable bias. We consider this a reason to include $\ln(income)$ as a regressor in other models, too.

Regressions (3) and (4) are regression that aim to assees the effect of allowing for an interaction between $size$ and $HiEL$, without and with economic control variables. In both modesl, the interaction term and the dummy are not statistically significant. Thus, even with economic control variables we cannot the reject the null hypothesis, that the effect of the student-teacher ratios on test scores is the same for districts with high and districts with low share of english learning students.

Regression (5) includes a cubic term for the student-teacher ratio and omittes the interaction between $size$ and $HiEl$. The estimation results indicate that there is a nonlinear effect of the student-teacher ratio on test scores. (Can You verify this using an F-test of $H_0 : \beta_2 = \beta_3 = 0$?)

Consequently, regression (6) further explores whether the fraction of english learners is also accountable for the effect of the student-teacher ration by using $HiEL \times size$ and the interactions $HiEL \times size^2$ and $HiEL \times size^3$. All individual t-tests indicate that that there are significant effects. We check this using a robust F-test of $H_0 : \beta_6 = \beta_7 = \beta_8 = 0$.

```r
# check joint significance of interactions
linearHypothesis(TestScore_mod6,
                 c("size:HiEL=0", "I(size^2):HiEL=0", "I(size^3):HiEL=0"),
                 vcov. = vcovHC(TestScore_mod6, type = "HC1")
                 )
```

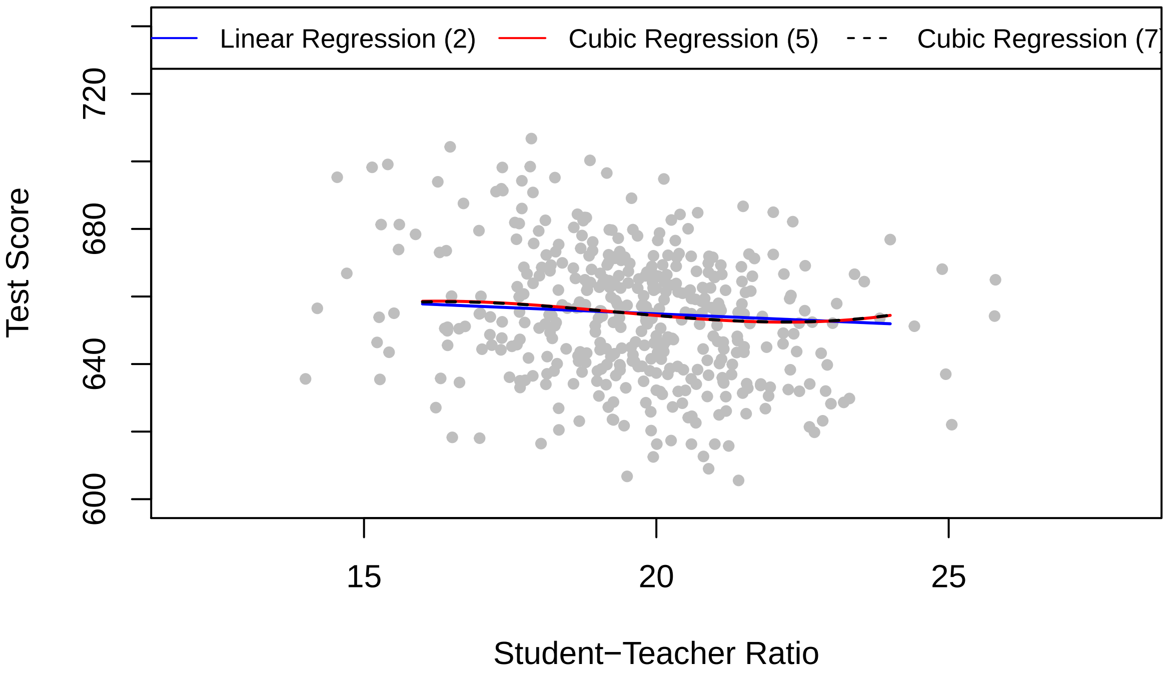
```
## Linear hypothesis test
##
## Hypothesis:
## size:HiEL = 0
## I(size^2):HiEL = 0
## I(size^3):HiEL = 0
##
## Model 1: restricted model
## Model 2: score ~ size + I(size^2) + I(size^3) + HiEL + HiEL:size + HiEL:I(size^2) +
##     HiEL:I(size^3) + lunch + log(income)
##
## Note: Coefficient covariance matrix supplied.
##
##   Res.Df Df      F  Pr(>F)
## 1    413
## 2    410  3 2.6903 0.04597 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

We find that the null can be rejected at the level of 5% and conclude that the regression function differs for districts with high and low percentage of english learners.

Specification (7) uses a continuous measure for the share of english learners instead of a dummy variable (and thus omitts the interaction terms). We observe only small changes to the coefficient estimates on the other regressors and thus conclude that the results observed for specification (5) are not sensitive to the way the percentage of english learners is measured.

We continue by reproducing figure 8.10 of the book using R for interpretation of the nonlinear specifications (2), (5) and (7).

