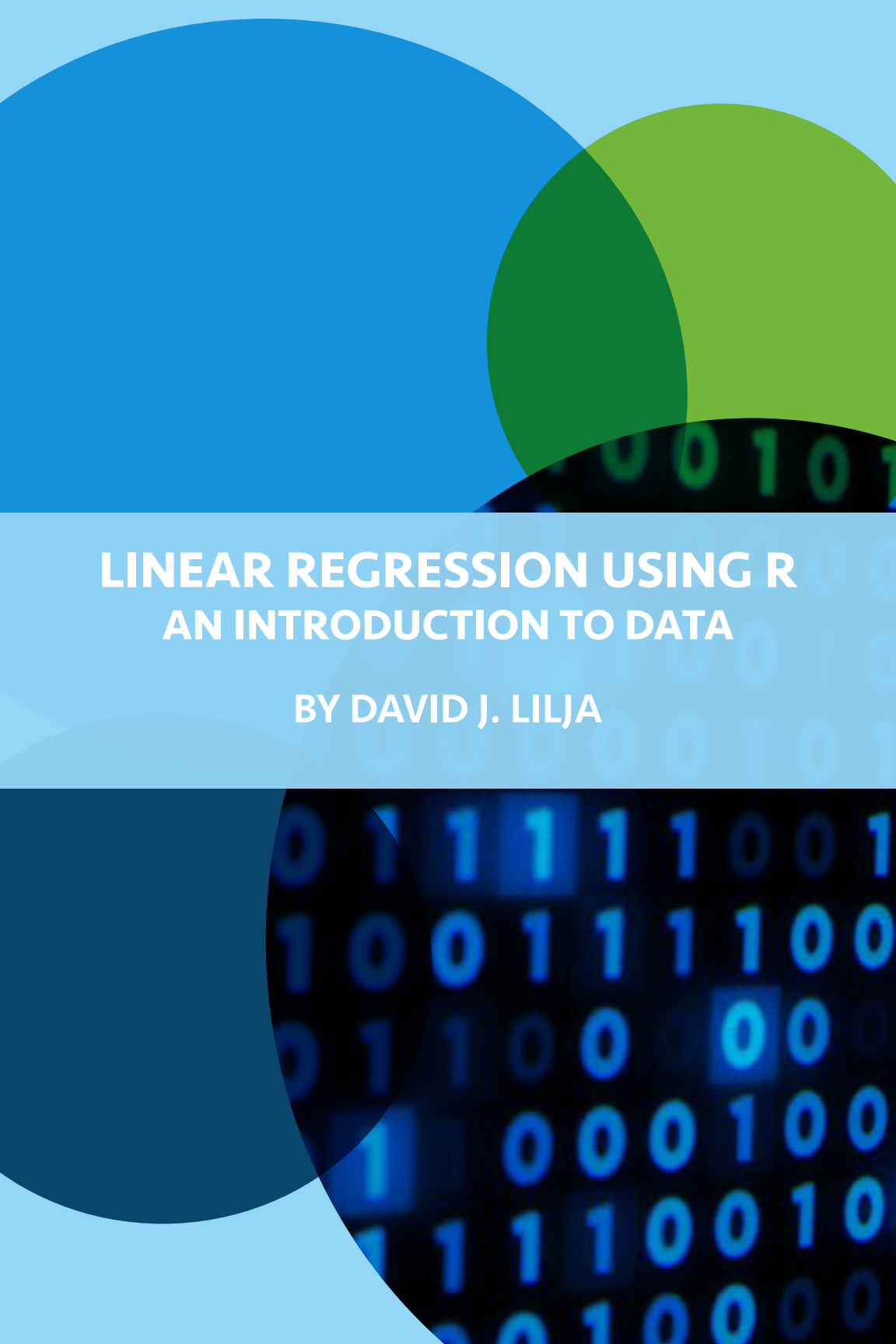
LINEAR REGRESSION USING R
AN INTRODUCTION TO DATA

BY DAVID J. LILJA



Linear Regression Using R

AN INTRODUCTION TO DATA MODELING

DAVID J. LILJA

University of Minnesota, Minneapolis

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Preface

Goals

Interest in what has become popularly known as data mining has expanded significantly in the past few years, as the amount of data generated continues to explode. Furthermore, computing systems' ever-increasing capabilities make it feasible to deeply analyze data in ways that were previously available only to individuals with access to expensive, high-performance computing systems.

Learning about the broad field of data mining really means learning a range of statistical tools and techniques. Regression modeling is one of those fundamental techniques, while the R programming language is widely used by statisticians, scientists, and engineers for a broad range of statistical analyses. A working knowledge of R is an important skill for anyone who is interested in performing most types of data analysis.

The primary goal of this tutorial is to explain, in step-by-step detail, how to develop linear regression models. It uses a large, publicly available data set as a running example throughout the text and employs the R programming language environment as the computational engine for developing the models.

This tutorial will not make you an expert in regression modeling, nor a complete programmer in R. However, anyone who wants to understand how to extract information from data needs a working knowledge of the basic concepts used to develop reliable regression models, and should also know how to use R. The specific focus, casual presentation, and detailed examples will help you understand the modeling process, using R as your computational tool.

All of the resources you will need to work through the examples in the book are readily available on the book web site (see p. ii). Furthermore, a fully functional R programming environment is available as a free, open-source download [13].

Audience

Students taking university-level courses on data science, statistical modeling, and related topics, plus professional engineers and scientists who want to learn how to perform linear regression modeling, are the primary audience for this tutorial. This tutorial assumes that you have at least some experience with programming, such as what you would typically learn while studying for any science or engineering degree. However, you do not need to be an expert programmer. In fact, one of the key advantages of R as a programming language for developing regression models is that it is easy to perform remarkably complex computations with only a few lines of code.

Acknowledgments

Writing a book requires a lot of time by yourself, concentrating on trying to say what you want to say as clearly as possible. But developing and publishing a book is rarely the result of just one person's effort. This book is no exception.

At the risk of omitting some of those who provided both direct and indirect assistance in preparing this book, I thank the following individuals for their help: Professor Phil Bones of the University of Canterbury in Christchurch, New Zealand, for providing me with a quiet place to work on this text in one of the most beautiful countries in the world, and for our many interesting conversations; Shane Nackerud and Kristi Jensen of the University of Minnesota Libraries for their logistical and financial support through the Libraries' Partnership for Affordable Content grant program; and Brian Conn, also of the University of Minnesota Libraries, for his insights into the numerous publishing options available for this type of text, and for steering me towards the Partnership for Affordable Content program. I also want to thank my copy editor, Ingrid Case, for gently and tactfully pointing out my errors and inconsistencies. Any errors that remain are

my own fault, most likely because I ignored Ingrid's advice. Finally, none of this would have happened without Sarah and her unwavering support.

Without these people, this book would be just a bunch of bits, moldering away on a computer disk drive somewhere.

Contents

1 Introduction

DATA mining is a phrase that has been popularly used to suggest the process of finding useful information from within a large collection of data. I like to think of data mining as encompassing a broad range of statistical techniques and tools that can be used to extract different types of information from your data. Which particular technique or tool to use depends on your specific goals.

One of the most fundamental of the broad range of data mining techniques that have been developed is *regression modeling*. Regression modeling is simply generating a mathematical model from measured data. This model is said to *explain* an output value given a new set of input values. *Linear regression modeling* is a specific form of regression modeling that assumes that the output can be explained using a linear combination of the input values.

A common goal for developing a regression model is to predict what the output value of a system should be for a new set of input values, given that you have a collection of data about similar systems. For example, as you gain experience driving a car, you begun to develop an intuitive sense of how long it might take you to drive somewhere if you know the type of car, the weather, an estimate of the traffic, the distance, the condition of the roads, and so on. What you really have done to make this estimate of driving time is constructed a multi-factor regression model in your mind. The inputs to your model are the type of car, the weather, etc. The output is how long it will take you to drive from one point to another. When you change any of the inputs, such as a sudden increase in traffic, you automatically re-estimate how long it will take you to reach the destination.

This type of model building and estimating is precisely what we are go-

ing to learn to do more formally in this tutorial. As a concrete example, we will use real performance data obtained from thousands of measurements of computer systems to develop a regression model using the R statistical software package. You will learn how to develop the model and how to evaluate how well it fits the data. You also will learn how to use it to predict the performance of other computer systems.

As you go through this tutorial, remember that what you are developing is just a model. It will hopefully be useful in understanding the system and in predicting future results. However, do not confuse a model with the real system. The real system will always produce the correct results, regardless of what the model may say the results should be.

1.1 What is a Linear Regression Model?

Suppose that we have measured the performance of several different computer systems using some standard benchmark program. We can organize these measurements into a table, such as the example data shown in Table 1.1. The details of each system are recorded in a single row. Since we measured the performance of n different systems, we need n rows in the table.

Table 1.1: An example of computer system performance data.

System	Inputs			Output
	Clock (MHz)	Cache (kB)	Transistors (M)	Performance
1	1500	64	2	98
2	2000	128	2.5	134
...	...	...	...	...
i	...	...	...	...
...	...	...	...	...
n	1750	32	4.5	113

The first column in this table is the index number (or name) from 1 to n that we have arbitrarily assigned to each of the different systems measured. Columns 2-4 are the *input parameters*. These are called the *independent variables* for the system we will be modeling. The specific values of the

input parameters were set by the experimenter when the system was measured, or they were determined by the system configuration. In either case, we know what the values are and we want to measure the performance obtained for these input values. For example, in the first system, the processor's clock was 1500 MHz, the cache size was 64 kbytes, and the processor contained 2 million transistors. The last column is the performance that was measured for this system when it executed a standard benchmark program. We refer to this value as the *output* of the system. More technically, this is known as the system's *dependent variable* or the system's *response*.

The goal of regression modeling is to use these n independent measurements to determine a mathematical function, $f()$, that describes the relationship between the input parameters and the output, such as:

$$performance = f(Clock, Cache, Transistors) \tag{1.1}$$

This function, which is just an ordinary mathematical equation, is the regression model. A regression model can take on any form. However, we will restrict ourselves to a function that is a linear combination of the input parameters. We will explain later that, while the function is a linear combination of the input parameters, the parameters themselves do not need to be linear. This linear combination is commonly used in regression modeling and is powerful enough to model most systems we are likely to encounter.

In the process of developing this model, we will discover how important each of these inputs are in determining the output value. For example, we might find that the performance is heavily dependent on the clock frequency, while the cache size and the number of transistors may be much less important. We may even find that some of the inputs have essentially no impact on the output making it completely unnecessary to include them in the model. We also will be able to use the model we develop to predict the performance we would expect to see on a system that has input values that did not exist in any of the systems that we actually measured. For instance, Table 1.2 shows three new systems that were not part of the set of systems that we previously measured. We can use our regression model to predict the performance of each of these three systems to replace the question marks in the table.

Table 1.2: An example in which we want to predict the performance of new systems $n+1$, $n+2$, and $n+3$ using the previously measured results from the other n systems.

System	Inputs			Output
	Clock (MHz)	Cache (kB)	Transistors (M)	Performance
1	1500	64	2	98
2	2000	128	2.5	134
...	...	...	...	...
i	...	...	...	...
...	...	...	...	...
n	1750	32	4.5	113
$n+1$	2500	256	2.8	?
$n+2$	1560	128	1.8	?
$n+3$	900	64	1.5	?

As a final point, note that, since the regression model is a linear combination of the input values, the values of the model parameters will automatically be scaled as we develop the model. As a result, the units used for the inputs and the output are arbitrary. In fact, we can rescale the values of the inputs and the output before we begin the modeling process and still produce a valid model.

1.2 What is R?

R is a computer language developed specifically for statistical computing. It is actually more than that, though. R provides a complete environment for interacting with your data. You can directly use the functions that are provided in the environment to process your data without writing a complete program. You also can write your own programs to perform operations that do not have built-in functions, or to repeat the same task multiple times, for instance.

R is an object-oriented language that uses vectors and matrices as its basic operands. This feature makes it quite useful for working on large sets of data using only a few lines of code. The R environment also provides ex-

cellent graphical tools for producing complex plots relatively easily. And, perhaps best of all, it is free. It is an open source project developed by many volunteers. You can learn more about the history of R, and download a copy to your own computer, from the R Project web site [13].

As an example of using R, here is a copy of a simple interaction with the R environment.

```
> x <- c(2,4,6,8,10,12,14,16)
> x
[1]  2  4  6  8 10 12 14 16
> mean(x)
[1] 9
> var(x)
[1] 24
>
```

In this listing, the "`>`" character indicates that R is waiting for input. The line `x <- c(2, 4, 6, 8, 10, 12, 14, 16)` concatenates all of the values in the argument into a vector and assigns that vector to the variable `x`. Simply typing `x` by itself causes R to print the contents of the vector. Note that R treats vectors as a matrix with a single row. Thus, the "`[1]`" preceding the values is R's notation to show that this is the first row of the matrix `x`. The next line, `mean(x)`, calls a function in R that computes the arithmetic mean of the input vector, `x`. The function `var(x)` computes the corresponding variance.

This book will not make you an expert in programming using the R computer language. Developing good regression models is an interactive process that requires you to dig in and play around with your data and your models. Thus, I am more interested in using R as a computing environment for doing statistical analysis than as a programming language. Instead of teaching you the language's syntax and semantics directly, this tutorial will introduce what you need to know about R as you need it to perform the specific steps to develop a regression model. You should already have some programming expertise so that you can follow the examples in the remainder of the book. However, you do not need to be an expert programmer.

1.3 What's Next?

Before beginning any sort of data analysis, you need to understand your data. Chapter 2 describes the sample data that will be used in the examples throughout this tutorial, and how to read this data into the R environment. Chapter 3 introduces the simplest regression model consisting of a single independent variable. The process used to develop a more complex regression model with multiple independent input variables is explained in Chapter 4. Chapter 5 then shows how to use this multi-factor regression model to predict the system response when given new input data. Chapter 6 explains in more detail the routines used to read a file containing your data into the R environment. The process used to develop a multi-factor regression model is summarized in Chapter 7 along with some suggestions for further reading. Finally, Chapter 8 provides some experiments you might want to try to expand your understanding of the modeling process.

2 | Understand Your Data

GOOD data is the basis of any sort of regression model, because we use this data to actually construct the model. If the data is flawed, the model will be flawed. It is the old maxim of *garbage in, garbage out*. Thus, the first step in regression modeling is to ensure that your data is reliable. There is no universal approach to verifying the quality of your data, unfortunately. If you collect it yourself, you at least have the advantage of knowing its provenance. If you obtain your data from somewhere else, though, you depend on the source to ensure data quality. Your job then becomes verifying your source's reliability and correctness as much as possible.