```
# scatterplot
plot(CASchools$size,
     CASchools$score,
     xlim = c(12,28),
     ylim = c(600,740),
     pch=20,
     col="gray",
     xlab="Student-Teacher Ratio",
     ylab = "Test Score")

# add a legend
legend("top",
       legend = c("Linear Regression (2)","Cubic Regression (5)", "Cubic Regression (7)"),
       cex = 0.8,
       ncol = 3,
       lty = c(1,1,2),
       col = c("blue","red","black")
       )

# data for use with predict()
new_data <- data.frame("size"=seq(16,24,0.05),
                       "english"=mean(CASchools$english),
                       "lunch"=mean(CASchools$lunch),
                       "income"=mean(CASchools$income),
                       "HiEL"=mean(CASchools$HiEL)
                       )

# add estimated regression function for model (2)
fitted <- predict(TestScore_mod2, newdata = new_data)

lines(new_data$size,
      fitted,
      lwd=1.5,
      col="blue")

# add estimated regression function for model (5)
fitted <- predict(TestScore_mod5, newdata = new_data)

lines(new_data$size,
      fitted,
      lwd=1.5,
      col="red")

# add estimated regression function for model (7)
fitted <- predict(TestScore_mod7, newdata = new_data)

lines(new_data$size,
      fitted,
      col="black",
      lwd=1.5,
      lty=2)
```

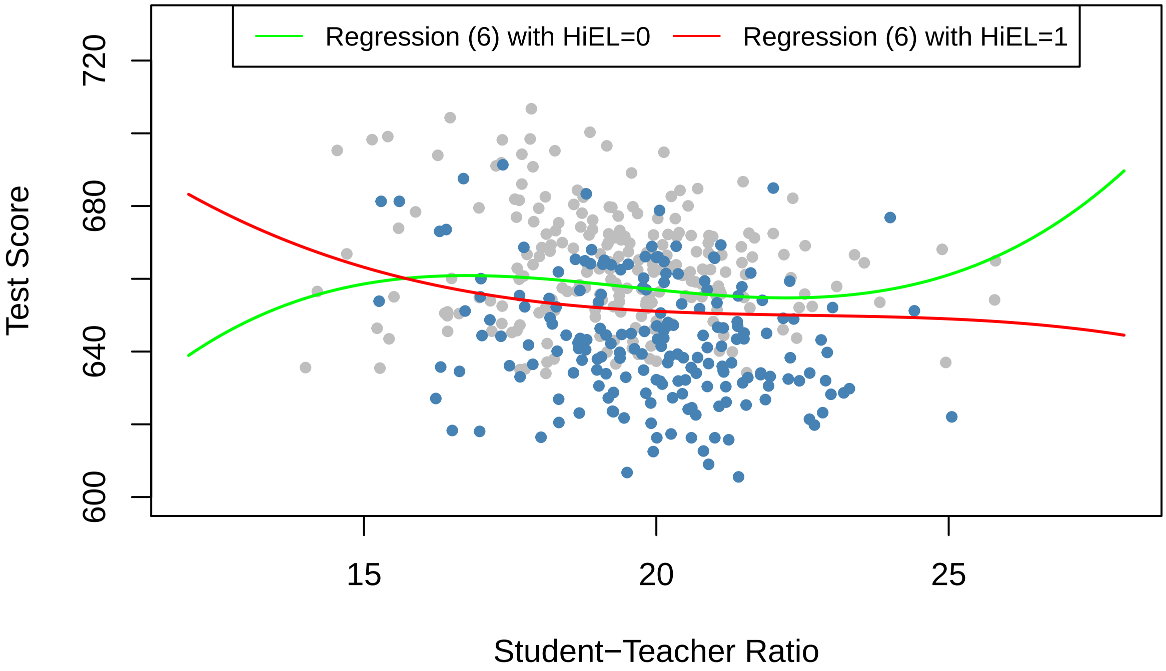


Note that for the figure above all regressors except for *size* are set to their sample averages. We see that the cubic regressions (5) and (7) are almost identical. They indicate that the relation between test scores and the student-teacher ratio has only a small amount of nonlinearity since they do not deviate much from the regression function of (2).

The next code chunk reproduces figure 8.11 of the book. We use `plot()` and `points()` to color observations depending on *HiEL*. Again, the regression lines are drawn based on predictions using average sample averages of all regressors except for *size*.