2.1 || Missing Values

Any large collection of data is probably incomplete. That is, it is likely that there will be cells without values in your data table. These missing values may be the result of an error, such as the experimenter simply forgetting to fill in a particular entry. They also could be missing because that particular system configuration did not have that parameter available. For example, not every processor tested in our example data had an L2 cache. Fortunately, R is designed to gracefully handle missing values. R uses the notation `NA` to indicate that the corresponding value is not available.

Most of the functions in R have been written to appropriately ignore `NA` values and still compute the desired result. Sometimes, however, you must explicitly tell the function to ignore the `NA` values. For example, calling the `mean()` function with an input vector that contains `NA` values causes it to return `NA` as the result. To compute the mean of the input vector while

ignoring the `NA` values, you must explicitly tell the function to remove the `NA` values using `mean(x, na.rm=TRUE)`.

2.2 || Sanity Checking and Data Cleaning

Regardless of where you obtain your data, it is important to do some *sanity checks* to ensure that nothing is drastically flawed. For instance, you can check the minimum and maximum values of key input parameters (i.e., columns) of your data to see if anything looks obviously wrong. One of the exercises in Chapter 8 encourages you explore other approaches for verifying your data. R also provides good plotting functions to quickly obtain a visual indication of some of the key relationships in your data set. We will see some examples of these functions in Section 3.1.

If you discover obvious errors or flaws in your data, you may have to eliminate portions of that data. For instance, you may find that the performance reported for a few system configurations is hundreds of times larger than that of all of the other systems tested. Although it is possible that this data is correct, it seems more likely that whoever recorded the data simply made a transcription error. You may decide that you should delete those results from your data. It is important, though, not to throw out data that looks strange without good justification. Sometimes the most interesting conclusions come from data that on first glance appeared flawed, but was actually hiding an interesting and unsuspected phenomenon. This process of checking your data and putting it into the proper format is often called *data cleaning*.

It also is always appropriate to use your knowledge of the system and the relationships between the inputs and the output to inform your model building. For instance, from our experience, we expect that the clock rate will be a key parameter in any regression model of computer systems performance that we construct. Consequently, we will want to make sure that our models include the clock parameter. If the modeling methodology suggests that the clock is not important in the model, then using the methodology is probably an error. We additionally may have deeper insights into the physical system that suggest how we should proceed in developing a model. We will see a specific example of applying our insights about the effect of caches on system performance when we begin constructing more

complex models in Chapter 4.

These types of sanity checks help you feel more comfortable that your data is valid. However, keep in mind that it is impossible to prove that your data is flawless. As a result, you should always look at the results of any regression modeling exercise with a healthy dose of skepticism and think carefully about whether or not the results make sense. Trust your intuition. If the results don't feel right, there is quite possibly a problem lurking somewhere in the data or in your analysis.

2.3 || The Example Data

I obtained the input data used for developing the regression models in the subsequent chapters from the publicly available *CPU DB* database [2]. This database contains design characteristics and measured performance results for a large collection of commercial processors. The data was collected over many years and is nicely organized using a common format and a standardized set of parameters. The particular version of the database used in this book contains information on 1,525 processors.

Many of the database's parameters (columns) are useful in understanding and comparing the performance of the various processors. Not all of these parameters will be useful as predictors in the regression models, however. For instance, some of the parameters, such as the column labeled *Instruction set width*, are not available for many of the processors. Others, such as the *Processor family*, are common among several processors and do not provide useful information for distinguishing among them. As a result, we can eliminate these columns as possible predictors when we develop the regression model.

On the other hand, based on our knowledge of processor design, we know that the clock frequency has a large effect on performance. It also seems likely that the parallelism-related parameters, specifically, the number of threads and cores, could have a significant effect on performance, so we will keep these parameters available for possible inclusion in the regression model.

Technology-related parameters are those that are directly determined by the particular fabrication technology used to build the processor. The number of transistors and the die size are rough indicators of the size and com-

plexity of the processor's logic. The feature size, channel length, and FO4 (fanout-of-four) delay are related to gate delays in the processor's logic. Because these parameters both have a direct effect on how much processing can be done per clock cycle and effect the critical path delays, at least some of these parameters could be important in a regression model that describes performance.

Finally, the memory-related parameters recorded in the database are the separate L1 instruction and data cache sizes, and the unified L2 and L3 cache sizes. Because memory delays are critical to a processor's performance, all of these memory-related parameters have the potential for being important in the regression models.

The reported performance metric is the score obtained from the SPEC CPU integer and floating-point benchmark programs from 1992, 1995, 2000, and 2006 [6–8]. This performance result will be the regression model's output. Note that performance results are not available for every processor running every benchmark. Most of the processors have performance results for only those benchmark sets that were current when the processor was introduced into the market. Thus, although there are more than 1,500 lines in the database representing more than 1,500 unique processor configurations, a much smaller number of results are reported for each individual benchmark.

2.4 || Data Frames

The fundamental object used for storing tables of data in R is called a *data frame*. We can think of a data frame as a way of organizing data into a large table with a row for each system measured and a column for each parameter. An interesting and useful feature of R is that all the columns in a data frame do not need to be the same data type. Some columns may consist of numerical data, for instance, while other columns contain textual data. This feature is quite useful when manipulating large, heterogeneous data files.

To access the CPU DB data, we first must read it into the R environment. R has built-in functions for reading data directly from files in the *csv* (comma separated values) format and for organizing the data into data frames. The specifics of this reading process can get a little messy, depend-

ing on how the data is organized in the file. We will defer the specifics of reading the CPU DB file into R until Chapter 6. For now, we will use a function called `extract_data()`, which was specifically written for reading the CPU DB file.

To use this function, copy both the **all-data.csv** and **read-data.R** files into a directory on your computer (you can download both of these files from this book's web site shown on p. ii). Then start the R environment and set the local directory in R to be this directory using the *File -> Change dir* pull-down menu. Then use the *File -> Source R code* pull-down menu to read the **read-data.R** file into R. When the R code in this file completes, you should have six new data frames in your R environment workspace: `int92.dat`, `fp92.dat`, `int95.dat`, `fp95.dat`, `int00.dat`, `fp00.dat`, `int06.dat`, and `fp06.dat`.

The data frame `int92.dat` contains the data from the CPU DB database for all of the processors for which performance results were available for the SPEC Integer 1992 (Int1992) benchmark program. Similarly, `fp92.dat` contains the data for the processors that executed the Floating-Point 1992 (Fp1992) benchmarks, and so on. I use the `.dat` suffix to show that the corresponding variable name is a data frame.

Simply typing the name of the data frame will cause R to print the entire table. For example, here are the first few lines printed after I type `int92.dat`, truncated to fit within the page:

```
         nperf      perf clock threads cores  ...
1    9.662070  68.60000   100       1     1 ...
2    7.996196  63.10000   125       1     1 ...
3   16.363872  90.72647   166       1     1 ...
4   13.720745  82.00000   175       1     1 ...
...
```

The first row is the header, which shows the name of each column. Each subsequent row contains the data corresponding to an individual processor. The first column is the index number assigned to the processor whose data is in that row. The next columns are the specific values recorded for that parameter for each processor. The function `head(int92.dat)` prints out just the header and the first few rows of the corresponding data frame. It gives you a quick glance at the data frame when you interact with your data.

Table 2.1shows the complete list of column names available in these

data frames. Note that the column names are listed vertically in this table, simply to make them fit on the page.

Table 2.1: The names and definitions of the columns in the data frames containing the data from CPU DB.

Column number	Column name	Definition
1	(blank)	Processor index number
2	nperf	Normalized performance
3	perf	SPEC performance
4	clock	Clock frequency (MHz)
5	threads	Number of hardware threads available
6	cores	Number of hardware cores available
7	TDP	Thermal design power
8	transistors	Number of transistors on the chip (M)
9	dieSize	The size of the chip
10	voltage	Nominal operating voltage
11	featureSize	Fabrication feature size
12	channel	Fabrication channel size
13	FO4delay	Fan-out-four delay
14	L1icache	Level 1 instruction cache size
15	L1dcache	Level 1 data cache size
16	L2cache	Level 2 cache size
17	L3cache	Level 3 cache size

2.5 || Accessing a Data Frame

We access the individual elements in a data frame using square brackets to identify a specific cell. For instance, the following accesses the data in the cell in row 15, column 12:

```
> int92.dat[15,12]
[1] 180
```

We can also access cells by name by putting quotes around the name:

```
> int92.dat["71","perf"]
[1] 105.1
```

This expression returns the data in the row labeled `71` and the column labeled `perf`. Note that this is not row 71, but rather the row that contains the data for the processor whose name is `71`.

We can access an entire column by leaving the first parameter in the square brackets empty. For instance, the following prints the value in every row for the column labeled `clock`:

```
> int92.dat[,"clock"]
 [1] 100 125 166 175 190 ...
```

Similarly, this expression prints the values in all of the columns for row 36:

```
> int92.dat[36,]
      nperf     perf clock threads cores ...
36 13.07378 79.86399    80       1     1  ...
```

The functions `nrow()` and `ncol()` return the number of rows and columns, respectively, in the data frame:

```
> nrow(int92.dat)
[1] 78
> ncol(int92.dat)
[1] 16
```

Because R functions can typically operate on a vector of any length, we can use built-in functions to quickly compute some useful results. For example, the following expressions compute the minimum, maximum, mean, and standard deviation of the `perf` column in the `int92.dat` data frame:

```
> min(int92.dat[,"perf"])
[1] 36.7
> max(int92.dat[,"perf"])
[1] 366.857
> mean(int92.dat[,"perf"])
[1] 124.2859
> sd(int92.dat[,"perf"])
[1] 78.0974
```

This square-bracket notation can become cumbersome when you do a substantial amount of interactive computation within the R environment. R provides an alternative notation using the `$` symbol to more easily access a column. Repeating the previous example using this notation:

```
> min(int92.dat$perf)
[1] 36.7
> max(int92.dat$perf)
[1] 366.857
> mean(int92.dat$perf)
[1] 124.2859
> sd(int92.dat$perf)
[1] 78.0974
```

This notation says to use the data in the column named `perf` from the data frame named `int92.dat`. We can make yet a further simplification using the `attach` function. This function makes the corresponding data frame local to the current workspace, thereby eliminating the need to use the potentially awkward `$` or square-bracket indexing notation. The following example shows how this works:

```
> attach(int92.dat)
> min(perf)
[1] 36.7
> max(perf)
[1] 366.857
> mean(perf)
[1] 124.2859
> sd(perf)
[1] 78.0974
```

To change to a different data frame within your local workspace, you must first `detach` the current data frame:

```
> detach(int92.dat)
> attach(fp00.dat)
> min(perf)
[1] 87.54153
> max(perf)
[1] 3369
> mean(perf)
[1] 1217.282
> sd(perf)
[1] 787.4139
```

Now that we have the necessary data available in the R environment, and some understanding of how to access and manipulate this data, we are

ready to generate our first regression model.

3 | One-Factor Regression

THE simplest linear regression model finds the relationship between one input variable, which is called the *predictor* variable, and the output, which is called the system's *response*. This type of model is known as a *one-factor* linear regression. To demonstrate the regression-modeling process, we will begin developing a one-factor model for the SPEC Integer 2000 (Int2000) benchmark results reported in the CPU DB data set. We will expand this model to include multiple input variables in Chapter 4.

3.1 || Visualize the Data

The first step in this one-factor modeling process is to determine whether or not it *looks* as though a linear relationship exists between the predictor and the output value. From our understanding of computer system design - that is, from our *domain-specific knowledge* - we know that the clock frequency strongly influences a computer system's performance. Consequently, we must look for a roughly linear relationship between the processor's performance and its clock frequency. Fortunately, R provides powerful and flexible plotting functions that let us visualize this type relationship quite easily.

This R function call:

```
> plot(int00.dat[,"clock"],int00.dat[,"perf"], main="Int2000",
    xlab="Clock", ylab="Performance")
```

generates the plot shown in Figure 3.1. The first parameter in this function call is the value we will plot on the x-axis. In this case, we will plot the `clock` values from the `int00.dat` data frame as the independent variable

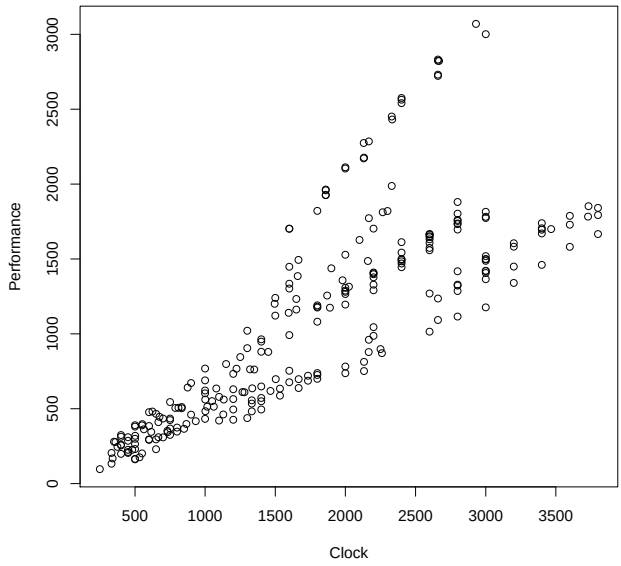

Figure 3.1: A scatter plot of the performance of the processors that were tested using the Int2000 benchmark versus the clock frequency.

on the x-axis. The dependent variable is the `perf` column from `int00.dat`, which we plot on the y-axis. The function argument `main="Int2000"` provides a title for the plot, while `xlab="Clock"` and `ylab="Performance"` provide labels for the x- and y-axes, respectively.

This figure shows that the performance tends to increase as the clock frequency increases, as we expected. If we superimpose a straight line on this scatter plot, we see that the relationship between the predictor (the clock frequency) and the output (the performance) is roughly linear. It is not perfectly linear, however. As the clock frequency increases, we see a larger spread in performance values. Our next step is to develop a regression model that will help us quantify the degree of linearity in the relationship between the output and the predictor.

3.2 || The Linear Model Function

We use regression models to predict a system's behavior by extrapolating from previously measured output values when the system is tested with known input parameter values. The simplest regression model is a straight line. It has the mathematical form:

$$y = a_0 + a_1 x_1 \tag{3.1}$$

where x_1 is the input to the system, a_0 is the y-intercept of the line, a_1 is the slope, and y is the output value the model predicts.

R provides the function `lm()` that generates a linear model from the data contained in a data frame. For this one-factor model, R computes the values of a_0 and a_1 using the method of least squares. This method finds the line that most closely fits the measured data by minimizing the distances between the line and the individual data points. For the data frame `int00.dat`, we compute the model as follows:

```
> attach(int00.dat)
> int00.lm <- lm(perf ~ clock)
```

The first line in this example attaches the `int00.dat` data frame to the current workspace. The next line calls the `lm()` function and assigns the resulting *linear model object* to the variable `int00.lm`. We use the suffix `.lm` to emphasize that this variable contains a linear model. The argument in the `lm()` function, `(perf ~ clock)`, says that we want to find a model where the predictor `clock` explains the output `perf`.