```
# scatterplot

# observations with HiEL = 0
plot(CASchools$size[CASchools$HiEL==0],
     CASchools$score[CASchools$HiEL==0],
     xlim = c(12,28),
     ylim = c(600,730),
     pch=20,
     col="gray",
     xlab="Student-Teacher Ratio",
     ylab = "Test Score")
```

```r
# observations with HiEL = 1
points(CASchools$size[CASchools$HiEL==1],
       CASchools$score[CASchools$HiEL==1],
       col="steelblue",
       pch=20)

# add a legend
legend("top",
       legend = c("Regression (6) with HiEL=0", "Regression (6) with HiEL=1"),
       cex = 0.8,
       ncol = 2,
       lty = c(1,1),
       col = c("green","red")
       )

# data for use with predict()
new_data <- data.frame("size"=seq(12,28,0.05),
                       "english"=mean(CASchools$english),
                       "lunch"=mean(CASchools$lunch),
                       "income"=mean(CASchools$income),
                       "HiEL"=0
                       )

# add estimated regression function for model (6) with HiEL=0
fitted <- predict(TestScore_mod6, newdata = new_data)

lines(new_data$size,
      fitted,
      lwd=1.5,
      col="green")

# add estimated regression function for model (6) with HiEL=1
new_data$HiEL=1

fitted <- predict(TestScore_mod6, newdata = new_data)

lines(new_data$size,
      fitted,
      lwd=1.5,
      col="red")
```



From the regression output we see that (6) finds statistically significant coefficients on the interaction terms $HiEL:size$, $HiEL:size^2$ and $HiEL:size^3$ i.e. there is evidence that the nonlinear relationship connecting test scores and student-teacher ration depends on the amount of English learning students in the district. However, the figure shows that this difference is not/ of practical importance and is a good example of why one should be careful when inpreting nonlinear models: though the two regression functions look different, we see that the slope of both functions, that is for both districts with high and districs with low share of English learning students, is almost identical for student-teacher ratios between 17 and 23. Since this range includes almost 90% of all observations, we can be confident about this.

One might be tempted to object since both functions show opposing slopes for student-teacher ratios below 15 and beyond 24. Two things can be set aginst that:

1. The data has only few observations with low and high values of the student-teacher ratio so there is only little information to be exploited when estimating the model. This means the estimated function is less precise in the extremes of the dataset
2. Such a behaviour is a typical caveat when using cubic functions since they generally show extreme behaviour for extreme observations. Think of the graph of $f(x) = x^3$.

We thus conclude that there is no dependence of the relation between class size and test scores on the percentage of English learners in the district.

Summary

We are now able to answer the three question posed at the beginning of this section.

1. Considering the linear models, the percentage of English learners has only little influence on the effect of test scores of changing the student-teacher ratio. This result keeps valid if we control for economic background of the students. While the cubic specification (6) provides evidence, the strength of the effect is negligible.
2. When controlling for the students' economic backgroumd we find evidence of nonlinearities in the relationship between student-teacher ratio and test scores.

3. The linear specification (2) predicts that a reduction of the student-teacher ratio by two students per teacher leads to an improvement in test scores of about $-0.73 \times (-2) = 1.46$ points. Since the model is linear, this effect is independent of the class size. Asssume that the student-teacher ratio is 20. For example, model (5) predicts that the reduction increases test scores by

   $$64.33 * 18 + 18^2 * (-3.42) + 18^3 * (0.059) - (64.33 * 20 + 20^2 * (-3.42) + 20^3 * (0.059)) \approx 3.3$$

   points. if the ratio is 22, a reduction to 20 leads to a predicted improvement in test scores of

   $$64.33 * 20 + 20^2 * (-3.42) + 20^3 * (0.059) - (64.33 * 22 + 22^2 * (-3.42) + 22^3 * (0.059)) \approx 2.4$$

   points. This suggests that the effect is stronger in smaller classes.

Chapter 9

Assessing Studies Based on Multiple Regression

t.b.d.

Bibliography