Typing the variable's name, `int00.lm`, by itself causes R to print the argument with which the function `lm()` was called, along with the computed coefficients for the regression model.

```
> int00.lm

Call:
lm(formula = perf ~ clock)

Coefficients:
(Intercept)        clock
    51.7871       0.5863
```

In this case, the y-intercept is $a_0 = 51.7871$ and the slope is $a_1 = 0.5863$. Thus, the final regression model is:

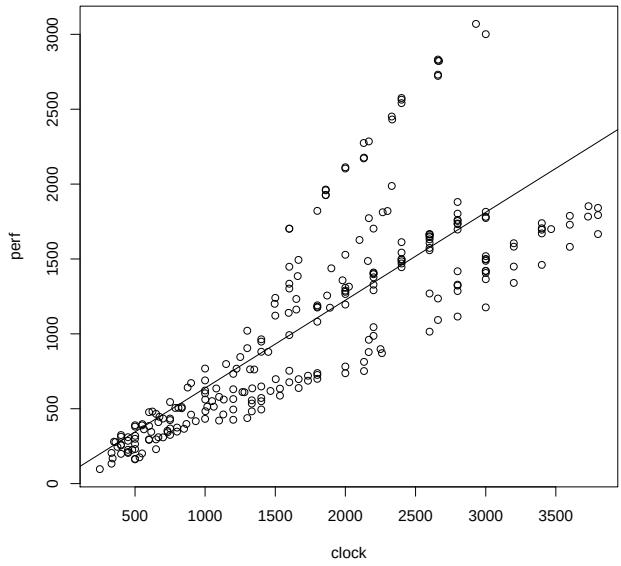

Figure 3.2: The one-factor linear regression model superimposed on the data from Figure 3.1.

$$perf = 51.7871 + 0.5863 * clock. \tag{3.2}$$

The following code plots the original data along with the fitted line, as shown in Figure 3.2. The function `abline()` is short for *(a,b)-line*. It plots a line on the active plot window, using the slope and intercept of the linear model given in its argument.

```
> plot(clock,perf)
> abline(int00.lm)
```

3.3 || Evaluating the Quality of the Model

The information we obtain by typing `int00.lm` shows us the regression model's basic values, but does not tell us anything about the model's quality. In fact, there are many different ways to evaluate a regression model's

quality. Many of the techniques can be rather technical, and the details of them are beyond the scope of this tutorial. However, the function `summary()` extracts some additional information that we can use to determine how well the data fit the resulting model. When called with the model object `int00.lm` as the argument, `summary()` produces the following information:

```
> summary(int00.lm)

Call:
lm(formula = perf ~ clock)

Residuals:
    Min      1Q  Median      3Q     Max
-634.61 -276.17  -30.83   75.38 1299.52

Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept) 51.78709   53.31513   0.971    0.332
clock        0.58635    0.02697  21.741   <2e-16 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1


Residual standard error: 396.1 on 254 degrees of freedom
Multiple R-squared:  0.6505,    Adjusted R-squared:  0.6491
F-statistic: 472.7 on 1 and 254 DF,  p-value: < 2.2e-16
```

Let's examine each of the items presented in this summary in turn.

```
> summary(int00.lm)

Call:
lm(formula = perf ~ clock)
```

These first few lines simply repeat how the `lm()` function was called. It is useful to look at this information to verify that you actually called the function as you intended.

```
Residuals:
    Min      1Q  Median      3Q     Max
-634.61 -276.17  -30.83   75.38 1299.52
```

The *residuals* are the differences between the actual measured values and the corresponding values on the fitted regression line. In Figure 3.2, each data point's residual is the distance that the individual data point is above (positive residual) or below (negative residual) the regression line. `Min` is the minimum residual value, which is the distance from the regression line

to the point furthest below the line. Similarly, `Max` is the distance from the regression line of the point furthest above the line. `Median` is the median value of all of the residuals. The `1Q` and `3Q` values are the points that mark the first and third quartiles of all the sorted residual values.

How should we interpret these values? If the line is a good fit with the data, we would expect residual values that are normally distributed around a mean of zero. (Recall that a normal distribution is also called a Gaussian distribution.) This distribution implies that there is a decreasing probability of finding residual values as we move further away from the mean. That is, a good model's residuals should be roughly balanced around and not too far away from the mean of zero. Consequently, when we look at the residual values reported by `summary()`, a good model would tend to have a median value near zero, minimum and maximum values of roughly the same magnitude, and first and third quartile values of roughly the same magnitude. For this model, the residual values are not too far off what we would expect for Gaussian-distributed numbers. In Section 3.4, we present a simple visual test to determine whether the residuals appear to follow a normal distribution.

```
Coefficients:
             Estimate Std. Error t value Pr(>|t|)
(Intercept) 51.78709   53.31513   0.971    0.332
clock        0.58635    0.02697  21.741   <2e-16 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

This portion of the output shows the estimated coefficient values. These values are simply the fitted regression model values from Equation 3.2. The `Std. Error` column shows the statistical *standard error* for each of the coefficients. For a good model, we typically would like to see a standard error that is at least five to ten times smaller than the corresponding coefficient. For example, the standard error for `clock` is 21.7 times smaller than the coefficient value (0.58635/0.02697 = 21.7). This large ratio means that there is relatively little variability in the slope estimate, a_1. The standard error for the intercept, a_0, is 53.31513, which is roughly the same as the estimated value of 51.78709 for this coefficient. These similar values suggest that the estimate of this coefficient for this model can vary significantly.

The last column, labeled `Pr(>|t|)`, shows the probability that the corresponding coefficient is *not* relevant in the model. This value is also known

as the *significance* or p-value of the coefficient. In this example, the probability that `clock` is not relevant in this model is 2×10^{-16} - a tiny value. The probability that the intercept is not relevant is 0.332, or about a one-in-three chance that this specific intercept value is not relevant to the model. There is an intercept, of course, but we are again seeing indications that the model is not predicting this value very well.

The symbols printed to the right in this summary - that is, the asterisks, periods, or spaces - are intended to give a quick visual check of the coefficients' significance. The line labeled `Signif. codes:` gives these symbols' meanings. Three asterisks (***) means $0 < p \leq 0.001$, two asterisks (**) means $0.001 < p \leq 0.01$, and so on.

R uses the column labeled `t value` to compute the p-values and the corresponding significance symbols. You probably will not use these values directly when you evaluate your model's quality, so we will ignore this column for now.

```
Residual standard error: 396.1 on 254 degrees of freedom
Multiple R-squared:  0.6505,    Adjusted R-squared:  0.6491
F-statistic: 472.7 on 1 and 254 DF,  p-value: < 2.2e-16
```

These final few lines in the output provide some statistical information about the quality of the regression model's fit to the data. The `Residual standard error` is a measure of the total variation in the residual values. If the residuals are distributed normally, the first and third quantiles of the previous residuals should be about 1.5 times this standard error.

The number of `degrees of freedom` is the total number of measurements or *observations* used to generate the model, minus the number of coefficients in the model. This example had 256 unique rows in the data frame, corresponding to 256 independent measurements. We used this data to produce a regression model with two coefficients: the slope and the intercept. Thus, we are left with (256 - 2 = 254) degrees of freedom.

The `Multiple R-squared` value is a number between 0 and 1. It is a statistical measure of how well the model describes the measured data. We compute it by dividing the total variation that the model explains by the data's total variation. Multiplying this value by 100 gives a value that we can interpret as a percentage between 0 and 100. The reported R^2 of 0.6505 for this model means that the model explains 65.05 percent of the data's variation. Random chance and measurement errors creep in, so the model

will never explain all data variation. Consequently, you should not ever expect an R^2 value of exactly one. In general, values of R^2 that are closer to one indicate a better-fitting model. However, a good model does not necessarily require a large R^2 value. It may still accurately predict future observations, even with a small R^2 value.

The `Adjusted R-squared` value is the R^2 value modified to take into account the number of predictors used in the model. The adjusted R^2 is always smaller than the R^2 value. We will discuss the meaining of the adjusted R^2 in Chapter 4, when we present regression models that use more than one predictor.

The final line shows the `F-statistic`. This value compares the current model to a model that has one fewer parameters. Because the one-factor model already has only a single parameter, this test is not particularly useful in this case. It is an interesting statistic for the multi-factor models, however, as we will discuss later.

3.4 || Residual Analysis

The `summary()` function provides a substantial amount of information to help us evaluate a regression model's fit to the data used to develop that model. To dig deeper into the model's quality, we can analyze some additional information about the observed values compared to the values that the model predicts. In particular, *residual analysis* examines these residual values to see what they can tell us about the model's quality.

Recall that the residual value is the difference between the actual measured value stored in the data frame and the value that the fitted regression line predicts for that corresponding data point. Residual values greater than zero mean that the regression model predicted a value that was too small compared to the actual measured value, and negative values indicate that the regression model predicted a value that was too large. A model that fits the data well would tend to over-predict as often as it under-predicts. Thus, if we plot the residual values, we would expect to see them distributed uniformly around zero for a well-fitted model.

The following function calls produce the residuals plot for our model, shown in Figure 3.3.

```
> plot(fitted(int00.lm),resid(int00.lm))
```

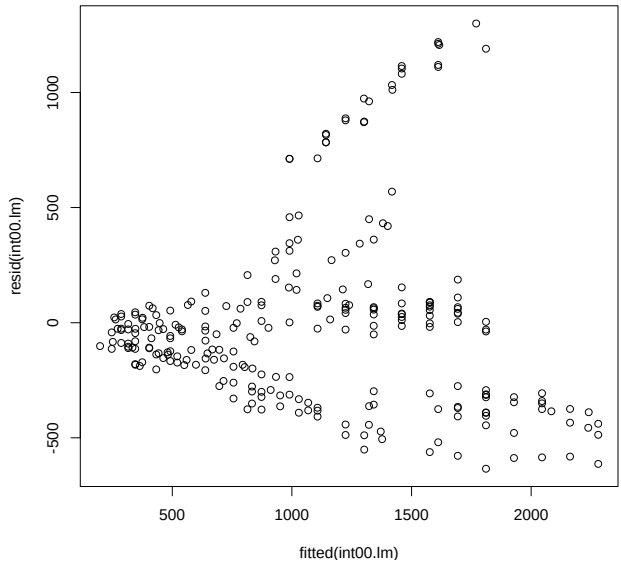

Figure 3.3: The residual values versus the input values for the one-factor model developed using the Int2000 data.

In this plot, we see that the residuals tend to increase as we move to the right. Additionally, the residuals are not uniformly scattered above and below zero. Overall, this plot tells us that using the clock as the sole predictor in the regression model does not sufficiently or fully explain the data. In general, if you observe any sort of clear trend or pattern in the residuals, you probably need to generate a better model. This does not mean that our simple one-factor model is useless, though. It only means that we may be able to construct a model that produces tighter residual values and better predictions.

Another test of the residuals uses the *quantile-versus-quantile*, or *Q-Q*, plot. Previously we said that, if the model fits the data well, we would expect the residuals to be normally (Gaussian) distributed around a mean of zero. The Q-Q plot provides a nice visual indication of whether the residuals from the model are normally distributed. The following function

calls generate the Q-Q plot shown in Figure 3.4:

```
> qqnorm(resid(int00.lm))
> qqline(resid(int00.lm))
```

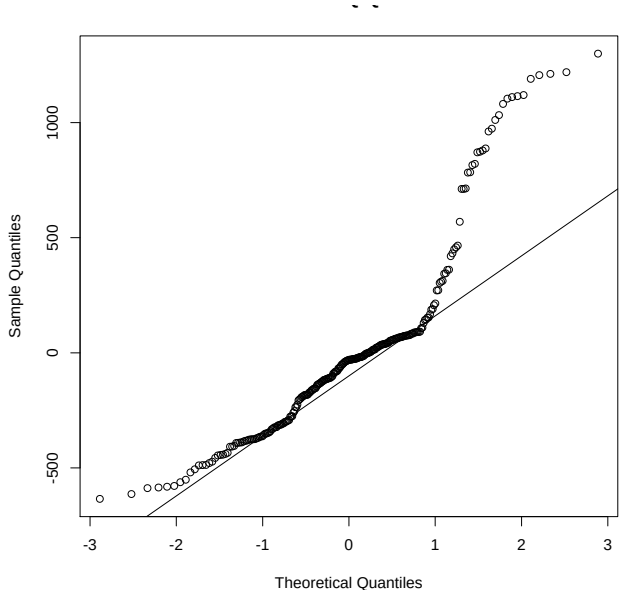

Figure 3.4: The Q-Q plot for the one-factor model developed using the Int2000 data.

If the residuals were normally distributed, we would expect the points plotted in this figure to follow a straight line. With our model, though, we see that the two ends diverge significantly from that line. This behavior indicates that the residuals are not normally distributed. In fact, this plot suggests that the distribution's tails are "heavier" than what we would expect from a normal distribution. This test further confirms that using only the clock as a predictor in the model is insufficient to explain the data.

Our next step is to learn to develop regression models with multiple input factors. Perhaps we will find a more complex model that is better able to explain the data.

4 | Multi-factor Regression

A multi-factor regression model is a generalization of the simple one-factor regression model discussed in Chapter 3. It has n factors with the form:

$$y = a_0 + a_1x_1 + a_2x_2 + ...a_nx_n, \tag{4.1}$$

where the x_i values are the inputs to the system, the a_i coefficients are the model parameters computed from the measured data, and y is the output value predicted by the model. Everything we learned in Chapter 3 for one-factor models also applies to the multi-factor models. To develop this type of multi-factor regression model, we must also learn how to select specific predictors to include in the model

4.1 || Visualizing the Relationships in the Data

Before beginning model development, it is useful to get a visual sense of the relationships within the data. We can do this easily with the following function call:

```
> pairs(int00.dat, gap=0.5)
```

The `pairs()` function produces the plot shown in Figure 4.1. This plot provides a pairwise comparison of all the data in the `int00.dat` data frame. The `gap` parameter in the function call controls the spacing between the individual plots. Set it to zero to eliminate any space between plots.

As an example of how to read this plot, locate the box near the upper left corner labeled `perf`. This is the value of the performance measured for the `int00.dat` data set. The box immediately to the right of this one is a scatter

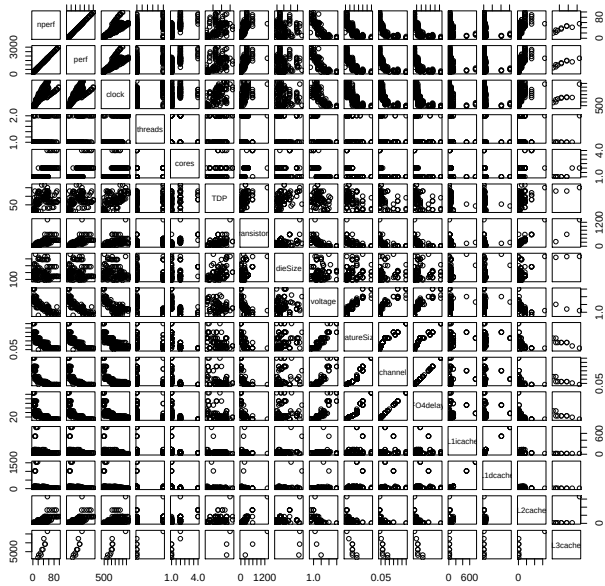

Figure 4.1: All of the pairwise comparisons for the Int2000 data frame.

plot, with `perf` data on the vertical axis and `clock` data on the horizontal axis. This is the same information we previously plotted in Figure 3.1. By scanning through these plots, we can see any obviously significant relationships between the variables. For example, we quickly observe that there is a somewhat proportional relationship between `perf` and `clock`. Scanning down the `perf` column, we also see that there might be a weakly inverse relationship between `perf` and `featureSize`.

Notice that there is a perfect linear correlation between `perf` and `nperf`. This relationship occurs because `nperf` is a simple rescaling of `perf`. The reported benchmark performance values in the database - that is, the `perf` values - use different scales for different benchmarks. To directly compare the values that our models will predict, it is useful to rescale `perf` to the range [0,100]. Do this quite easily, using this R code:

```
max_perf = max(perf)
min_perf = min(perf)
range = max_perf - min_perf
nperf = 100 * (perf - min_perf) / range
```

Note that this rescaling has no effect on the models we will develop, because it is a linear transformation of `perf`. For convenience and consistency, we use `nperf` in the remainder of this tutorial.

4.2 || Identifying Potential Predictors

The first step in developing the multi-factor regression model is to identify all possible predictors that we could include in the model. To the novice model developer, it may seem that we should include all factors available in the data as predictors, because more information is likely to be better than not enough information. However, a good regression model explains the relationship between a system's inputs and output as simply as possible. Thus, we should use the smallest number of predictors necessary to provide good predictions. Furthermore, using too many or redundant predictors builds the random noise in the data into the model. In this situation, we obtain an *over-fitted* model that is very good at predicting the outputs from the specific input data set used to *train* the model. It does not accurately model the overall system's response, though, and it will not appropriately predict the system output for a broader range of inputs than those on which it was trained. Redundant or unnecessary predictors also can lead to numerical instabilities when computing the coefficients.

We must find a balance between including too few and too many predictors. A model with too few predictors can produce biased predictions. On the other hand, adding more predictors to the model will always cause the R^2 value to increase. This can confuse you into thinking that the additional predictors generated a better model. In some cases, adding a predictor will improve the model, so the increase in the R^2 value makes sense. In some cases, however, the R^2 value increases simply because we've better modeled the random noise.

The *adjusted* R^2 attempts to compensate for the regular R^2's behavior by changing the R^2 value according to the number of predictors in the model. This adjustment helps us determine whether adding a predictor improves the fit of the model, or whether it is simply modeling the noise

better. It is computed as:

$$R^2_{adjusted} = 1 - \frac{n-1}{n-m}(1 - R^2) \tag{4.2}$$

where n is the number of observations and m is the number of predictors in the model. If adding a new predictor to the model increases the previous model's R^2 value by more than we would expect from random fluctuations, then the adjusted R^2 will increase. Conversely, it will decrease if removing a predictor decreases the R^2 by more than we would expect due to random variations. Recall that the goal is to use as few predictors as possible, while still producing a model that explains the data well.

Because we do not know *a priori* which input parameters will be useful predictors, it seems reasonable to start with all of the columns available in the measured data as the set of potential predictors. We listed all of the column names in Table 2.1. Before we throw all these columns into the modeling process, though, we need to step back and consider what we know about the underlying system, to help us find any parameters that we should obviously exclude from the start.

There are two output columns: `perf` and `nperf`. The regression model can have only one output, however, so we must choose only one column to use in our model development process. As discussed in Section 4.1, `nperf` is a linear transformation of `perf` that shifts the output range to be between 0 and 100. This range is useful for quickly obtaining a sense of future predictions' quality, so we decide to use `nperf` as our model's output and ignore the `perf` column.

Almost all the remaining possible predictors appear potentially useful in our model, so we keep them available as potential predictors for now. The only exception is `TDP`. The name of this factor, *thermal design power*, does not clearly indicate whether this could be a useful predictor in our model, so we must do a little additional research to understand it better. We discover [10] that thermal design power is "the average amount of power in watts that a cooling system must dissipate. Also called the 'thermal guideline' or 'thermal design point,' the TDP is provided by the chip manufacturer to the system vendor, who is expected to build a case that accommodates the chip's thermal requirements." From this definition, we conclude that `TDP` is not really a parameter that will directly affect per-

formance. Rather, it is a specification provided by the processor's manufacturer to ensure that the system designer includes adequate cooling capability in the final product. Thus, we decide not to include `TDP` as a potential predictor in the regression model.

In addition to excluding some apparently unhelpful factors (such as TDP) at the beginning of the model development process, we also should consider whether we should include any additional parameters. For example, the terms in a regression model add linearly to produce the predicted output. However, the individual terms themselves can be nonlinear, such as $a_i x_i^m$, where m does not have to be equal to one. This flexibility lets us include additional powers of the individual factors. We should include these non-linear terms, though, only if we have some physical reason to suspect that the output could be a nonlinear function of a particular input.

For example, we know from our prior experience modeling processor performance that empirical studies have suggested that cache miss rates are roughly proportional to the square root of the cache size [5]. Consequently, we will include terms for the square root ($m = {}^1/_2$) of each cache size as possible predictors. We must also include first-degree terms ($m = 1$) of each cache size as possible predictors. Finally, we notice that only a few of the entries in the `int00.dat` data frame include values for the L3 cache, so we decide to exclude the L3 cache size as a potential predictor. Exploiting this type of domain-specific knowledge when selecting predictors ultimately can help produce better models than blindly applying the model development process.

The final list of potential predictors that we will make available for the model development process is shown in Table 4.1.

Table 4.1: The list of potential predictors to be used in the model development process.

$clock$	$threads$	$cores$	$transistors$
$dieSize$	$voltage$	$featureSize$	$channel$
$FO4delay$	$L1icache$	$\sqrt{L1icache}$	$L1dcache$
$\sqrt{L1dcache}$	$L2cache$	$\sqrt{L2cache}$	

4.3 || The Backward Elimination Process

We are finally ready to develop the multi-factor linear regression model for the `int00.dat` data set. As mentioned in the previous section, we must find the right balance in the number of predictors that we use in our model. Too many predictors will train our model to follow the data's random variations (noise) too closely. Too few predictors will produce a model that may not be as accurate at predicting future values as a model with more predictors.

We will use a process called *backward elimination* [1] to help decide which predictors to keep in our model and which to exclude. In backward elimination, we start with all possible predictors and then use `lm()` to compute the model. We use the `summary()` function to find each predictor's significance level. The predictor with the least significance has the largest p-value. If this value is larger than our predetermined significance threshold, we remove that predictor from the model and start over. A typical threshold for keeping predictors in a model is $p = 0.05$, meaning that there is at least a 95 percent chance that the predictor is meaningful. A threshold of $p = 0.10$ also is not unusual. We repeat this process until the significance levels of all of the predictors remaining in the model are below our threshold.

Note that backward elimination is not the only approach to developing regression models. A complementary approach is *forward selection*. In this approach, we successively add potential predictors to the regression model as long as their significance levels in the computed model remain below the predefined threshold. This process continues, one at a time for each potential predictor, until all of the predictors have been tested. Other approaches include *step-wise regression*, *all possible regressions*, and *automated selection* approaches.

All of these approaches have their advantages and disadvantages, their supporters and detractors. I prefer the backward elimination process because it is usually straightforward to determine which factor we should drop at each step of the process. Determining which factor to try at each step is more difficult with forward selection. Backward elimination has a further advantage, in that several factors together may have better predictive power than any subset of these factors. As a result, the backward elimination process is more likely to include these factors as a group in the

final model than is the forward selection process.

The automated procedures have a very strong allure because, as technologically savvy individuals, we tend to believe that this type of automated process will likely test a broader range of possible predictor combinations than we could test manually. However, these automated procedures lack intuitive insights into the underlying physical nature of the system being modeled. Intuition can help us answer the question of whether this is a reasonable model to construct in the first place.

As you develop your models, continually ask yourself whether the model "makes sense." Does it make sense that factor i is included but factor j is excluded? Is there a physical explanation to support the inclusion or exclusion of any potential factor? Although the automated methods can simplify the process, they also make it too easy for you to forget to think about whether or not each step in the modeling process makes sense.

4.4 An Example of the Backward Elimination Process

We previously identified the list of possible predictors that we can include in our models, shown in Table 4.1. We start the backward elimination process by putting all these potential predictors into a model for the `int00.dat` data frame using the `lm()` function.

```
> int00.lm <- lm(nperf ~ clock + threads + cores + transistors +
    dieSize + voltage + featureSize + channel + FO4delay +
    L1icache + sqrt(L1icache) + L1dcache + sqrt(L1dcache) +
    L2cache + sqrt(L2cache), data=int00.dat)
```

This function call assigns the resulting linear model object to the variable `int00.lm`. As before, we use the suffix `.lm` to remind us that this variable is a linear model developed from the data in the corresponding data frame, `int00.dat`. The arguments in the function call tell `lm()` to compute a linear model that explains the output `nperf` as a function of the predictors separated by the "+" signs. The argument `data=int00.dat` explicitly passes to the `lm()` function the name of the data frame that should be used when developing this model. This `data=` argument is not necessary if we `attach()` the data frame `int00.dat` to the current workspace. However, it is useful to

explicitly specify the data frame that `lm()` should use, to avoid confusion when you manipulate multiple models simultaneously.

The `summary()` function gives us a great deal of information about the linear model we just created:

```
> summary(int00.lm)

Call:
lm(formula = nperf ~ clock + threads + cores + transistors +
    dieSize + voltage + featureSize + channel + FO4delay +
    L1icache + sqrt(L1icache) + L1dcache + sqrt(L1dcache) +
    L2cache + sqrt(L2cache), data = int00.dat)

Residuals:
    Min      1Q  Median      3Q     Max
-10.804  -2.702   0.000   2.285   9.809

Coefficients:
                Estimate Std. Error t value Pr(>|t|)
(Intercept)    -2.108e+01  7.852e+01  -0.268  0.78927
clock           2.605e-02  1.671e-03  15.594  < 2e-16 ***
threads        -2.346e+00  2.089e+00  -1.123  0.26596
cores           2.246e+00  1.782e+00   1.260  0.21235
transistors    -5.580e-03  1.388e-02  -0.402  0.68897
dieSize         1.021e-02  1.746e-02   0.585  0.56084
voltage        -2.623e+01  7.698e+00  -3.408  0.00117 **
featureSize     3.101e+01  1.122e+02   0.276  0.78324
channel         9.496e+01  5.945e+02   0.160  0.87361
FO4delay       -1.765e-02  1.600e+00  -0.011  0.99123
L1icache        1.102e+02  4.206e+01   2.619  0.01111 *
sqrt(L1icache) -7.390e+02  2.980e+02  -2.480  0.01593 *
L1dcache       -1.114e+02  4.019e+01  -2.771  0.00739 **
sqrt(L1dcache)  7.492e+02  2.739e+02   2.735  0.00815 **
L2cache        -9.684e-03  1.745e-03  -5.550 6.57e-07 ***
sqrt(L2cache)   1.221e+00  2.425e-01   5.034 4.54e-06 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 4.632 on 61 degrees of freedom
  (179 observations deleted due to missingness)
Multiple R-squared:  0.9652,    Adjusted R-squared:  0.9566
F-statistic: 112.8 on 15 and 61 DF,  p-value: < 2.2e-16
```

Notice a few things in this summary: First, a quick glance at the residuals shows that they are roughly balanced around a median of zero, which is what we like to see in our models. Also, notice the line, `(179 observations deleted due to missingness)`. This tells us that in 179 of the rows in the data frame - that is, in 179 of the processors for which performance re-

sults were reported for the Int2000 benchmark - some of the values in the columns that we would like to use as potential predictors were missing. These `NA` values caused R to automatically remove these data rows when computing the linear model.

The total number of observations used in the model equals the number of degrees of freedom remaining - 61 in this case - plus the total number of predictors in the model. Finally, notice that the R^2 and adjusted R^2 values are relatively close to one, indicating that the model explains the `nperf` values well. Recall, however, that these large R^2 values may simply show us that the model is good at modeling the noise in the measurements. We must still determine whether we should retain all these potential predictors in the model.

To continue developing the model, we apply the backward elimination procedure by identifying the predictor with the largest p-value that exceeds our predetermined threshold of $p = 0.05$. This predictor is `FO4delay`, which has a p-value of 0.99123. We can use the `update()` function to eliminate a given predictor and recompute the model in one step. The notation "`.~.`" means that `update()` should keep the left- and right-hand sides of the model the same. By including "`- FO4delay`," we also tell it to remove that predictor from the model, as shown in the following:

```
> int00.lm <- update(int00.lm, .~. - FO4delay, data = int00.dat)
> summary(int00.lm)

Call:
lm(formula = nperf ~ clock + threads + cores + transistors +
    dieSize + voltage + featureSize + channel + L1icache +
    sqrt(L1icache) + L1dcache + sqrt(L1dcache) + L2cache +
    sqrt(L2cache), data = int00.dat)

Residuals:
    Min      1Q  Median      3Q     Max
-10.795  -2.714   0.000   2.283   9.809

Coefficients:
                Estimate Std. Error t value Pr(>|t|)
(Intercept)    -2.088e+01  7.584e+01  -0.275 0.783983
clock           2.604e-02  1.563e-03  16.662  < 2e-16 ***
threads        -2.345e+00  2.070e+00  -1.133 0.261641
cores           2.248e+00  1.759e+00   1.278 0.206080
transistors    -5.556e-03  1.359e-02  -0.409 0.684020
dieSize         1.013e-02  1.571e-02   0.645 0.521488
voltage        -2.626e+01  7.302e+00  -3.596 0.000642 ***
featureSize     3.104e+01  1.113e+02   0.279 0.781232
```

```
channel          8.855e+01  1.218e+02   0.727 0.469815
L1icache         1.103e+02  4.041e+01   2.729 0.008257 **
sqrt(L1icache) -7.398e+02  2.866e+02  -2.581 0.012230 *
L1dcache        -1.115e+02  3.859e+01  -2.889 0.005311 **
sqrt(L1dcache)   7.500e+02  2.632e+02   2.849 0.005937 **
L2cache         -9.693e-03  1.494e-03  -6.488 1.64e-08 ***
sqrt(L2cache)    1.222e+00  1.975e-01   6.189 5.33e-08 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 4.594 on 62 degrees of freedom
  (179 observations deleted due to missingness)
Multiple R-squared:  0.9652,    Adjusted R-squared:  0.9573
F-statistic: 122.8 on 14 and 62 DF,  p-value: < 2.2e-16
```

We repeat this process by removing the next potential predictor with the largest p-value that exceeds our predetermined threshold, `featureSize`. As we repeat this process, we obtain the following sequence of possible models.

Remove `featureSize`:

```
> int00.lm <- update(int00.lm, .~. - featureSize, data=int00.dat)
> summary(int00.lm)

Call:
lm(formula = nperf ~ clock + threads + cores + transistors +
    dieSize + voltage + channel + L1icache + sqrt(L1icache) +
    L1dcache + sqrt(L1dcache) + L2cache + sqrt(L2cache), data =
    int00.dat)

Residuals:
     Min       1Q   Median       3Q      Max
-10.5548  -2.6442   0.0937   2.2010  10.0264

Coefficients:
                Estimate Std. Error t value Pr(>|t|)
(Intercept)    -3.129e+01  6.554e+01  -0.477 0.634666
clock           2.591e-02  1.471e-03  17.609  < 2e-16 ***
threads        -2.447e+00  2.022e+00  -1.210 0.230755
cores           1.901e+00  1.233e+00   1.541 0.128305
transistors    -5.366e-03  1.347e-02  -0.398 0.691700
dieSize         1.325e-02  1.097e-02   1.208 0.231608
voltage        -2.519e+01  6.182e+00  -4.075 0.000131 ***
channel         1.188e+02  5.504e+01   2.158 0.034735 *
L1icache        1.037e+02  3.255e+01   3.186 0.002246 **
sqrt(L1icache) -6.930e+02  2.307e+02  -3.004 0.003818 **
L1dcache       -1.052e+02  3.106e+01  -3.387 0.001223 **
sqrt(L1dcache)  7.069e+02  2.116e+02   3.341 0.001406 **
L2cache        -9.548e-03  1.390e-03  -6.870 3.37e-09 ***
sqrt(L2cache)   1.202e+00  1.821e-01   6.598 9.96e-09 ***
```

```
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Residual standard error: 4.56 on 63 degrees of freedom
  (179 observations deleted due to missingness)
Multiple R-squared:  0.9651,    Adjusted R-squared:  0.958
F-statistic: 134.2 on 13 and 63 DF,  p-value: < 2.2e-16
```

Remove `transistors`:

```
> int00.lm <- update(int00.lm, .~. - transistors, data=int00.dat)
> summary(int00.lm)

Call:
lm(formula = nperf ~ clock + threads + cores + dieSize + voltage +
    channel + L1icache + sqrt(L1icache) + L1dcache +
    sqrt(L1dcache) + L2cache + sqrt(L2cache), data = int00.dat)

Residuals:
    Min      1Q  Median      3Q     Max
-9.8861 -3.0801 -0.1871  2.4534 10.4863

Coefficients:
                Estimate Std. Error t value Pr(>|t|)
(Intercept)    -7.789e+01  4.318e+01  -1.804 0.075745 .
clock           2.566e-02  1.422e-03  18.040  < 2e-16 ***
threads        -1.801e+00  1.995e+00  -0.903 0.369794
cores           1.805e+00  1.132e+00   1.595 0.115496
dieSize         1.111e-02  8.807e-03   1.262 0.211407
voltage        -2.379e+01  5.734e+00  -4.148 9.64e-05 ***
channel         1.512e+02  3.918e+01   3.861 0.000257 ***
L1icache        8.159e+01  2.006e+01   4.067 0.000128 ***
sqrt(L1icache) -5.386e+02  1.418e+02  -3.798 0.000317 ***
L1dcache       -8.422e+01  1.914e+01  -4.401 3.96e-05 ***
sqrt(L1dcache)  5.671e+02  1.299e+02   4.365 4.51e-05 ***
L2cache        -8.700e-03  1.262e-03  -6.893 2.35e-09 ***
sqrt(L2cache)   1.069e+00  1.654e-01   6.465 1.36e-08 ***
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Residual standard error: 4.578 on 67 degrees of freedom
  (176 observations deleted due to missingness)
Multiple R-squared:  0.9657,    Adjusted R-squared:  0.9596
F-statistic: 157.3 on 12 and 67 DF,  p-value: < 2.2e-16
```

Remove `threads`:

```
> int00.lm <- update(int00.lm, .~. - threads, data=int00.dat)
> summary(int00.lm)

Call:
```

```
lm(formula = nperf ~ clock + cores + dieSize + voltage + channel +
    L1icache + sqrt(L1icache) + L1dcache + sqrt(L1dcache) +
    L2cache + sqrt(L2cache), data = int00.dat)

Residuals:
    Min      1Q  Median      3Q     Max
-9.7388 -3.2326  0.1496  2.6633 10.6255

Coefficients:
                 Estimate Std. Error t value Pr(>|t|)
(Intercept)    -8.022e+01  4.304e+01  -1.864 0.066675 .
clock           2.552e-02  1.412e-03  18.074  < 2e-16 ***
cores           2.271e+00  1.006e+00   2.257 0.027226 *
dieSize         1.281e-02  8.592e-03   1.491 0.140520
voltage        -2.299e+01  5.657e+00  -4.063 0.000128 ***
channel         1.491e+02  3.905e+01   3.818 0.000293 ***
L1icache        8.131e+01  2.003e+01   4.059 0.000130 ***
sqrt(L1icache) -5.356e+02  1.416e+02  -3.783 0.000329 ***
L1dcache       -8.388e+01  1.911e+01  -4.390 4.05e-05 ***
sqrt(L1dcache)  5.637e+02  1.297e+02   4.346 4.74e-05 ***
L2cache        -8.567e-03  1.252e-03  -6.844 2.71e-09 ***
sqrt(L2cache)   1.040e+00  1.619e-01   6.422 1.54e-08 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 4.572 on 68 degrees of freedom
  (176 observations deleted due to missingness)
Multiple R-squared:  0.9653,    Adjusted R-squared:  0.9597
F-statistic:   172 on 11 and 68 DF,  p-value: < 2.2e-16
```

Remove `dieSize`:

```
> int00.lm <- update(int00.lm, .~. - dieSize, data=int00.dat)
> summary(int00.lm)

Call:
lm(formula = nperf ~ clock + cores + voltage + channel + L1icache
    + sqrt(L1icache) + L1dcache + sqrt(L1dcache) + L2cache +
    sqrt(L2cache), data = int00.dat)

Residuals:
     Min       1Q   Median       3Q      Max
-10.0240  -3.5195   0.3577   2.5486  12.0545

Coefficients:
                 Estimate Std. Error t value Pr(>|t|)
(Intercept)    -5.822e+01  3.840e+01  -1.516 0.133913
clock           2.482e-02  1.246e-03  19.922  < 2e-16 ***
cores           2.397e+00  1.004e+00   2.389 0.019561 *
voltage        -2.358e+01  5.495e+00  -4.291 5.52e-05 ***
channel         1.399e+02  3.960e+01   3.533 0.000726 ***
L1icache        8.703e+01  1.972e+01   4.412 3.57e-05 ***
```

```
sqrt(L1icache) -5.768e+02  1.391e+02  -4.146 9.24e-05 ***
L1dcache       -8.903e+01  1.888e+01  -4.716 1.17e-05 ***
sqrt(L1dcache)  5.980e+02  1.282e+02   4.665 1.41e-05 ***
L2cache        -8.621e-03  1.273e-03  -6.772 3.07e-09 ***
sqrt(L2cache)   1.085e+00  1.645e-01   6.598 6.36e-09 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 4.683 on 71 degrees of freedom
  (174 observations deleted due to missingness)
Multiple R-squared:  0.9641,    Adjusted R-squared:  0.959
F-statistic: 190.7 on 10 and 71 DF,  p-value: < 2.2e-16
```

At this point, the p-values for all of the predictors are less than 0.02, which is less than our predetermined threshold of 0.05. This tells us to stop the backward elimination process. Intuition and experience tell us that ten predictors are a rather large number to use in this type of model. Nevertheless, all of these predictors have p-values below our significance threshold, so we have no reason to exclude any specific predictor. We decide to include all ten predictors in the final model:

$$\begin{aligned} nperf = &- 58.22 + 0.02482clock + 2.397cores \\ &- 23.58voltage + 139.9channel + 87.03L1icache \\ &- 576.8\sqrt{L1icache} - 89.03L1dcache + 598\sqrt{L1dcache} \\ &- 0.008621L2cache + 1.085\sqrt{L2cache}. \end{aligned}$$

Looking back over the sequence of models we developed, notice that the number of degrees of freedom in each subsequent model increases as predictors are excluded, as expected. In some cases, the number of degrees of freedom increases by more than one when only a single predictor is eliminated from the model. To understand how an increase of more than one is possible, look at the sequence of values in the lines labeled `the number of observations dropped due to missingness`. These values show how many rows the `update()` function dropped because the value for one of the predictors in those rows was missing and had the `NA` value. When the backward elimination process removed that predictor from the model, at least some of those rows became ones we can use in computing the next version of the model, thereby increasing the number of degrees of freedom.

Also notice that, as predictors drop from the model, the R^2 values stay very close to 0.965. However, the adjusted R^2 value tends to increase very slightly with each dropped predictor. This increase indicates that the model with fewer predictors and more degrees of freedom tends to explain the data slightly better than the previous model, which had one more predictor. These changes in R^2 values are very small, though, so we should not read too much into them. It is possible that these changes are simply due to random data fluctuations. Nevertheless, it is nice to see them behaving as we expect.

Roughly speaking, the F-test compares the current model to a model with one fewer predictor. If the current model is better than the reduced model, the p-value will be small. In all of our models, we see that the p-value for the F-test is quite small and consistent from model to model. As a result, this F-test does not particularly help us discriminate between potential models.

4.5 || Residual Analysis

To check the validity of the assumptions used to develop our model, we can again apply the residual analysis techniques that we used to examine the one-factor model in Section 3.4.

This function call:

```
> plot(fitted(int00.lm),resid(int00.lm))
```

produces the plot shown in Figure 4.2. We see that the residuals appear to be somewhat uniformly scattered about zero. At least, we do not see any obvious patterns that lead us to think that the residuals are not well behaved. Consequently, this plot gives us no reason to believe that we have produced a poor model.

The Q-Q plot in Figure 4.3 is generated using these commands:

```
> qqnorm(resid(int00.lm))
> qqline(resid(int00.lm))
```

We see the that residuals roughly follow the indicated line. In this plot, we can see a bit more of a pattern and some obvious nonlinearities, leading us to be slightly more cautious about concluding that the residuals are

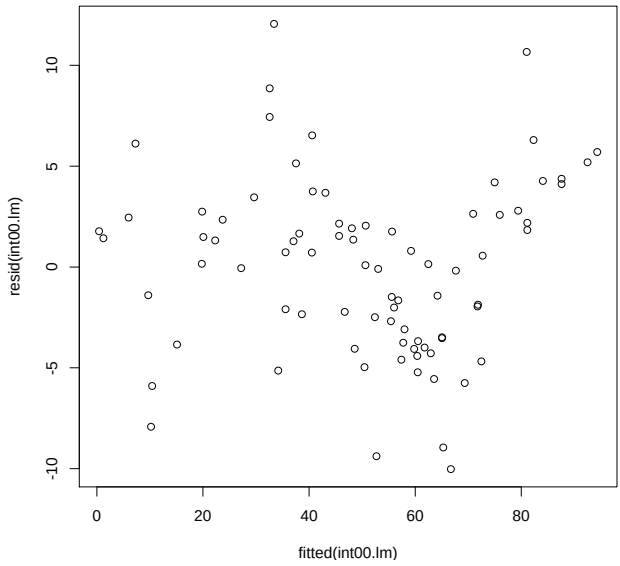

Figure 4.2: The fitted versus residual values for the multi-factor model developed from the Int2000 data.

normally distributed. We should not necessarily reject the model based on this one test, but the results should serve as a reminder that all models are imperfect.

4.6 || When Things Go Wrong

Sometimes when we try to develop a model using the backward elimination process, we get results that do not appear to make any sense. For an example, let's try to develop a multi-factor regression model for the Int1992 data using this process. As before, we begin by including all of the potential predictors from Table 4.1 in the model. When we try that for Int1992, however, we obtain the following result:

```
> int92.lm<-lm(nperf ~ clock + threads + cores + transistors +
    dieSize + voltage + featureSize + channel + FO4delay +
```

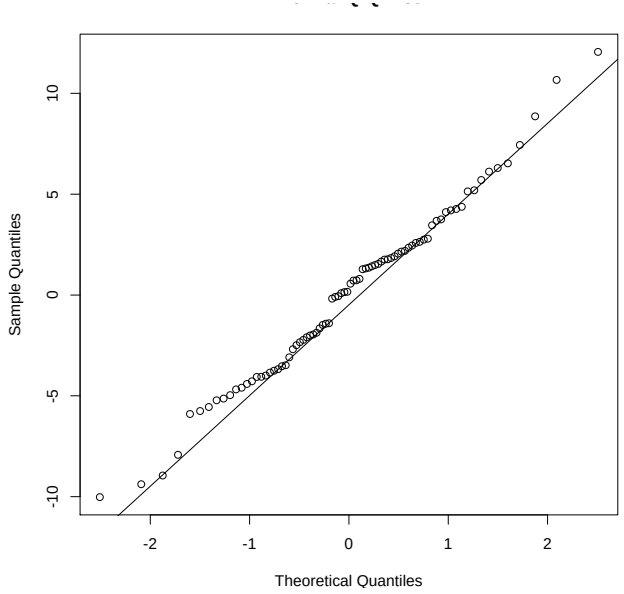

Figure 4.3: The Q-Q plot for the multi-factor model developed from the Int2000 data.

```
    L1icache + sqrt(L1icache) + L1dcache + sqrt(L1dcache) +
    L2cache + sqrt(L2cache))
> summary(int92.lm)

Call:
lm(formula = nperf ~ clock + threads + cores + transistors +
    dieSize + voltage + featureSize + channel + FO4delay +
    L1icache + sqrt(L1icache) + L1dcache + sqrt(L1dcache) +
    L2cache + sqrt(L2cache))

Residuals:
     14      15      16      17      18      19
 0.4096  1.3957 -2.3612  0.1498 -1.5513  1.9575

Coefficients: (14 not defined because of singularities)
               Estimate Std. Error t value Pr(>|t|)
(Intercept)    -25.93278    6.56141  -3.952   0.0168 *
clock            0.35422    0.02184  16.215 8.46e-05 ***
threads               NA         NA      NA       NA
cores                 NA         NA      NA       NA
transistors           NA         NA      NA       NA
```

```
dieSize                NA          NA       NA        NA
voltage                NA          NA       NA        NA
featureSize            NA          NA       NA        NA
channel                NA          NA       NA        NA
FO4delay               NA          NA       NA        NA
L1icache               NA          NA       NA        NA
sqrt(L1icache)         NA          NA       NA        NA
L1dcache               NA          NA       NA        NA
sqrt(L1dcache)         NA          NA       NA        NA
L2cache                NA          NA       NA        NA
sqrt(L2cache)          NA          NA       NA        NA
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 1.868 on 4 degrees of freedom
  (72 observations deleted due to missingness)
Multiple R-squared:  0.985,     Adjusted R-squared:  0.9813
F-statistic: 262.9 on 1 and 4 DF,  p-value: 8.463e-05
```

Notice that every predictor but `clock` has `NA` for every entry. Furthermore, we see a line that says that fourteen coefficients were "not defined because of singularities." This statement means that R could not compute a value for those coefficients because of some anomalies in the data. (More technically, it could not invert the matrix used in the least-squares minimization process.)

The first step toward resolving this problem is to notice that 72 observations were deleted due to "missingness," leaving only four degrees of freedom. We use the function `nrow(int92.dat)` to determine that there are 78 total rows in this data frame. These 78 separate observations sum up to the two predictors used in the model, plus four degrees of freedom, plus 72 deleted rows. When we tried to develop the model using `lm()`, however, some of our data remained unused.

To determine why these rows were excluded, we must do a bit of sanity checking to see what data anomalies may be causing the problem. The function `table()` provides a quick way to summarize a data vector, to see if anything looks obviously out of place. Executing this function on the `clock` column, we obtain the following:

```
> table(clock)
clock
 48  50  60  64  66  70  75  77  80  85  90  96  99 100 101 110
    118 120 125 133 150 166 175 180 190 200 225 231 233 250 266
    275 291 300 333 350
  1   3   4   1   5   1   4   1   2   1   2   1   2  10   1   1
```

```
    1   3   4   4   3   2   2   1   1   4   1   1   2   2   2   1
    1   1   1   1
```

The top line shows the unique values that appear in the column. The list of numbers directly below that line is the count of how many times that particular value appeared in the column. For example, `48` appeared once, while `50` appeared three times and `60` appeared four times. We see a reasonable range of values with minimum (`48`) and maximum (`350`) values that are not unexpected. Some of the values occur only once; the most frequent value occurs ten times, which again does not seem unreasonable. In short, we do not see anything obviously amiss with these results. We conclude that the problem likely is with a different data column.

Executing the `table()` function on the next column in the data frame `threads` produces this output:

```
> table(threads)
threads
 1
78
```

Aha! Now we are getting somewhere. This result shows that all of the 78 entries in this column contain the same value: `1`. An input factor in which all of the elements are the same value has no predictive power in a regression model. If every row has the same value, we have no way to distinguish one row from another. Thus, we conclude that `threads` is not a useful predictor for our model and we eliminate it as a potential predictor as we continue to develop our Int1992 regression model.

We continue by executing `table()` on the column labeled `cores`. This operation shows that this column also consists of only a single value, `1`. Using the `update()` function to eliminate these two predictors from the model gives the following:

```
> int92.lm <- update(int92.lm, .~. - threads - cores)
> summary(int92.lm)

Call:
lm(formula = nperf ~ clock + transistors + dieSize + voltage +
    featureSize + channel + FO4delay + L1icache + sqrt(L1icache) +
    L1dcache + sqrt(L1dcache) + L2cache + sqrt(L2cache))

Residuals:
     14      15      16      17      18      19
 0.4096  1.3957 -2.3612  0.1498 -1.5513  1.9575
```

```
Coefficients: (12 not defined because of singularities)
               Estimate Std. Error t value Pr(>|t|)
(Intercept)   -25.93278    6.56141  -3.952   0.0168 *
clock           0.35422    0.02184  16.215 8.46e-05 ***
transistors          NA         NA      NA       NA
dieSize              NA         NA      NA       NA
voltage              NA         NA      NA       NA
featureSize          NA         NA      NA       NA
channel              NA         NA      NA       NA
FO4delay             NA         NA      NA       NA
L1icache             NA         NA      NA       NA
sqrt(L1icache)       NA         NA      NA       NA
L1dcache             NA         NA      NA       NA
sqrt(L1dcache)       NA         NA      NA       NA
L2cache              NA         NA      NA       NA
sqrt(L2cache)        NA         NA      NA       NA
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Residual standard error: 1.868 on 4 degrees of freedom
  (72 observations deleted due to missingness)
Multiple R-squared:  0.985,     Adjusted R-squared:  0.9813
F-statistic: 262.9 on 1 and 4 DF,  p-value: 8.463e-05
```

Unfortunately, eliminating these two predictors from consideration has not solved the problem. Notice that we still have only four degrees of freedom, because 72 observations were again eliminated. This small number of degrees of freedom indicates that there must be at least one more column with insufficient data.

By executing `table()` on the remaining columns, we find that the column labeled `L2cache` has only three unique values, and that these appear in a total of only ten rows:

```
> table(L2cache)
L2cache
 96 256 512
  6   2   2
```

Although these specific data values do not look out of place, having only three unique values can make it impossible for `lm()` to compute the model coefficients. Dropping `L2cache` and `sqrt(L2cache)` as potential predictors finally produces the type of result we expect:

```
> int92.lm <- update(int92.lm, .~. - L2cache - sqrt(L2cache))
> summary(int92.lm)
```

```
Call:
lm(formula = nperf ~ clock + transistors + dieSize + voltage +
    featureSize + channel + FO4delay + L1icache + sqrt(L1icache) +
    L1dcache + sqrt(L1dcache))

Residuals:
    Min      1Q  Median      3Q     Max
-7.3233 -1.1756  0.2151  1.0157  8.0634

Coefficients:
                Estimate Std. Error t value Pr(>|t|)
(Intercept)     -58.51730   17.70879  -3.304  0.00278 **
clock             0.23444    0.01792  13.084 6.03e-13 ***
transistors      -0.32032    1.13593  -0.282  0.78018
dieSize           0.25550    0.04800   5.323 1.44e-05 ***
voltage           1.66368    1.61147   1.032  0.31139
featureSize     377.84287   69.85249   5.409 1.15e-05 ***
channel        -493.84797   88.12198  -5.604 6.88e-06 ***
FO4delay          0.14082    0.08581   1.641  0.11283
L1icache          4.21569    1.74565   2.415  0.02307 *
sqrt(L1icache)  -12.33773    7.76656  -1.589  0.12425
L1dcache         -5.53450    2.10354  -2.631  0.01412 *
sqrt(L1dcache)   23.89764    7.98986   2.991  0.00602 **
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 3.68 on 26 degrees of freedom
  (40 observations deleted due to missingness)
Multiple R-squared:  0.985,     Adjusted R-squared:  0.9786
F-statistic:   155 on 11 and 26 DF,  p-value: < 2.2e-16
```

We now can proceed with the normal backward elimination process. We begin by eliminating the predictor that has the largest p-value above our preselected threshold, which is `transistors` in this case. Eliminating this predictor gives the following:

```
> int92.lm <- update(int92.lm, .~. -transistors)
> summary(int92.lm)

Call:
lm(formula = nperf ~ clock + dieSize + voltage + featureSize +
    channel + FO4delay + L1icache + sqrt(L1icache) + L1dcache +
    sqrt(L1dcache))

Residuals:
     Min       1Q   Median       3Q      Max
-13.2935  -3.6068  -0.3808   2.4535  19.9617

Coefficients:
                Estimate Std. Error t value Pr(>|t|)
```

```
(Intercept)    -16.73899   24.50101  -0.683 0.499726
clock            0.19330    0.02091   9.243 2.77e-10 ***
dieSize          0.11457    0.02728   4.201 0.000219 ***
voltage          0.40317    2.85990   0.141 0.888834
featureSize     11.08190  104.66780   0.106 0.916385
channel        -37.23928  104.22834  -0.357 0.723379
FO4delay        -0.13803    0.14809  -0.932 0.358763
L1icache         7.84707    3.33619   2.352 0.025425 *
sqrt(L1icache) -16.28582   15.38525  -1.059 0.298261
L1dcache       -14.31871    2.94480  -4.862 3.44e-05 ***
sqrt(L1dcache)  48.26276    9.41996   5.123 1.64e-05 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 7.528 on 30 degrees of freedom
  (37 observations deleted due to missingness)
Multiple R-squared:  0.9288,    Adjusted R-squared:  0.9051
F-statistic: 39.13 on 10 and 30 DF,  p-value: 1.802e-14
```

After eliminating this predictor, however, we see something unexpected. The p-values for `voltage` and `featureSize` increased dramatically. Furthermore, the adjusted R-squared value dropped substantially, from 0.9786 to 0.9051. These unexpectedly large changes make us suspect that `transistors` may actually be a useful predictor in the model even though at this stage of the backward elimination process it has a high p-value. So, we decide to put `transistors` back into the model and instead drop `voltage`, which has the next highest p-value. These changes produce the following result:

```
> int92.lm <- update(int92.lm, .~. +transistors -voltage)
> summary(int92.lm)

Call:
lm(formula = nperf ~ clock + dieSize + featureSize + channel +
    FO4delay + L1icache + sqrt(L1icache) + L1dcache +
    sqrt(L1dcache) +
    transistors)

Residuals:
     Min       1Q   Median       3Q      Max
-10.0828  -1.3106   0.1447   1.5501   8.7589

Coefficients:
                Estimate Std. Error t value Pr(>|t|)
(Intercept)     -50.28514   15.27839  -3.291 0.002700 **
clock             0.21854    0.01718  12.722 3.71e-13 ***
dieSize           0.20348    0.04401   4.623 7.77e-05 ***
featureSize     409.68604   67.00007   6.115 1.34e-06 ***
channel        -490.99083   86.23288  -5.694 4.18e-06 ***
FO4delay          0.12986    0.09159   1.418 0.167264
```

```
L1icache          1.48070    1.21941   1.214 0.234784
sqrt(L1icache)   -5.15568    7.06192  -0.730 0.471413
L1dcache         -0.45668    0.10589  -4.313 0.000181 ***
sqrt(L1dcache)    4.77962    2.45951   1.943 0.062092 .
transistors       1.54264    0.88345   1.746 0.091750 .
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 3.96 on 28 degrees of freedom
  (39 observations deleted due to missingness)
Multiple R-squared:  0.9813,    Adjusted R-squared:  0.9746
F-statistic: 146.9 on 10 and 28 DF,  p-value: < 2.2e-16
```

The adjusted R-squared value now is 0.9746, which is much closer to the adjusted R-squared value we had before dropping `transistors`. Continuing with the backward elimination process, we first drop `sqrt(L1icache)` with a p-value of 0.471413, then `FO4delay` with a p-value of 0.180836, and finally `sqrt(L1dcache)` with a p-value of 0.071730.

After completing this backward elimination process, we find that the following predictors belong in the final model for Int1992:

$$clock \quad transistors \quad dieSize \quad featureSize$$
$$channel \quad L1icache \quad L1dcache$$

As shown below, all of these predictors have p-values below our threshold of 0.05. Additionally, the adjusted R-square looks quite good at 0.9722.

```
> int92.lm <- update(int92.lm, .~. -sqrt(L1dcache))
> summary(int92.lm)

Call:
lm(formula = nperf ~ clock + dieSize + featureSize + channel +
    L1icache + L1dcache + transistors, data = int92.dat)

Residuals:
     Min       1Q   Median       3Q      Max
-10.1742  -1.5180   0.1324   1.9967  10.1737

Coefficients:
              Estimate Std. Error t value Pr(>|t|)
(Intercept)  -34.17260    5.47413  -6.243 6.16e-07 ***
clock          0.18973    0.01265  15.004 9.21e-16 ***
dieSize        0.11751    0.02034   5.778 2.31e-06 ***
featureSize  305.79593   52.76134   5.796 2.20e-06 ***
channel     -328.13544   53.04160  -6.186 7.23e-07 ***
L1icache       0.78911    0.16045   4.918 2.72e-05 ***
L1dcache      -0.23335    0.03222  -7.242 3.80e-08 ***
```

```
transistors    3.13795    0.51450   6.099 9.26e-07 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 4.141 on 31 degrees of freedom
  (39 observations deleted due to missingness)
Multiple R-squared:  0.9773,    Adjusted R-squared:  0.9722
F-statistic:   191 on 7 and 31 DF,  p-value: < 2.2e-16
```

This example illustrates that you cannot always look at only the p-values to determine which potential predictors to eliminate in each step of the backward elimination process. You also must be careful to look at the broader picture, such as changes in the adjusted R-squared value and large changes in the p-values of other predictors, after each change to the model.

5 | Predicting Responses

PREDICTION is typically the primary goal of most regression modeling projects. That is, the model developer wants to use the model to estimate or predict the system's response if it were operated with input values that were never actually available in any of the measured systems. For instance, we might want to use the model we developed using the Int2000 data set to predict the performance of a new processor with a clock frequency, a cache size, or some other parameter combination that does not exist in the data set. By inserting this new combination of parameter values into the model, we can compute the new processor's expected performance when executing that benchmark program.

Because the model was developed using measured data, the coefficient values necessarily are only estimates. Consequently, any predictions we make with the model are also only estimates. The `summary()` function produces useful statistics about the regression model's quality, such as the R^2 and adjusted R^2 values. These statistics offer insights into how well the model explains variation in the data. The best indicator of any regression model's quality, however, is how well it predicts output values. The R environment provides some powerful functions that help us predict new values from a given model and evaluate the quality of these predictions.

5.1 || Data Splitting for Training and Testing

In Chapter 4 we used all of the data available in the `int00.dat` data frame to select the appropriate predictors to include in the final regression model. Because we computed the model to fit this particular data set, we cannot now use this same data set to test the model's predictive capabilities. That

would be like copying exam answers from the answer key and then using that same answer key to grade your exam. Of course you would get a perfect result. Instead, we must use one set of data to *train* the model and another set of data to *test* it.

The difficulty with this train-test process is that we need separate but similar data sets. A standard way to find these two different data sets is to split the available data into two parts. We take a random portion of all the available data and call it our *training set*. We then use this portion of the data in the `lm()` function to compute the specific values of the model's coefficients. We use the remaining portion of the data as our *testing set* to see how well the model predicts the results, compared to this test data.

The following sequence of operations splits the `int00.dat` data set into the training and testing sets:

```
rows <- nrow(int00.dat)
f <- 0.5
upper_bound <- floor(f * rows)
permuted_int00.dat <- int00.dat[sample(rows), ]
train.dat <- permuted_int00.dat[1:upper_bound, ]
test.dat <- permuted_int00.dat[(upper_bound+1):rows, ]
```

The first line assigns the total number of rows in the `int00.dat` data frame to the variable `rows`. The next line assigns to the variable `f` the fraction of the entire data set we wish to use for the training set. In this case, we somewhat arbitrarily decide to use half of the data as the training set and the other half as the testing set. The `floor()` function rounds its argument value down to the nearest integer. So the line `upper_bound <- floor(f * rows)` assigns the middle row's index number to the variable `upper_bound`.

The interesting action happens in the next line. The `sample()` function returns a permutation of the integers between 1 and n when we give it the integer value n as its input argument. In this code, the expression `sample(rows)` returns a vector that is a permutation of the integers between 1 and `rows`, where `rows` is the total number of rows in the `int00.dat` data frame. Using this vector as the row index for this data frame gives a random permutation of all of the rows in the data frame, which we assign to the new data frame, `permuted_int00.dat`. The next two lines assign the lower portion of this new data frame to the training data set and the top portion to the testing data set, respectively. This randomization process ensures that we obtain a new random selection of the rows in the train-and-test data sets

every time we execute this sequence of operations.

5.2 || Training and Testing

With the data set partitioned into two randomly selected portions, we can train the model on the first portion, and test it on the second portion. Figure 5.1shows the overall flow of this training and testing process. We next explain the details of this process to train and test the model we previously developed for the Int2000 benchmark results.

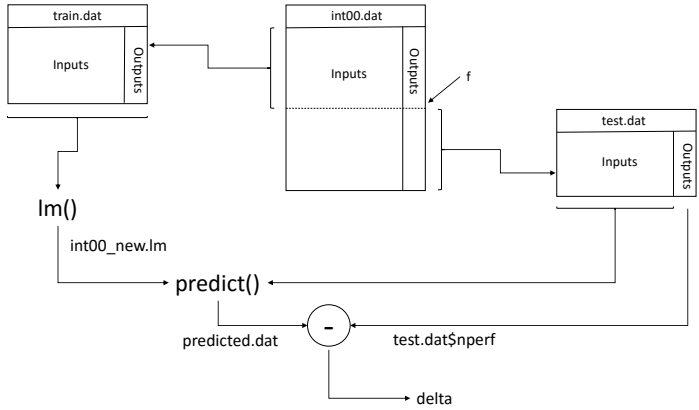

Figure 5.1: The training and testing process for evaluating the predictions produced by a regression model.

The following statement calls the `lm()` function to generate a regression model using the predictors we identified in Chapter 4 and the `train.dat` data frame we extracted in the previous section. It then assigns this model to the variable `int00_new.lm`. We refer to this process of computing the model's coefficients as *training* the regression model.

```
int00_new.lm <- lm(nperf ~ clock + cores + voltage + channel +
    L1icache + sqrt(L1icache) + L1dcache + sqrt(L1dcache) +
    L2cache + sqrt(L2cache), data = train.dat)
```

The `predict()` function takes this new model as one of its arguments. It uses this model to compute the predicted outputs when we use the `test.dat` data frame as the input, as follows:

```
predicted.dat <- predict(int00_new.lm, newdata=test.dat)
```

We define the difference between the predicted and measured performance for each processor i to be $\Delta_i = Predicted_i - Measured_i$, where $Predicted_i$ is the value predicted by the model, which is stored in the data frame `predicted.dat`, and $Measured_i$ is the actual measured performance response, which we previously assigned to the `test.dat` data frame. The following statement computes the entire vector of these Δ_i values and assigns the vector to the variable `delta`.

```
delta <- predicted.dat - test.dat$nperf
```

Note that we use the `$` notation to select the column with the output value, `nperf`, from the `test.dat` data frame.

The mean of these Δ differences for n different processors is:

$$\bar{\Delta} = \frac{1}{n}\sum_{i=1}^{n}\Delta_i \tag{5.1}$$

A confidence interval computed for this mean will give us some indication of how well a model trained on the `train.dat` data set predicted the performance of the processors in the `test.dat` data set. The `t.test()` function computes a confidence interval for the desired confidence level of these Δ_i values as follows:

```
> t.test(delta, conf.level = 0.95)

        One Sample t-test

data:  delta
t = -0.65496, df = 41, p-value = 0.5161
alternative hypothesis: true mean is not equal to 0
95 percent confidence interval:
 -2.232621  1.139121
sample estimates:
 mean of x
-0.5467502
```

If the prediction were perfect, then $\Delta_i = 0$. If $\Delta_i > 0$, then the model predicted that the performance would be greater than it actually was. A

$\Delta_i < 0$, on the other hand, means that the model predicted that the performance was lower than it actually was. Consequently, if the predictions were reasonably good, we would expect to see a tight confidence interval around zero. In this case, we obtain a 95 percent confidence interval of [-2.23, 1.14]. Given that $nperf$ is scaled to between 0 and 100, this is a reasonably tight confidence interval that includes zero. Thus, we conclude that the model is reasonably good at predicting values in the `test.dat` data set when trained on the `train.dat` data set.

Another way to get a sense of the predictions' quality is to generate a scatter plot of the Δ_i values using the `plot()` function:

```
plot(delta)
```

This function call produces the plot shown in Figure 5.2. Good predictions would produce a tight band of values uniformly scattered around zero. In this figure, we do see such a distribution, although there are a few outliers that are more than ten points above or below zero.

It is important to realize that the `sample()` function will return a different random permutation each time we execute it. These differing permutations will partition different processors (i.e., rows in the data frame) into the train and test sets. Thus, if we run this experiment again with exactly the same inputs, we will likely get a different confidence interval and Δ_i scatter plot. For example, when we repeat the same test five times with identical inputs, we obtain the following confidence intervals: [-1.94, 1.46], [-1.95, 2.68], [-2.66, 3.81], [-6.13, 0.75], [-4.21, 5.29]. Similarly, varying the fraction of the data we assign to the train and test sets by changing $f = 0.5$ also changes the results.

It is good practice to run this type of experiment several times and observe how the results change. If you see the results vary wildly when you re-run these tests, you have good reason for concern. On the other hand, a series of similar results does not necessarily mean your results are good, only that they are consistently reproducible. It is often easier to spot a bad model than to determine that a model is good.

Based on the repeated confidence interval results and the corresponding scatter plot, similar to Figure 5.2, we conclude that this model is reasonably good at predicting the performance of a set of processors when the model is trained on a different set of processors executing the same benchmark

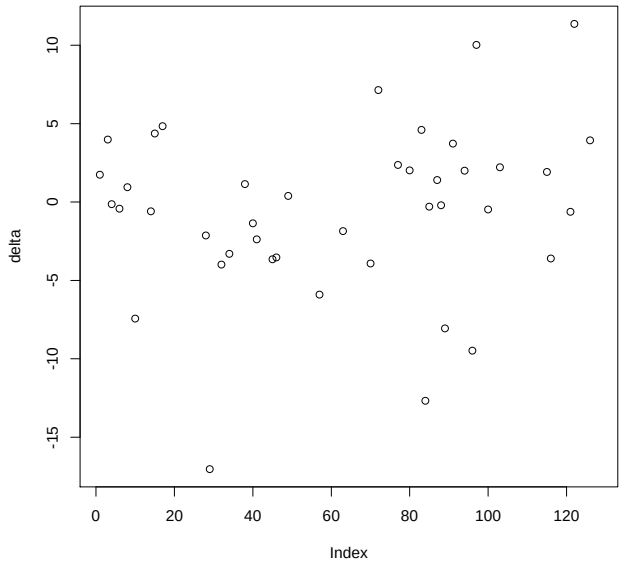

Figure 5.2: An example scatter plot of the differences between the predicted and actual performance results for the Int2000 benchmark when using the data-splitting technique to train and test the model.

program. It is not perfect, but it is also not too bad. Whether the differences are large enough to warrant concern is up to you.

5.3 || Predicting Across Data Sets

As we saw in the previous section, data splitting is a useful technique for testing a regression model. If you have other data sets, you can use them to further test your new model's capabilities.

In our situation, we have several additional benchmark results in the data file that we can use for these tests. As an example, we use the model we developed from the Int2000 data to predict the Fp2000 benchmark's performance.

We first train the model developed using the Int2000 data, `int00.lm`,

using all the Int2000 data available in the `int00.dat` data frame. We then predict the Fp2000 results using this model and the `fp00.dat` data. Again, we assign the differences between the predicted and actual results to the vector `delta`. Figure 5.3 shows the overall data flow for this training and testing. The corresponding R commands are:

```
> int00.lm <- lm(nperf ~ clock + cores + voltage + channel +
    L1icache + sqrt(L1icache) + L1dcache + sqrt(L1dcache) +
    L2cache + sqrt(L2cache), data = int00.dat)
> predicted.dat <- predict(int00.lm, newdata=fp00.dat)
> delta <- predicted.dat - fp00.dat$nperf
> t.test(delta, conf.level = 0.95)

        One Sample t-test

data:  delta
t = 1.5231, df = 80, p-value = 0.1317
alternative hypothesis: true mean is not equal to 0
95 percent confidence interval:
 -0.4532477  3.4099288
sample estimates:
mean of x
 1.478341
```

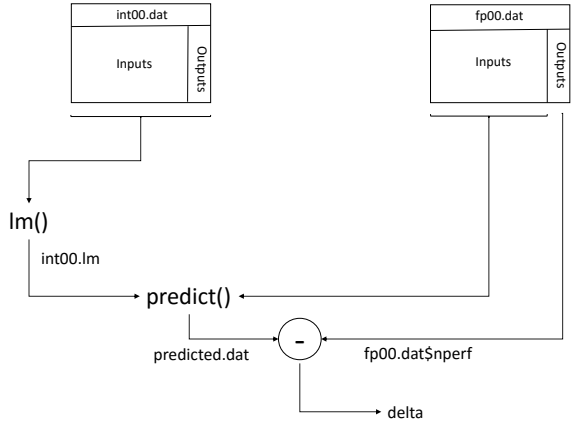

Figure 5.3: Predicting the Fp2000 results using the model developed with the Int2000 data.

The resulting confidence interval for the `delta` values contains zero and

is relatively small. This result suggests that the model developed using the Int2000 data is reasonably good at predicting the Fp2000 benchmark program's results. The scatter plot in Figure 5.4 shows the resulting `delta` values for each of the processors we used in the prediction. The results tend to be randomly distributed around zero, as we would expect from a good regression model. Note, however, that some of the values differ significantly from zero. The maximum positive deviation is almost 20, and the magnitude of the largest negative value is greater than 43. The confidence interval suggests relatively good results, but this scatter plot shows that not all the values are well predicted.

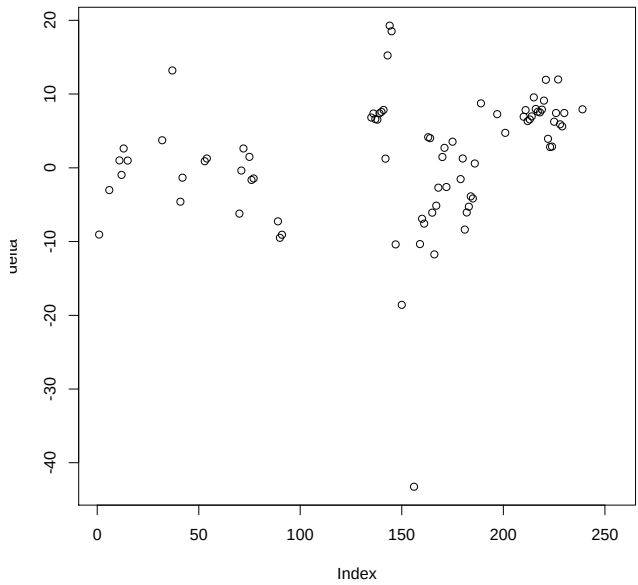

Figure 5.4: A scatter plot of the differences between the predicted and actual performance results for the Fp2000 benchmark when predicted using the Int2000 regression model.

As a final example, we use the Int2000 regression model to predict the results of the benchmark program's future Int2006 version. The R code to

compute this prediction is:

```
> int00.lm <- lm(nperf ~ clock + cores + voltage + channel +
    L1icache + sqrt(L1icache) + L1dcache + sqrt(L1dcache) +
    L2cache + sqrt(L2cache), data = int00.dat)
> predicted.dat <- predict(int00.lm, newdata=int06.dat)
> delta <- predicted.dat - int06.dat$nperf
> t.test(delta, conf.level = 0.95)

        One Sample t-test

data:  delta
t = 49.339, df = 168, p-value < 2.2e-16
alternative hypothesis: true mean is not equal to 0
95 percent confidence interval:
 48.87259 52.94662
sample estimates:
mean of x
  50.9096
```

In this case, the confidence interval for the `delta` values does not include zero. In fact, the mean value of the differences is 50.9096, which indicates that the average of the model-predicted values is substantially larger than the actual average value. The scatter plot shown in Figure 5.5 further confirms that the predicted values are all much larger than the actual values.

This example is a good reminder that models have their limits. Apparently, there are more factors that affect the performance of the next generation of the benchmark programs, Int2006, than the model we developed using the Int2000 results captures. To develop a model that better predicts future performance, we would have to uncover those factors. Doing so requires a deeper understanding of the factors that affect computer performance, which is beyond the scope of this tutorial.

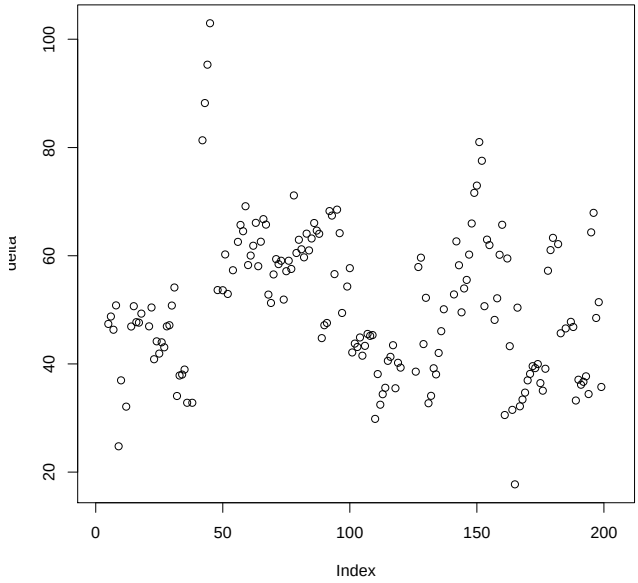

Figure 5.5: A scatter plot of the differences between the predicted and actual performance results for the Int2006 benchmark, predicted using the Int2000 regression model.

6 | Reading Data into the R Environment

As we have seen, the R environment provides some powerful functions to quickly and relatively easily develop and test regression models. Ironically, simply reading the data into R in a useful format can be one of the most difficult aspects of developing a model. R does not lack good input-output capabilities, but data often comes to the model developer in a messy form. For instance, the data format may be inconsistent, with missing fields and incorrectly recorded values. Getting the data into the format necessary for analysis and modeling is often called *data cleaning*. The specific steps necessary to "clean" data are heavily dependent on the data set and are thus beyond the scope of this tutorial. Suffice it to say that you should carefully examine your data before you use it to develop any sort of regression model. Section 2.2 provides a few thoughts on data cleaning.

In Chapter 2, we provided the functions used to read the example data into the R environment, but with no explanation about how they worked. In this chapter, we will look at these functions in detail, as specific examples of how to read a data set into R. Of course, the details of the functions you may need to write to input your data will necessarily change to match the specifics of your data set.

6.1 || Reading CSV files

Perhaps the simplest format for exchanging data among computer systems is the *de facto* standard *comma separated values*, or *csv*, file. R provides a function to directly read data from a csv file and assign it to a data frame:

```
> processors <- read.csv("all-data.csv")
```

The name between the quotes is the name of the csv-formatted file to be read. Each file line corresponds to one data record. Commas separate the individual data fields in each record. This function assigns each data record to a new row in the data frame, and assigns each data field to the corresponding column. When this function completes, the variable `processors` contains all the data from the file `all-data.csv` nicely organized into rows and columns in a data frame.

If you type `processors` to see what is stored in the data frame, you will get a long, confusing list of data. Typing

```
> head(processors)
```

will show a list of column headings and the values of the first few rows of data. From this list, we can determine which columns to extract for our model development. Although this is conceptually a simple problem, the execution can be rather messy, depending on how the data was collected and organized in the file.

As with any programming language, R lets you define your own functions. This feature is useful when you must perform a sequence of operations multiple times on different data pieces, for instance. The format for defining a function is:

```
function-name <- function(a1, a2, ...) {
R expressions
return(object)
}
```

where `function-name` is the function name you choose and `a1, a2, ...` is the list of arguments in your function. The R system evaluates the expressions in the body of the definition when the function is called. A function can return any type of data object using the `return()` statement.

We will define a new function called `extract_data` to extract all the rows that have a result for the given benchmark program from the `processors`

data frame. For instance, calling the function as follows:

```
> int92.dat <- extract_data("Int1992")
> fp92.dat <- extract_data("Fp1992")
> int95.dat <- extract_data("Int1995")
> fp95.dat <- extract_data("Fp1995")
> int00.dat <- extract_data("Int2000")
> fp00.dat <- extract_data("Fp2000")
> int06.dat <- extract_data("Int2006")
> fp06.dat <- extract_data("Fp2006")
```

extracts every row that has a result for the given benchmark program and assigns it to the corresponding data frame, `int92.dat`, `fp92.dat`, and so on.

We define the `extract_data` function as follows:

```
extract_data <- function(benchmark) {

temp <- paste(paste("Spec",benchmark,sep=""), "..average.base.",
    sep="")

perf <- get_column(benchmark,temp)

max_perf <- max(perf)
min_perf <- min(perf)
range <- max_perf - min_perf
nperf <- 100 * (perf - min_perf) / range

clock <- get_column(benchmark,"Processor.Clock..MHz.")
threads <- get_column(benchmark,"Threads.core")
cores <- get_column(benchmark,"Cores")
TDP <- get_column(benchmark,"TDP")
transistors <- get_column(benchmark,"Transistors..millions.")
dieSize <- get_column(benchmark,"Die.size..mm.2.")
voltage <- get_column(benchmark,"Voltage..low.")
featureSize <- get_column(benchmark,"Feature.Size..microns.")
channel <- get_column(benchmark,"Channel.length..microns.")
FO4delay <- get_column(benchmark,"FO4.Delay..ps.")
L1icache <- get_column(benchmark,"L1..instruction...on.chip.")
L1dcache <- get_column(benchmark,"L1..data...on.chip.")
L2cache <- get_column(benchmark,"L2..on.chip.")
L3cache <- get_column(benchmark,"L3..on.chip.")

return(data.frame(nperf, perf, clock, threads, cores, TDP,
    transistors, dieSize, voltage, featureSize, channel, FO4delay,
    L1icache, L1dcache, L2cache, L3cache))
 }
```

The first line with the `paste` functions looks rather complicated. However, it simply forms the name of the column with the given benchmark results. For example, when `extract_data` is called with `Int2000` as the ar-

gument, the nested `paste` functions simply concatenate the strings `"Spec"`, `"Int2000"`, and `"..average.base."`. The final string corresponds to the name of the column in the `processors` data frame that contains the performance results for the `Int2000` benchmark, `"SpecInt2000..average.base."`.

The next line calls the function `get_column`, which selects all the rows with the desired column name. In this case, that column contains the actual performance result reported for the given benchmark program, `perf`. The next four lines compute the normalized performance value, `nperf`, from the `perf` value we obtained from the data frame. The following sequence of calls to `get_column` extracts the data for each of the predictors we intend to use in developing the regression model. Note that the second parameter in each case, such as `"Processor.Clock..MHz."`, is the name of a column in the `processors` data frame. Finally, the `data.frame()` function is a predefined R function that assembles all its arguments into a single data frame. The new function we have just defined, `extract_data()`, returns this new data frame.

Next, we define the `get_column()` function to return all the data in a given column for which the given benchmark program has been defined:

```
get_column <- function(x,y) {

benchmark <- paste(paste("Spec",x,sep=""), "..average.base.",
    sep="")
ix <- !is.na(processors[,benchmark])
return(processors[ix,y])
}
```

The argument `x` is a string with the name of the benchmark program, and `y` is a string with the name of the desired column. The nested `paste()` functions produce the same result as the `extract_data()` function. The `is.na()` function performs the interesting work. This function returns a vector with "`1`" values corresponding to the row numbers in the `processors` data frame that have `NA` values in the column selected by the `benchmark` index. If there is a value in that location, `is.na()` will return a corresponding value that is a `0`. Thus, `is.na` indicates which rows are missing performance results for the benchmark of interest. Inserting the exclamation point in front of this function complements its output. As a result, the variable `ix` will contain a vector that identifies every row that contains performance results for the indicated benchmark program. The function then extracts the selected

rows from the `processors` data frame and returns them.

These types of data extraction functions can be somewhat tricky to write, because they depend so much on the specific format of your input file. The functions presented in this chapter are a guide to writing your own data extraction functions.

7 | Summary

LINEAR regression modeling is one of the most basic of a broad collection of data mining techniques. It can demonstrate the relationships between the inputs to a system and the corresponding output. It also can be used to predict the output given a new set of input values. While the specifics for developing a regression model will depend on the details of your data, there are several key steps to keep in mind when developing a new model using the R programming environment:

1. **Read your data into the R environment.**

   As simple as it sounds, one of the trickiest tasks oftentimes is simply reading your data into R. Because you may not have controlled how data was collected, or in what format, be prepared to spend some time writing new functions to parse your data and load it into an R data frame. Chapter 6 provides an example of reading a moderately complicated csv file into R.

2. **Sanity check your data.**

   Once you have your data in the R environment, perform some sanity checks to make sure that there is nothing obviously wrong with the data. The types of checks you should perform depend on the specifics of your data. Some possibilities include:

   - Finding the values' minimum, maximum, average, and standard deviation in each data frame column.
   - Looking for any parameter values that seem suspiciously outside the expected limits.

- Determining the fraction of missing (`NA`) values in each column to ensure that there is sufficient data available.
- Determining the frequency of categorical parameters, to see if any unexpected values pop up.
- Any other data-specific tests.

Ultimately, you need to feel confident that your data set's values are reasonable and consistent.

3. **Visualize your data.**

   It is always good to plot your data, to get a basic sense of its shape and ensure that nothing looks out of place. For instance, you may expect to see a somewhat linear relationship between two parameters. If you see something else, such as a horizontal line, you should investigate further. Your assumption about a linear relationship could be wrong, or the data may be corrupted (see item no. 2 above). Or perhaps something completely unexpected is going on. Regardless, you must understand what might be happening before you begin developing the model. The `pairs()` function is quite useful for performing this quick visual check, as described in Section 4.1.

4. **Identify the potential predictors.**

   Before you can begin the backward elimination process, you must identify the set of all possible predictors that could go into your model. In the simplest case, this set consists of all of the available columns in your data frame. However, you may know that some of the columns will not be useful, even before you begin constructing the model. For example, a column containing only a few valid entries probably is not useful in a model. Your knowledge of the system may also give you good reason to eliminate a parameter as a possible predictor, much as we eliminated TDP as a possible predictor in Section 4.2, or to include some of the parameters' non-linear functions as possible predictors, as we did when we added the square root of the cache size terms to our set of possible predictors.

5. **Select the predictors.**

Once you have identified the potential predictors, use the backward elimination process described in Section 4.3 to select the predictors you'll include in the final model, based on the significance threshold you decide to use.

6. **Validate the model.**

   Examine your model's R^2 value and the adjusted-R^2 value. Use residual analysis to further examine the model's quality. You also should split your data into training and testing sets, and then see how well your model predicts values from the test set.

7. **Predict.**

   Now that you have a model that you feel appropriately explains your data, you can use it to predict previously unknown output values.

A deep body of literature is devoted to both statistical modeling and the R language. If you want to learn more about R as a programming language, many good books are available, including [11, 12, 15, 16]. These books focus on specific statistical ideas and use R as the computational language [1, 3, 4, 14]. Finally, this book [9] gives an introduction to computer performance measurement.

As you continue to develop your data-mining skills, remember that what you have developed is only a model. Ideally, it is a useful tool for explaining the variations in your measured data and understanding the relationships between inputs and output. But like all models, it is only an approximation of the real underlying system, and is limited in what it can tell us about that system. Proceed with caution.

8 A Few Things to Try Next

HERE are a few suggested exercises to help you learn more about regression modeling using R.

1. Show how you would clean the data set for one of the selected benchmark results (Int1992, Int1995, etc.). For example, for every column in the data frame, you could:

   - Compute the average, variance, minimum, and maximum.
   - Sort the column data to look for outliers or unusual patterns.
   - Determine the fraction of NA values for each column.

   How else could you verify that the data looks reasonable?

2. Plot the processor performance versus the clock frequency for each of the benchmark results, similar to Figure 3.1.

3. Develop a one-factor linear regression model for all the benchmark results. What input factor should you use as the predictor?

4. Superimpose your one-factor models on the corresponding scatter plots of the data (see Figure 3.2).

5. Evaluate the quality of the one-factor models by discussing the residuals, the p-values of the coefficients, the residual standard errors, the R^2 values, the F-statistic, and by performing appropriate residual analysis.

6. Generate a pair-wise comparison plot for each of the benchmark results, similar to Figure 4.1.

7. Develop a multi-factor linear regression model for each of the benchmark results. Which predictors are the same and which are different across these models? What other similarities and differences do you see across these models?

8. Evaluate the multi-factor models' quality by discussing the residuals, the p-values of the coefficients, the residual standard errors, the R^2 values, the F-statistic, and by performing appropriate residual analysis.

9. Use the regression models you've developed to complete the following tables, showing how well the models from each row predict the benchmark results in each column. Specifically, fill in the x and y values so that x is the mean of the `delta` values for the predictions and y is the width of the corresponding 95 percent confidence interval. You need only predict forwards in time. For example, it is reasonable to use the model developed with Int1992 data to predict Int2006 results, but it does not make sense to use a model developed with Int2006 data to predict Int1992 results.

	Int1992	Int1995	Int2000	Int2006
Int1992	x ($\pm$ y)	x ($\pm$ y)	x ($\pm$ y)	x ($\pm$ y)
Int1995		x ($\pm$ y)	x ($\pm$ y)	x ($\pm$ y)
Int2000			x ($\pm$ y)	x ($\pm$ y)
Int2006				x ($\pm$ y)
Fp1992	x ($\pm$ y)	x ($\pm$ y)	x ($\pm$ y)	x ($\pm$ y)
Fp1995		x ($\pm$ y)	x ($\pm$ y)	x ($\pm$ y)
Fp2000			x ($\pm$ y)	x ($\pm$ y)
Fp2006				x ($\pm$ y)

	Fp1992	Fp1995	Fp2000	Fp2006
Int1992	x ($\pm$ y)	x ($\pm$ y)	x ($\pm$ y)	x ($\pm$ y)
Int1995		x ($\pm$ y)	x ($\pm$ y)	x ($\pm$ y)
Int2000			x ($\pm$ y)	x ($\pm$ y)
Int2006				x ($\pm$ y)
Fp1992	x ($\pm$ y)	x ($\pm$ y)	x ($\pm$ y)	x ($\pm$ y)
Fp1995		x ($\pm$ y)	x ($\pm$ y)	x ($\pm$ y)
Fp2000			x ($\pm$ y)	x ($\pm$ y)
Fp2006				x ($\pm$ y)

10. What can you say about these models' predictive abilities, based on the results from the previous problem? For example, how well does a model developed for the integer benchmarks predict the same-year performance of the floating-point benchmarks? What about predictions across benchmark generations?

11. In the discussion of data splitting, we defined the value f as the fraction of the complete data set used in the training set. For the Fp2000 data set, plot a 95 percent confidence interval for the mean of `delta` for f = [0.1, 0.2, ..., 0.9]. What value of f gives the best result (i.e., the smallest confidence interval)? Repeat this test $n = 5$ times to see how the best value of f changes.

12. Repeat the previous problem, varying f for all the other data sets.

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Update History

Edition 1.0 – The original version.
Edition 1.1

1. Corrected a few small typographical errors.
2. Extended the discussion of the backward elimination process in Section 4.6.

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Linear Regression Using R: An Introduction to Data Modeling presents one of the fundamental data modeling techniques in an informal tutorial style. Learn how to predict system outputs from measured data using a detailed step-by-step process to develop, train, and test reliable regression models. Key modeling and programming concepts are intuitively described using the R programming language. All of the necessary resources are freely available online.

David J. Lilja is the Schnell Professor of Electrical and Computer Engineering, and a graduate faculty in Computer Science, Scientific Computation, and Data Science, at the University of Minnesota in Minneapolis. He is a Fellow of IEEE and AAAS, and is the author of *Measuring Computer Performance: A Practitioner's Guide.*

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